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DESCRIPTION

SEQUENCE LISTING

[0001] The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on May 26, 2016, is named MXI_543PC_Sequence_Listing.txt and is 417,528 bytes in size.

BACKGROUND

[0002] OX40 (TNFRSF4), also known as ACT35, IMD16, TXGP1L, and CD134, is a 50-kD type I transmembrane glycoprotein in the TNFSFR family of costimulatory receptors expressed on activated CD4+ T cells. In the context of cancer, OX40-expressing activated T cells are found in tumor infiltrating lymphocytes. OX40 and its ligand, OX40-L, play a crucial role in inducing and maintaining T-cell responses. Recent studies have demonstrated the utility of enhancing anti-tumor T cell function to fight cancer, with key components of an effective response including the activation of CD4+ T cells and promoting survival signals through memory and effector T cells. Given the ongoing need for improved strategies for treating diseases such as cancer through, e.g., enhancing immune responses such as T cell responses, novel agents that modulate T cell responses, such as those that target OX40, as well as therapies (e.g., combination therapies) that use such agents, would be therapeutically beneficial.

[0003] WO200907935 describes isolated binding molecules that bind to the human OX40, nucleic acid molecules encoding an amino acid sequence of the binding molecules, vectors comprising the nucleic acid molecules, host cells containing the vectors, methods of making the binding molecules, pharmaceutical compositions containing the binding molecules, and methods of using the binding molecules or compositions.

SUMMARY

[0004] Provided herein are antibodies, such as human monoclonal antibodies, that specifically bind OX40 and have desirable functional properties. These properties include high affinity binding to human OX40 and cynomolgus OX40 and the ability to stimulate antigen-specific T cell responses, e.g., in tumor-bearing subjects. Also provided herein are methods of detecting OX40 in a sample.

[0005] In one aspect, the invention provides isolated monoclonal antibodies which bind to OX40, as defined in the claims. In other aspects, the invention provides nucleic acids as defined in the claims, and expression vectors comprising these nucleic acids. In a further aspect, the invention provides cells as defined in the claims. The invention also provides, in another aspect, pharmaceutical compositions as defined in the claims. In a further aspect, the invention provides antibodies and pharmaceutical compositions for use in methods of treating cancer, as defined in the claims.

[0006] The antibodies specifically bind to OX40 and exhibit at least one of the following properties:

1. (1) binding to soluble human OX40, e.g., with a K_D of 10 nM or less (e.g., 0.01 nM to 10 nM), e.g., as measured by Biacore;
2. (2) binding to membrane bound human OX40, e.g., with an EC_{50} of 1 nM or less (e.g., 0.01 nM to 1 nM), e.g., as measured by FACS;
3. (3) binding to cynomolgus OX40, e.g., binding to membrane bound cynomolgus OX40, e.g., with an EC_{50} of 10 nM or less (e.g., 0.01 nM to 10 nM), e.g., as measured by FACS;
4. (4) inducing or enhancing T cell activation, as evidenced by (i) increased IL-2 and/or IFN- γ production in OX40-expressing T cells and/or (ii) enhanced T cell proliferation;
5. (5) inhibiting the binding of OX40 ligand to OX40, e.g., with an EC_{50} of 1 nM or less as measured by FACS, e.g., in an assay with hOX40-293 cells;

6. (6) binding to an epitope on the extracellular portion of mature human OX40 (SEQ ID NO: 2), e.g., an epitope within the region DVVSSKPKCPCTWCNLR (SEQ ID NO: 178) or DSYKPGVDCAPCPGHHFSPGDNQACKPWTNCTLAGK (SEQ ID NO: 179);
7. (7) competing for binding to human OX40 with 3F4, 14B6-1, 14B6-2, 23H3, 18E9, 8B11, 20B3, and 20C1;
8. (8) competing for binding to human OX40 with 6E1-1, 6E1-2, 14A2-1, and 14A2-2.

[0007] The anti-OX40 antibodies stimulate an anti-tumor immune response, for example, an antigen-specific T cell response. In certain embodiments, the antibodies increase cytokine production (e.g., IL-2 and/or IFN- γ) in OX40-expressing T cells and/or increase T cell proliferation. In certain embodiments, the antibodies bind to the C1q component of human complement. In certain embodiments, the antibodies induce NK cell-mediated lysis of activated CD4+ T cells. In certain embodiments, the antibody promotes macrophage-mediated phagocytosis of OX40 expressing cells. In certain embodiments, the antibody inhibits regulatory T cell-mediated suppression of CD4+ T cell proliferation.

[0008] In certain embodiments, the anti-OX40 antibodies bind to Fc receptors, such as one or more activating Fc γ Rs. In certain embodiments, the antibodies induce or enhance T cell activation through multivalent crosslinking.

[0009] The isolated monoclonal antibodies specifically bind to OX40 and comprise the three variable heavy chain CDRs and the three variable light chain CDRs that are in the variable heavy chain and variable light chain pair of SEQ ID NOs: 318 and 94.

[0010] The claimed monoclonal antibodies bind to OX40 and comprise:

heavy chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 87, 317, and 89, respectively, and light chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 90-92, respectively. Non-claimed aspects of the disclosure also include antibodies that comprise;

1. (a) heavy chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 11-13, respectively, and light chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 14-16, respectively;
2. (b) heavy chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 19-21, respectively, and light chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 22-24, respectively;
3. (c) heavy chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 19-21, respectively, and light chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 25-27, respectively;
4. (d) heavy chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 31-33, respectively, and light chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 34-36, respectively;
5. (e) heavy chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 39-41, respectively, and light chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 42-44, respectively;
6. (f) heavy chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 39-41, respectively, and light chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 45-47, respectively;
7. (g) heavy chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 51-53, respectively, and light chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 54-56, respectively;
8. (h) heavy chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 59-61, respectively, and light chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 62-64, respectively;
9. (i) heavy chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 67-69, respectively, and light chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 70-72, respectively;
10. (j) heavy chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 75-77, respectively, and light chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 78-80, respectively;
11. (k) heavy chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 75-77, respectively, and light chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 81-83, respectively; or
12. (l) heavy chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 87-89, respectively, and light chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 90-92, respectively.

[0011] Provided herein are non-claimed monoclonal antibodies, or antigen binding portions thereof, which bind to OX40 and comprise heavy and light chain variable regions, wherein the heavy chain variable region comprises an amino acid

sequence which is at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOs: 17, 28, 37, 48, 57, 65, 73, 84, and 93.

[0012] Provided herein are non-claimed isolated monoclonal antibodies, or antigen binding portions thereof, which bind to OX40 and comprise heavy and light chain variable regions, wherein the light chain variable region comprises an amino acid sequence which is at least 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence selected from the group consisting of SEQ ID NOs: 18, 29, 30, 38, 49, 50, 58, 66, 74, 85, 86, and 94.

[0013] Provided herein are non-claimed isolated monoclonal antibodies, or antigen binding portions thereof, which bind to OX40 and comprise heavy and light chain variable region sequences at least 85% identical, for example, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical, to the amino acid sequences selected from the group consisting of: 17 and 18; 28 and 29; 28 and 30; 37 and 38; 48 and 49; 48 and 50; 57 and 58; 65 and 66; 73 and 74; 84 and 85; 84 and 86; 93 and 94.

[0014] In some embodiments, the claimed isolated monoclonal antibodies bind to OX40 and comprise heavy chain and light chain sequences at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequences selected from the group consisting of: SEQ ID NOs: 124 and 116.

[0015] In certain embodiments, the claimed isolated monoclonal antibodies (a) bind to the same epitope on OX40 as 20C1, and (b) inhibit binding of 20C1 to OX40 on activated T cells by at least 50%, 60%, 70%, 80% or 90% as measured by, e.g., FACS.

[0016] In certain embodiments, the anti-OX40 antibodies bind within the regions DVVSSKPCKPCTWCNLR (SEQ ID NO: 178) or DSYKPGVDCAPCPPGHFSPGDNQACKPWTNCTLAGK (SEQ ID NO: 179) of mature extracellular portion of human OX40 (SEQ ID NO: 2). In some embodiments, the anti-OX40 antibodies, described herein, bind to both human and cynomolgus OX40. In some embodiments, the anti-OX40 antibodies, described herein, do not bind to mouse and/or rat OX40.

[0017] In certain embodiments, the anti-OX40 antibodies are IgG1, IgG2, IgG3, or IgG4 antibodies, or variants thereof. In certain embodiments, the anti-OX40 antibodies are human or humanized antibodies. In certain embodiments, the anti-OX40 antibodies comprise an Fc having enhanced binding to an activating FcγR.

[0018] Provided herein are isolated monoclonal antibodies which bind to OX40 comprising a modified heavy chain constant region that comprises an IgG2 hinge and at least one of CH1, CH2 and CH3 that is not of an IgG2 isotype.

[0019] In certain embodiments, the heavy chain of the claimed anti-OX40 antibodies comprises an amino acid sequence consisting of SEQ ID NO: 124, or a heavy chain that differs therefrom in at most 10 amino acids or is at least 95%, 96%, 97%, 98% or 99% identical to an amino acid sequence of SEQ ID NO: 124.

[0020] In certain embodiments, the light chain of the claimed anti-OX40 antibodies comprises an amino acid sequence consisting of SEQ ID NO: 116, or a light chain that differs therefrom in at most 10 amino acids or is at least 95%, 96%, 97%, 98% or 99% identical to an amino acid sequence of SEQ ID NO: 116.

[0021] In certain embodiments, the anti-OX40 antibodies are not immunogenic.

[0022] In certain embodiments, the anti-OX40 antibodies lack an amino acid sequence that undergoes isomerization. For instance, if the amino acid sequence Asp-Gly is present in the heavy and/or light chain CDR sequences of the antibody, the sequence is substituted with an amino acid sequence that does not undergo isomerization. The antibody comprises the heavy chain variable region CDR2 sequence set forth in SEQ ID NO: 88, but wherein the Gly in the Asp-Gly sequence (AIDTDGGTFYADSVRG; SEQ ID NO: 88) is replaced with an amino acid sequence that does not undergo isomerization, i.e. Asp-Ala.

[0023] In some embodiments, the claimed antibodies comprise an amino acid sequence selected from the group consisting of SEQ ID NOs: 294-296. Non-claimed aspects of the disclosure provided herein are antibodies which bind to OX40 comprising an amino acid selected from the group consisting of SEQ ID NOs: 282-293. Such antibodies comprise

a heavy chain consisting of an amino acid sequence selected from the group consisting of SEQ ID NOs: 282-293.

[0024] Provided herein are bispecific molecules comprising the anti-OX40 antibody linked to a molecule having a second binding specificity.

[0025] Provided herein are nucleic acids encoding the heavy and/or light chain variable regions of the anti-OX40 antibodies, expression vectors comprising the nucleic acid molecules, and cells transformed with the expression vectors.

[0026] Provided herein are immunoconjugates comprising the anti-OX40 antibodies described herein, linked to an agent.

[0027] Provided herein are compositions comprising the anti-OX40 antibodies and a carrier.

[0028] Provided herein are kits comprising the anti-OX40 antibodies, and instructions for use. In certain cases, the kits further comprise an anti-CTLA4 antibody, anti-PD-1, or anti-PD-L1 antibody.

[0029] Provided herein is a method of preparing the anti-OX40 antibodies, comprising expressing an anti-OX40 antibody in a cell and isolating the antibody from the cell.

[0030] Provided herein is the anti-OX40 antibody for use in a method of stimulating an antigen-specific T cell response comprising contacting the T cell with an anti-OX40 antibody such that an antigen-specific T cell response is stimulated.

[0031] Provided herein is the anti-OX40 antibody for use in a method of activating or co-stimulating a T cell, e.g., an effector T cell, comprising contacting a cell, e.g., an effector T cell, with an anti-OX40 antibody, and CD3, wherein the effector T cell is activated or co-stimulated.

[0032] Provided herein is the anti-OX40 antibody for use in a method of increasing IL-2 and/or IFN- γ production in and/or proliferation of a T cell comprising contacting the T cell with an effective amount of an anti-OX40 antibody.

[0033] Provided herein is the anti-OX40 antibody for use in a method of increasing IL-2 and/or IFN- γ production in T cells in a subject comprising administering an effective amount of an anti-OX40 antibody, bispecific molecule or conjugate comprising the anti-OX40 antibody, or composition comprising the anti-OX40 antibody, to increase IL-2 and/or IFN- γ production from the T cells.

[0034] Provided herein is the anti-OX40 antibody for use in a method of reducing or depleting the number of T regulatory cells in a tumor of a subject in need thereof comprising administering an effective amount of an anti-OX40 antibody, bispecific molecule or conjugate wherein the antibody, or antigen binding portion thereof, has effector or enhanced effector function, to reduce the number of T regulatory cells in the tumor.

[0035] Provided herein is the anti-OX40 antibody for use in a method of stimulating an immune response in a subject comprising administering an effective amount of an anti-OX40 antibody, bispecific molecule or conjugate to the subject such that an immune response in the subject is stimulated. In certain embodiments, the subject has a tumor and an immune response against the tumor is stimulated.

[0036] Provided herein is the anti-OX40 antibody for use in a method of inhibiting the growth of tumor cells in a subject comprising administering to the subject an anti-OX40 antibody, bispecific molecule or conjugate such that growth of the tumor is inhibited in the subject.

[0037] Provided herein is the anti-OX40 antibody or pharmaceutical composition for use in a method of treating cancer, e.g., by immunotherapy, comprising administering to a subject in need thereof a therapeutically effective amount of an anti-OX40 antibody, bispecific molecule or conjugate comprising the anti-OX40 antibody, or composition comprising the anti-OX40 antibody, to treat the cancer. In certain embodiments, the cancer is selected from the group consisting of: bladder cancer, breast cancer, uterine/cervical cancer, ovarian cancer, prostate cancer, testicular cancer, esophageal

cancer, gastrointestinal cancer, pancreatic cancer, colorectal cancer, colon cancer, kidney cancer, head and neck cancer, lung cancer, stomach cancer, germ cell cancer, bone cancer, liver cancer, thyroid cancer, skin cancer, neoplasm of the central nervous system, lymphoma, leukemia, myeloma, sarcoma, and virus-related cancer. In certain embodiments, the cancer is a metastatic cancer, refractory cancer, or recurrent cancer.

[0038] In certain embodiments, the methods described herein further comprise administering one or more additional therapeutics with an anti-OX40 antibody, for example, an anti-PD1 antibody, a LAG-3 antibody, a CTLA-4 antibody, and/or a PD-L1 antibody.

[0039] Provided herein is a non-claimed method of detecting the presence of OX40 in a sample comprising contacting the sample with an anti-OX40 antibody, or an antigen binding portion thereof, under conditions that allow for formation of a complex between the antibody, or antigen binding portion thereof, and OX40, and detecting the formation of a complex.

[0040] Provided herein are the anti-OX40 antibodies described herein for use in for treating cancer, stimulating an immune response in a subject, stimulating an antigen-specific T cell response, activating or co-stimulating a T cell, increasing the production of cytokines, such as IL-2 and/or

[0041] IFN- γ , in and/or proliferation of a T cell, reducing or depleting the number of T regulatory cells in a tumor, and/or inhibiting the growth of tumor cells. Also provided herein are the anti-OX40 antibodies described herein for use in preparing a medicament for stimulating an immune response in a subject, stimulating an antigen-specific T cell response, activating or co-stimulating a T cell, increasing IL-2 and/or IFN- γ production in and/or proliferation of a T cell, reducing or depleting the number of T regulatory cells in a tumor, and/or inhibiting the growth of tumor cells.

[0042] Provided herein is the anti-OX40 antibody or pharmaceutical composition for use in a method of treating a solid tumor in a human subject, the method comprising administering to the subject an effective amount of an anti-OX40 antibody comprising CDR1, CDR2 and CDR3 domains of the heavy chain variable region having the sequence set forth in SEQ ID NO: 318, and CDR1, CDR2 and CDR3 domains of the light chain variable region having the sequence set forth in SEQ ID NO: 94, wherein the method comprises at least one administration cycle, wherein the cycle is a period of two weeks, wherein for each of the at least one cycles, one dose of the anti-OX40 antibody is administered at a dose of 1 mg/kg body weight; a fixed dose of 20, 40, 80, 160, or 320 mg; a dose of about 1 mg/kg body weight; or a fixed dose of about 20, 40, 80, 160, or 320 mg.

[0043] In one embodiment, the method comprises further administering an anti-PD-1 antibody comprising CDR1, CDR2 and CDR3 domains of the heavy chain variable region having the sequence set forth in SEQ ID NO: 301, and CDR1, CDR2 and CDR3 domains of the light chain variable region having the sequence set forth in SEQ ID NO: 302, wherein the method comprises at least one administration cycle, wherein the cycle is a period of two, three, or four weeks, wherein for each of the at least one cycles, one dose of the anti-OX40 antibody is administered at a dose of 1 mg/kg body weight; a fixed dose of 20, 40, 80, 160, or 320 mg; a dose of about 1 mg/kg body weight; or a fixed dose of about 20, 40, 80, 160, or 320 mg, and one dose of the anti-PD-1 antibody is administered at a dose of 240, 360, or 480 mg or a dose of about 240, 360, or 480 mg.

[0044] In another embodiment, the method comprises further administering an anti-CTLA-4 antibody comprising CDR1, CDR2 and CDR3 domains of the heavy chain variable region having the sequence set forth in SEQ ID NO: 309, and CDR1, CDR2 and CDR3 domains of the light chain variable region having the sequence set forth in SEQ ID NO: 310, wherein the method comprises at least one administration cycle, wherein the cycle is a period of three weeks, wherein for each of the at least one cycles, one dose of the anti-OX40 antibody is administered at a dose of 1 mg/kg body weight; a fixed dose of 20, 40, 80, 160, or 320 mg; a dose of about 1 mg/kg body weight; or a fixed dose of about 20, 40, 80, 160, or 320 mg, and one dose of the anti-CTLA-4 antibody is administered at a dose of 1 mg/kg or a dose of about 1 mg/kg, wherein the anti-OX40 antibody is administered together with the anti-CTLA-4 antibody for at least one cycle, followed by anti-OX40 antibody monotherapy for at least one cycle. In some embodiments, the treatment consists of 8 cycles. In one embodiment, the anti-OX40 antibody is administered together with the anti-CTLA-4 antibody for the first 4 cycles, followed by anti-OX40 antibody monotherapy for the last 4 cycles.

[0045] In some embodiments, the anti-OX40 antibody comprises heavy and light chain sequences set forth in SEQ ID NOs: 124 and 116, respectively.

[0046] In certain embodiments, the anti-OX40 antibody, or anti-OX40 antibody and anti-PD-1 or anti-CTLA-4 antibody, are formulated for intravenous administration. In some embodiments, the anti-OX40 and anti-PD-1 or anti-CTLA-4 antibody are formulated together. In other embodiments, the anti-OX40 and anti-PD-1 or anti-CTLA-4 antibody are formulated separately.

[0047] In some embodiments, the treatment consists of 8 cycles. In one embodiment, the anti-OX40 antibody, or anti-OX40 antibody and anti-PD-1 or anti-CTLA-4 antibody, are administered on Day 1 of each cycle.

[0048] In certain embodiments, the anti-OX40 antibody is administered prior to administration of the anti-PD-1 or anti-CTLA-4 antibody. In one embodiment, the anti-OX40 antibody is administered within about 30 minutes prior to administration of the anti-PD-1 or anti-CTLA-4 antibody. In other embodiments, the anti-OX40 antibody is administered after administration of the anti-PD-1 or anti-CTLA-4 antibody. In yet other embodiments, the anti-OX40 antibody is administered concurrently with the anti-PD-1 or anti-CTLA-4 antibody.

[0049] In certain embodiments, the treatment produces at least one therapeutic effect chosen from a reduction in size of a tumor, reduction in number of metastatic lesions over time, complete response, partial response, and stable disease. In some embodiments, the tumor is associated with a cancer selected from the group consisting of: cervical cancer, bladder cancer, colorectal cancer, and ovarian cancer.

[0050] Other features and advantages of the instant disclosure will be apparent from the following detailed description and examples, which should not be construed as limiting.

BRIEF DESCRIPTION OF THE FIGURES

[0051] The antibodies of the claimed invention are designated "OX40.21" in the following description of the figures. Antibodies other than those claimed are disclosed below for reference purposes and to fully understand the invention.

Figure 1A shows the nucleotide sequence (SEQ ID NO: 126) and amino acid sequence (SEQ ID NO: 17) of the heavy chain variable region of the 3F4 human monoclonal antibody. The CDR1 (SEQ ID NO: 11), CDR2 (SEQ ID NO: 12) and CDR3 (SEQ ID NO: 13) regions are delineated and the V, D and J germline derivations are indicated.

Figure 1B shows the nucleotide sequence (SEQ ID NO: 127) and amino acid sequence (SEQ ID NO: 18) of the kappa light chain variable region of the 3F4 human monoclonal antibody. The CDR1 (SEQ ID NO: 14), CDR2 (SEQ ID NO: 15) and CDR3 (SEQ ID NO: 16) regions are delineated and the V and J germline derivations are indicated.

Figure 2A shows the nucleotide sequence (SEQ ID NO: 128) and amino acid sequence (SEQ ID NO: 28) of the heavy chain variable region of the 14B6 (14B6-1 and 14B6-2) human monoclonal antibody. The CDR1 (SEQ ID NO: 19), CDR2 (SEQ ID NO: 20) and CDR3 (SEQ ID NO: 21) regions are delineated and the V, D and J germline derivations are indicated.

Figure 2B shows the nucleotide sequence (SEQ ID NO: 129) and amino acid sequence (SEQ ID NO: 29) of the kappa light chain variable region of the 14B6-1 human monoclonal antibody. The CDR1 (SEQ ID NO: 22), CDR2 (SEQ ID NO: 23) and CDR3 (SEQ ID NO: 24) regions are delineated and the V and J germline derivations are indicated.

Figure 2C shows the nucleotide sequence (SEQ ID NO: 130) and amino acid sequence (SEQ ID NO: 30) of the kappa light chain variable region of the 14B6-2 human monoclonal antibody. The CDR1 (SEQ ID NO: 26), CDR2 (SEQ ID NO: 27) and CDR3 (SEQ ID NO: 28) regions are delineated and the V and J germline derivations are indicated.

Figure 3A shows the nucleotide sequence (SEQ ID NO: 131) and amino acid sequence (SEQ ID NO: 37) of the heavy chain variable region of the 23H3 human monoclonal antibody. The CDR1 (SEQ ID NO: 31), CDR2 (SEQ ID NO: 32) and CDR3 (SEQ ID NO: 33) regions are delineated and the V, D and J germline derivations are indicated.

Figure 3B shows the nucleotide sequence (SEQ ID NO: 132) and amino acid sequence (SEQ ID NO: 38) of the kappa

light chain variable region of the 23H3 human monoclonal antibody. The CDR1 (SEQ ID NO: 34), CDR2 (SEQ ID NO: 35) and CDR3 (SEQ ID NO: 36) regions are delineated and the V and J germline derivations are indicated.

Figure 4A shows the nucleotide sequence (SEQ ID NO: 133) and amino acid sequence (SEQ ID NO: 48) of the heavy chain variable region of the 6E1 (6E1-1 and 6E1-2) human monoclonal antibody. The CDR1 (SEQ ID NO: 39), CDR2 (SEQ ID NO: 40) and CDR3 (SEQ ID NO: 41) regions are delineated and the V, D and J germline derivations are indicated.

Figure 4B shows the nucleotide sequence (SEQ ID NO: 134) and amino acid sequence (SEQ ID NO: 49) of the kappa light chain variable region of the 6E1-1 human monoclonal antibody. The CDR1 (SEQ ID NO: 42), CDR2 (SEQ ID NO: 43) and CDR3 (SEQ ID NO: 44) regions are delineated and the V and J germline derivations are indicated.

Figure 4C shows the nucleotide sequence (SEQ ID NO: 135) and amino acid sequence (SEQ ID NO: 50) of the kappa light chain variable region of the 6E1-2 human monoclonal antibody. The CDR1 (SEQ ID NO: 45), CDR2 (SEQ ID NO: 46) and CDR3 (SEQ ID NO: 47) regions are delineated and the V and J germline derivations are indicated.

Figure 5A shows the nucleotide sequence (SEQ ID NO: 136) and amino acid sequence (SEQ ID NO: 57) of the heavy chain variable region of the 18E9 human monoclonal antibody. The CDR1 (SEQ ID NO: 51), CDR2 (SEQ ID NO: 52) and CDR3 (SEQ ID NO: 53) regions are delineated and the V, D and J germline derivations are indicated.

Figure 5B shows the nucleotide sequence (SEQ ID NO: 137) and amino acid sequence (SEQ ID NO: 58) of the kappa light chain variable region of the 18E9 human monoclonal antibody. The CDR1 (SEQ ID NO: 54), CDR2 (SEQ ID NO: 55) and CDR3 (SEQ ID NO: 56) regions are delineated and the V and J germline derivations are indicated.

Figure 6A shows the nucleotide sequence (SEQ ID NO: 138) and amino acid sequence (SEQ ID NO: 65) of the heavy chain variable region of the 8B11 human monoclonal antibody. The CDR1 (SEQ ID NO: 59), CDR2 (SEQ ID NO: 60) and CDR3 (SEQ ID NO: 61) regions are delineated and the V, D and J germline derivations are indicated.

Figure 6B shows the nucleotide sequence (SEQ ID NO: 139) and amino acid sequence (SEQ ID NO: 66) of the kappa light chain variable region of the 8B11 human monoclonal antibody. The CDR1 (SEQ ID NO: 62), CDR2 (SEQ ID NO: 63) and CDR3 (SEQ ID NO: 64) regions are delineated and the V and J germline derivations are indicated.

Figure 7A shows the nucleotide sequence (SEQ ID NO: 140) and amino acid sequence (SEQ ID NO: 73) of the heavy chain variable region of the 20B3 human monoclonal antibody. The CDR1 (SEQ ID NO: 67), CDR2 (SEQ ID NO: 68) and CDR3 (SEQ ID NO: 69) regions are delineated and the V, D and J germline derivations are indicated.

Figure 7B shows the nucleotide sequence (SEQ ID NO: 141) and amino acid sequence (SEQ ID NO: 74) of the kappa light chain variable region of the 20B3 human monoclonal antibody. The CDR1 (SEQ ID NO: 70), CDR2 (SEQ ID NO: 71) and CDR3 (SEQ ID NO: 72) regions are delineated and the V and J germline derivations are indicated.

Figure 8A shows the nucleotide sequence (SEQ ID NO: 142) and amino acid sequence (SEQ ID NO: 84) of the heavy chain variable region of the 14A2 (14A2-1 and 14A2-2) human monoclonal antibody. The CDR1 (SEQ ID NO: 75), CDR2 (SEQ ID NO: 76) and CDR3 (SEQ ID NO: 77) regions are delineated and the V, D and J germline derivations are indicated.

Figure 8B shows the nucleotide sequence (SEQ ID NO: 143) and amino acid sequence (SEQ ID NO: 85) of the kappa light chain variable region of the 14A2-1 human monoclonal antibody. The CDR1 (SEQ ID NO: 78), CDR2 (SEQ ID NO: 79) and CDR3 (SEQ ID NO: 80) regions are delineated and the V and J germline derivations are indicated.

Figure 8C shows the nucleotide sequence (SEQ ID NO: 144) and amino acid sequence (SEQ ID NO: 86) of the kappa light chain variable region of the 14A2-2 human monoclonal antibody. The CDR1 (SEQ ID NO: 81), CDR2 (SEQ ID NO: 82) and CDR3 (SEQ ID NO: 83) regions are delineated and the V and J germline derivations are indicated.

Figure 9A shows the nucleotide sequence (SEQ ID NO: 145) and amino acid sequence (SEQ ID NO: 93) of the heavy chain variable region of the 20C1 human monoclonal antibody. The CDR1 (SEQ ID NO: 87), CDR2 (SEQ ID NO: 88) and CDR3 (SEQ ID NO: 89) regions are delineated and the V, D and J germline derivations are indicated.

Figure 9B shows the nucleotide sequence (SEQ ID NO: 146) and amino acid sequence (SEQ ID NO: 94) of the kappa light chain variable region of the 20C1 human monoclonal antibody. The CDR1 (SEQ ID NO: 90), CDR2 (SEQ ID NO: 91) and CDR3 (SEQ ID NO: 92) regions are delineated and the V and J germline derivations are indicated.

Figure 10A shows the nucleotide sequence (SEQ ID NO: 176) and amino acid sequence (SEQ ID NO: 124) of the heavy chain of the OX40.21 human monoclonal antibody. The nucleotide sequence (SEQ ID NO: 168) and amino acid sequence (SEQ ID NO: 116) of the light chain is shown in Figure 10B.

Figures 11A-11D show binding curves and EC₅₀s (in nM) of various anti-OX40 antibodies for activated human T cells, with hlgG1 and secondary antibodies serving as controls, as assessed by FACS.

Figures 12A-12C show binding curves and EC₅₀s (in nM) of various anti-OX40 antibodies for activated cynomolgus T cells, with hlgG1 and secondary antibodies serving as controls, as assessed by FACS.

Figures 13A-13C show binding curves and K_Ds of the anti-OX40 antibody, OX40.21, for activated human T cells, HEK293 cells overexpressing human OX40, and CHO cells overexpressing cynomolgus monkey OX40, as assessed by Scatchard analysis.

Figures 14A shows immunohistological staining of various acetone-fixed frozen human tissue sections with the anti-OX40 antibodies OX40.8, OX40.6, and OX40.16. Images show representative staining at an antibody concentration of 1 µg/ml for hyperplastic tonsil and 5 µg/ml for other tissues, with the exception of OX40.16 at 10 µg/ml in the endocardium and valves. While all three antibodies positively stained a small subset of lymphocytes in the tonsil, OX40.8 also stained myofilament-like structures in the heart and OX40.6 stained the cardiac muscles, endothelium/subendothelium matrix in small arteries in the tonsil, and endocardium and valves in the heart. GC, germinal center; MZ, mantle zone.

Figure 14B shows immunostaining of various acetone-fixed frozen human tissue sections with the anti-OX40 antibody OX40.21 (a variant of OX40.16). Images show representative staining at an antibody concentration of 5 µg/ml. The antibody positively stained a small subset of lymphocytes in the tonsil and thymus. The positive cells in the tonsil were distributed in the germinal center, mantle zone, and inter-follicular region, while the positive cells in the thymus were primarily localized in the medulla. No specific staining was observed in the heart, liver, kidney, and lung. GC, germinal center; Me, medulla; MZ, mantle zone.

Figure 15A shows the distribution of OX40+ tumor infiltrating lymphocytes in hepatocellular carcinoma (HCC), colorectal carcinoma (CRC), head and neck squamous cell carcinoma (HNSCC), and melanoma (Mel). A manual score of 12 to 20 cases for each tumor type was performed by estimation of number of positive cells under the 20x objective of a microscope. Minimum, <1 cells per 20x objective field; Mild, 1~<10 cells per 20x objective field; Moderate, 10~<50 cells per 20x objective field; Marked, 50~<200 cells per 20x objective; Intense, >200 cells per 20x objective field.

Figures 15B and 15C shows immunohistological staining for CD3, FoxP3, and OX40 on adjacent FFPE sections from colorectal carcinoma (CRC) and head and neck squamous cell carcinoma (HNSCC) samples. Figure 15B is a low power view, showing that both OX40+ and FoxP3+ TILs are a small fraction of CD3+ TILs and primarily distributed in tumor stroma. Figure 15C is a higher power view showing potential partial co-localization of OX40+ and FoxP3+ (Treg) TILs in CRC.

Figure 16 shows the ability of various anti-OX40 antibodies to inhibit the binding of OX40 ligand (OX40-L) to human OX40-transfected 293 cells ("hOX40-293 cells"), with hlgG1 as the control.

Figure 17 summarizes the OX40-L blocking relationships between various anti-OX40 antibodies.

Figure 18 shows the ability of various anti-OX40 antibodies to inhibit the binding of the anti-OX40 antibody clone L106 to hOX40-293 cells, as assessed by FACS, with PE-labeled L106 only, PE-labeled mlgG1, and unstained cells as controls.

Figures 19A-19C show the ability of various anti-OX40 antibodies to inhibit the binding of allophycocyanin (APC)-conjugated OX40.1 antibody to hOX40-293 (Figures 19A and 19B) or hOX40-HT1080 cells (Figure 19C), as assessed by FACS. hlgG1 and/or hlgG4 were used as controls.

Figures 19D-19G show the ability of various anti-OX40 antibodies to inhibit the binding of biotin-conjugated OX40.4 or OX40.5 antibody to hOX40-293 cells. hlgG1 and streptavidin-APC were used as controls.

Figure 19H summarize the epitope bins in relation to OX40.1 based on results shown in Figures 19A-19C.

Figure 191 summarizes the epitope bins in relation to OX40.5 or OX40.4 based on results shown in Figures 19D-19G.

Figure 20A shows that OX40.21 binds only to non-reduced human OX40, regardless of the presence of N-linked sugars.

Figures 20B and 20C show two N-glycopeptides that were identified by peptide mapping after deglycosylation: 60% occupancy for both AspN118 (Figure 20B) and AspN12 (Figure 20C).

Figure 20D depicts the regions in OX40 bound by OX40.16, OX40.21, and OX40.8.

Figure 20E shows the identification of the peptides recognized by OX40.16, OX40.21, and OX40.8 by LC-MS.

Figures 21A-21D show the effects of various anti-OX40 antibodies on human primary CD4+ T cell proliferation when co-cultured with CHO-CD3-CD32A cells. CHO cells only, T cells only, CHO cells co-cultured with T cells only, and hIgG1 were used as controls.

Figures 22A-22D show the effects of various anti-OX40 antibodies on interferon gamma (IFN- γ) secretion from human primary CD4+ T cells co-cultured with CHO-CD3-CD32A cells. CHO cells only, T cells only, CHO cells co-cultured with T cells only, and hIgG1 were used as controls.

Figures 23A-23F show the effects of various anti-OX40 antibodies on the stimulation of IL-2 secretion from primary T cells in cultures of staphylococcus enterotoxin B (SEB)-activated human peripheral blood mononuclear cells (PBMCs), which were isolated from different donors.

Figure 24 shows the effects of various anti-OX40 antibodies on NK92 cell induced lysis of activated CD4+ cells.

Figures 25A and 25B show the effects of various anti-OX40 antibodies on primary NK cell-mediated lysis of activated CD4+ T cells isolated from two donors by NK:target cell ratios.

Figure 26 shows the effects of various anti-OX40 antibodies on the phagocytosis of hOX40-293 cells by primary human macrophages.

Figure 27 shows the level of binding of the human complement C1q component to OX40.21. IgG1 and IgG1.1 (effectorless) were used as controls.

Figures 28A-28C show that OX40 is expressed in tumor infiltrating lymphocytes, with a pattern generally limited to CD4+ cells with minimal expression on CD8+ cells.

Figure 28D shows that OX40 is expressed by CD4+ T cells and regulatory T cells in mouse SalN tumors.

Figure 28E shows that OX40 is expressed by CD4+ T cells, CD8+ T cells, and regulatory T cells in mouse MC38 tumors.

Figure 29 shows the ability of various anti-OX40 antibodies to reverse regulatory T (Treg) cell-mediated suppression of human CD4+ T cells. In both the presence and absence of Treg cells, anti-OX40 antibodies increased the proliferation of T responder (Tresp) cells compared to the IgG1 isotype control.

Figures 30A and 30B show the clearance of intravenously administered OX40.6 antibody from monkeys. Two of the monkeys showed accelerated clearance, which correlated with the formation of anti-drug antibodies.

Figure 31 is a graph depicting T-cell proliferation results for percentage antigenicity for various anti-OX40 antibodies, as well as quality control samples QC-1, QC-2, and QC-3.

Figures 32A-32C show the effects of different isotypes of the chimeric OX86 antibody (an antibody having the rat variable regions of OX86 and mouse constant region that does not block the interaction between OX40 and OX40-L, i.e., a non-blocking antibody) on anti-tumor activity measured by changes in tumor volumes in individual mice treated with these isotypes (mIgG1 and mIgG2 isotypes) in a MC38 colon adenocarcinoma model: (Figure 32A) control mouse IgG1 antibody ("control"), (Figure 32B) OX86 mIgG1 antibody ("OX-40 mIgG1"), (Figure 32C) OX86 mIgG2 antibody ("OX-40 mIgG2a").

Figures 33A-33C show the effects of different isotypes (mIgG1 and mIgG2a) of the OX86 antibody on the number of CD4+ regulatory T cells in tumors and the periphery, and on cell numbers in the spleen.

Figures 34A-34C show the effects of chimeric OX86 antibodies with a human IgG1 on anti-tumor activity measured by changes in tumor volumes in individual mice treated with the indicated antibodies in the MC38 colon adenocarcinoma model: (Figure 34A) human IgG1 isotype control ("Isotype"), (Figure 34B) OX86-hIgG1 chimeric antibody ("OX86-hG1"), (Figure 34C) OX86-hIgG1-S267E antibody ("OX86-hG1-S267E"). The S267E substitution in hIgG1 increases its effector function by increasing binding to FcRs (CD32A and CD32B). OX86-hIgG1 exhibited potent anti-tumor activity.

Figures 35A-35D show the effects of chimeric OX86 hIgG1 antibody on regulatory T cell depletion.

Figures 36A-36E show the effects of a blocking (i.e., blocks the interaction between OX40 and OX40 ligand) hamster anti-mouse OX40 antibody (8E5) at different dosages on anti-tumor activity by changes in tumor volumes in individual mice treated with the indicated antibodies in the subcutaneous mouse CT-26 tumor model. (Figure 36A) hamster Ig control, (Figure 36B) 8E5 at 10 mg/kg, (Figure 36C) 8E5 at 3 mg/kg, (Figure 36D) 8E5 at 1 mg/kg, (Figure 36E) 8E5 at 0.3 mg/kg.

Figures 37A-37D show the effects of combination therapy with the OX86-rG1 antibody and an anti-PDI antibody on anti-tumor activity measured by changes in tumor volumes in individual mice treated with the indicated antibodies and combination in the MC38 colon adenocarcinoma model: (Figure 37A) isotype control, (Figure 37B) anti-PDI antibody, (Figure 37C) OX86-rG1 ("anti-OX40"), (Figure 37D) OX86-rG1 + anti-PDI antibody ("anti-OX40 + anti-PDI").

Figures 38A and 38B show the *ex vivo* recall response to KLH, CD69+ expressing CD4+CD8- T cells at Days 22 and 41, respectively. Animals were immunized with KLH on Study Day 1. Data points represent individual animal (males and females) results as a percentage of CD4+CD8- T cells. Horizontal bars represent group means.

Figure 39 shows antibody binding to anti-his Fab captured FcγR-his proteins. Binding responses are plotted as a percentage of the theoretical R_{max} assuming a 1:1 mAb:FcγR binding stoichiometry. The bars for each antibody are shown in the order provided by the color legends at the bottom of the slide.

Figure 40 shows antibody binding to anti-his Fab captured FcγR-his proteins. Binding responses are plotted as a percentage of the theoretical R_{max} assuming a 1:1 mAb:FcγR binding stoichiometry. The bars for each antibody are shown in the order provided by the color legends at the bottom of the slide.

Figures 41A-41D show the effects of combination therapy with an agonistic anti-OX40 antibody (OX86-rG1) and an anti-CTLA-4 antibody (9D9-mG2b) on anti-tumor activity measured by changes in tumor volumes in individual mice treated with the indicated antibodies and combination in the CT26 colon adenocarcinoma model: (Figure 41A) isotype control, (Figure 41B) anti-CTLA-4 antibody, (Figure 41C) OX86-rG1, (Figure 41D) OX86-rG1 + anti-CTLA-4 antibody.

Figure 42 is a schematic of the Phase 1/2a clinical trial protocol.

Figure 43 is a schematic of the study visit schedule for the Phase 1/2a clinical trial.

DETAILED DESCRIPTION

[0052] Described herein are isolated antibodies, particularly monoclonal antibodies, e.g., human monoclonal antibodies, which specifically bind to OX40 and thereby activate downstream OX40 signaling ("agonist anti-OX40 antibodies"). The antibodies described

herein are characterized by particular functional features and/or comprise particular structural features, such as CDR regions comprising specific amino acid sequences. Provided herein are isolated antibodies, methods of making such anti-OX40 antibodies, immunoconjugates, and bispecific molecules comprising such antibodies, and pharmaceutical compositions formulated to contain the antibodies. Also provided herein are methods of using the antibodies for immune response enhancement, alone or in combination with other immunostimulatory agents (e.g., antibodies) and/or cancer therapies. Accordingly, the anti-OX40 antibodies described herein may be used in a treatment in a wide variety of therapeutic applications, including, for example, inhibiting tumor growth and treating viral infections.

Definitions

[0053] In order that the present description may be more readily understood, certain terms are first defined. Additional definitions are set forth throughout the detailed description.

[0054] The term "OX40" as used herein refers to a receptor that is a member of the TNF-receptor superfamily, which binds to OX40 ligand (OX40-L). OX40 is also referred to as tumor necrosis factor receptor superfamily, member 4 (TNFRSF4), ACT35, IMD16, TXGP1L, and CD134. The term "OX40" includes any variants or isoforms of OX40 which are naturally expressed by cells. Accordingly, antibodies described herein may cross-react with OX40 from species other than human (e.g., cynomolgus OX40). Alternatively, the antibodies may be specific for human OX40 and may not exhibit any cross-reactivity with other species. OX40 or any variants and isoforms thereof, may either be isolated from cells or tissues which naturally express them or be recombinantly produced using well-known techniques in the art and/or those described herein.

[0055] The amino acid sequence of human OX40 precursor (Accession No. NP_003318.1) is set forth in SEQ ID NO: 1. The amino acid sequence of the extracellular domain of mature human OX40 is set forth in SEQ ID NO: 2. The amino acid sequence of cynomolgus OX40 is set forth in SEQ ID NO: 3. The amino acid sequence of human OX40-L is set forth in SEQ ID NO: 4.

[0056] The terms "Programmed Death 1," "Programmed Cell Death 1," "Protein PD-1," "PD-1," PD1, "PDCD1," "hPD-1" and "hPD-I," as used herein, are used interchangeably, and include variants, isoforms, species homologs of human PD-1, and analogs having at least one common epitope with PD-1. The complete PD-1 sequence can be found under GenBank Accession No. U64863.

[0057] The term "cytotoxic T lymphocyte-associated antigen-4," "CTLA-4," "CTLA4," "CTLA-4 antigen" and "CD152" (see, e.g., Murata (1999) Am. J. Pathol. 155:453-460) are used interchangeably, and include variants, isoforms, species homologs of human CTLA-4, and analogs having at least one common epitope with CTLA-4 (see, e.g., Balzano (1992) Int. J. Cancer Suppl. 7:28-32). A complete sequence of human CTLA-4 is set forth in GenBank Accession No. LI 5006.

[0058] The term "antibody" as used to herein may include whole antibodies and any antigen binding fragments (*i.e.*, "antigen-binding portions") or single chains thereof. An "antibody" refers, in one embodiment, to a glycoprotein comprising at least two heavy (H) chains and two light (L) chains inter-connected by disulfide bonds, or an antigen binding portion thereof. Each heavy chain is comprised of a heavy chain variable region (abbreviated herein as V_H) and a heavy chain constant region. In certain naturally occurring IgG, IgD, and IgA antibodies, the heavy chain constant region is comprised of three domains, CH1, CH2 and CH3. In certain naturally occurring antibodies, each light chain is comprised of a light chain variable region (abbreviated herein as V_L) and a light chain constant region. The light chain constant region is comprised of one domain, CL. The V_H and V_L regions can be further subdivided into regions of hypervariability, termed complementarity determining regions (CDR), interspersed with regions that are more conserved, termed framework regions (FR). Each V_H and V_L is composed of three CDRs and four FRs, arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4. The variable regions of the heavy and light chains contain a binding domain that interacts with an antigen. The constant regions of the antibodies may mediate the binding of the immunoglobulin to host tissues or factors, including various cells of the immune system (*e.g.*, effector cells) and the first component (C1q) of the classical complement system.

[0059] Antibodies typically bind specifically to their cognate antigen with high affinity, reflected by a dissociation constant (K_D) of 10^{-7} to 10^{-11} M or less. Any K_D greater than about 10^{-6} M is generally considered to indicate nonspecific binding. As used herein, an antibody that "binds specifically" to an antigen refers to an antibody that binds to the antigen and substantially identical antigens with high affinity, which means having a K_D of 10^{-7} M or less, preferably 10^{-8} M or less, even more preferably 5×10^{-9} M or less, and most preferably between 10^{-8} M and 10^{-10} M or less, but does not bind with high affinity to unrelated antigens. An antigen is "substantially identical" to a given antigen if it exhibits a high degree of sequence identity to the given antigen, for example, if it exhibits at least 80%, at least 90%, preferably at least 95%, more preferably at least 97%, or even more preferably at least 99% sequence identity to the sequence of the given antigen. By way of example, an antibody that binds specifically to human OX40 may cross-react with OX40 from certain non-human primate species (*e.g.*, cynomolgus monkey), but may not cross-react with OX40 from other species

(e.g., murine OX40), or with an antigen other than OX40.

[0060] An immunoglobulin may be from any of the commonly known isotypes, including but not limited to IgA, secretory IgA, IgG and IgM. The IgG isotype is divided in subclasses in certain species: IgG1, IgG2, IgG3 and IgG4 in humans, and IgG1, IgG2a, IgG2b and IgG3 in mice. In certain embodiments, the anti-OX40 antibodies described herein are of the IgG1 or IgG2 subtype. Immunoglobulins, e.g., IgG1, exist in several allotypes, which differ from each other in at most a few amino acids. "Antibody" may include, by way of example, both naturally occurring and non-naturally occurring antibodies; monoclonal and polyclonal antibodies; chimeric and humanized antibodies; human and nonhuman antibodies; wholly synthetic antibodies; and single chain antibodies.

[0061] The term "antigen-binding portion" of an antibody, as used herein, refers to one or more fragments of an antibody that retain the ability to specifically bind to an antigen (e.g., human OX40). It has been shown that the antigen-binding function of an antibody can be performed by fragments of a full-length antibody. Examples of binding fragments encompassed within the term "antigen-binding portion" of an antibody, e.g., an anti-OX40 antibody described herein, include (i) a Fab fragment, a monovalent fragment consisting of the V_L , V_H , CL and CH1 domains; (ii) a $F(ab')_2$ 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_H and CH1 domains; (iv) a Fv fragment consisting of the V_L and V_H domains of a single arm of an antibody, (v) a dAb fragment (Ward et al., (1989) Nature 341:544-546), which consists of a V_H domain; and (vi) an isolated complementarity determining region (CDR) or (vii) 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_L and V_H , are coded for by separate genes, they can be joined, using recombinant methods, by a synthetic linker that enables them to be made as a single protein chain in which the V_L and V_H regions pair to form monovalent molecules (known as single chain Fv (scFv); see e.g., Bird et al. (1988) Science 242:423-426; and Huston et al. (1988) Proc. Natl. Acad. Sci. USA 85:5879-5883). Such single chain antibodies are also intended to be encompassed within the term "antigen-binding portion" of an antibody. These and other potential constructs are described at Chan & Carter (2010) Nat. Rev. Immunol. 10:301. These antibody fragments are obtained using conventional techniques known to those with skill in the art, and the fragments are screened for utility in the same manner as are intact antibodies. Antigen-binding portions can be produced by recombinant DNA techniques, or by enzymatic or chemical cleavage of intact immunoglobulins.

[0062] A "bispecific" or "bifunctional antibody" is an artificial hybrid antibody having two different heavy/light chain pairs and two different binding sites. Bispecific antibodies can be produced by a variety of methods including fusion of hybridomas or linking of Fab' fragments. See, e.g., Songsivilai & Lachmann, Clin. Exp. Immunol. 79:315-321 (1990); Kostelny et al., J. Immunol. 148, 1547-1553 (1992).

[0063] The term "monoclonal antibody," as used herein, refers to an antibody that displays a single binding specificity and affinity for a particular epitope or a composition of antibodies in which all antibodies display a single binding specificity and affinity for a particular epitope. Typically such monoclonal antibodies will be derived from a single cell or nucleic acid encoding the antibody, and will be propagated without intentionally introducing any sequence alterations. Accordingly, the term "human monoclonal antibody" refers to a monoclonal antibody that has variable and optional constant regions derived from human germline immunoglobulin sequences. In one embodiment, human monoclonal antibodies are produced by a hybridoma, for example, obtained by fusing a B cell obtained from a transgenic or transchromosomal non-human animals (e.g., a transgenic mouse having a genome comprising a human heavy chain transgene and a light chain), to an immortalized cell.

[0064] The term "recombinant human antibody," as used herein, includes all human antibodies that are prepared, expressed, created or isolated by recombinant means, such as (a) antibodies isolated from an animal (e.g., a mouse) that is transgenic or transchromosomal for human immunoglobulin genes or a hybridoma prepared therefrom, (b) antibodies isolated from a host cell transformed to express the antibody, e.g., from a transfectoma, (c) antibodies isolated from a recombinant, combinatorial human antibody library, and (d) antibodies prepared, expressed, created or isolated by any other means that involve splicing of human immunoglobulin gene sequences to other DNA sequences. Such recombinant human antibodies comprise variable and constant regions that utilize particular human germline immunoglobulin sequences are encoded by the germline genes, but include subsequent rearrangements and mutations that occur, for example, during antibody maturation. As known in the art (see, e.g., Lonberg (2005) Nature Biotech. 23(9):1117-1125), the variable region contains the antigen binding domain, which is encoded by various genes that rearrange to form an antibody specific for a foreign antigen. In addition to rearrangement, the variable region can

be further modified by multiple single amino acid changes (referred to as somatic mutation or hypermutation) to increase the affinity of the antibody to the foreign antigen. The constant region will change in further response to an antigen (*i.e.*, isotype switch). Therefore, the rearranged and somatically mutated nucleic acid sequences that encode the light chain and heavy chain immunoglobulin polypeptides in response to an antigen may not be identical to the original germline sequences, but instead will be substantially identical or similar (*i.e.*, have at least 80% identity).

[0065] A "human" antibody (HuMAb) refers to an antibody having variable regions in which both the framework and CDR regions are derived from human germline immunoglobulin sequences. Furthermore, if the antibody contains a constant region, the constant region also is derived from human germline immunoglobulin sequences. The antibodies described herein may include amino acid residues not encoded by human germline immunoglobulin sequences (*e.g.*, mutations introduced by random or site-specific mutagenesis *in vitro* or by somatic mutation *in vivo*). However, the term "human antibody", as used herein, is not intended to include antibodies in which CDR sequences derived from the germline of another mammalian species, such as a mouse, have been grafted onto human framework sequences. The terms "human" antibodies and "fully human" antibodies are used synonymously.

[0066] A "humanized" antibody refers to an antibody in which some, most or all of the amino acids outside the CDR domains of a non-human antibody are replaced with corresponding amino acids derived from human immunoglobulins. In one embodiment of a humanized form of an antibody, some, most, or all of the amino acids outside the CDR domains have been replaced with amino acids from human immunoglobulins, whereas some, most or all amino acids within one or more CDR regions are unchanged. Small additions, deletions, insertions, substitutions or modifications of amino acids are permissible as long as they do not abrogate the ability of the antibody to bind to a particular antigen. A "humanized" antibody retains an antigenic specificity similar to that of the original antibody.

[0067] A "chimeric antibody" refers to an antibody in which the variable regions are derived from one species and the constant regions are derived from another species, such as an antibody in which the variable regions are derived from a mouse antibody and the constant regions are derived from a human antibody.

[0068] As used herein, "isotype" refers to the antibody class (*e.g.*, IgG1, IgG2, IgG3, IgG4, IgM, IgA1, IgA2, IgD, and IgE antibody) that is encoded by the heavy chain constant region genes.

[0069] "Allotype" refers to naturally occurring variants within a specific isotype group, which variants differ in a few amino acids (see, *e.g.*, Jefferis et al. (2009) mAbs 1:1). Antibodies described herein may be of any allotype. As used herein, antibodies referred to as "IgG1f" or "IgG1.1f" isotype are IgG1 and effectorless IgG1.1 antibodies, respectively, of the allotype "f," *i.e.*, having 214R, 356E and 358M according to the EU index as in Kabat, as shown, *e.g.*, in SEQ ID NO: 5 (see underlined residues in SEQ ID NO: 5 of Table 23).

[0070] The phrases "an antibody recognizing an antigen" and "an antibody specific for an antigen" are used interchangeably herein with the term "an antibody which binds specifically to an antigen."

[0071] An "isolated antibody," as used herein, is intended to refer to an antibody that is substantially free of other antibodies having different antigenic specificities (*e.g.*, an isolated antibody that specifically binds to OX40 is substantially free of antibodies that specifically bind antigens other than OX40). An isolated antibody that specifically binds to an epitope of OX40 may, however, have cross-reactivity to other OX40 proteins from different species.

[0072] As used herein, an antibody that "inhibits binding of OX40-L to OX40" is intended to refer to an antibody that inhibits the binding of OX40-L to OX40, *e.g.*, in binding assays using hOX40-293 cells, with an EC₅₀ of about 1 µg/mL or less, such as about 0.9 µg/mL or less, about 0.85 µg/mL or less, about 0.8 µg/mL or less, about 0.75 µg/mL or less, about 0.7 µg/mL or less, about 0.65 µg/mL or less, about 0.6 µg/mL or less, about 0.55 µg/mL or less, about 0.5 µg/mL or less, about 0.45 µg/mL or less, about 0.4 µg/mL or less, about 0.35 µg/mL or less, about 0.3 µg/mL or less, about 0.25 µg/mL or less, about 0.2 µg/mL or less, about 0.15 µg/mL or less, or about 0.1 µg/mL or less, in art-recognized methods, *e.g.*, the FACS-based binding assays described herein.

[0073] An "effector function" refers to the interaction of an antibody Fc region with an Fc receptor or ligand, or a biochemical event that results therefrom. Exemplary "effector functions" include C1q binding, complement dependent cytotoxicity (CDC), Fc receptor binding, FcγR-mediated effector functions such as ADCC and antibody dependent cell-

mediated phagocytosis (ADCP), and downregulation of a cell surface receptor (e.g., the B cell receptor; BCR). Such effector functions generally require the Fc region to be combined with a binding domain (e.g., an antibody variable domain).

[0074] An "Fc receptor" or "FcR" is a receptor that binds to the Fc region of an immunoglobulin. FcRs that bind to an IgG antibody comprise receptors of the FcγR family, including allelic variants and alternatively spliced forms of these receptors. The FcγR family consists of three activating (FcγRI, FcγRIII, and FcγRIV in mice; FcγRIA, FcγRIIA, and FcγRIIIA in humans) and one inhibitory (FcγRIIB) receptor. Various properties of human FcγRs are summarized in Table 1. The majority of innate effector cell types coexpress one or more activating FcγR and the inhibitory FcγRIIB, whereas natural killer (NK) cells selectively express one activating Fc receptor (FcγRIII in mice and FcγRIIIA in humans) but not the inhibitory FcγRIIB in mice and humans. Human IgG1 binds to most human Fc receptors and is considered equivalent to murine IgG2a with respect to the types of activating Fc receptors that it binds to.

Table 1. Properties of human FcγRs

Fcγ	Allelic variants	Affinity for human IgG	Isotype preference	Cellular distribution
FcγRI	None described	High ($K_D \sim 10$ nM)	IgG1=3>4>>2	Monocytes, macrophages, activated neutrophils, dendritic cells?
FcγRIIA	H131	Low to medium	IgG 1>3>2>4	Neutrophils, monocytes, macrophages, eosinophils, dendritic cells, platelets
	R131	Low	IgG 1>3>4>2	
FcγRIIIA	V158	Medium	IgG1=3>>4>2	NK cells, monocytes, macrophages, mast cells, eosinophils, dendritic cells?
	F158	Low	IgG1=3>>4>2	
FcγRIIB	1232	Low	IgG 1=3=4>2	B cells, monocytes, macrophages, dendritic cells, mast cells
	T232	Low	IgG1=3=4>2	

[0075] An "Fc region" (fragment crystallizable region) or "Fc domain" or "Fc" refers to the C-terminal region of the heavy chain of an antibody that mediates the binding of the immunoglobulin to host tissues or factors, including binding to Fc receptors located on various cells of the immune system (e.g., effector cells) or to the first component (C1q) of the classical complement system. Thus, an Fc region comprises the constant region of an antibody excluding the first constant region immunoglobulin domain (e.g., CH1 or CL). In IgG, IgA and IgD antibody isotypes, the Fc region comprises C_{H2} and C_{H3} constant domains in each of the antibody's two heavy chains; IgM and IgE Fc regions comprise three heavy chain constant domains (C_H domains 2-4) in each polypeptide chain. For IgG, the Fc region comprises immunoglobulin domains Cy2 and Cy3 and the hinge between Cy1 and Cy2. Although the boundaries of the Fc region of an immunoglobulin heavy chain might vary, the human IgG heavy chain Fc region is usually defined to stretch from an amino acid residue at position C226 or P230 (or amino acid between these two amino acids) to the carboxy-terminus of the heavy chain, wherein the numbering is according to the EU index as in Kabat. Kabat et al. (1991) Sequences of Proteins of Immunological Interest, National Institutes of Health, Bethesda, MD; see also Figs. 3C-3F of U.S. Pat. App. Pub. No. 2008/0248028. The C_{H2} domain of a human IgG Fc region extends from about amino acid 231 to about amino acid 340, whereas the C_{H3} domain is positioned on C-terminal side of a C_{H2} domain in an Fc region, i.e., it extends from about amino acid 341 to about amino acid 447 of an IgG. As used herein, the Fc region may be a native sequence Fc, including any allotypic variant, or a variant Fc (e.g., a non-naturally occurring Fc). Fc may also refer to this region in isolation or in the context of an Fc-comprising protein polypeptide such as a "binding protein comprising an Fc region," also referred to as an "Fc fusion protein" (e.g., an antibody or immunoadhesin).

[0076] A "hinge", "hinge domain" or "hinge region" or "antibody hinge region" refers to the domain of a heavy chain constant region that joins the CH1 domain to the CH2 domain and includes the upper, middle, and lower portions of the hinge (Roux et al. J. Immunol. 1998 161:4083). The hinge provides varying levels of flexibility between the binding and effector regions of an antibody and also provides sites for intermolecular, disulfide bonding between the two heavy chain constant regions. As used herein, a hinge starts at Glu216 and ends at Gly237 for all IgG isotypes (Roux et al., 1998 J Immunol 161:4083). The sequences of wildtype IgG1, IgG2, IgG3 and IgG4 hinges are shown in Tables 2 and 23.

Table 2. Hinge region amino acids

Ig Type	C-terminal C _H 1*	Upper Hinge	Middle Hinge	Lower Hinge
IgG1	VDKRV (SEQ ID NO: 186)	EPKSCDKTHT (SEQ ID NO: 188)	CPPCP (SEQ ID NO: 192)	APELLGG (SEQ ID NO: 200)
IgG2	VDKTV (SEQ ID NO: 187)	ERK	CCVECPPCP (SEQ ID NO: 193)	APPVAG (SEQ ID NO: 201)
IgG3 (17-15-15)	VDKRV (SEQ ID NO: 186)	ELKTPLGDTTHT (SEQ ID NO: 189)	CPRCP (EPKSCDTPPPCPRCP) ₃ (SEQ ID NO: 194)	APELLGG (SEQ ID NO: 200)
IgG3 (17-15-15)	VDKRV (SEQ ID NO: 186)	ELKTPLGDTTHT (SEQ ID NO: 189)	CPRCP (EPKSCDTPPPCPRCP) ₂ (SEQ ID NO: 195)	APELLGG (SEQ ID NO: 200)
IgG3 (17-15)	VDKRV (SEQ ID NO: 186)	ELKTPLGDTTHT (SEQ ID NO: 189)	CPRCP (EPKSCDTPPPCPRCP) ₁ (SEQ ID NO: 196)	APELLGG (SEQ ID NO: 200)
IgG3 (15-15-15)	VDKRV (SEQ ID NO: 186)	EPKS (SEQ ID NO: 190)	CDTPPPCPRCP (EPKSCDTPPPCPRCP) ₂ (SEQ ID NO: 197)	APELLGG (SEQ ID NO: 200)
IgG3 (15)	VDKRV (SEQ ID NO: 186)	EPKS (SEQ ID NO: 190)	CDTPPPCPRCP (SEQ ID NO: 198)	APELLGG (SEQ ID NO: 200)
IgG4	VDKRV (SEQ ID NO: 186)	ESKYGPP (SEQ ID NO: 191)	CPSCP (SEQ ID NO: 199)	APEFLGG (SEQ ID NO: 200)

* C-terminal amino acid sequences of the CH1 domains.

[0077] The term "hinge" includes wild-type hinges (such as those set forth in Table 23), as well as variants thereof (e.g., non-naturally-occurring hinges or modified hinges). For example, the term "IgG2 hinge" includes wildtype IgG2 hinge, as shown in Table 23, and variants having 1, 2, 3, 4, 5, 1-3, 1-5, 3-5 and/or at most 5, 4, 3, 2, or 1 mutations, e.g., substitutions, deletions or additions. Exemplary IgG2 hinge variants include IgG2 hinges in which 1, 2, 3 or all 4 cysteines (C219, C220, C226 and C229) are changed to another amino acid. In a specific embodiment, an IgG2 comprises a C219S substitution. In certain embodiments, a hinge is a hybrid hinge that comprises sequences from at least two isotypes. For example, a hinge may comprise the upper, middle or lower hinge from one isotype and the remainder of the hinge from one or more other isotypes. For example, a hinge can be an IgG2/IgG1 hinge, and may comprise, e.g., the upper and middle hinges of IgG2 and the lower hinge of IgG1. A hinge may have effector function or be deprived of effector function. For example, the lower hinge of wildtype IgG1 provides effector function.

[0078] The term "CH1 domain" refers to the heavy chain constant region linking the variable domain to the hinge in a heavy chain constant domain. As used herein, a CH1 domain starts at A118 and ends at V215. The term "CH1 domain" includes wildtype CH1 domains (such as having SEQ ID NO: 202 for IgG1 and SEQ ID NO: 203 for IgG2; Table 23), as well as variants thereof (e.g., non-naturally-occurring CH1 domains or modified CH1 domains). For example, the term "CH1 domain" includes wildtype CH1 domains and variants having 1, 2, 3, 4, 5, 1-3, 1-5, 3-5 and/or at most 5, 4, 3, 2, or 1 mutations, e.g., substitutions, deletions or additions. Exemplary CH1 domains include CH1 domains with mutations

that modify a biological activity of an antibody, such as ADCC, CDC or half-life. Modifications to the CH1 domain that affect a biological activity of an antibody are provided herein.

[0079] The term "CH2 domain" refers to the heavy chain constant region linking the hinge to the CH3 domain in a heavy chain constant domain. As used herein, a CH2 domain starts at P238 and ends at K340. The term "CH2 domain" includes wildtype CH2 domains (such as having SEQ ID NO: 204 for IgG1 and SEQ ID NO: 205 for IgG2; Table 23), as well as variants thereof (e.g., non-naturally occurring CH2 domains or modified CH2 domains). For example, the term "CH2 domain" includes wildtype CH2 domains and variants having 1, 2, 3, 4, 5, 1-3, 1-5, 3-5 and/or at most 5, 4, 3, 2, or 1 mutations, e.g., substitutions, deletions or additions. Exemplary CH2 domains include CH2 domains with mutations that modify a biological activity of an antibody, such as ADCC, CDC or half-life. In certain embodiments, a CH2 domain comprises the substitutions A330S/P331S that reduce effector function. Other modifications to the CH2 domain that affect a biological activity of an antibody are provided herein.

[0080] The term "CH3 domain" refers to the heavy chain constant region that is C-terminal to the CH2 domain in a heavy chain constant domain. As used herein, a CH3 domain starts at G341 and ends at K447. The term "CH3 domain" includes wildtype CH3 domains (such as having SEQ ID NO: 206 for IgG1 and SEQ ID NO: 207 for IgG2; Table 23), as well as variants thereof (e.g., non-naturally occurring CH3 domains or modified CH3 domains). For example, the term "CH3 domain" includes wildtype CH3 domains and variants having 1, 2, 3, 4, 5, 1-3, 1-5, 3-5 and/or at most 5, 4, 3, 2, or 1 mutations, e.g., substitutions, deletions or additions. Exemplary CH3 domains include CH3 domains with mutations that modify a biological activity of an antibody, such as ADCC, CDC or half-life. Modifications to the CH3 domain that affect a biological activity of an antibody are provided herein.

[0081] A "native sequence Fc region" or "native sequence Fc" comprises an amino acid sequence that is identical to the amino acid sequence of an Fc region found in nature. Native sequence human Fc regions include a native sequence human IgG1 Fc region; native sequence human IgG2 Fc region; native sequence human IgG3 Fc region; and native sequence human IgG4 Fc region as well as naturally occurring variants thereof. Native sequence Fcs include the various allotypes of Fcs (see, e.g., Jefferis et al. (2009) mAbs 1:1).

[0082] The term "epitope" or "antigenic determinant" refers to a site on an antigen (e.g., OX40) to which an immunoglobulin or antibody specifically binds. Epitopes within protein antigens can be formed both from contiguous amino acids (usually a linear epitope) or noncontiguous amino acids juxtaposed by tertiary folding of the protein (usually a conformational epitope). Epitopes formed from contiguous amino acids are typically, but not always, retained on exposure to denaturing solvents, whereas epitopes formed by tertiary folding are typically lost on treatment with denaturing solvents. An epitope typically includes at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15 amino acids in a unique spatial conformation. Methods for determining what epitopes are bound by a given antibody (*i.e.*, epitope mapping) are well known in the art and include, for example, immunoblotting and immunoprecipitation assays, wherein overlapping or contiguous peptides (e.g., from OX40) are tested for reactivity with a given antibody (e.g., an anti-OX40 antibody). Methods of determining spatial conformation of epitopes include techniques in the art and those described herein, for example, x-ray crystallography, 2-dimensional nuclear magnetic resonance and HDX-MS (see, e.g., Epitope Mapping Protocols in Methods in Molecular Biology, Vol. 66, G. E. Morris, Ed. (1996)).

[0083] The term "epitope mapping" refers to the process of identification of the molecular determinants on the antigen involved in antibody-antigen recognition.

[0084] The term "binds to the same epitope" with reference to two or more antibodies means that the antibodies bind to the same group of amino acid residues, as determined by a given method. Techniques for determining whether antibodies bind to the "same epitope on OX40" with the antibodies described herein include art-recognized epitope mapping methods, such as x-ray analyses of crystals of antigen:antibody complexes which provides atomic resolution of the epitope and hydrogen/deuterium exchange mass spectrometry (HDX-MS). Other methods monitor the binding of the antibody to antigen fragments (e.g., proteolytic fragments) or to mutated variations of the antigen where loss of binding due to a modification of an amino acid residue within the antigen sequence is often considered an indication of an epitope component (e.g., alanine scanning mutagenesis - Cunningham & Wells (1985) Science 244:1081). In addition, computational combinatorial methods for epitope mapping can also be used. These methods rely on the ability of the antibody of interest to affinity isolate specific short peptides from combinatorial phage display peptide libraries. Antibodies having the same or closely related VH and VL or the same CDR1, 2 and 3 sequences are expected to bind

to the same epitope.

[0085] Antibodies that "compete with another antibody for binding to a target" refer to antibodies that (partially or completely) inhibit the binding of the other antibody to the target. Whether two antibodies compete with each other for binding to a target, i.e., whether and to what extent one antibody inhibits the binding of the other antibody to a target, may be determined using known competition experiments. In certain embodiments, an antibody competes with, and inhibits binding of another antibody to a target by at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or 100%. The level of inhibition or competition may be different depending on which antibody is the "blocking antibody" (i.e., the cold antibody that is incubated first with the target). Competition assays can be conducted as described, for example, in Ed Harlow and David Lane, Cold Spring Harb Protoc ; 2006; doi:10.1101/pdb.prot4277 or in Chapter 11 of "Using Antibodies" by Ed Harlow and David Lane, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, USA 1999. Competing antibodies bind to the same epitope, an overlapping epitope, or to adjacent epitopes (e.g., as evidenced by steric hindrance).

[0086] Other art-recognized competitive binding assays include: solid phase direct or indirect radioimmunoassay (RIA), solid phase direct or indirect enzyme immunoassay (EIA), sandwich competition assay (see Stahli et al., Methods in Enzymology 9:242 (1983)); solid phase direct biotin-avidin EIA (see Kirkland et al., J. Immunol. 137:3614 (1986)); solid phase direct labeled assay, solid phase direct labeled sandwich assay (see Harlow and Lane, Antibodies: A Laboratory Manual, Cold Spring Harbor Press (1988)); solid phase direct label RIA using I-125 label (see Morel et al., Mol. Immunol. 25(1):7 (1988)); solid phase direct biotin-avidin EIA (Cheung et al., Virology 176:546 (1990)); and direct labeled RIA. (Moldenhauer et al., Scand. J. Immunol. 32:77 (1990)).

[0087] As used herein, the terms "specific binding," "selective binding," "selectively binds," and "specifically binds," refer to antibody binding to an epitope on a predetermined antigen but not to other antigens. Typically, the antibody (i) binds with an equilibrium dissociation constant (K_D) of approximately less than 10^{-7} M, such as approximately less than 10^{-8} M, 10^{-9} M or 10^{-10} M or even lower when determined by, e.g., surface plasmon resonance (SPR) technology in a BIACORE 2000 surface plasmon resonance (SPR) instrument using the predetermined antigen, e.g., recombinant human OX40, as the analyte and the antibody as the ligand, and (ii) binds to the predetermined antigen with an affinity that is at least two-fold greater than its affinity for binding to a non-specific antigen (e.g., BSA, casein) other than the predetermined antigen or a closely-related antigen. Accordingly, an antibody that "specifically binds to human OX40" refers to an antibody that binds to soluble or cell bound human OX40 with a K_D of 10^{-7} M or less, such as approximately less than 10^{-8} M, 10^{-9} M or 10^{-10} M or even lower. An antibody that "cross-reacts with cynomolgus OX40" refers to an antibody that binds to cynomolgus OX40 with a K_D of 10^{-7} M or less, such as approximately less than 10^{-8} M, 10^{-9} M or 10^{-10} M or even lower. In certain embodiments, antibodies that do not cross-react with OX40 from a non-human species (e.g., murine OX40) exhibit essentially undetectable binding against these proteins in standard binding assays.

[0088] The term " k_{assoc} " or " k_a ", as used herein, is intended to refer to the association rate constant of a particular antibody-antigen interaction, whereas the term " k_{dis} " or " k_d ", as used herein, is intended to refer to the dissociation rate constant of a particular antibody-antigen interaction. The term " K_D ", as used herein, is intended to refer to the equilibrium dissociation constant, which is obtained from the ratio of k_d to k_a (i.e., k_d/k_a) and is expressed as a molar concentration (M). K_D values for antibodies can be determined using methods well established in the art. A preferred method for determining the K_D of an antibody is by using surface plasmon resonance, preferably using a biosensor system such as a Biacore[®] SPR system or flow cytometry and Scatchard analysis.

[0089] As used herein, the term "high affinity" for an IgG antibody refers to an antibody having a K_D of 10^{-8} M or less, more preferably 10^{-9} M or less and even more preferably 10^{-10} M or less for a target antigen. However, "high affinity" binding can vary for other antibody isotypes. For example, "high affinity" binding for an IgM isotype refers to an antibody having a K_D of 10^{-7} M or less, more preferably 10^{-8} M or less.

[0090] The term "EC50" in the context of an *in vitro* or *in vivo* assay using an antibody or antigen binding fragment thereof, refers to the concentration of an antibody or an antigen-binding portion thereof that induces a response that is 50% of the maximal response, i.e., halfway between the maximal response and the baseline.

[0091] The term "binds to immobilized OX40," refers to the ability of an antibody described herein to bind to OX40, for example, expressed on the surface of a cell or attached to a solid support.

[0092] The term "cross-reacts," as used herein, refers to the ability of an antibody described herein to bind to OX40 from a different species. For example, an antibody described herein that binds human OX40 may also bind OX40 from another species (e.g., cynomolgus OX40). As used herein, cross-reactivity may be measured by detecting a specific reactivity with purified antigen in binding assays (e.g., SPR, ELISA) or binding to, or otherwise functionally interacting with, cells physiologically expressing OX40. Methods for determining cross-reactivity include standard binding assays as described herein, for example, by BIACORE® surface plasmon resonance (SPR) analysis using a BIACORE® 2000 SPR instrument (Biacore AB, Uppsala, Sweden), or flow cytometric techniques.

[0093] The term "naturally-occurring" as used herein as applied to an object refers to the fact that an object can be found in nature. For example, a polypeptide or polynucleotide sequence that is present in an organism (including viruses) that can be isolated from a source in nature and which has not been intentionally modified by man in the laboratory is naturally-occurring.

[0094] A "polypeptide" refers to a chain comprising at least two consecutively linked amino acid residues, with no upper limit on the length of the chain. One or more amino acid residues in the protein may contain a modification such as, but not limited to, glycosylation, phosphorylation or a disulfide bond. A "protein" may comprise one or more polypeptides.

[0095] The term "nucleic acid molecule," as used herein, is intended to include DNA molecules and RNA molecules. A nucleic acid molecule may be single-stranded or double-stranded, and may be cDNA.

[0096] Also provided are "conservative sequence modifications" of the sequences set forth herein, e.g., in Table 23, i.e., nucleotide and amino acid sequence modifications which do not abrogate the binding of the antibody encoded by the nucleotide sequence or containing the amino acid sequence, to the antigen. Such conservative sequence modifications include conservative nucleotide and amino acid substitutions, as well as, nucleotide and amino acid additions and deletions. For example, modifications can be introduced into a sequence in Table 23 by standard techniques known in the art, such as site-directed mutagenesis and PCR-mediated mutagenesis. Conservative sequence modifications include conservative amino acid substitutions, in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine, tryptophan), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an anti-OX40 antibody is preferably replaced with another amino acid residue from the same side chain family. Methods of identifying nucleotide and amino acid conservative substitutions that do not eliminate antigen binding are well-known in the art (see, e.g., Brummell et al., *Biochem.* 32:1180-1187 (1993); Kobayashi et al. *Protein Eng.* 12(10):879-884 (1999); and Burks et al. *Proc. Natl. Acad. Sci. USA* 94:412-417 (1997)). Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an anti-OX40 antibody coding sequence, such as by saturation mutagenesis, and the resulting modified anti-OX40 antibodies can be screened for improved binding activity.

[0097] For nucleic acids, the term "substantial homology" indicates that two nucleic acids, or designated sequences thereof, when optimally aligned and compared, are identical, with appropriate nucleotide insertions or deletions, in at least about 80% of the nucleotides, usually at least about 90% to 95%, and more preferably at least about 98% to 99.5% of the nucleotides. Alternatively, substantial homology exists when the segments will hybridize under selective hybridization conditions, to the complement of the strand.

[0098] For polypeptides, the term "substantial homology" indicates that two polypeptides, or designated sequences thereof, when optimally aligned and compared, are identical, with appropriate amino acid insertions or deletions, in at least about 80% of the amino acids, usually at least about 90% to 95%, and more preferably at least about 98% to 99.5% of the amino acids.

[0099] The percent identity between two sequences is a function of the number of identical positions shared by the sequences when the sequences are optimally aligned (*i.e.*, % homology = # of identical positions/total # of positions x 100), with optimal alignment determined taking into account the number of gaps, and the length of each gap, which need to be introduced for optimal alignment of the two sequences. The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm, as described in the non-limiting examples below.

[0100] The percent identity between two nucleotide sequences can be determined using the GAP program in the GCG software package (available at <http://www.gcg.com>), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. The percent identity between two nucleotide or amino acid sequences can also be determined using the algorithm of E. Meyers and W. Miller (CABIOS, 4:11-17 (1989)) which has been incorporated into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4. In addition, the percent identity between two amino acid sequences can be determined using the Needleman and Wunsch (J. Mol. Biol. (48):444-453 (1970)) algorithm which has been incorporated into the GAP program in the GCG software package (available at <http://www.gcg.com>), using either a Blossum 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6.

[0101] The nucleic acid and protein sequences described herein can further be used as a "query sequence" to perform a search against public databases to, for example, identify related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul, et al. (1990) J. Mol. Biol. 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to the nucleic acid molecules described herein. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to the protein molecules described herein. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al., (1997) Nucleic Acids Res. 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (*e.g.*, XBLAST and NBLAST) can be used. See www.ncbi.nlm.nih.gov.

[0102] The nucleic acids may be present in whole cells, in a cell lysate, or in a partially purified or substantially pure form. A nucleic acid is "isolated" or "rendered substantially pure" when purified away from other cellular components or other contaminants, *e.g.*, other cellular nucleic acids (*e.g.*, the other parts of the chromosome) or proteins, by standard techniques, including alkaline/SDS treatment, CsCl banding, column chromatography, agarose gel electrophoresis and others well known in the art. See, F. Ausubel, et al., ed. Current Protocols in Molecular Biology, Greene Publishing and Wiley Interscience, New York (1987).

[0103] Nucleic acids, *e.g.*, cDNA, may be mutated, in accordance with standard techniques to provide gene sequences. For coding sequences, these mutations, may affect amino acid sequence as desired. In particular, DNA sequences substantially homologous to or derived from native V, D, J, constant, switches and other such sequences described herein are contemplated.

[0104] The term "vector" as used herein, is intended to refer to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid," which refers to a circular double stranded DNA loop into which additional DNA segments may be ligated. Another type of vector is a viral vector, wherein additional DNA segments may be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) can be integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "recombinant expression vectors" (or simply, "expression vectors") In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" may be used interchangeably as the plasmid is the most commonly used form of vector. However, also included are other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

[0105] The term "recombinant host cell" (or simply "host cell"), as used herein, is intended to refer to a cell that

comprises a nucleic acid that is not naturally present in the cell, and maybe a cell into which a recombinant expression vector has been introduced. It should be understood that such terms are intended to refer not only to the particular subject cell but to the progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term "host cell" as used herein.

[0106] As used herein, the term "antigen" refers to any natural or synthetic immunogenic substance, such as a protein, peptide, or hapten. An antigen may be OX40 or a fragment thereof. An antigen may also be a tumor antigen, against which protective or therapeutic immune responses are desired, e.g., antigens expressed by a tumor cell (e.g., for use as a tumor vaccine to be administered in combination with an anti-OX40 antibody). Antigens include tumor-associated antigens for the prevention or treatment of cancers. Examples of tumor-associated antigens include, but are not limited to, sequences comprising all or part of the sequences of β hCG, gp100 or Pmel17, HER2/neu, WT1, mesothelin, CEA, gp100, MART1, TRP-2, melan-A, NY-ESO-1, NY-BR-1, NY-CO-58, MN (gp250), idiotype, MAGE-1, MAGE-3, MAGE-A3, Tyrosinase, Telomerase, SSX2 and MUC-1 antigens, and germ cell derived tumor antigens. Tumor associated antigens also include the blood group antigens, for example, Le^a, Le^b, LeX, LeY, H-2, B-1, B-2 antigens. Alternatively, more than one antigen can be included in a construct. For example, a MAGE antigen can be combined with other antigens such as melanin A, tyrosinase, and gp100 along with adjuvants such as GM-CSF or IL-12, and linked to an anti-APC antibody.

[0107] Sequences of the foregoing antigens are well known in the art. For example, an example of a MAGE-3 cDNA sequence is provided in US 6,235,525 (Ludwig Institute for Cancer Research); examples of NY-ESO-1 nucleic acid and protein sequences are provided in US 5,804,381 and US 6,069,233 (Ludwig Institute for Cancer Research); examples of Melan-A nucleic acid and protein sequences are provided in US 5,620,886 and US 5,854,203 (Ludwig Institute for Cancer Research); examples of NY-BR-1 nucleic acid and protein sequences are provided in US 6,774,226 and US 6,911,529 (Ludwig Institute for Cancer Research) and examples of NY-CO-58 nucleic acid and protein sequences are provided in WO 02/90986 (Ludwig Institute for Cancer Research); an example of an amino acid sequence for the HER-2/neu protein is available at GENBANK[®] Accession No. AAA58637; and a nucleotide sequence (mRNA) for human carcinoembryonic antigen-like 1 (CEA-1) is available at GENBANK[®] Accession No. NM020219.

[0108] An "immune response" refers to a biological response within a vertebrate against foreign agents, which response protects the organism against these agents and diseases caused by them. An immune response is mediated by the action of a cell of the immune system (for example, a T lymphocyte, B lymphocyte, natural killer (NK) cell, macrophage, eosinophil, mast cell, dendritic cell or neutrophil) and soluble macromolecules produced by any of these cells or the liver (including antibodies, cytokines, and complement) that results in selective targeting, binding to, damage to, destruction of, and/or elimination from the vertebrate's body of invading pathogens, cells or tissues infected with pathogens, cancerous or other abnormal cells, or, in cases of autoimmunity or pathological inflammation, normal human cells or tissues. An immune reaction includes, e.g., activation or inhibition of a T cell, e.g., an effector T cell or a Th cell, such as a CD4+ or CD8+ T cell, or the inhibition of a Treg cell.

[0109] An "immunomodulator" or "immunoregulator" refers to an agent, e.g., a component of a signaling pathway, that may be involved in modulating, regulating, or modifying an immune response. "Modulating," "regulating," or "modifying" an immune response refers to any alteration in a cell of the immune system or in the activity of such cell (e.g., an effector T cell). Such modulation includes stimulation or suppression of the immune system which may be manifested by an increase or decrease in the number of various cell types, an increase or decrease in the activity of these cells, or any other changes which can occur within the immune system. Both inhibitory and stimulatory immunomodulators have been identified, some of which may have enhanced function in a tumor microenvironment. In preferred embodiments, the immunomodulator is located on the surface of a T cell. An "immunomodulatory target" or "immunoregulatory target" is an immunomodulator that is targeted for binding by, and whose activity is altered by the binding of, a substance, agent, moiety, compound or molecule. Immunomodulatory targets include, for example, receptors on the surface of a cell ("immunomodulatory receptors") and receptor ligands ("immunomodulatory ligands").

[0110] "Immunotherapy" refers to the treatment of a subject afflicted with, or at risk of contracting or suffering a recurrence of, a disease by a method comprising inducing, enhancing, suppressing or otherwise modifying an immune response.

[0111] "Immunostimulating therapy" or "immunostimulatory therapy" refers to a therapy that results in increasing (inducing or enhancing) an immune response in a subject for, e.g., treating cancer.

[0112] "Potentiating an endogenous immune response" means increasing the effectiveness or potency of an existing immune response in a subject. This increase in effectiveness and potency may be achieved, for example, by overcoming mechanisms that suppress the endogenous host immune response or by stimulating mechanisms that enhance the endogenous host immune response.

[0113] "T effector" ("T_{eff}") cells refers to T cells (e.g., CD4+ and CD8+ T cells) with cytolytic activities as well as T helper (Th) cells, which secrete cytokines and activate and direct other immune cells, but does not include regulatory T cells (Treg cells). Anti-OX40 antibodies described herein activate T_{eff} cells, e.g., CD4+ and CD8+ T_{eff} cells.

[0114] An increased ability to stimulate an immune response or the immune system, can result from an enhanced agonist activity of T cell costimulatory receptors and/or an enhanced antagonist activity of inhibitory receptors. An increased ability to stimulate an immune response or the immune system may be reflected by a fold increase of the EC₅₀ or maximal level of activity in an assay that measures an immune response, e.g., an assay that measures changes in cytokine or chemokine release, cytolytic activity (determined directly on target cells or indirectly via detecting CD107a or granzymes) and proliferation. The ability to stimulate an immune response or the immune system activity may be enhanced by at least 10%, 30%, 50%, 75%, 2 fold, 3 fold, 5 fold or more.

[0115] As used herein, the term "linked" refers to the association of two or more molecules. The linkage can be covalent or non-covalent. The linkage also can be genetic (*i.e.*, recombinantly fused). Such linkages can be achieved using a wide variety of art recognized techniques, such as chemical conjugation and recombinant protein production.

[0116] As used herein, "administering" refers to the physical introduction of a composition comprising a therapeutic agent to a subject, using any of the various methods and delivery systems known to those skilled in the art. Preferred routes of administration for antibodies described herein include intravenous, intraperitoneal, intramuscular, subcutaneous, spinal or other parenteral routes of administration, for example by injection or infusion. The phrase "parenteral administration" as used herein means modes of administration other than enteral and topical administration, usually by injection, and includes, without limitation, intravenous, intraperitoneal, intramuscular, intraarterial, intrathecal, intralymphatic, intralesional, intracapsular, intraorbital, intracardiac, intradermal, transtracheal, subcutaneous, subcuticular, intraarticular, subcapsular, subarachnoid, intraspinal, epidural and intrasternal injection and infusion, as well as *in vivo* electroporation. Alternatively, an antibody described herein can be administered via a non-parenteral route, such as a topical, epidermal or mucosal route of administration, for example, intranasally, orally, vaginally, rectally, sublingually or topically. Administering can also be performed, for example, once, a plurality of times, and/or over one or more extended periods.

[0117] As used herein, the term "T cell-mediated response" refers to a response mediated by T cells, including effector T cells (e.g., CD8⁺ cells) and helper T cells (e.g., CD4⁺ cells). T cell mediated responses include, for example, T cell cytotoxicity and proliferation.

[0118] As used herein, the term "cytotoxic T lymphocyte (CTL) response" refers to an immune response induced by cytotoxic T cells. CTL responses are mediated primarily by CD8⁺ T cells.

[0119] As used herein, the terms "inhibits" or "blocks" (e.g., referring to inhibition/blocking of binding of OX40-L to OX40 on cells) are used interchangeably and encompass both partial and complete inhibition/blocking. In certain embodiments, the anti-OX40 antibody inhibits binding of OX40-L to OX40 by at least about 50%, for example, about 60%, 70%, 80%, 90%, 95%, 99%, or 100%, determined, e.g., as further described herein. In certain embodiments, the anti-OX40 antibody inhibits binding of OX40-L to OX40 by no more than 50%, for example, by about 40%, 30%, 20%, 10%, 5% or 1%, determined, e.g., as further described herein.

[0120] As used herein, the term "inhibits growth" of a tumor includes any measurable decrease in the growth of a tumor, e.g., the inhibition of growth of a tumor by at least about 10%, for example, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 99%, or 100%.

[0121] As used herein, "cancer" refers a broad group of diseases characterized by the uncontrolled growth of abnormal cells in the body. Unregulated cell division may result in the formation of malignant tumors or cells that invade neighboring tissues and may metastasize to distant parts of the body through the lymphatic system or bloodstream.

[0122] The terms "treat," "treating," and "treatment," as used herein, refer to any type of intervention or process performed on, or administering an active agent to, the subject with the objective of reversing, alleviating, ameliorating, inhibiting, or slowing down or preventing the progression, development, severity or recurrence of a symptom, complication, condition or biochemical indicia associated with a disease. Prophylaxis refers to administration to a subject who does not have a disease, to prevent the disease from occurring or minimize its effects if it does.

[0123] A "hematological malignancy" includes a lymphoma, leukemia, myeloma or a lymphoid malignancy, as well as a cancer of the spleen and the lymph nodes. Exemplary lymphomas include both B cell lymphomas (a B-cell hematological cancer) and T cell lymphomas. B-cell lymphomas include both Hodgkin's lymphomas and most non-Hodgkin's lymphomas. Non-limiting examples of B cell lymphomas include diffuse large B-cell lymphoma, follicular lymphoma, mucosa-associated lymphatic tissue lymphoma, small cell lymphocytic lymphoma (overlaps with chronic lymphocytic leukemia), mantle cell lymphoma (MCL), Burkitt's lymphoma, mediastinal large B cell lymphoma, Waldenström macroglobulinemia, nodal marginal zone B cell lymphoma, splenic marginal zone lymphoma, intravascular large B-cell lymphoma, primary effusion lymphoma, lymphomatoid granulomatosis. Non-limiting examples of T cell lymphomas include extranodal T cell lymphoma, cutaneous T cell lymphomas, anaplastic large cell lymphoma, and angioimmunoblastic T cell lymphoma. Hematological malignancies also include leukemia, such as, but not limited to, secondary leukemia, chronic lymphocytic leukemia, acute myelogenous leukemia, chronic myelogenous leukemia, and acute lymphoblastic leukemia. Hematological malignancies further include myelomas, such as, but not limited to, multiple myeloma and smoldering multiple myeloma. Other hematological and/or B cell- or T-cell-associated cancers are encompassed by the term hematological malignancy.

[0124] The term "effective dose" or "effective dosage" is defined as an amount sufficient to achieve or at least partially achieve a desired effect. A "therapeutically effective amount" or "therapeutically effective dosage" of a drug or therapeutic agent is any amount of the drug that, when used alone or in combination with another therapeutic agent, promotes disease regression evidenced by a decrease in severity of disease symptoms, an increase in frequency and duration of disease symptom-free periods, or a prevention of impairment or disability due to the disease affliction.

[0125] In reference to solid tumors, an effective amount comprises an amount sufficient to cause a tumor to shrink and/or to decrease the growth rate of the tumor (such as to suppress tumor growth) or to prevent or delay other unwanted cell proliferation. In certain embodiments, an effective amount is an amount sufficient to delay tumor development. In some embodiments, an effective amount is an amount sufficient to prevent or delay tumor recurrence. An effective amount can be administered in one or more administrations. The effective amount of the drug or composition may: (i) reduce the number of cancer cells; (ii) reduce tumor size; (iii) inhibit, retard, slow to some extent and may stop cancer cell infiltration into peripheral organs; (iv) inhibit, *i.e.*, slow to some extent and may stop, tumor metastasis; (v) inhibit tumor growth; (vi) prevent or delay occurrence and/or recurrence of tumor; and/or (vii) relieve to some extent one or more of the symptoms associated with the cancer. In one example, an "effective amount" is the amount of anti-OX40 antibody and the amount of anti-PD-1 antibody (e.g., nivolumab) or anti-CTLA-4 antibody (e.g., ipilimumab), in combination, clinically proven to affect a significant decrease in cancer or slowing of progression of cancer, such as an advanced solid tumor. As used herein, the terms "fixed dose", "flat dose" and "flat-fixed dose" are used interchangeably and refer to a dose that is administered to a patient without regard for the weight or body surface area (BSA) of the patient. The fixed or flat dose is therefore not provided as a mg/kg dose, but rather as an absolute amount of the agent.

[0126] As used herein, a "body surface area (BSA)-based dose" refers to a dose that is adjusted to the body-surface area (BSA) of the individual patient. A BSA-based dose may be provided as mg/kg body weight. Various calculations have been published to arrive at the BSA without direct measurement, the most widely used of which is the Du Bois formula (see Du Bois D, Du Bois EF (Jun 1916) Archives of Internal Medicine 17 (6): 863-71; and Verbräecken, J. et al. (Apr 2006). Metabolism - Clinical and Experimental 55 (4): 515-24). Other exemplary BSA formulas include the Mosteller formula (Mosteller RD. N Engl J Med., 1987; 317:1098), the Haycock formula (Haycock GB, et al., J Pediatr 1978, 93:62-66), the Gehan and George formula (Gehan EA, George SL, Cancer Chemother Rep 1970, 54:225-235),

the Boyd formula (Current, JD (1998), The Internet Journal of Anesthesiology 2 (2); and Boyd, Edith (1935), University of Minnesota. The Institute of Child Welfare, Monograph Series, No. x. London: Oxford University Press), the Fujimoto formula (Fujimoto S, et al., Nippon Eiseigaku Zasshi 1968;5:443-50), the Takahira formula (Fujimoto S, et al., Nippon Eiseigaku Zasshi 1968;5:443-50), and the Schlich formula (Schlich E, et al., Ernährungs Umschau 2010;57:178-183).

[0127] A "prophylactically effective amount" or a "prophylactically effective dosage" of a drug, is an amount of the drug that, when administered alone or in combination with another therapeutic agent to a subject at risk of developing a disease or of suffering a recurrence of disease, inhibits the development or recurrence of the disease. The ability of a therapeutic or prophylactic agent to promote disease regression or inhibit the development or recurrence of the disease can be evaluated using a variety of methods known to the skilled practitioner, such as in human subjects during clinical trials, in animal model systems predictive of efficacy in humans, or by assaying the activity of the agent in *in vitro* assays.

[0128] By way of example, an anti-cancer agent is a drug that slows cancer progression or promotes cancer regression in a subject. In preferred embodiments, a therapeutically effective amount of the drug promotes cancer regression to the point of eliminating the cancer. "Promoting cancer regression" means that administering an effective amount of the drug, alone or in combination with an anti-neoplastic agent, results in a reduction in tumor growth or size, necrosis of the tumor, a decrease in severity of at least one disease symptom, an increase in frequency and duration of disease symptom-free periods, a prevention of impairment or disability due to the disease affliction, or otherwise amelioration of disease symptoms in the patient. Pharmacological effectiveness refers to the ability of the drug to promote cancer regression in the patient. Physiological safety refers to an acceptably low level of toxicity, or other adverse physiological effects at the cellular, organ and/or organism level (adverse effects) resulting from administration of the drug.

[0129] By way of example for the treatment of tumors, a therapeutically effective amount or dosage of the drug preferably inhibits cell growth or tumor growth by at least about 20%, more preferably by at least about 40%, even more preferably by at least about 60%, and still more preferably by at least about 80% relative to untreated subjects. In the most preferred embodiments, a therapeutically effective amount or dosage of the drug completely inhibits cell growth or tumor growth, *i.e.*, preferably inhibits cell growth or tumor growth by 100%. The ability of a compound to inhibit tumor growth can be evaluated using the assays described *infra*. Alternatively, this property of a composition can be evaluated by examining the ability of the compound to inhibit cell growth, such inhibition can be measured *in vitro* by assays known to the skilled practitioner. In other preferred embodiments described herein, tumor regression may be observed and may continue for a period of at least about 20 days, more preferably at least about 40 days, or even more preferably at least about 60 days.

[0130] The terms "patient" and "subject" refer to any human or non-human animal that receives either prophylactic or therapeutic treatment. For example, the methods and compositions described herein can be used to treat a subject or patient having cancer, such as an advanced solid tumor. The term "non-human animal" includes all vertebrates, *e.g.*, mammals and non-mammals, such as non-human primates, sheep, dog, cow, chickens, amphibians, reptiles, *etc.*

[0131] Various aspects described herein are described in further detail in the following subsections.

I. Anti-OX40 antibodies

[0132] Described herein are antibodies, *e.g.*, fully human antibodies, which are characterized by particular functional features or properties. For example, the antibodies specifically bind human OX40. Additionally, antibodies may cross react with OX40 from one or more non-human primates, such as cynomolgus OX40. Such antibodies are useful in the treatment of cancer when used as monotherapy, or when used in combination with an immuno-oncology agent, such as an anti-PD-1 antibody (*e.g.*, nivolumab) or anti-CTLA-4 antibody (*e.g.*, ipilimumab).

[0133] Anti-OX40 antibodies described herein exhibit one or more or all of the following functional properties:

1. (1) binding to soluble human OX40, *e.g.*, with a K_D of 10 nM or less (*e.g.*, 0.01 nM to 10 nM), *e.g.*, as measured by BIACORE® SPR analysis;
2. (2) binding to membrane bound human OX40, *e.g.*, with an EC_{50} of 1 nM or less (*e.g.*, 0.01 nM to 1 nM), *e.g.*, as

measured by FACS;

3. (3) binding to cynomolgus OX40, e.g., binding to membrane bound cynomolgus OX40, e.g., with an EC₅₀ of 10 nM or less (e.g., 0.01 nM to 10 nM), e.g., as measured by FACS;
4. (4) inducing or enhancing T cell activation, as evidenced by (i) increased IL-2 and/or IFN- γ production in OX40-expressing T cells and/or (ii) enhanced T cell proliferation;
5. (5) inhibiting the binding of OX40 ligand to OX40, e.g., with an EC₅₀ of 1 nM or less as measured by FACS, e.g., in an assay with hOX40-293 cells;
6. (6) binding to an epitope on the extracellular portion of mature human OX40 (SEQ ID NO: 2), e.g., an epitope within the region DVVSSKPKCPCTWCNLR (SEQ ID NO: 178) or DSYKPGVDCAPCPGHHFSPGDNQACKPWTNCTLAGK (SEQ ID NO: 179);
7. (7) competing for binding to human OX40 with 3F4, 14B6-1, 14B6-2, 23H3, 18E9, 8B11, 20B3, and 20C1;
8. (8) competing for binding to human OX40 with 6E1-1, 6E1-2, 14A2-1, and 14A2-2.

[0134] Preferably, the antibodies bind to OX40 with high affinity, for example, with a K_D of 10⁻⁷ M or less, 10⁻⁸ M or less, 10⁻⁹ M or less, 10⁻¹⁰ M or less, 10⁻¹¹ M or less, 10⁻¹² M or less, 10⁻¹² M to 10⁻⁷ M, 10⁻¹¹ M to 10⁻⁷ M, 10⁻¹⁰ M to 10⁻⁷ M, or 10⁻⁹ M to 10⁻⁷ M. In certain embodiments, an anti-OX40 antibody binds to soluble human OX40, e.g., as determined by BIACORE® SPR analysis, with a K_D of 10⁻⁷ M or less, 10⁻⁸ M or less, 10⁻⁹ M (1 nM) or less, 10⁻¹⁰ M or less, 10⁻¹² M to 10⁻⁷ M, 10⁻¹¹ M to 10⁻⁷ M, 10⁻¹⁰ M to 10⁻⁷ M, 10⁻⁹ M to 10⁻⁷ M, or 10⁻⁸ M to 10⁻⁷ M. In certain embodiments, the anti-OX40 antibody binds to bound (e.g., cell membrane bound) human OX40, such as on activated human T cells, e.g., as determined by flow cytometry, with a K_D of 10⁻⁷ M or less, 10⁻⁸ M or less, 10⁻⁹ M (1 nM) or less, 10⁻¹⁰ M or less, 10⁻¹² M to 10⁻⁷ M, 10⁻¹¹ M to 10⁻⁸ M, 10⁻¹⁰ M to 10⁻⁸ M, 10⁻⁹ M to 10⁻⁸ M, 10⁻¹¹ M to 10⁻⁹ M, or 10⁻¹⁰ M to 10⁻⁹ M. In certain embodiments, an anti-OX40 antibody binds to bound (e.g., cell membrane bound) human OX40, such as on activated human T cells, e.g., as determined by FACS, with an EC₅₀ of 10⁻⁷ M or less, 10⁻⁸ M or less, 10⁻⁹ M (1 nM) or less, 10⁻¹⁰ M or less, 10⁻¹² M to 10⁻⁷ M, 10⁻¹¹ M to 10⁻⁸ M, 10⁻¹⁰ M to 10⁻⁸ M, 10⁻⁹ M to 10⁻⁸ M, 10⁻¹¹ M to 10⁻⁹ M, or 10⁻¹⁰ M to 10⁻⁹ M. In certain embodiments, the anti-OX40 antibody binds to soluble human OX40 with a K_D of 10⁻⁷ M or less, 10⁻⁸ M or less, 10⁻⁹ M (1 nM) or less, 10⁻¹⁰ M or less, 10⁻¹² M to 10⁻⁷ M, 10⁻¹¹ M to 10⁻⁷ M, 10⁻¹⁰ M to 10⁻⁷ M, 10⁻⁹ M to 10⁻⁷ M, or 10⁻⁸ M to 10⁻⁷ M, and to cell membrane bound human OX40 with a K_D or EC₅₀ of 10⁻⁷ M or less, 10⁻⁸ M or less, 10⁻⁹ M (1 nM) or less, 10⁻¹⁰ M or less, 10⁻¹² M to 10⁻⁷ M, 10⁻¹¹ M to 10⁻⁸ M, 10⁻¹⁰ M to 10⁻⁸ M, 10⁻⁹ M to 10⁻⁸ M, 10⁻¹¹ M to 10⁻⁹ M, or 10⁻¹⁰ M to 10⁻⁹ M.

[0135] Anti-OX40 antibodies described herein may bind to cynomolgus OX40, e.g., bind to membrane bound cynomolgus OX40, e.g., with an EC₅₀ of 100 nM or less, 10 nM or less, 100 nM to 0.01 nM, 100 nM to 0.1 nM, 100 nM to 1 nM, or 10 nM to 1 nM, e.g., as measured by FACS (e.g., as described in the Examples).

[0136] Anti-OX40 antibodies described herein may stimulate or enhance an immune response, e.g., by activating T_{eff} cells, limiting the suppression of T_{eff} cells by Treg cells, depleting and/or inhibiting tumor Treg cells and/or activating NK cells, e.g., in the tumor. For example, the anti-OX40 antibodies may activate or costimulate T_{eff} cells as evidenced, e.g., by enhanced cytokine (e.g., IL-2 and IFN- γ) secretion and/or enhanced proliferation. In certain embodiments, CD3 stimulation is also provided. In certain embodiments, the OX40 antibody increases IL-2 secretion by a factor of 50%, 100% (i.e., 2 fold), 3 fold, 4 fold, 5 fold or more, optionally with a maximum of up to 10 fold, 30 fold, 100 fold, as measured, e.g., on primary human T cells or T cells expressing human OX40 (e.g., as further described in the Examples). In certain embodiments, the OX40 antibody increases IFN- γ secretion by a factor of 50%, 100% (i.e., 2 fold), 3 fold, 4 fold, 5 fold or more, optionally with a maximum of up to 10 fold, 30 fold, 100 fold, as measured, e.g., on primary human T cells or T cells expressing human OX40 (e.g., as further described in the Examples).

[0137] Anti-OX40 antibodies described herein may inhibit binding of human OX40L to human OX40 on cells, e.g., 293 cells expressing human OX40 (i.e., hOX40-293 cells), e.g., with an EC₅₀ of 10 nM or less, 1 nM or less, 0.01 nM to 10 nM, 0.1 nM to 10 nM, or 0.1 nM to 1 nM (see Example 6).

[0138] Anti-OX40 antibodies described herein bind to an epitope on OX40, as determined, for example, by binding to fragments of human OX40. For example, in certain embodiments, the antibody binds to all or a portion of the sequence DVVSSKPKPCTWCNLR (SEQ ID NO: 178) of human OX40 (SEQ ID NO: 2) as determined, for example, by HDX or by binding of the antibodies to fragments of human OX40, followed by enzymatic cleavage (see Example 11). In other embodiments, the antibody binds to all or a portion of the sequence DSYKPGVDCAPCPGHHFSPGDNQACKPWTNCTLAGK (SEQ ID NO: 179) of human OX40 (SEQ ID NO: 2).

[0139] In certain embodiments, the anti-OX40 antibodies described herein bind to all or a portion of the sequence SQNTVCRPCGPGFYNDVSSKPKPCTWCNLR (SEQ ID NO: 182).

[0140] In other embodiments, the anti-OX40 antibodies described herein bind to all or a portion of the sequence PCKPCTWCNLR (SEQ ID NO: 183).

[0141] In yet other embodiments, the anti-OX40 antibodies that bind to all or a portion of the sequence DVVSSKPKPCTWCNLR (SEQ ID NO: 178) further bind to all or a portion of the sequence QLCTATQDTVCR (SEQ ID NO: 184).

[0142] In additional embodiments, the anti-OX40 antibodies described herein bind to all or a portion of the sequence SQNTVCRPCGPGFYNDVSSKPKPCTWCNLR (SEQ ID NO: 185).

[0143] Anti-OX40 antibodies described herein may compete for binding to OX40 with (or inhibit binding of) anti-OX40 antibodies comprising CDRs or variable regions described herein, e.g., 3F4, 14B6-1, 14B6-2, 23H3, 6E1-1, 6E1-2, 18E9, 8B11, 20B3, 14A2-1, 14A2-2, and/or 20C1. In certain embodiments, anti-OX40 antibodies inhibit binding of 3F4, 14B6-1, 14B6-2, 23H3, 6E1-1, 6E1-2, 18E9, 8B11, 20B3, 14A2-1, 14A2-2, and/or 20C1 to human OX40 by at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or by 100%. In certain non-claimed embodiments, 3F4, 14B6-1, 14B6-2, 23H3, 6E1-1, 6E1-2, 18E9, 8B11, 20B3, 14A2-1, 14A2-2, and 20C1 inhibit binding of anti-OX40 antibodies to human OX40 by at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or by 100%.

[0144] In certain embodiments, the antibodies induce or enhance T cell activation with multivalent crosslinking through, e.g., FcR binding. In certain embodiments, the antibodies are multivalent, e.g., bivalent. In certain embodiments, the antibodies are not monovalent.

[0145] In certain embodiments, the antibodies have 1, 2, 3, 4, 5, or 6 of the following features:

1. (1) binding to soluble human OX40, e.g., with a K_D of 10 nM or less (e.g., 0.01 nM to 10 nM), e.g., as measured by BIACORE® SPR analysis;
2. (2) binding to membrane bound human OX40, e.g., with an EC_{50} of 1 nM or less (e.g., 0.01 nM to 1 nM), e.g., as measured by FACS;
3. (3) binding to cynomolgus OX40, e.g., binding to membrane bound cynomolgus OX40, e.g., with an EC_{50} of 10 nM or less (e.g., 0.01 nM to 10 nM), e.g., as measured by FACS;
4. (4) inducing or enhancing T cell activation, as evidenced by (i) increased IL-2 and/or IFN- γ production in OX40-expressing T cells and/or (ii) enhanced T cell proliferation;
5. (5) inhibiting the binding of OX40 ligand to OX40, e.g., with an EC_{50} of 1 nM or less as measured by FACS, e.g., in an assay with hOX40-293 cells;
6. (6) binding to an epitope on the extracellular portion of mature human OX40 (SEQ ID NO: 2), e.g., an epitope within the region DVVSSKPKPCTWCNLR (SEQ ID NO: 178) or DSYKPGVDCAPCPGHHFSPGDNQACKPWTNCTLAGK (SEQ ID NO: 179);
7. (7) competing for binding to human OX40 with 3F4, 14B6-1, 14B6-2, 23H3, 18E9, 8B11, 20B3, and 20C1;
8. (8) competing for binding to human OX40 with 6E1-1, 6E1-2, 14A2-1, and 14A2-2.

[0146] Accordingly, an antibody that exhibits one or more of these functional properties (e.g., biochemical, immunochemical, cellular, physiological or other biological activities, or the like) as determined according to methodologies known to the art and described herein, will be understood to relate to a statistically significant difference

in the particular activity relative to that seen in the absence of the antibody (e.g., or when a control antibody of irrelevant specificity is present). Preferably, the anti-OX40 antibody increases a measured parameter (e.g., T cell proliferation, cytokine production) by at least 10% of the measured parameter, more preferably by at least 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 100% (i.e., 2 fold), 3 fold, 5 fold, or 10 fold. Conversely, the antibody may decrease a measured parameter (e.g., tumor volume, OX40-L binding to OX40, quantity of regulatory T cells in tumors) by at least 10% of the measured parameter, more preferably by at least 20%, 30%, 40%, 50%, 60%, 70%, 80% or 90%, 95%, or 99%.

[0147] Standard assays to evaluate the binding ability of the antibodies toward OX40 of various species are known in the art, including for example, ELISAs, Western blots, and RIAs. Suitable assays are described in detail in the Examples. The binding kinetics (e.g., binding affinity) of the antibodies also can be assessed by standard assays known in the art, such as by BIACORE[®] SPR analysis. Assays to evaluate the effects of the antibodies on functional properties of OX40 (e.g., ligand binding, T cell proliferation, cytokine production) are described in further detail *infra* and in the Examples.

[0148] In certain embodiments, the anti-OX40 antibodies are not native antibodies or are not naturally-occurring antibodies, e.g., anti-OX40 antibodies with post-translational modifications that are different from those of antibodies that are naturally occurring, such as by having more, less, or a different type of post-translational modification.

II. Exemplary anti-OX40 antibodies

[0149] The claimed antibodies have a V_H and V_L sequence set forth in SEQ ID NO: 318 and 94 respectively. Particular antibodies also described herein are antibodies, e.g., monoclonal antibodies, having the CDR and/or variable region sequences of antibodies 3F4, 14B6-1, 14B6-2, 23H3, 6E1-1, 6E1-2, 18E9, 8B11, 20B3, 14A2-1, 14A2-2, and 20C1, isolated and structurally characterized as described in Example 1, as well as antibodies having at least 80% identity (e.g., at least 85%, at least 90%, at least 95%, or at least 99% identity) to the variable region or CDR sequences of antibodies 3F4, 14B6-1, 14B6-2, 23H3, 6E1-1, 6E1-2, 18E9, 8B11, 20B3, 14A2-1, 14A2-2, and 20C1. The V_H amino acid sequences of 3F4, 14B6 (14B6-1 and 14B6-2), 23H3, 6E1 (6E1-1 and 6E1-2), 18E9, 8B11, 20B3, 14A2 (14A2-1 and 14A2-2), and 20C1 are set forth in SEQ ID NOs: 17, 28, 37, 48, 57, 65, 73, 84, and 93, respectively. The V_L amino acid sequences of 3F4, 14B6-1, 14B6-2, 23H3, 6E1-1, 6E1-2, 18E9, 8B11, 20B3, 14A2-1, 14A2-2, and 20C1 are set forth in SEQ ID NOs: 18, 29, 30, 38, 49, 50, 58, 66, 74, 85, 86, and 94, respectively.

[0150] Accordingly, provided herein are non-claimed antibodies, or antigen binding portion thereof, comprising heavy and light chain variable regions, wherein the heavy chain variable region comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 17, 28, 37, 48, 57, 65, 73, 84, and 93.

[0151] Also provided are non-claimed antibodies, or antigen binding portions thereof, comprising heavy and light chain variable regions, wherein the light chain variable region comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 18, 29, 30, 38, 49, 50, 58, 66, 74, 85, and 86.

[0152] Provided herein are non-claimed antibodies, or antigen-binding portion thereof, comprising: heavy and light chain variable region sequences comprising SEQ ID NOs: 17 and 18; 28 and 29; 28 and 30; 37 and 38; 48 and 49; 48 and 50; 57 and 58; 65 and 66; 73 and 74; 84 and 85; 84 and 86; 93 and 94.

[0153] Non-claimed anti-OX40 antibodies described herein may comprise the heavy and light chain CDR1s, CDR2s and CDR3s of 3F4, 14B6-1, 14B6-2, 23H3, 6E1-1, 6E1-2, 18E9, 8B11, 20B3, 14A2-1, 14A2-2, and 20C1, or combinations thereof. The amino acid sequences of the V_H CDR1s of 3F4, 14B6 (14B6-1 and 14B6-2), 23H3, 6E1 (6E1-1 and 6E1-2), 18E9, 8B11, 20B3, 14A2 (14A2-1 and 14A2-2), and 20C1 are set forth in SEQ ID NOs: 11, 19, 31, 39, 51, 59, 67, 75, and 87, respectively. The amino acid sequences of the V_H CDR2s of 3F4, 14B6 (14B6-1 and 14B6-2), 23H3, 6E1 (6E1-1 and 6E1-2), 18E9, 8B11, 20B3, 14A2 (14A2-1 and 14A2-2), and 20C1 are set forth in SEQ ID NOs: 12, 20, 32, 40, 52, 60, 68, 76, and 88, respectively. The amino acid sequences of the V_H CDR3s of 3F4, 14B6 (14B6-1 and 14B6-2), 23H3, 6E1 (6E1-1 and 6E1-2), 18E9, 8B11, 20B3, 14A2 (14A2-1 and 14A2-2), and 20C1 are set forth in SEQ ID NOs: 13, 21, 33, 41, 53, 61, 69, 77, and 89. The amino acid sequences of the V_L CDR1s of 3F4, 14B6-

1, 14B6-2, 23H3, 6E1-1, 6E1-2, 18E9, 8B11, 20B3, 14A2-1, 14A2-2, and 20C1 are set forth in SEQ ID NOs: 14, 22, 25, 34, 42, 45, 54, 62, 70, 78, 81, and 90, respectively. The amino acid sequences of the V_L CDR2s of 3F4, 14B6-1, 14B6-2, 23H3, 6E1-1, 6E1-2, 18E9, 8B11, 20B3, 14A2-1, 14A2-2, and 20C1 are set forth in SEQ ID NOs: 15, 23, 26, 35, 43, 46, 55, 63, 71, 79, 82, and 91, respectively. The amino acid sequences of the V_L CDR3s of 3F4, 14B6-1, 14B6-2, 23H3, 6E1-1, 6E1-2, 18E9, 8B11, 20B3, 14A2-1, 14A2-2, and 20C1 are set forth in SEQ ID NOs: 16, 24, 27, 36, 44, 47, 56, 64, 72, 80, 83, and 92, respectively. The CDR regions are delineated using the Kabat system (Kabat, E. A., et al. (1991) Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242).

[0154] Given that each of these antibodies bind to OX40 and that antigen-binding specificity is provided primarily by the CDR1, 2 and 3 regions, the V_H CDR1, 2 and 3 sequences and V_L CDR1, 2 and 3 sequences can be "mixed and matched" (*i.e.*, CDRs from different antibodies can be mixed and match, although each antibody must contain a V_H CDR1, 2 and 3 and a V_L CDR1, 2 and 3) to create other anti-OX40 binding antibodies. OX40 binding of such "mixed and matched" antibodies can be tested using the binding assays described above and in the Examples (*e.g.*, ELISAs). Preferably, when V_H CDR sequences are mixed and matched, the CDR1, CDR2 and/or CDR3 sequence from a particular V_H sequence is replaced with a structurally similar CDR sequence(s). Likewise, when V_L CDR sequences are mixed and matched, the CDR1, CDR2 and/or CDR3 sequence from a particular V_L sequence preferably is replaced with a structurally similar CDR sequence(s). It will be readily apparent to the ordinarily skilled artisan that novel V_H and V_L sequences can be created by substituting one or more V_H and/or V_L CDR region sequences with structurally similar sequences from the CDR sequences disclosed herein for monoclonal antibodies 3F4, 14B6-1, 14B6-2, 23H3, 6E1-1, 6E1-2, 18E9, 8B11, 20B3, 14A2-1, 14A2-2, and 20C1. "Mixed and matched" antibodies having binding affinity, bioactivity and/or other properties equivalent or superior to the specific antibodies disclosed herein may be selected for use in the methods of the present invention.

[0155] Provided herein are non-claimed isolated antibodies, or antigen binding portion thereof comprising:

1. (a) a heavy chain variable region CDR1 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 11, 19, 31, 39, 51, 59, 67, 75, and 87;
2. (b) a heavy chain variable region CDR2 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 12, 20, 32, 40, 52, 60, 68, 76, and 88;
3. (c) a heavy chain variable region CDR3 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 13, 21, 33, 41, 53, 61, 69, 77, and 89;
4. (d) a light chain variable region CDR1 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 14, 22, 25, 34, 42, 45, 54, 62, 70, 78, 81, and 90;
5. (e) a light chain variable region CDR2 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 15, 23, 26, 35, 43, 46, 55, 63, 71, 79, 82, and 91; and
6. (f) a light chain variable region CDR3 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 16, 24, 27, 36, 44, 47, 56, 64, 72, 80, 83, and 92;

wherein the antibody specifically binds to human OX40.

[0156] The claimed antibody comprises heavy and light chain variable regions, wherein the antibody comprises:

heavy chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 87, 317, and 89, respectively, and light chain CDR1, CDR2, and CDR3 sequences comprising SEQ ID NOs: 90-92, respectively;

wherein the antibody specifically binds to human OX40.

[0157] A V_H domain, or one or more CDRs thereof, described herein may be linked to a constant domain for forming a heavy chain, *e.g.*, a full length heavy chain. Similarly, a V_L domain, or one or more CDRs thereof, described herein may be linked to a constant domain for forming a light chain, *e.g.*, a full length light chain. A full length heavy chain (with the exception of the C-terminal lysine (K) or with the exception of the C-terminal glycine and lysine (GK), which may be absent) and full length light chain combine to form a full length antibody. N-terminal glutamine and glutamate residues may also be converted to pyroglutamate residues on both light and heavy chains.

[0158] A VH domain described herein may be fused to the constant domain of a human IgG, e.g., IgG1, IgG2, IgG3 or IgG4, which are either naturally-occurring or modified, e.g., as further described herein. For example, a heavy chain may comprise the amino acid sequence of any VH domain described herein fused to the human IgG1 amino acid sequence set forth in SEQ ID NO: 5.

[0159] The human IgG1 constant domain may also be that of an allotypic variant. For example, an allotypic variant of IgG1 comprises an R107K, E189D and M191L (underlined above, with numbering according to that in SEQ ID NO: 6). Within the full length heavy region, these amino acid substitutions are numbered R214K, E356D and M358L.

[0160] A VL domain described herein may be fused to the constant domain of a human kappa or lambda light chain. For example, a light chain may comprise the amino acid sequence of any VL domain described herein fused to the human IgG1 kappa light chain amino acid sequence set forth in SEQ ID NO: 7.

[0161] In certain embodiments, the heavy chain constant region comprises a lysine or another amino acid at the C-terminus, e.g., it comprises the following last amino acids: LSPGK (SEQ ID NO: 8) for the heavy chain. In certain embodiments, the heavy chain constant region is lacking one or more amino acids at the C-terminus, and has, e.g., the C-terminal sequence LSPG (SEQ ID NO: 9) or LSP.

[0162] The amino acid sequences of heavy and light chains of the claimed and non-claimed antibodies are set forth in Table 23 and correspond to SEQ ID NOs: 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 124 and 125 for the heavy chains and SEQ ID NOs: 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, and 122 for the light chains.

[0163] Heavy and light chains comprising an amino acid sequence that is at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, 80%, 75% or 70% identical to any of the heavy or light chains set forth in Table 23 (or their variable regions), e.g., SEQ ID NOs: 95 and 96; 97 and 98; 99 and 100; 101 and 102; 103 and 104; 105 and 106; 107 and 108; 109 and 110; 111 and 112; 113 and 114; 115 and 116; 117 and 118; 119 and 120; 121 and 122; 123 and 116; 124 and 116; and 125 and 116 may be used for forming anti-human OX40 antibodies having the desired characteristics, e.g., those further described herein. Exemplary variants are those comprising an allotypic variation, e.g., in the constant domain, and/or a mutation in the variable or constant regions, such as the mutations disclosed herein. Heavy and light chains comprising an amino acid sequence that differs in at most 1-30, 1-25, 1-20, 1-15, 1-10, 1-5, 1-4, 1-3, 1-2 or 1 amino acid (by substitution, addition or deletion) from any of the heavy or light chains set forth in Table 23 (or their variable regions) may be used for forming anti-human OX40 antibodies having the desired characteristics, e.g., those further described herein.

[0164] In various embodiments, the antibodies described above exhibit one or more, two or more, three or more, four or more, five or more, six, or all of the following functional properties:

1. (1) binding to soluble human OX40, e.g., with a K_D of 10 nM or less (e.g., 0.01 nM to 10 nM), e.g., as measured by Biacore;
2. (2) binding to membrane bound human OX40, e.g., with an EC_{50} of 1 nM or less (e.g., 0.01 nM to 1 nM), e.g., as measured by FACS;
3. (3) binding to cynomolgus OX40, e.g., binding to membrane bound cynomolgus OX40, e.g., with an EC_{50} of 10 nM or less (e.g., 0.01 nM to 10 nM), e.g., as measured by FACS;
4. (4) inducing or enhancing T cell activation, as evidenced by (i) increased IL-2 and/or IFN- γ production in OX40-expressing T cells and/or (ii) enhanced T cell proliferation;
5. (5) inhibiting the binding of OX40 ligand to OX40, e.g., with an EC_{50} of 1 nM or less as measured by FACS, e.g., in an assay with hOX40-293 cells;
6. (6) binding to an epitope on the extracellular portion of mature human OX40 (SEQ ID NO: 2), e.g., an epitope within the region DVVSSKPKCPCTWCNLR (SEQ ID NO: 178) or DSYKPGVDCAPCPGHFSPGDNQACKPWTNCTLAGK (SEQ ID NO: 179);
7. (7) competing for binding to human OX40 with 3F4, 14B6-1, 14B6-2, 23H3, 18E9, 8B11, 20B3, and 20C1;
8. (8) competing for binding to human OX40 with 6E1-1, 6E1-2, 14A2-1, and 14A2-2.

[0165] Such antibodies include, for example, human antibodies, humanized antibodies, or chimeric antibodies.

[0166] In certain embodiments, the anti-OX40 antibodies described herein bind to amino acid residues within the following region of mature human OX40 (SEQ ID NO: 2):

DVVSSKPCKPCTWCNLR (SEQ ID NO: 178),

corresponding to amino acid residues 46-62 of mature human OX40 (SEQ ID NO: 2).

[0167] In certain embodiments, the anti-OX40 antibodies described herein bind to amino acid residues within the following region of mature human OX40 (SEQ ID NO: 2):

DSYKPGVDCAPCPGHHFSPGDNQACKPWTNCTLAGK (SEQ ID NO: 179),

corresponding to amino acid residues 89-124 of mature human OX40 (SEQ ID NO: 2).

[0168] In certain embodiments, the anti-OX40 antibodies described herein that bind to all or a portion of the sequence DVVSSKPCKPCTWCNLR (SEQ ID NO: 178) bind to all or a portion of the sequence SQNTVCRPCGPGFYNDVVSSKPCKPCTWCNLR (SEQ ID NO: 182).

[0169] In other embodiments, the anti-OX40 antibodies described herein that bind to all or a portion of the sequence DVVSSKPCKPCTWCNLR (SEQ ID NO: 178) bind to all or a portion of the sequence PCKPCTWCNLR (SEQ ID NO: 183).

[0170] In yet other embodiments, the anti-OX40 antibodies that bind to all or a portion of the sequence DVVSSKPCKPCTWCNLR (SEQ ID NO: 178) further bind to all or a portion of the sequence QLCTATQDTVCR (SEQ ID NO: 184).

[0171] In additional embodiments, the anti-OX40 antibodies described herein that bind to all or a portion of the sequence DVVSSKPCKPCTWCNLR (SEQ ID NO: 178) further bind to all or a portion of the sequence SQNTVCRPCGPGFYN (SEQ ID NO: 185).

Modified heavy chain constant domains

[0172] The heavy chain constant region of anti-OX40 antibodies described herein may be of any isotype, e.g., IgG1, IgG2, IgG3 and IgG4, or combinations thereof and/or modifications thereof. In certain embodiments, anti-OX40 antibodies comprise a modified heavy chain constant region that alters the properties of the antibody.

[0173] As discussed further herein and in the Examples, cross-linking of anti-OX40 antibodies with unmodified hlgG1 constant regions (hlgG1 isotype antibodies) induce OX40 signaling and promote T cell activation, and specifically to promote T cell proliferation, IFN- γ secretion, and IL-2 secretion. Cross-linking can occur by, e.g., binding to human CD32A Fc γ receptors (Fc γ Rs) expressed on the surface of transfected CHO cells in an assay utilizing co-cultures of CHO-CD3-CD32A cells and human primary CD4 T cells. Cross-linking can also occur, e.g., by adding a soluble polyclonal anti-human Fc γ antibody in cultures of staphylococcus enterotoxin B (SEB)-activated human peripheral blood mononuclear cells (PBMCs).

[0174] Anti-OX40 antibodies with modified heavy chain constant regions (e.g., IgG1 constant region wherein the CH1/hinge region is replaced with an hlgG2 CH1/hinge region) may have the ability to alter the activities of the antibodies relative to antibodies with a fully IgG1 heavy chain constant region. Exemplary activities that may be altered include, but are not limited to, (1) T cell activation in the presence or absence of cross-linking, (2) T cell proliferation in the presence or absence of cross-linking, and/or (3) cytokine secretion (e.g., IFN- γ , IL-2) in the presence or absence of cross-linking. The methods described in the Examples can be used to determine whether the anti-OX40 antibodies with modified heavy chain constant regions exhibit these altered activities (see, e.g., Example 27). In preferred embodiments, these altered activities do not markedly affect the antigen-binding properties of the antibodies, which can be assessed using, e.g., FACS, SPR).

[0175] Accordingly, provided herein are methods of altering the activity of anti-OX40 antibodies comprising providing an

anti-OX40 antibody that has a non-IgG2 hinge, and replacing the non-IgG2 hinge with an IgG2 hinge. In certain embodiments, a modified heavy chain constant region comprises a hinge of the IgG2 isotype (an "IgG2 hinge") and a CH1, CH2 and CH3 domain. In certain embodiments, a modified heavy chain constant region comprises an IgG2 hinge and a CH1, CH2 and CH3 domain, wherein at least one of the CH1, CH2 and CH3 domains is not of the IgG2 isotype. The IgG2 hinge may be a wildtype IgG2 hinge, e.g., a wildtype human IgG2 hinge (e.g., ERKCCVECPPCPAPPVAG; SEQ ID NO: 208) or a variant thereof, provided that the IgG2 hinge retains the ability to confer to the antibody an altered activity relative to the same antibody that comprises a non-IgG2 hinge. In certain embodiments, an IgG2 hinge variant retains similar rigidity or stiffness to that of a wildtype IgG2 hinge. The rigidity of a hinge can be determined, e.g., by computer modeling, electron microscopy, spectroscopy such as Nuclear Magnetic Resonance (NMR), X-ray crystallography (B-factors), or Sedimentation Velocity Analytical ultracentrifugation (AUC) to measure or compare the radius of gyration of antibodies comprising the hinge. A hinge may have similar or higher rigidity relative to another hinge if an antibody comprising the hinge has a value obtained from one of the tests described in the previous sentence that differs from the value of the same antibody with a different hinge, e.g., an IgG1 hinge, in less than 5%, 10%, 25%, 50%, 75%, or 100%. A person of skill in the art would be able to determine from the tests whether a hinge has at least similar rigidity to that of another hinge by interpreting the results of these tests. An exemplary human IgG2 hinge variant is an IgG2 hinge that comprises a substitution of one or more of the four cysteine residues (i.e., C219, C220, C226 and C229). A cysteine may be replaced by a serine. An exemplary IgG2 hinge is a human IgG2 hinge comprising a C219S mutation (e.g., ERKSCVECPPCPAPPVAG; SEQ ID NO: 209). Other IgG2 hinge variants that may be used include human IgG2 hinges comprising a C220, C226 and/or C229 substitution, e.g., a C220S, C226S or C229S mutation (which may be combined with a C219S mutation). An IgG2 hinge may also be an IgG2 hinge in which a portion of the hinge is that of another isotype (i.e., it is a chimeric hinge), provided that the rigidity of the chimeric hinge is at least similar to that of a wildtype IgG2 hinge. For example, an IgG2 hinge may be an IgG2 hinge in which the lower hinge (as defined in Table 2) is of an IgG1 isotype, and is, e.g., a wildtype IgG1 lower hinge. Additional IgG2 hinge mutations that may be used in an IgG2 hinge include the SE (S267E), SELF (S267E/L328F), SDIE (S239D/I332E),

[0176] SEFF and GASDALIE (G236A/S239D/A330L/I332E) mutations.

[0177] A "hybrid" or "chimeric" hinge is referred to as being of a specific isotype if more than half of the consecutive amino acids of the hinge are from that isotype. For example, a hinge having an upper and middle hinge of IgG2 and the lower hinge of IgG1 is considered to be an IgG2 hinge.

[0178] In certain embodiments, an anti-OX40 antibody comprises a modified heavy chain constant region that comprises an IgG2 hinge comprising one of the following sequences:

ERKCCVECPPCPAPPVAG (SEQ ID NO: 208);

ERKSCVECPPCPAPPVAG (SEQ ID NO: 209);

ERKCSVECPPCPAPPVAG (SEQ ID NO: 210);

ERKXCVCPPCPAPPVAG (SEQ ID NO: 211);

ERKCXVECPPCPAPPVAG (SEQ ID NO: 212);

ERKCCVECPPCPAPPVAGX (SEQ ID NO: 213);

ERKSCVECPPCPAPPVAGX (SEQ ID NO: 214);

ERKCSVECPPCPAPPVAGX (SEQ ID NO: 215);

ERKXCVCPPCPAPPVAGX (SEQ ID NO: 216);

ERKCXVECPPCPAPPVAGX (SEQ ID NO: 217);

ERKCCVECPPCPAPELLGG (SEQ ID NO: 218);

ERKSCVECPPCPAPELLGG (SEQ ID NO: 219);

ERKCCSVECPPCPAPELLGG (SEQ ID NO: 220);

ERKXCVECPPCPAPPELLGG (SEQ ID NO: 221);

ERKCXVECPPCPAPPELLGG (SEQ ID NO: 222);

ERKCCVECPPCPAPPELLG (SEQ ID NO: 223);

ERKSCVECPPCPAPPELLG (SEQ ID NO: 224);

ERKCCSVECPPCPAPPELLG (SEQ ID NO: 225);

ERKXCVECPPCPAPPELLG (SEQ ID NO: 226);

ERKCXVECPPCPAPPELLG (SEQ ID NO: 227);

ERKCCVECPPCPAP (SEQ ID NO: 228);

ERKSCVECPPCPAP (SEQ ID NO: 229);

ERKCSVECPPCPAP (SEQ ID NO: 230);

ERKXCVECPPCPAP (SEQ ID NO: 231); or

ERKCXVECPPCPAP (SEQ ID NO: 232),

wherein X is any amino acid, except a cysteine,

or any of the above sequences, in which 1-5, 1-3, 1-2 or 1 amino acid is inserted between amino acid residues CVE and CPP. In certain embodiments, THT or GGG is inserted. In certain embodiments, 1, 1-2, or 1-3 amino acids are inserted between the hinge and CH2 domain. For example, a glycine may be inserted between the hinge and CH2 domain.

[0179] In certain embodiments, the hinge comprises SEQ ID NO: 208, 209, 210, 211, or 212, wherein 1, 2, 3 or all 4 amino acids P233, V234, A235 and G237 (corresponding to the C-terminal 4 amino acids "PVAG" (SEQ ID NO: 233) are deleted or substituted with another amino acid, e.g., the amino acids of the C-terminus of the IgG1 hinge (ELLG (SEQ ID NO: 234) or ELLGG (SEQ ID NO: 235)). In certain embodiments, the hinge comprises SEQ ID NO: 208, 209, 210, 211, or 212, wherein V234, A235 and G237 are deleted or substituted with another amino acid. In certain embodiments, the hinge comprises SEQ ID NO: 208, 209, 210, 211, or 212, wherein A235 and G237 are deleted or substituted with another amino acid. In certain embodiments, the hinge comprises SEQ ID NO: 208, 209, 210, 211, or 212, wherein G237 is deleted or substituted with another amino acid. In certain embodiments, the hinge comprises SEQ ID NO: 447, 448, 449, 450, or 451, wherein V234 and A235 are deleted or substituted with another amino acid. Substitution of PVAG (SEQ ID NO: 233) in an IgG2 with the corresponding amino acids of an IgG1 hinge, i.e., (ELLG (SEQ ID NO: 234) or ELLGG (SEQ ID NO: 235)) to obtain a hybrid hinge, e.g., shown above, that provides a hinge having the advantages of an IgG2 hinge and the effector function of IgG1 hinges.

[0180] In certain embodiments, a modified heavy chain constant region comprises a hinge that consists of or consists essentially of one of the sequences shown above, e.g., any one of SEQ ID NOs: 208-232, and in certain embodiments, does not comprise additional hinge amino acid residues.

[0181] In certain embodiments, a modified heavy chain constant region comprises a CH1 domain that is a wildtype CH1 domain of the IgG1 or IgG2 isotype ("IgG1 CH1 domain" or "IgG2 CH1 domain," respectively). CH1 domains of the isotypes IgG3 and IgG4 ("IgG3 CH1 domain" and "IgG2 CH1 domain," respectively) may also be used. A CH1 domain may also be a variant of a wildtype CH1 domain, e.g., a variant of a wildtype IgG1, IgG2, IgG3 or IgG4 CH1 domain. Exemplary variants of CH1 domains include A114C and T173C and/or C131, e.g., C131S.

[0182] In certain embodiments, a modified heavy chain constant region comprises a CH2 domain that is a wildtype CH2 domain of the IgG1, IgG2, IgG3 or IgG4 isotype ("IgG1 CH2 domain," "IgG2 CH2 domain," "IgG3 CH2 domain," or "IgG4 CH2 domain," respectively). A CH2 domain may also be a variant of a wildtype CH2 domain, e.g., a variant of a wildtype IgG1, IgG2, IgG3 or IgG4 CH2 domain. Exemplary variants of CH2 domains include variants that modulate a biological activity of the Fc region of an antibody, such as ADCC or CDC or modulate the half-life of the antibody or its stability. In one embodiment, the CH2 domain is a human IgG1 CH2 domain with an A330S and P331S mutation,

wherein the CH2 domain has reduced effector function relative to the same CH2 mutation without the mutations. Other mutations are further set forth herein elsewhere.

[0183] In certain embodiments, a modified heavy chain constant region comprises a CH3 domain that is a wildtype CH3 domain of the IgG1, IgG2, IgG3 or IgG4 isotype ("IgG1 CH3 domain," "IgG2 CH3 domain," "IgG3 CH3 domain," or "IgG4 CH3 domain," respectively). A CH3 domain may also be a variant of a wildtype CH3 domain, e.g., a variant of a wildtype IgG1, IgG2, IgG3 or IgG4 CH3 domain. Exemplary variants of CH3 domains include variants that modulate a biological activity of the Fc region of an antibody, such as ADCC or CDC or modulate the half-life of the antibody or its stability.

[0184] Generally, variants of the CH1, hinge, CH2 or CH3 domains may comprise 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more mutations, and/or at most 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 mutation, or 1-10 or 1-5 mutations, or comprise an amino acid sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to that of the corresponding wildtype domain (CH1, hinge, CH2, or CH3 domain, respectively), provided that the heavy chain constant region comprising the specific variant retains the necessary biological activity.

[0185] Table 3 sets forth exemplary human heavy chain constant regions comprising a human CH1, hinge, CH2 and/or CH3 domains, wherein each domain is either a wildtype domain or a variant thereof that provides the desired biological activity to the heavy chain constant region. An unfilled cell in Table 3 indicates that the domain is present or not, and if present can be of any isotype, e.g., IgG1, IgG2, IgG3 or IgG4. For example, an antibody comprising the heavy chain constant region 1 in Table 3 is an antibody that comprises a heavy chain constant region comprising at least an IgG2 hinge, and which may also comprise a CH1, CH2 and/or CH3 domain, and if present, which CH1, CH2 and/or CH3 domain is of an IgG1, IgG2, IgG3 or IgG4 isotype. As another example for understanding Table 3, an antibody comprising a heavy chain constant region 8 is an antibody comprising a heavy chain constant region comprising an IgG1 CH1 domain, and IgG2 hinge, an IgG1 CH2 domain, and which may or may not also comprise a CH3 domain, which if present, may be of an IgG1, IgG2, IgG3 or IgG4 isotype.

Table 3. Exemplary configurations of human heavy chain constant regions

MHCCR*	CH1	Hinge	CH2	CH3
1		IgG2		
2	IgG1	IgG2		
3	IgG2	IgG2		
4		IgG2	IgG1	
5		IgG2	IgG2	
6		IgG2		IgG1
7		IgG2		IgG2
8	IgG1	IgG2	IgG1	
9	IgG1	IgG2	IgG2	
10	IgG2	IgG2	IgG1	
11	IgG2	IgG2	IgG2	
12	IgG1	IgG2		IgG1
13	IgG1	IgG2		IgG2
14	IgG2	IgG2		IgG1
15	IgG2	IgG2		IgG2
16		IgG2	IgG1	IgG1
17		IgG2	IgG1	IgG2
18		IgG2	IgG2	IgG1
19		IgG2	IgG2	IgG2
20	IgG1	IgG2	IgG1	IgG1
21	IgG1	IgG2	IgG1	IgG2
22	IgG1	IgG2	IgG2	IgG1

MHCCR*	CH1	Hinge	CH2	CH3
23	IgG1	IgG2	IgG2	IgG2
24	IgG2	IgG2	IgG1	IgG1
25	IgG2	IgG2	IgG1	IgG2
26	IgG2	IgG2	IgG2	IgG1
27	IgG2	IgG2	IgG2	IgG2
* Modified heavy chain constant region				

[0186] In certain embodiments, an anti-OX40 antibody comprises a heavy chain constant region shown in Table 3 and may have altered activity relative to the same antibody comprising a heavy chain constant region that does not comprise that specific heavy chain constant region. In certain embodiments, an antibody comprising a heavy chain constant region shown in Table 3 or 4 may have an altered activity relative to the same antibody comprising a heavy chain constant region that does not comprise an IgG2 hinge or the same IgG2 hinge. In certain embodiments, an antibody comprising a heavy chain constant region shown in Table 3 or 4 may have an altered activity relative to the same antibody comprising a heavy chain constant region that comprises a non- IgG2 hinge, and comprises, e.g., an IgG1, IgG3 or IgG4 hinge. In certain embodiments, an antibody comprising a heavy chain constant region shown in Table 3 or 4 may have an altered activity relative to the same antibody comprising a heavy chain constant region that does not comprise one or more of the same CH1, hinge, CH2 or CH3 domain. For example, in certain embodiments, an antibody comprising a heavy chain constant region shown in Table 3 or 4 may have an altered activity relative to the same antibody comprising a heavy chain constant region that does not comprise an IgG2 hinge and a CH1, CH2 and/or CH3 domain of the specific isotype. For example, an antibody comprising a heavy chain constant region 22 shown in Table 3, may have an altered activity relative to (i) the same antibody comprising a heavy chain constant region that does not comprise an IgG2 hinge, and comprises, e.g., a non-IgG2 hinge (e.g., an IgG1, IgG3 or IgG4 hinge); (ii) the same antibody comprising a heavy chain constant region that does not comprise an IgG2 hinge and an IgG1 CH1, and comprises, e.g., a non-IgG2 hinge and/or a non-IgG1 CH1; (iii) the same antibody comprising a heavy chain constant region that does not comprise an IgG2 hinge and an IgG2 CH2, and comprises, e.g., a non-IgG2 hinge and/or a non-IgG2 CH2; (iv) the same antibody comprising a heavy chain constant region that does not comprise an IgG2 hinge and an IgG1 CH3, and comprises, e.g., a non-IgG2 hinge and/or a non-IgG1 CH3; (v) the same antibody comprising a heavy chain constant region that does not comprise an IgG2 hinge, an IgG1 CH1 and an IgG2 CH2, and comprises, e.g., a non-IgG2 hinge and/or a non-IgG1 CH1 and/or a non-IgG2 CH2; (vi) the same antibody comprising a heavy chain constant region that does not comprise an IgG2 hinge, an IgG1 CH1 and an IgG1 CH3, and comprises, e.g., a non-IgG2 hinge and/or a non-IgG1 CH1 and/or a non-IgG1 CH3; (vii) the same antibody comprising a heavy chain constant region that does not comprise an IgG2 hinge, an IgG2 CH2 and an IgG1 CH3, and comprises, e.g., a non-IgG2 hinge and/or a non-IgG2 CH and/or a non-IgG1 CH3; (viii) or the same antibody comprising a heavy chain constant region that does not comprise an IgG2 hinge, an IgG1 CH1, IgG2 CH2 and an IgG1 CH3, and comprises, e.g., a non-IgG2 hinge and/or a non-IgG1 CH1 and/or a non-IgG2 CH2 and/or a non-IgG1 CH3.

[0187] Exemplary modified heavy chain constant regions that may be linked to anti-OX40 variable regions, e.g., the variable regions described herein, are provided in Table 4, which sets forth the identity of each of the domains.

Table 4: Exemplary modified heavy chain constant regions

Modified heavy chain constant region	CH1	Hinge	CH2	CH3	SEQ ID NO of whole MHCCR
IgG1-IgG2-IgG1f	IgG1 wildtype SEQ ID NO: 202	IgG2/IgG1 SEQ ID NO:240	IgG1 wildtype SEQ ID NO:204	IgG1 wildtype SEQ ID NO:204	SEQ ID NO:244
IgG1-IgG2-IgG1f2	IgG1 wildtype SEQ ID	IgG2 wildtype SEQ ID NO:238	IgG1 wildtype SEQ ID	IgG1 wildtype SEQ ID NO:206	SEQ ID NO:245

Modified heavy chain constant region	CH1	Hinge	CH2	CH3	SEQ ID NO of whole MHCCR
	NO:202		NO:204		
IgG1-IgG2CS-IgG1f	IgG1 wildtype SEQ ID NO:202	IgG2C219S/IgG1 SEQ ID NO:241	IgG1 wildtype SEQ ID NO:204	IgG1 wildtype SEQ ID NO:206	SEQ ID NO:246
IgG1-IgG2CS-IgG1f2	IgG1 wildtype SEQ ID NO:202	IgG2 C219S SEQ ID NO:239	IgG1 wildtype SEQ ID NO:204	IgG1 wildtype SEQ ID NO:206	SEQ ID NO:247
IgG2-IgG1f	IgG2 wildtype SEQ ID NO:203	IgG2/IgG1 SEQ ID NO:240	IgG1 wildtype SEQ ID NO:204	IgG1 wildtype SEQ ID NO:206	SEQ ID NO:248
IgG2-IgG1f2	IgG2 wildtype SEQ ID NO:203	IgG2 wildtype SEQ ID NO:238	IgG1 wildtype SEQ ID NO:204	IgG1 wildtype SEQ ID NO:206	SEQ ID NO:249
IgG2CS-IgG1f	IgG2 wildtype SEQ ID NO:203	IgG2C219S/IgG1 SEQ ID NO:241	IgG1 wildtype SEQ ID NO:204	IgG1 wildtype SEQ ID NO:206	SEQ ID NO:250
IgG2CS-IgG1f2	IgG2 wildtype SEQ ID	IgG2 C219S SEQ ID NO:239	IgG1 wildtype SEQ ID	IgG1 wildtype SEQ ID NO:206	SEQ ID NO:251
	NO:203		NO:204		
IgG1-IgG2-IgG1.1f	IgG1 wildtype SEQ ID NO:202	IgG2 wildtype SEQ ID NO:238	IgG1 A330S/P331S SEQ ID NO:243	IgG1 wildtype SEQ ID NO:206	SEQ ID NO:252
IgG1-IgG2CS-IgG1.1f	IgG1 wildtype SEQ ID NO:202	IgG2 C219S SEQ ID NO:239	IgG1 A330S/P331S SEQ ID NO:243	IgG1 wildtype SEQ ID NO:206	SEQ ID NO:253
IgG2-IgG1.1f	IgG2 wildtype SEQ ID NO:203	IgG2 wildtype SEQ ID NO:238	IgG1 A330S/P331S SEQ ID NO:243	IgG1 wildtype SEQ ID NO:206	SEQ ID NO:254
IgG2CS-IgG1.1f	IgG2 wildtype SEQ ID	IgG2 C219S SEQ ID NO:239	IgG1 A330S/P331S SEQ ID	IgG1 wildtype SEQ ID NO:206	SEQ ID NO:255

Modified heavy chain constant region	CH1	Hinge	CH2	CH3	SEQ ID NO of whole MHCCR
	SEQ ID NO:203		SEQ ID NO:243		

[0188] Additional exemplary modified heavy chain constant regions are provided in Table 5.

Table 5.

Constructs	SEQ ID NO of constant region	Description
IgG1f	256	wild type IgG1f
IgG1.1f	257	standard inert IgG1.1f
IgG2.3	258	IgG2 A-form (C219S)
IgG2.5	259	IgG2 B-form (C131S)
IgG2.3G1-KH	260	CH1, upper hinge and lower hinge/upper CH2 of IgG2.3, all else IgG1f
IgG2.5G1-KH	261	CH1, upper hinge and lower hinge/upper CH2 of IgG2.5, all else IgG1f
IgG2.3G1-AY	262	CH1 and upper hinge of IgG2.3, all else IgG1f
IgG2.5G1-AY	263	CH1 and upper hinge of IgG2.5, all else IgG1f
IgG2.3G1.1f-KH	264	CH1, upper hinge and lower hinge/upper CH2 of IgG2.3, all else IgG1.1f
IgG2.5G1.1f-KH	265	CH1, upper hinge and lower hinge/upper CH2 of IgG2.5, all else IgG1.1f
IgG2.5G1-V27	266	IgG2-B-form variant
IgG2.3G1-V27	297	hHC-IgG2-C219S/hHC-IgG1f-S267E

[0189] In certain embodiments, an anti-OX40 antibody comprises a modified heavy chain constant region comprising an IgG2 hinge comprising any one of SEQ ID NOs: 238, 239, 240, 241, and 208-232 or a variant thereof, such as an IgG2 hinge comprising an amino acid sequence that (i) differs from any one of SEQ ID NOs: 238, 239, 240, 241, and 208-232 in 1, 2, 3, 4 or 5 amino acids substitutions, additions or deletions; (ii) differs from any one of SEQ ID NOs: 238, 239, 240, 241, and 208-232 in at most 5, 4, 3, 2, or 1 amino acids substitutions, additions or deletions; (iii) differs from any one of SEQ ID NOs: 238, 239, 240, 241, and 208-232 in 1-5, 1-3, 1-2, 2-5 or 3-5 amino acids substitutions, additions or deletions and/or (iv) comprises an amino acid sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NOs: 238, 239, 240, 241, and 208-232, wherein in any of (i)-(iv), an amino acid substitution may be a conservative amino acid substitution or a non-conservative amino acid substitution; and wherein the modified heavy chain constant region provides an altered activity to an anti-OX40 antibody relative to another heavy chain constant region, e.g., a heavy chain constant region that comprises a non-IgG2 hinge or relative to the same modified heavy chain constant region that comprises a non-IgG2 hinge.

[0190] In certain embodiments, an anti-OX40 antibody comprises a modified heavy chain constant region comprising an IgG1 CH1 domain comprising SEQ ID NO: 202 or an IgG2 CH1 domain comprising SEQ ID NO: 203, or a variant of SEQ ID NO: 202 or 203, which variant (i) differs from SEQ ID NO: 202 or 203 in 1, 2, 3, 4 or 5 amino acids substitutions, additions or deletions; (ii) differs from SEQ ID NO: 202 or 203 in at most 5, 4, 3, 2, or 1 amino acids substitutions, additions or deletions; (iii) differs from SEQ ID NO: 202 or 203 in 1-5, 1-3, 1-2, 2-5 or 3-5 amino acids substitutions, additions or deletions and/or (iv) comprises an amino acid sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 202 or 203, wherein in any of (i)-(iv), an amino acid substitution may be a conservative amino acid substitution or a non-conservative amino acid substitution; and wherein the anti-OX40 antibody comprising a modified heavy chain constant region may have an altered activity relative to that of the anti-OX40 antibody but with another heavy chain constant region, e.g., a heavy chain constant region that

comprises a non-IgG2 hinge or relative to the same modified heavy chain constant region that comprises a non-IgG2 hinge.

[0191] In certain embodiments, an anti-OX40 antibody comprises a modified heavy chain constant region comprising an IgG1 CH2 domain comprising SEQ ID NO: 204 or 298, or a variant of SEQ ID NO: 204 or 298, which variant (i) differs from SEQ ID NO: 204 or 298 in 1, 2, 3, 4 or 5 amino acids substitutions, additions or deletions; (ii) differs from SEQ ID NO: 204 or 298 in at most 5, 4, 3, 2, or 1 amino acids substitutions, additions or deletions; (iii) differs from SEQ ID NO: 204 or 298 in 1-5, 1-3, 1-2, 2-5 or 3-5 amino acids substitutions, additions or deletions and/or (iv) comprises an amino acid sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 204 or 298, wherein in any of (i)-(iv), an amino acid substitution may be a conservative amino acid substitution or a non-conservative amino acid substitution; and wherein the modified heavy chain constant region may provide an altered activity to an anti-OX40 antibody relative to that of another heavy chain constant region, e.g., a heavy chain constant region that comprises a non-IgG2 hinge or relative to the same modified heavy chain constant region that comprises a non-IgG2 hinge.

[0192] In certain embodiments, an anti-OX40 antibody comprises a modified heavy chain constant region comprising an IgG1 CH3 domain comprising SEQ ID NO: 206, or a variant of SEQ ID NO: 206, which variant (i) differs from SEQ ID NO: 206 in 1, 2, 3, 4 or 5 amino acids substitutions, additions or deletions; (ii) differs from SEQ ID NO: 206 in at most 5, 4, 3, 2, or 1 amino acids substitutions, additions or deletions; (iii) differs from SEQ ID NO: 206 in 1-5, 1-3, 1-2, 2-5 or 3-5 amino acids substitutions, additions or deletions and/or (iv) comprises an amino acid sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 206, wherein in any of (i)-(iv), an amino acid substitution may be a conservative amino acid substitution or a non-conservative amino acid substitution; and wherein the modified heavy chain constant region may provide an altered activity relative to that of another heavy chain constant region, e.g., a heavy chain constant region that comprises a non-IgG2 hinge or relative to the same modified heavy chain constant region that comprises a non-IgG2 hinge.

[0193] Modified heavy chain constant regions may also comprise a combination of the CH1, hinge, CH2 and CH3 domains described above.

[0194] In certain embodiments, an anti-OX40 antibody comprises a modified heavy chain constant region comprising any one of SEQ ID NOs: 244-281, or a variant of any one of SEQ ID NOs: 244-281, which variant (i) differs from any one of SEQ ID NOs: 244-281 in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more amino acids substitutions, additions or deletions; (ii) differs from any one of SEQ ID NOs: 244-281 in at most 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 amino acids substitutions, additions or deletions; (iii) differs from any one of SEQ ID NOs: 244-281 in 1-5, 1-3, 1-2, 2-5, 3-5, 1-10, or 5-10 amino acids substitutions, additions or deletions and/or (iv) comprises an amino acid sequence that is at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NOs: 244-281, wherein in any of (i)-(iv), an amino acid substitution may be a conservative amino acid substitution or a non-conservative amino acid substitution; and wherein the modified heavy chain constant region may provide an altered activity relative to that of another heavy chain constant region, e.g., a heavy chain constant region that comprises a non-IgG2 hinge or relative to the same modified heavy chain constant region that comprises a non-IgG2 hinge.

[0195] Modified heavy chain constant regions may have (i) similar, reduced or increased effector function (e.g., binding to an FcγR) relative to a wildtype heavy chain constant region and or (ii) similar, reduced or increased half-life (or binding to the FcRn receptor) relative to a wildtype heavy chain constant region.

III. Antibodies Having Particular Germline Sequences

[0196] As discussed in the Examples of the present disclosure, human antibodies specific for OX40 have been prepared that comprise a heavy chain variable region that is the product of or derived from human germline VH 1-08 gene, VH 6-6 gene, VH 5-51 gene, VH 3-9 gene, VH DP44 gene, VH 3-30.3 gene, VH 3-10 gene, and/or VH 3-13 gene. Accordingly, provided herein are isolated monoclonal antibodies specific for human OX40, comprising a heavy chain variable region that is the product of or derived from a human VH germline gene selected from the group consisting of: VH 1-08 gene, VH 6-6 gene, VH 5-51 gene, VH 3-9 gene, VH DP44 gene, VH 3-30.3 gene, VH 3-10 gene, and VH 3-13 gene.

[0197] Human antibodies specific for OX40 have been prepared that comprise a light chain variable region that is the product of or derived from human germline VK L5 gene, VK L6 gene, VK L15 gene, VK A27 gene, and/or VK O14/O4 gene. Accordingly, provided herein are isolated monoclonal antibodies comprising a light chain variable region that is the product of or derived from a human VK germline gene selected from the group consisting of: VK L5 gene, VK L6 gene, VK L15 gene, VK A27 gene, and VK O14/O4 gene.

[0198] Preferred non-claimed antibodies described herein are those comprising a heavy chain variable region that is the product of or derived from one of the above-listed human germline VH genes and also comprising a light chain variable region that is the product of or derived from one of the above-listed human germline VK genes.

[0199] As used herein, a human antibody comprises heavy or light chain variable regions that is "the product of" or "derived from" a particular germline sequence if the variable regions of the antibody are obtained from a system that uses human germline immunoglobulin genes. Such systems include immunizing a transgenic mouse carrying human immunoglobulin genes with the antigen of interest or screening a human immunoglobulin gene library displayed on phage with the antigen of interest. A human antibody that is "the product of" or "derived from" a human germline immunoglobulin sequence can be identified as such by comparing the amino acid sequence of the human antibody to the amino acid sequences of human germline immunoglobulins and selecting the human germline immunoglobulin sequence that is closest in sequence (*i.e.*, greatest % identity) to the sequence of the human antibody. A human antibody that is "the product of" or "derived from" a particular human germline immunoglobulin sequence may contain amino acid differences as compared to the germline sequence, due to, for example, naturally-occurring somatic mutations or intentional introduction of site-directed mutation. However, a selected human antibody typically is at least 90% identical in amino acids sequence to an amino acid sequence encoded by a human germline immunoglobulin gene and contains amino acid residues that identify the human antibody as being human when compared to the germline immunoglobulin amino acid sequences of other species (e.g., murine germline sequences). In certain cases, a human antibody may be at least 95%, or even at least 96%, 97%, 98%, or 99% identical in amino acid sequence to the amino acid sequence encoded by the germline immunoglobulin gene. Typically, a human antibody derived from a particular human germline sequence will display no more than 10 amino acid differences from the amino acid sequence encoded by the human germline immunoglobulin gene. In certain cases, the human antibody may display no more than 5, or even no more than 4, 3, 2, or 1 amino acid difference from the amino acid sequence encoded by the germline immunoglobulin gene.

IV. Homologous Antibodies

[0200] Provided herein are non-claimed antibodies having heavy and light chain variable regions comprising amino acid sequences that are homologous to the amino acid sequences of the preferred antibodies described herein, and wherein the antibodies retain the desired functional properties of the anti-OX40 antibodies described herein.

[0201] The non-claimed antibody can be, for example, a human antibody, a humanized antibody or a chimeric antibody.

[0202] The non-claimed anti-OX40 antibody, or antigen binding portion thereof, may comprise a heavy chain and a light chain, wherein:

1. (a) the heavy chain comprises an amino acid sequence that is at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to an amino acid sequence consisting of SEQ ID NO: 124, or comprises 1, 2, 3, 4, 5, 1-2, 1-3, 1-4, 1-5, 1-10, 1-15, 1-20, 1-25, or 1-50 amino acid changes (*i.e.*, amino acid substitutions, additions or deletions) relative to an amino acid sequence consisting of SEQ ID NO: 124;
2. (b) the light chain comprises an amino acid sequence that is at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to an amino acid sequence consisting of SEQ ID NO: 116, or comprises 1, 2, 3, 4, 5, 1-2, 1-3, 1-4, 1-5, 1-10, 1-15, 1-20, 1-25, or 1-50 amino acid changes (*i.e.*, amino acid substitutions, additions or deletions) relative to an amino acid sequence consisting of SEQ ID NO: 116;
3. (c) the antibody specifically binds to OX40, and
4. (d) the antibody exhibits 1, 2, 3, 4, 5, 6, or all of the following functional properties:
 1. (1) binding to soluble human OX40, e.g., with a K_D of 10 nM or less (e.g., 0.01 nM to 10 nM), e.g., as

measured by Biacore;

2. (2) binding to membrane bound human OX40, e.g., with an EC₅₀ of 1 nM or less (e.g., 0.01 nM to 1 nM), e.g., as measured by FACS;
3. (3) binding to cynomolgus OX40, e.g., binding to membrane bound cynomolgus OX40, e.g., with an EC₅₀ of 10 nM or less (e.g., 0.01 nM to 10 nM), e.g., as measured by FACS;
4. (4) inducing or enhancing T cell activation, as evidenced by (i) increased IL-2 and/or IFN- γ production in OX40-expressing T cells and/or (ii) enhanced T cell proliferation;
5. (5) inhibiting the binding of OX40 ligand to OX40, e.g., with an EC₅₀ of 1 nM or less as measured by FACS, e.g., in an assay with hOX40-293 cells;
6. (6) binding to an epitope on the extracellular portion of mature human OX40 (SEQ ID NO: 2), e.g., an epitope within the region DVVSSKPCPKCTWCNLR (SEQ ID NO: 178) or DSYKPGVDCAPCPGHFSPGDNQACKPWTNCTLAGK (SEQ ID NO: 179);
7. (7) competing for binding to human OX40 with 3F4, 14B6-1, 14B6-2, 23H3, 18E9, 8B11, 20B3, and 20C1;
8. (8) competing for binding to human OX40 with 6E1-1, 6E1-2, 14A2-1, and 14A2-2.

[0203] Non-claimed antibodies having sequences with homology to the V_H and V_L regions of SEQ ID NOs: 124 and 116, or CDRs can be obtained by mutagenesis (e.g., site-directed or PCR-mediated mutagenesis) of nucleic acid molecules encoding SEQ ID NO: 124 and/or SEQ ID NO: 116, followed by testing of the encoded altered antibody for retained function (*i.e.*, the functions set forth in (1) through (7) above) using the functional assays described herein.

V. Antibodies with Conservative Modifications

[0204] Conservative amino acid substitutions may be made in the Fc region. In certain embodiments, the anti-OX40 antibody comprises a combination of conservative and non-conservative amino acid modification.

VI. Competing antibodies and same epitope binding antibodies

[0205] Also provided herein are non-claimed antibodies that compete for binding to OX40 with the anti-OX40 antibodies described herein (e.g., antibodies 3F4, 14B6-1, 14B6-2, 23H3, 6E1-1, 6E1-2, 18E9, 8B11, 20B3, 14A2-1, 14A2-2, and 20C1). Such competing antibodies can be identified based on their ability to competitively inhibit binding to OX40 of one or more of monoclonal antibodies 3F4, 14B6-1, 14B6-2, 23H3, 6E1-1, 6E1-2, 18E9, 8B11, 20B3, 14A2-1, 14A2-2, and 20C1 in standard OX40 binding assays. For example, standard ELISA assays or competitive ELISA assays can be used in which a recombinant human OX40 protein is immobilized on a plate, various concentrations of unlabeled first antibody are added, the plate is washed, labeled second antibody is added, washed, and the amount of bound label is measured. If the increasing concentration of the unlabeled (first) antibody (also referred to as the "blocking antibody") inhibits the binding of the labeled (second) antibody, the first antibody is said to inhibit the binding of the second antibody to the target on the plate, or is said to compete with the binding of the second antibody. Additionally or alternatively, BIACORE® SPR analysis can be used to assess the ability of the antibodies to compete. The ability of a test antibody to inhibit the binding of an anti-OX40 antibody described herein to OX40 demonstrates that the test antibody can compete with the antibody for binding to OX40.

[0206] Accordingly, provided herein are anti-OX40 antibodies that inhibit the binding of the anti-OX40 antibodies described herein to OX40 on cells, e.g., activated T cells, by at least 10%, 20%, 30%, 40%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%, by using, e.g., FACS as described in the Examples.

[0207] Provided herein are non-claimed anti-OX40 antibodies which bind to the same epitope as one or more of the anti-OX40 antibodies described herein (e.g., antibodies 3F4, 14B6-1, 14B6-2, 23H3, 6E1-1, 6E1-2, 18E9, 8B11, 20B3, 14A2-1, 14A2-2, and 20C1), as determined using art-recognized epitope mapping techniques, such as those described below.

[0208] Art-recognized epitope mapping techniques include, for example, structural methods, such as X-ray crystal structure determination (e.g., WO2005/044853), molecular modeling and nuclear magnetic resonance (NMR) spectroscopy, including NMR determination of the H-D exchange rates of labile amide hydrogens in OX40 when free and when bound in a complex with an antibody of interest (Zinn-Justin et al. *Biochemistry* 1992;31:11335-47; Zinn-Justin et al. *Biochemistry* 1993;32:6884-91).

[0209] For X-ray crystallography, crystallization may be accomplished using any known method in the art (e.g. Giege et al. *Acta Crystallogr* 1994;D50:339-50; McPherson, *Eur J Biochem* 1990;189:1-23), including microbatch (e.g. Chayen, *Structure* 1997;5:1269-74), hanging-drop vapor diffusion (e.g. McPherson, *J Biol Chem* 1976;251:6300-3), seeding and dialysis. It is desirable to use a protein preparation having a concentration of at least about 1 mg/mL and preferably about 10 mg/mL to about 20 mg/mL. Crystallization may be best achieved in a precipitant solution containing polyethylene glycol 1000-20,000 (PEG; average molecular weight ranging from about 1000 to about 20,000 Da), preferably about 5000 to about 7000 Da, more preferably about 6000 Da, with concentrations ranging from about 10% to about 30% (w/v). It may also be desirable to include a protein stabilizing agent, e.g., glycerol at a concentration ranging from about 0.5% to about 20%. A suitable salt, such as sodium chloride, lithium chloride or sodium citrate may also be desirable in the precipitant solution, preferably in a concentration ranging from about 1 mM to about 1000 mM. The precipitant is preferably buffered to a pH of from about 3.0 to about 5.0, preferably about 4.0. Specific buffers useful in the precipitant solution may vary and are well-known in the art (Scopes, *Protein Purification: Principles and Practice*, Third ed., (1994) Springer-Verlag, New York). Examples of such buffers include, but are not limited to, HEPES, Tris, MES and acetate. Crystals may be grow at a wide range of temperatures, including 2°C, 4°C, 8°C and 26°C. Antibody:antigen crystals may be studied using well-known X-ray diffraction techniques and may be refined using computer software such as X-PLOR (Yale University, 1992, distributed by Molecular Simulations, Inc.; see e.g. Blundell & Johnson, *Meth. Enzymol.* 1985; 114 & 115, H. W. Wyckoff et al., eds., Academic Press; U.S. Patent Application Publication No. 2004/0014194), and BUSTER (Bricogne, *Acta Cryst* 1993;D49:37-60; Bricogne, *Meth Enzymol* 1997;276A:361-423; Carter & Sweet, eds.; Roversi et al., *Acta Cryst.* 2000;D56:1313-23).

[0210] Other epitope mapping methods monitor the binding of the antibody to antigen fragments or mutated variations of the antigen where loss of binding due to a modification of an amino acid residue within the antigen sequence is often considered an indication of an epitope component. One such method is alanine scanning mutagenesis, as described, e.g., by Cunningham and Wells, *Science* 1989;244:1081-5. Another suitable method is deep mutational scanning (see, e.g., Araya et al., *Trends in Biotechnology* 2011;29:435-42; Forsyth et al., *mAbs* 2013;5:523-32).

[0211] Additionally or alternatively, computational combinatorial methods for epitope mapping, including the mapping of conformational discontinuous epitopes, can be used.

[0212] Additionally or alternatively, epitope mapping can be achieved by testing binding of an antibody to peptides comprising fragments of OX40, e.g., non-denatured or denatured fragments. A series of overlapping peptides encompassing the sequence of OX40 (e.g., human OX40) may be synthesized and screened for binding, e.g., in a direct ELISA, a competitive ELISA (where the peptide is assessed for its ability to prevent binding of an antibody to OX40 bound to a well of a microtiter plate) or on a chip. Other methods rely on the ability of an antibody of interest to affinity isolate specific short peptides (either in native three dimensional form or in denatured form) from combinatorial phage display peptide libraries. The peptides are then regarded as leads for the definition of the epitope recognized by the antibody used to screen the peptide library.

[0213] Epitopes also can be identified by MS-based protein footprinting, such as Hydrogen/deuterium exchange mass spectrometry (HDX-MS) and Fast Photochemical Oxidation of Proteins (FPOP). HDX-MS may be conducted, for example, as described in the Examples herein and by Wei et al., *Drug Discovery Today* 2014;19:95. FPOP may be conducted, for example, as described by Hambley et al. (*J American Soc Mass Spectrometry* 2005;16:2057).

[0214] Antibodies that compete for binding with the anti-OX40 antibodies described herein may be produced and identified using art-known methods. For example, mice may be immunized with human OX40 as described herein, hybridomas produced, and the resulting monoclonal antibodies screened for the ability to compete with an antibody described herein for binding to OX40 using the methods described above.

[0215] Antibodies that bind to the same epitope as the anti-OX40 antibodies described herein may be produced by

immunizing mice with a smaller fragment of OX40 containing the epitope to which the antibody binds. The epitope or region comprising the epitope can be identified using the methods described above. Alternatively, the method of Jespers et al. (Biotechnology 1994;12:899) may be used to guide the selection of antibodies recognizing the same epitope and therefore exhibiting similar properties to the anti-OX40 antibodies described herein. For example, using phage display, first the heavy chain of the anti-OX40 antibody is paired with a repertoire of (preferably human) light chains to select a OX40-binding antibody, and then the new light chain is paired with a repertoire of (preferably human) heavy chains to select a (preferably human) OX40-binding antibody recognizing the same epitope or epitope region on OX40 as an anti-OX40 antibody described herein. Alternatively variants of an antibody described herein can be obtained by mutagenesis of cDNA encoding the heavy and light chains of the antibody.

[0216] In some embodiments, provided herein are antibodies which bind to all or a portion of the sequence DVVSSKPCKPCTWCNLR (SEQ ID NO: 178), corresponding to amino acid residues 46-62 of mature human OX40 (SEQ ID NO: 2), as determined by the methods in the Examples.

[0217] In certain embodiments, the anti-OX40 antibodies described herein that bind to all or a portion of the sequence SQNTVCRPCGPGFYNDVSSKPCKPCTWCNLR (SEQ ID NO: 182), as determined by the methods in the Examples.

[0218] In other embodiments, the anti-OX40 antibodies described herein that bind to all or a portion of the sequence PCKPCTWCNLR (SEQ ID NO: 183), as determined by the methods in the Examples.

[0219] In yet other embodiments, the anti-OX40 antibodies that bind to all or a portion of the sequence DVVSSKPCKPCTWCNLR (SEQ ID NO: 178) further bind to all or a portion of the sequence QLCTATQDTVCR (SEQ ID NO: 184), as determined by the methods in the Examples.

[0220] In additional embodiments, the anti-OX40 antibodies described herein that bind to all or a portion of the sequence SQNTVCRPCGPGFYNDVSSKPCKPCTWCNLR (SEQ ID NO: 185), as determined by the methods in the Examples.

[0221] In additional embodiments, the anti-OX40 antibody binds within the region DSYKPGVDCAPCPGPHFSPGDNQACKPWTNCTLAGK (SEQ ID NO: 179), corresponding to amino acid residues 89-124 of mature human OX40 (SEQ ID NO: 2), as determined by the methods in the Examples.

VII. Engineered and Modified Antibodies

Targeted antigen binding

[0222] In various embodiments, the antibodies described herein are modified to selectively block antigen binding in tissues and environments where antigen binding would be detrimental, but allow antigen binding where it would be beneficial. In one embodiment, a blocking peptide "mask" is generated that specifically binds to the antigen binding surface of the antibody and interferes with antigen binding, which mask is linked to each of the binding arms of the antibody by a peptidase cleavable linker. See, e.g., U.S. Pat. No. 8,518,404 to CytomX. Such constructs are useful for treatment of cancers in which protease levels are greatly increased in the tumor microenvironment compared with non-tumor tissues. Selective cleavage of the cleavable linker in the tumor microenvironment allows disassociation of the masking/blocking peptide, enabling antigen binding selectively in the tumor, rather than in peripheral tissues in which antigen binding might cause unwanted side effects.

[0223] Alternatively, in a related embodiment, a bivalent binding compound ("masking ligand") comprising two antigen binding domains is developed that binds to both antigen binding surfaces of the (bivalent) antibody and interfere with antigen binding, in which the two binding domains masks are linked to each other (but not the antibody) by a cleavable linker, for example cleavable by a peptidase. See, e.g., Int'l Pat. App. Pub. No. WO 2010/077643 to Tegopharm Corp. Masking ligands may comprise, or be derived from, the antigen to which the antibody is intended to bind, or may be independently generated. Such masking ligands are useful for treatment of cancers in which protease levels are greatly increased in the tumor microenvironment compared with non-tumor tissues. Selective cleavage of the cleavable linker in the tumor microenvironment allows disassociation of the two binding domains from each other, reducing the avidity

for the antigen-binding surfaces of the antibody. The resulting dissociation of the masking ligand from the antibody enables antigen binding selectively in the tumor, rather than in peripheral tissues in which antigen binding might cause unwanted side effects.

Fcs and modified Fcs

[0224] In addition to the activity of a therapeutic antibody arising from binding of the antigen binding domain to the antigen (e.g. blocking of a cognate ligand or receptor protein in the case of antagonist antibodies, or induced signaling in the case of agonist antibodies), the Fc portion of the antibody interact with the immune system generally in complex ways to elicit any number of biological effects. Effector functions, such as the Fc region of an immunoglobulin, are responsible for many important antibody functions, such as antigen-dependent cellular cytotoxicity (ADCC), complement dependent cytotoxicity (CDC), and antibody-dependent cell-mediated phagocytosis (ADCP), result in killing of target cells, albeit by different mechanisms. There are five major classes, or isotypes, of heavy chain constant region (IgA, IgG, IgD, IgE, IgM), each with characteristic effector functions. These isotypes can be further subdivided into subclasses, for example, IgG is separated into four subclasses known as IgG1, IgG2, IgG3, and IgG4. IgG molecules interact with three classes of Fcγ receptors (FcγR) specific for the IgG class of antibody, namely FcγRI, FcγRII, and FcγRIII. The important sequences for the binding of IgG to the FcγR receptors have been reported to be located in the CH2 and CH3 domains. The serum half-life of an antibody is influenced by the ability of that antibody to bind to the neonatal Fc receptor (FcRn).

[0225] Anti-OX40 antibodies described herein may comprise the variable domains of the invention combined with constant domains comprising different Fc regions, selected based on the biological activities (if any) of the antibody for the intended use. Salfeld (2007) Nat. Biotechnol. 25:1369. Human IgGs, for example, can be classified into four subclasses, IgG1, IgG2, IgG3, and IgG4, and each these of these comprises an Fc region having a unique profile for binding to one or more of Fcγ receptors (activating receptors FcγRI (CD64), FcγRIIA, FcγRIIC (CD32); FcγRIIIA and FcγRIIIB (CD16) and inhibiting receptor FcγRIIB), and for the first component of complement (C1q). Human IgG1 and IgG3 bind to all Fcγ receptors; IgG2 binds to FcγRIIA_{H131}, and with lower affinity to FcγRIIA_{R131} FcγRIIIA_{V158}; IgG4 binds to FcγRI, FcγRIIA, FcγRIIB, FcγRIIC, and FcγRIIIA_{V158}; and the inhibitory receptor FcγRIIB has a lower affinity for IgG1, IgG2 and IgG3 than all other Fcγ receptors. Bruhns et al. (2009) Blood 113:3716. Studies have shown that FcγRI does not bind to IgG2, and FcγRIIIB does not bind to IgG2 or IgG4. *Id.* In general, with regard to ADCC activity, human IgG1 ≥ IgG3 >> IgG4 ≥ IgG2. As a consequence, for example, an IgG1 constant domain, rather than an IgG2 or IgG4, might be chosen for use in a drug where ADCC is desired; IgG3 might be chosen if activation of FcγRIIIA-expressing NK cells, monocytes, or macrophages; and IgG4 might be chosen if the antibody is to be used to desensitize allergy patients. IgG4 may also be selected if it is desired that the antibody lack all effector function.

[0226] Accordingly, anti-OX40 variable regions described herein may be linked (e.g., covalently linked or fused) to an Fc, e.g., an IgG1, IgG2, IgG3 or IgG4 Fc, which may be of any allotype or isoallotype, e.g., for IgG1: G1m, G1m1(a), G1m2(x), G1m3(f), G1m17(z); for IgG2: G2m, G2m23(n); for IgG3: G3m, G3m21(gl), G3m28(g5), G3m11(b0), G3m5(b1), G3m13(b3), G3m14(b4), G3m10(b5), G3m15(s), G3m16(t), G3m6(c3), G3m24(c5), G3m26(u), G3m27(v); . See, e.g., Jefferis et al. (2009) mAbs 1:1). Selection of allotype may be influenced by the potential immunogenicity concerns, e.g. to minimize the formation of anti-drug antibodies.

[0227] In certain embodiments, anti-OX40 variable regions described herein are linked to an Fc that binds to one or more activating Fc receptors (FcγI/CD64, FcγIIa/CD32 or FcγIIIa/CD16), and thereby stimulate ADCC and may cause T cell depletion. In particular embodiments, anti-OX40 variable regions described herein are linked to an Fc that causes depletion. In other embodiments, anti-OX40 variable regions described herein are linked to a human IgG1 or IgG3 Fc, i.e., the antibodies are of the IgG1 or IgG3 isotype. In other embodiments, anti-OX40 antibodies are depleting antibodies. For example, they may deplete T_{reg} cells that are in the tumor microenvironment (and thereby enhance anti-tumor activity), but not significantly deplete T_{eff} cells that are in the tumor microenvironment and mediate the anti-tumor effect, and/or not significantly deplete T_{reg} and T_{eff} cells that are outside of the tumor, e.g., in the periphery. In other embodiments, anti-OX40 antibodies are of an isotype, (either naturally occurring or non-naturally occurring (e.g., including mutation(s)) isotype that stimulate T_{reg} cell depletion or elimination at the tumor site and concomitant activation of T_{eff} cells. In other embodiments, anti-OX40 antibodies create an elevated T_{eff} to T_{reg} ratio at the tumor site,

which is indicative of potent anti-tumor activity, and preferably without significantly depleting T_{reg} and T_{eff} cells that are outside of the tumor, e.g., in the periphery.

[0228] In certain embodiments, anti-OX40 antibodies block the immunosuppressive activity of T_{regs}. In other embodiments, anti-OX40 antibodies have an Fc receptor with reduced or eliminated FcR binding, e.g., reduced binding to activating FcRs. In certain embodiments, anti-OX40 antibodies have an Fc that binds to or has enhanced binding to FcRIIb, which can provide enhanced agonism. See, e.g., WO 2012/087928; Li & Ravetch (2011) Science 333:1030; Wilson et al. (2011) Cancer Cell 19:101; White et al. (2011) J. Immunol. 187:1754.

[0229] Anti-OX40 variable regions described herein may be linked to a non-naturally occurring Fc region, e.g., an effectorless or mostly effectorless Fc (e.g., human IgG2 or IgG4) or, alternatively, an Fc with enhanced binding to one or more activating Fc receptors (FcγI, FcγIIa or FcγIIIa), such as to enhance T_{reg} depletion in the tumor environment.

[0230] Variable regions described herein may be linked to an Fc comprising one or more modification, typically to alter one or more functional properties of the antibody, such as serum half-life, complement fixation, Fc receptor binding, and/or antigen-dependent cellular cytotoxicity. Furthermore, an antibody described herein may be chemically modified (e.g., one or more chemical moieties can be attached to the antibody) or it may be modified to alter its glycosylation, to alter one or more functional properties of the antibody. Each of these embodiments is described in further detail below. The numbering of residues in the Fc region is that of the EU index of Kabat. Sequence variants disclosed herein are provided with reference to the residue number followed by the amino acid that is substituted in place of the naturally occurring amino acid, optionally preceded by the naturally occurring residue at that position. Where multiple amino acids may be present at a given position, e.g. if sequences differ between naturally occurring isotypes, or if multiple mutations may be substituted at the position, they are separated by slashes (e.g. "X/Y/Z").

[0231] For example, one may make modifications in the Fc region in order to generate an Fc variant with (a) increased or decreased antibody-dependent cell-mediated cytotoxicity (ADCC), (b) increased or decreased complement mediated cytotoxicity (CDC), (c) increased or decreased affinity for C1q and/or (d) increased or decreased affinity for a Fc receptor relative to the parent Fc. Such Fc region variants will generally comprise at least one amino acid modification in the Fc region. Combining amino acid modifications is thought to be particularly desirable. For example, the variant Fc region may include two, three, four, five, etc substitutions therein, e.g. of the specific Fc region positions identified herein. Exemplary Fc sequence variants are disclosed herein, and are also provided at U.S. Pat. Nos. 5,624,821; 6,277,375; 6,737,056; 6,194,551; 7,317,091; 8,101,720; PCT Patent Publications WO 00/42072; WO 01/58957; WO 04/016750; WO 04/029207; WO 04/035752; WO 04/074455; WO 04/099249; WO 04/063351; WO 05/070963; WO 05/040217, WO 05/092925 and WO 06/020114.

Reducing Effector Function

[0232] ADCC activity may be reduced by modifying the Fc region. In certain embodiments, sites that affect binding to Fc receptors may be removed, preferably sites other than salvage receptor binding sites. In other embodiments, an Fc region may be modified to remove an ADCC site. ADCC sites are known in the art; see, for example, Sarmay et al. (1992) Molec. Immunol. 29 (5): 633-9 with regard to ADCC sites in IgG1. In one embodiment, the G236R and L328R variant of human IgG1 effectively eliminates Fc γ R binding. Horton et al. (2011) J. Immunol. 186:4223 and Chu et al. (2008) Mol. Immunol. 45:3926. In other embodiments, the Fc having reduced binding to FcγRs comprised the amino acid substitutions L234A, L235E and G237A. Gross et al. (2001) Immunity 15:289.

[0233] CDC activity may also be reduced by modifying the Fc region. Mutations at IgG1 positions D270, K322, P329 and P331, specifically alanine mutations D270A, K322A, P329A and P331A, significantly reduce the ability of the corresponding antibody to bind C1q and activate complement. Idusogie et al. (2000) J. Immunol. 164:4178; WO 99/51642. Modification of position 331 of IgG1 (e.g. P331S) has been shown to reduce complement binding. Tao et al. (1993) J. Exp. Med. 178:661 and Canfield & Morrison (1991) J. Exp. Med. 173:1483. In another example, one or more amino acid residues within amino acid positions 231 to 239 are altered to thereby reduce the ability of the antibody to fix complement. WO 94/29351.

[0234] In some embodiments, the Fc with reduced complement fixation has the amino acid substitutions A330S and

P331S. Gross et al. (2001) Immunity 15:289.

[0235] For uses where effector function is to be avoided altogether, e.g. when antigen binding alone is sufficient to generate the desired therapeutic benefit, and effector function only leads to (or increases the risk of) undesired side effects, IgG4 antibodies may be used, or antibodies or fragments lacking the Fc region or a substantial portion thereof can be devised, or the Fc may be mutated to eliminate glycosylation altogether (e.g. N297A). Alternatively, a hybrid construct of human IgG2 (C_H1 domain and hinge region) and human IgG4 (C_H2 and C_H3 domains) has been generated that is devoid of effector function, lacking the ability to bind the FcγRs (like IgG2) and unable to activate complement (like IgG4). Rother et al. (2007) Nat. Biotechnol. 25:1256. See also Mueller et al. (1997) Mol. Immunol. 34:441; Labrijn et al. (2008) Curr. Op. Immunol. 20:479 (discussing Fc modifications to reduce effector function generally).

[0236] In other embodiments, the Fc region is altered by replacing at least one amino acid residue with a different amino acid residue to reduce all effector function(s) of the antibody. For example, one or more amino acids selected from amino acid residues 234, 235, 236, 237, 297, 318, 320 and 322 can be replaced with a different amino acid residue such that the antibody has decreased affinity for an effector ligand but retains the antigen-binding ability of the parent antibody. The effector ligand to which affinity is altered can be, for example, an Fc receptor (residues 234, 235, 236, 237, 297) or the C1 component of complement (residues 297, 318, 320, 322). U.S. Patent Nos. 5,624,821 and 5,648,260, both by Winter et al.

[0237] One early patent application proposed modifications in the IgG Fc region to decrease binding to FcγRI to decrease ADCC (234A; 235E; 236A; G237A) or block binding to complement component C1q to eliminate CDC (E318A or V/K320A and K322A/Q). WO 88/007089. See also Duncan & Winter (1988) Nature 332:563; Chappel et al. (1991) Proc. Nat'l Acad. Sci. (USA) 88:9036; and Sonderrmann et al. (2000) Nature 406:267 (discussing the effects of these mutations on FcγRIII binding).

[0238] Fc modifications reducing effector function also include substitutions, insertions, and deletions at positions 234, 235, 236, 237, 267, 269, 325, and 328, such as 234G, 235G, 236R, 237K, 267R, 269R, 325L, and 328R. An Fc variant may comprise 236R/328R. Other modifications for reducing FcγR and complement interactions include substitutions 297A, 234A, 235A, 237A, 318A, 228P, 236E, 268Q, 309L, 330S, 331 S, 220S, 226S, 229S, 238S, 233P, and 234V. These and other modifications are reviewed in Strohl (2009) Current Opinion in Biotechnology 20:685-691. Effector functions (both ADCC and complement activation) can be reduced, while maintaining neonatal FcR binding (maintaining half-life), by mutating IgG residues at one or more of positions 233 - 236 and 327 - 331, such as E233P, L234V, L235A, optionally G236Δ, A327G, A330S and P331S in IgG1; E233P, F234V, L235A, optionally G236Δ in IgG4; and A330S and P331S in IgG2. See Armour et al. (1999) Eur. J. Immunol. 29:2613; WO 99/58572. Other mutations that reduce effector function include L234A and L235A in IgG1 (Alegre et al. (1994) Transplantation 57:1537); V234A and G237A in IgG2 (Cole et al. (1997) J. Immunol. 159:3613; see also U.S. Pat. No. 5,834,597); and S228P and L235E for IgG4 (Reddy et al. (2000) J. Immunol. 164:1925). Another combination of mutations for reducing effector function in a human IgG1 include L234F, L235E and P331S. Oganessian et al. (2008) Acta Crystallogr. D. Biol. Crystallogr. 64:700. See generally Labrijn et al. (2008) Curr. Op. Immunol. 20:479. Additional mutations found to decrease effector function in the context of an Fc (IgG1) fusion protein (abatacept) are C226S, C229S and P238S (EU residue numbering). Davis et al. (2007) J. Immunol. 34:2204.

[0239] Other Fc variants having reduced ADCC and/or CDC are disclosed at Glaesner et al. (2010) Diabetes Metab. Res. Rev. 26:287 (F234A and L235A to decrease ADCC and ADCP in an IgG4); Hutchins et al. (1995) Proc. Nat'l Acad. Sci. (USA) 92:11980 (F234A, G237A and E318A in an IgG4); An et al. (2009) MAbs 1:572 and U.S. Pat. App. Pub. 2007/0148167 (H268Q, V309L, A330S and P331S in an IgG2); McEarchern et al. (2007) Blood 109:1185 (C226S, C229S, E233P, L234V, L235A in an IgG1); Vafa et al. (2014) Methods 65:114 (V234V, G237A, P238S, H268A, V309L, A330S, P331S in an IgG2).

[0240] In certain embodiments, an Fc is chosen that has essentially no effector function, i.e., it has reduced binding to FcγRs and reduced complement fixation. An exemplary Fc, e.g., IgG1 Fc, that is effectorless comprises the following five mutations: L234A, L235E, G237A, A330S and P331S. Gross et al. (2001) Immunity 15:289. Exemplary heavy chains comprising these mutations are set forth in the Sequence Listing, as detailed at Table 23 (e.g. SEQ ID NO: 11). These five substitutions may be combined with N297A to eliminate glycosylation as well.

Enhancing Effector Function

[0241] Alternatively, ADCC activity may be increased by modifying the Fc region. With regard to ADCC activity, human IgG1 $\geq$ IgG3 $\gg$ IgG4 $\geq$ IgG2, so an IgG1 constant domain, rather than an IgG2 or IgG4, might be chosen for use in a drug where ADCC is desired. Alternatively, the Fc region may be modified to increase antibody dependent cellular cytotoxicity (ADCC) and/or to increase the affinity for an Fc γ receptor by modifying one or more amino acids at the following positions: 234, 235, 236, 238, 239, 240, 241, 243, 244, 245, 247, 248, 249, 252, 254, 255, 256, 258, 262, 263, 264, 265, 267, 268, 269, 270, 272, 276, 278, 280, 283, 285, 286, 289, 290, 292, 293, 294, 295, 296, 298, 299, 301, 303, 305, 307, 309, 312, 313, 315, 320, 322, 324, 325, 326, 327, 329, 330, 331, 332, 333, 334, 335, 337, 338, 340, 360, 373, 376, 378, 382, 388, 389, 398, 414, 416, 419, 430, 433, 434, 435, 436, 437, 438 or 439. See WO 2012/142515; see also WO 00/42072. Exemplary substitutions include 236A, 239D, 239E, 268D, 267E, 268E, 268F, 324T, 332D, and 332E. Exemplary variants include 239D/332E, 236A/332E, 236A/239D/332E, 268F/324T, 267E/268F, 267E/324T, and 267E/268F/324T. For example, human IgG1 Fcs comprising the G236A variant, which can optionally be combined with I332E, have been shown to increase the Fc γ IIA / Fc γ IIb binding affinity ratio approximately 15-fold. Richards et al. (2008) Mol. Cancer Therap. 7:2517; Moore et al. (2010) mAbs 2:181. Other modifications for enhancing Fc γ R and complement interactions include but are not limited to substitutions 298A, 333A, 334A, 326A, 247I, 339D, 339Q, 280H, 290S, 298D, 298V, 243L, 292P, 300L, 396L, 305I, and 396L. These and other modifications are reviewed in Strohl (2009) Current Opinion in Biotechnology 20:685-691. Specifically, both ADCC and CDC may be enhanced by changes at position E333 of IgG1, e.g. E333A. Shields et al. (2001) J. Biol. Chem. 276:6591. The use of P247I and A339D/Q mutations to enhance effector function in an IgG1 is disclosed in WO2006/020114, and D280H, K290S $\pm$ S298D/V is disclosed in WO2004/074455. The K326A/W and E333A/S variants have been shown to increase effector function in human IgG1, and E333S in IgG2. Idusogie et al. (2001) J. Immunol. 166:2571.

[0242] Specifically, the binding sites on human IgG1 for Fc γ R1, Fc γ RII, Fc γ RIII and Fc γ Rn have been mapped, and variants with improved binding have been described. Shields et al. (2001) J. Biol. Chem. 276:6591-6604. Specific mutations at positions 256, 290, 298, 333, 334 and 339 were shown to improve binding to Fc γ RIII, including the combination mutants T256A/S298A, S298A/E333A, S298A/K224A and S298A/E333A/K334A (having enhanced Fc γ RIIIa binding and ADCC activity). Other IgG1 variants with strongly enhanced binding to Fc γ RIIIa have been identified, including variants with S239D/I332E and S239D/I332E/A330L mutations which showed the greatest increase in affinity for Fc γ RIIIa, a decrease in Fc γ RIIb binding, and strong cytotoxic activity in cynomolgus monkeys. Lazar et al. (2006) Proc. Nat'l Acad. Sci. (USA) 103:4005; Awan et al. (2010) Blood 115:1204; Desjarlais & Lazar (2011) Exp. Cell Res. 317:1278. Introduction of the triple mutations into antibodies such as alemtuzumab (CD52-specific), trastuzumab (HER2/neu-specific), rituximab (CD20-specific), and cetuximab (EGFR-specific) translated into greatly enhanced ADCC activity *in vitro*, and the S239D/I332E variant showed an enhanced capacity to deplete B cells in monkeys. Lazar et al. (2006) Proc. Nat'l Acad. Sci. (USA) 103:4005. In addition, IgG1 mutants containing L235V, F243L, R292P, Y300L, V305I and P396L mutations which exhibited enhanced binding to Fc γ RIIIa and concomitantly enhanced ADCC activity in transgenic mice expressing human Fc γ RIIIa in models of B cell malignancies and breast cancer have been identified. Stavenhagen et al. (2007) Cancer Res. 67:8882; U.S. Pat. No. 8,652,466; Nordstrom et al. (2011) Breast Cancer Res. 13:R123.

[0243] Different IgG isotypes also exhibit differential CDC activity (IgG3>IgG1>>IgG2 $\approx$ IgG4). Dangi et al. (1988) EMBO J. 7:1989. For uses in which enhanced CDC is desired, it is also possible to introduce mutations that increase binding to C1q. The ability to recruit complement (CDC) may be enhanced by mutations at K326 and/or E333 in an IgG2, such as K326W (which reduces ADCC activity) and E333S, to increase binding to C1q, the first component of the complement cascade. Idusogie et al. (2001) J. Immunol. 166:2571. Introduction of S267E / H268F / S324T (alone or in any combination) into human IgG1 enhances C1q binding. Moore et al. (2010) mAbs 2:181. The Fc region of the IgG1/IgG3 hybrid isotype antibody "113F" of Natsume et al. (2008) Cancer Res. 68:3863 (figure 1 therein) also confers enhanced CDC. See also Michaelsen et al. (2009) Scand. J. Immunol. 70:553 and Redpath et al. (1998) Immunology 93:595.

[0244] Additional mutations that can increase or decrease effector function are disclosed at Dall'Acqua et al. (2006) J. Immunol. 177:1129. See also Carter (2006) Nat. Rev. Immunol. 6:343; Presta (2008) Curr. Op. Immunol. 20:460.

[0245] Fc variants that enhance affinity for the inhibitory receptor Fc γ RIIb may also be used, e.g. to enhance

apoptosis-inducing or adjuvant activity. Li & Ravetch (2011) *Science* 333:1030; Li & Ravetch (2012) *Proc. Nat'l Acad. Sci. (USA)* 109:10966; U.S. Pat. App. Pub. 2014/0010812. Such variants may provide an antibody with immunomodulatory activities related to FcγR11b⁺ cells, including for example B cells and monocytes. In one embodiment, the Fc variants provide selectively enhanced affinity to FcγR11b relative to one or more activating receptors. Modifications for altering binding to FcγR11b include one or more modifications at a position selected from the group consisting of 234, 235, 236, 237, 239, 266, 267, 268, 325, 326, 327, 328, and 332, according to the EU index. Exemplary substitutions for enhancing FcγR11b affinity include but are not limited to 234D, 234E, 234F, 234W, 235D, 235F, 235R, 235Y, 236D, 236N, 237D, 237N, 239D, 239E, 266M, 267D, 267E, 268D, 268E, 327D, 327E, 328F, 328W, 328Y, and 332E. Exemplary substitutions include 235Y, 236D, 239D, 266M, 267E, 268D, 268E, 328F, 328W, and 328Y. Other Fc variants for enhancing binding to FcγRIIb include 235Y/267E, 236D/267E, 239D/268D, 239D/267E, 267E/268D, 267E/268E, and 267E/328F. Specifically, the S267E, G236D, S239D, L328F and I332E variants, including the S267E + L328F double variant, of human IgG1 are of particular value in specifically enhancing affinity for the inhibitory FcγR11b receptor. Chu et al. (2008) *Mol. Immunol.* 45:3926; U.S. Pat. App. Pub. 2006/024298; WO 2012/087928. Enhanced specificity for FcγRIIb (as distinguished from FcγRIIa^{R131}) may be obtained by adding the P238D substitution. Mimoto et al. (2013) *Protein. Eng. Des. & Selection* 26:589; WO 2012/115241.

[0246] In certain embodiments, the antibody is modified to increase its biological half-life. Various approaches are possible. For example, this may be done by increasing the binding affinity of the Fc region for FcRn. In one embodiment, the antibody is altered within the CH1 or CL region to contain a salvage receptor binding epitope taken from two loops of a CH2 domain of an Fc region of an IgG, as described in U.S. Patent Nos. 5,869,046 and 6,121,022 by Presta et al. Other exemplary Fc variants that increase binding to FcRn and/or improve pharmacokinetic properties include substitutions at positions 259, 308, and 434, including for example 259I, 308F, 428L, 428M, 434S, 434H, 434P, 434Y, and 434M. Other variants that increase Fc binding to FcRn include: 250E, 250Q, 428L, 428F, 250Q/428L (Hinton et al., 2004, *J. Biol. Chem.* 279(8): 6213-6216, Hinton et al. 2006 *Journal of Immunology* 176:346-356), 256A, 272A, 305A, 307A, 311A, 312A, 378Q, 380A, 382A, 434A (Shields et al. *Journal of Biological Chemistry*, 2001, 276(9):6591-6604), 252F, 252Y, 252W, 254T, 256Q, 256E, 256D, 433R, 434F, 434Y, 252Y/254T/256E, 433K/434F/436H (Dall'Acqua et al. *Journal of Immunology*, 2002, 169:5171-5180, Dall'Acqua et al., 2006, *Journal of Biological Chemistry* 281:23514-23524). See U.S. Pat. No. 8,367,805.

[0247] Modification of certain conserved residues in IgG Fc (I253/H310/Q311/H433/N434), such as the N434A variant (Yeung et al. (2009) *J. Immunol.* 182:7663), has been proposed as a way to increase FcRn affinity, thus increasing the half-life of the antibody in circulation. WO 98/023289. The combination Fc variant comprising M428L and N434S has been shown to increase FcRn binding and increase serum half-life up to five-fold. Zalevsky et al. (2010) *Nat. Biotechnol.* 28:157. The combination Fc variant comprising T307A, E380A and N434A modifications also extends half-life of IgG1 antibodies. Petkova et al. (2006) *Int. Immunol.* 18:1759. In addition, combination Fc variants comprising M252Y/M428L, M428L/N434H, M428L/N434F, M428L/N434Y, M428L/N434A, M428L/N434M, and M428L/N434S variants have also been shown to extend half-life. WO 2009/086320.

[0248] Further, a combination Fc variant comprising M252Y, S254T and T256E, increases half-life-nearly 4-fold. Dall'Acqua et al. (2006) *J. Biol. Chem.* 281:23514. A related IgG1 modification providing increased FcRn affinity but reduced pH dependence (M252Y / S254T / T256E / H433K / N434F) has been used to create an IgG1 construct ("MST-HN Abdeg") for use as a competitor to prevent binding of *other* antibodies to FcRn, resulting in increased clearance of that *other* antibody, either endogenous IgG (e.g. in an autoimmune setting) or another exogenous (therapeutic) mAb. Vaccaro et al. (2005) *Nat. Biotechnol.* 23:1283; WO 2006/130834.

[0249] Other modifications for increasing FcRn binding are described in Yeung et al. (2010) *J. Immunol.* 182:7663-7671; 6,277,375; 6,821,505; WO 97/34631; WO 2002/060919.

[0250] In certain embodiments, hybrid IgG isotypes may be used to increase FcRn binding, and potentially increase half-life. For example, an IgG1/IgG3 hybrid variant may be constructed by substituting IgG1 positions in the CH2 and/or CH3 region with the amino acids from IgG3 at positions where the two isotypes differ. Thus a hybrid variant IgG antibody may be constructed that comprises one or more substitutions, e.g., 274Q, 276K, 300F, 339T, 356E, 358M, 384S, 392N, 397M, 422I, 435R, and 436F. In other embodiments described herein, an IgG1/IgG2 hybrid variant may be constructed by substituting IgG2 positions in the CH2 and/or CH3 region with amino acids from IgG1 at positions where the two isotypes differ. Thus a hybrid variant IgG antibody may be constructed that comprises one or more

substitutions, e.g., one or more of the following amino acid substitutions: 233E, 234L, 235L, -236G (referring to an insertion of a glycine at position 236), and 327A. See U.S. Pat. No. 8,629,113. A hybrid of IgG1/IgG2/IgG4 sequences has been generated that purportedly increases serum half-life and improves expression. U.S. Pat. No. 7,867,491 (sequence number 18 therein).

[0251] The serum half-life of the antibodies of the present invention can also be increased by pegylation. An antibody can be pegylated to, for example, increase the biological (e.g., serum) half-life of the antibody. To pegylate an antibody, the antibody, or fragment thereof, typically is reacted with a polyethylene glycol (PEG) reagent, such as a reactive ester or aldehyde derivative of PEG, under conditions in which one or more PEG groups become attached to the antibody or antibody fragment. Preferably, the pegylation is carried out via an acylation reaction or an alkylation reaction with a reactive PEG molecule (or an analogous reactive water-soluble polymer). As used herein, the term "polyethylene glycol" is intended to encompass any of the forms of PEG that have been used to derivatize other proteins, such as mono (C1-C10) alkoxy- or aryloxy-polyethylene glycol or polyethylene glycol-maleimide. In certain embodiments, the antibody to be pegylated is an aglycosylated antibody. Methods for pegylating proteins are known in the art and can be applied to the antibodies described herein. See for example, EP 0154316 by Nishimura et al. and EP 0401384 by Ishikawa et al.

[0252] Alternatively, under some circumstances it may be desirable to decrease the half-life of an antibody, rather than increase it. Modifications such as I253A (Hornick et al. (2000) J. Nucl. Med. 41:355) and H435A/R I253A or H310A (Kim et al. (2000) Eur. J. Immunol. 29:2819) in Fc of human IgG1 can decrease FcRn binding, thus decreasing half-life (increasing clearance) for use in situations where rapid clearance is preferred, such as medical imaging. See also Kenanova et al. (2005) Cancer Res. 65:622. Other means to enhance clearance include formatting the antigen binding domains of the present invention as antibody fragments lacking the ability to bind FcRn, such as Fab fragments. Such modification can reduce the circulating half-life of an antibody from a couple of weeks to a matter of hours. Selective PEGylation of antibody fragments can then be used to fine-tune (increase) the half-life of the antibody fragments if necessary. Chapman et al. (1999) Nat. Biotechnol. 17:780. Antibody fragments may also be fused to human serum albumin, e.g. in a fusion protein construct, to increase half-life. Yeh et al. (1992) Proc. Nat'l Acad. Sci. 89:1904. Alternatively, a bispecific antibody may be constructed with a first antigen binding domain of the present invention and a second antigen binding domain that binds to human serum albumin (HSA). See Int'l Pat. Appl. Pub. WO 2009/127691 and patent references cited therein. Alternatively, specialized polypeptide sequences can be added to antibody fragments to increase half-life, e.g. "XTEN" polypeptide sequences. Schellenberger et al. (2009) Nat. Biotechnol. 27:1186; Int'l Pat. Appl. Pub. WO 2010/091122.

Additional Fc Variants

[0253] When using an IgG4 constant domain, it is preferable to include the substitution S228P, which mimics the hinge sequence in IgG1 and thereby stabilizes IgG4 molecules, e.g. reducing Fab-arm exchange between the therapeutic antibody and endogenous IgG4 in the patient being treated. Labrijn et al. (2009) Nat. Biotechnol. 27:767; Reddy et al. (2000) J. Immunol. 164:1925.

[0254] A potential protease cleavage site in the hinge of IgG1 constructs can be eliminated by D221G and K222S modifications, increasing the stability of the antibody. WO 2014/043344.

[0255] The affinities and binding properties of an Fc variant for its ligands (Fc receptors) may be determined by a variety of *in vitro* assay methods (biochemical or immunological based assays) known in the art including but not limited to, equilibrium methods (e.g., enzyme-linked immunoabsorbent assay (ELISA), or radioimmunoassay (RIA)), or kinetics (e.g., BIACORE® SPR analysis), and other methods such as indirect binding assays, competitive inhibition assays, fluorescence resonance energy transfer (FRET), gel electrophoresis and chromatography (e.g., gel filtration). These and other methods may utilize a label on one or more of the components being examined and/or employ a variety of detection methods including but not limited to chromogenic, fluorescent, luminescent, or isotopic labels. A detailed description of binding affinities and kinetics can be found in Paul, W. E., ed., Fundamental Immunology, 4th Ed., Lippincott-Raven, Philadelphia (1999), which focuses on antibody-immunogen interactions.

[0256] In still other embodiments, the glycosylation of an antibody is modified to increase or decrease effector function.

For example, an aglycosylated antibody can be made that lacks all effector function by mutating the conserved asparagine residue at position 297 (e.g. N297A), thus abolishing complement and FcγRI binding. Bolt et al. (1993) Eur. J. Immunol. 23:403. See also Tao & Morrison (1989) J. Immunol. 143:2595 (using N297Q in IgG1 to eliminate glycosylation at position 297).

[0257] Although aglycosylated antibodies generally lack effector function, mutations can be introduced to restore that function. Aglycosylated antibodies, e.g. those resulting from N297A/C/D/or H mutations or produced in systems (e.g. *E. coli*) that do not glycosylate proteins, can be further mutated to restore FcγR binding, e.g. S298G and/or T299A/G/or H (WO 2009/079242), or E382V and M428I (Jung et al. (2010) Proc. Nat'l Acad. Sci (USA) 107:604).

[0258] Additionally, an antibody with enhanced ADCC can be made by altering glycosylation. For example, removal of fucose from heavy chain Asn297-linked oligosaccharides has been shown to enhance ADCC, based on improved binding to FcγRIIIa. Shields et al. (2002) JBC 277:26733; Niwa et al. (2005) J. Immunol. Methods 306: 151; Cardarelli et al. (2009) Clin. Cancer Res. 15:3376 (MDX-1401); Cardarelli et al. (2010) Cancer Immunol. Immunotherap. 59:257 (MDX-1342). Such low fucose antibodies may be produced, e.g., in knockout Chinese hamster ovary (CHO) cells lacking fucosyltransferase (*FUT8*) (Yamane-Ohnuki et al. (2004) Biotechnol. Bioeng. 87:614), or in other cells that generate afucosylated antibodies. See, e.g., Zhang et al. (2011) mAbs 3:289 and Li et al. (2006) Nat. Biotechnol. 24:210 (both describing antibody production in glycoengineered *Pichia pastoris*.); Mossner et al. (2010) Blood 115:4393; Shields et al. (2002) J. Biol. Chem. 277:26733; Shinkawa et al. (2003) J. Biol. Chem. 278:3466; EP 1176195B1. ADCC can also be enhanced as described in PCT Publication WO 03/035835, which discloses use of a variant CHO cell line, Lec13, with reduced ability to attach fucose to Asn(297)-linked carbohydrates, also resulting in hypofucosylation of antibodies expressed in that host cell (see also Shields, R.L. et al. (2002) J. Biol. Chem. 277:26733-26740). Alternatively, fucose analogs may be added to culture medium during antibody production to inhibit incorporation of fucose into the carbohydrate on the antibody (see, e.g., WO 2009/135181).

[0259] Increasing bisecting GlcNAc structures in antibody-linked oligosaccharides also enhances ADCC. PCT Publication WO 99/54342 by Umana et al. describes cell lines engineered to express glycoprotein-modifying glycosyl transferases (e.g., beta(1,4)-N-acetylglucosaminyltransferase III (GnTIII)) such that antibodies expressed in the engineered cell lines exhibit increased bisecting GlcNAc structures which results in increased ADCC activity of the antibodies (see also Umana et al. (1999) Nat. Biotech. 17:176-180).

[0260] Additional glycosylation variants have been developed that are devoid of galactose, sialic acid, fucose and xylose residues (so-called GNGN glycoforms), which exhibit enhanced ADCC and ADCP but decreased CDC, as well as others that are devoid of sialic acid, fucose and xylose (so-called G1/G2 glycoforms), which exhibit enhanced ADCC, ADCP and CDC. U.S. Pat. App. Pub. No. 2013/0149300. Antibodies having these glycosylation patterns are optionally produced in genetically modified *N. benthamiana* plants in which the endogenous xylosyl and fucosyl transferase genes have been knocked-out.

[0261] Glycoengineering can also be used to modify the anti-inflammatory properties of an IgG construct by changing the α2,6 sialyl content of the carbohydrate chains attached at Asn297 of the Fc regions, wherein an increased proportion of α2,6 sialylated forms results in enhanced anti-inflammatory effects. See Nimmerjahn et al. (2008) Ann. Rev. Immunol. 26:513. Conversely, reduction in the proportion of antibodies having α2,6 sialylated carbohydrates may be useful in cases where anti-inflammatory properties are not wanted. Methods of modifying α2,6 sialylation content of antibodies, for example by selective purification of α2,6 sialylated forms or by enzymatic modification, are provided at U.S. Pat. Appl. Pub. No. 2008/0206246. In other embodiments, the amino acid sequence of the Fc region may be modified to mimic the effect of α2,6 sialylation, for example by inclusion of an F241A modification (see, e.g., WO 2013/095966).

VIII. Antibody Physical Properties

[0262] Antibodies described herein can contain one or more glycosylation sites in either the light or heavy chain variable region. Such glycosylation sites may result in increased immunogenicity of the antibody or an alteration of the pK of the antibody due to altered antigen binding (Marshall et al (1972) Annu Rev Biochem 41:673-702; Gala and Morrison (2004) J. Immunol 172:5489-94; Wallick et al (1988) J ExpMed 168:1099-109; Spiro (2002) Glycobiology

12:43R-56R; Parekh et al (1985) Nature 316:452-7; Mimura et al. (2000) Mol Immunol 37:697-706). Glycosylation has been known to occur at motifs containing an N-X-S/T sequence. In some some embodiments, the anti-OX40 antibody does not contain variable region glycosylation. This can be achieved either by selecting antibodies that do not contain the glycosylation motif in the variable region or by mutating residues within the glycosylation region.

[0263] In certain embodiments, the antibodies described herein do not contain asparagine isomerism sites. The deamidation of asparagine may occur on N-G or D-G sequences and result in the creation of an isoaspartic acid residue that introduces a kink into the polypeptide chain and decreases its stability (isoaspartic acid effect). For instance, if the amino acid sequence Asp-Gly is present in the heavy and/or light chain CDR sequences of the antibody, the sequence is substituted with an amino acid sequence that does not undergo isomerization.

[0264] The antibody comprises the heavy chain variable region CDR2 sequence set forth in SEQ ID NO: 88, but wherein the Gly in the Asp-Gly sequence (AIDT DGGTFYADSVRG; SEQ ID NO: 88) is replaced with an amino acid sequence that does not undergo isomerization, i.e. Asp-Ala.

[0265] Each antibody will have a unique isoelectric point (pI), which generally falls in the pH range between 6 and 9.5. The pI for an IgG1 antibody typically falls within the pH range of 7-9.5 and the pI for an IgG4 antibody typically falls within the pH range of 6-8. There is speculation that antibodies with a pI outside the normal range may have some unfolding and instability under in vivo conditions. Thus, it is preferred to have an anti-OX40 antibody that contains a pI value that falls in the normal range. This can be achieved either by selecting antibodies with a pI in the normal range or by mutating charged surface residues.

[0266] Each antibody will have a characteristic melting temperature, with a higher melting temperature indicating greater overall stability in vivo (Krishnamurthy R and Manning M C (2002) Curr Pharm Biotechnol 3:361-71). Generally, it is preferred that the T_{M1} (the temperature of initial unfolding) be greater than 60° C, preferably greater than 65° C., even more preferably greater than 70° C. The melting point of an antibody can be measured using differential scanning calorimetry (Chen et al (2003) Pharm Res 20:1952-60; Ghirlando et al (1999) Immunol Lett 68:47-52) or circular dichroism (Murray et al. (2002) J. Chromatogr Sci 40:343-9). In a preferred embodiment, antibodies are selected that do not degrade rapidly. Degradation of an antibody can be measured using capillary electrophoresis (CE) and MALDI-MS (Alexander A J and Hughes D E (1995) Anal Chem 67:3626-32). In certain embodiments, the anti-OX40 antibodies disclosed herein (e.g., the OX40.21 antibody) have increased stability.

[0267] Accordingly, in other embodiments, antibodies are selected that have minimal aggregation effects, which can lead to the triggering of an unwanted immune response and/or altered or unfavorable pharmacokinetic properties. Generally, antibodies are acceptable with aggregation of 25% or less, preferably 20% or less, even more preferably 15% or less, even more preferably 10% or less and even more preferably 5% or less. Aggregation can be measured by several techniques, including size-exclusion column (SEC), high performance liquid chromatography (HPLC), and light scattering.

IX. Methods of Engineering Antibodies

[0268] As discussed herein, the anti-OX40 antibodies can be used to create new anti-OX40 antibodies by modifying the constant region(s) of the antibodies. Thus, in another embodiment, the structural features of anti-OX40 antibodies described herein are used to create structurally related anti-OX40 antibodies that retain at least one functional property of the antibodies described herein, such as binding to human OX40 and cynomolgus OX40.

[0269] Mutational methods have been described in the art. For example, PCT Publication WO 02/092780 by Short describes methods for creating and screening antibody mutations using saturation mutagenesis, synthetic ligation assembly, or a combination thereof. Alternatively, PCT Publication WO 03/074679 by Lazar et al. describes methods of using computational screening methods to optimize physiochemical properties of antibodies.

X. Nucleic Acid Molecules

[0270] Also provided herein are nucleic acid molecules that encode the antibodies described herein. The nucleic acids may be present in whole cells, in a cell lysate, or in a partially purified or substantially pure form. A nucleic acid is "isolated" or "rendered substantially pure" when purified away from other cellular components or other contaminants, e.g., other cellular nucleic acids (e.g., other chromosomal DNA, e.g., the chromosomal DNA that is linked to the isolated DNA in nature) or proteins, by standard techniques, including alkaline/SDS treatment, CsCl banding, column chromatography, restriction enzymes, agarose gel electrophoresis and others well known in the art. See, F. Ausubel, et al., ed. (1987) Current Protocols in Molecular Biology, Greene Publishing and Wiley Interscience, New York. A nucleic acid can be, for example, DNA or RNA and may or may not contain intronic sequences. In a certain embodiments, the nucleic acid is a cDNA molecule.

[0271] Nucleic acids provided herein can be obtained using standard molecular biology techniques. For antibodies expressed by hybridomas (e.g., hybridomas prepared from transgenic mice carrying human immunoglobulin genes as described further below), cDNAs encoding the light and heavy chains of the antibody made by the hybridoma can be obtained by standard PCR amplification or cDNA cloning techniques. For antibodies obtained from an immunoglobulin gene library (e.g., using phage display techniques), nucleic acid encoding the antibody can be recovered from the library.

An exemplary DNA sequence encoding the VH sequence of the claimed antibodies is set forth in SEQ ID NO: 176. An exemplary DNA sequence encoding the light chain sequence of the claimed antibodies is set forth in SEQ ID NO: 168.

[0272] Methods for making the anti-OX40 antibodies provided herein can include expressing the heavy chain and the light chains in a cell line comprising the nucleotide sequences encoding the heavy and light chains with a signal peptide. Host cells comprising these nucleotide sequences are also provided herein.

[0273] Once DNA fragments encoding VH and VL segments are obtained, these DNA fragments can be further manipulated by standard recombinant DNA techniques, for example 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 term "operatively linked", as used in this context, refers to the joining of the two DNA fragments such that the amino acid sequences they encode remain in-frame.

[0274] The isolated DNA encoding the VH region can be converted to a full-length heavy chain gene by operatively linking the VH-encoding DNA to another DNA molecule encoding heavy chain constant regions (hinge, CH1, CH2 and/or CH3). The sequences of human heavy chain constant region genes are known in the art (see e.g., Kabat, E. A., et al. (1991) Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242) 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, for example, an IgG1 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 constant region.

[0275] The isolated DNA encoding the VL region 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, E. A., et al. (1991) Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242) and DNA fragments encompassing these regions can be obtained by standard PCR amplification. The light chain constant region can be a kappa or lambda constant region.

[0276] To create a scFv gene, the VH- and VL-encoding DNA fragments are operatively linked to another fragment encoding a flexible linker, e.g., encoding the amino acid sequence (Gly₄ - Ser)₃, such that the VH and VL sequences can be expressed as a contiguous single-chain protein, with the VL and VH regions joined by the flexible linker (see e.g., Bird et al. (1988) Science 242:423-426; Huston et al. (1988) Proc. Natl. Acad. Sci. USA 85:5879-5883; McCafferty et al., (1990) Nature 348:552-554).

[0277] Also provided herein are non-claimed nucleic acid molecules encoding VH and VL sequences that are homologous to those of the 3F4, 14B6-1, 14B6-2, 23H3, 6E1-1, 6E1-2, 18E9, 8B11, 20B3, 14A2-1, 14A2-2, and 20C1 monoclonal antibodies. Exemplary nucleic acid molecules encode VH and VL sequences that are at least 70% identical,

for example, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% identical, to nucleic acid molecules encoding the VH and VL sequences of the 3F4, 14B6-1, 14B6-2, 23H3, 6E1-1, 6E1-2, 18E9, 8B11, 20B3, 14A2-1, 14A2-2, and 20C1 monoclonal antibodies. Also provided herein are nucleic acid molecules with conservative substitutions (i.e., substitutions that do not alter the resulting amino acid sequence upon translation of nucleic acid molecule), e.g., for codon optimization.

XI. Antibody Generation

[0278] Anti-OX40 antibodies described herein can be produced using a variety of known techniques, such as the standard somatic cell hybridization technique described by Kohler and Milstein, *Nature* 256: 495 (1975). Although somatic cell hybridization procedures are preferred, in principle, other techniques for producing monoclonal antibodies also can be employed, e.g., viral or oncogenic transformation of B lymphocytes, phage display technique using libraries of human antibody genes.

[0279] The preferred animal system for preparing hybridomas is the murine system. Hybridoma production in the mouse is a very well-established procedure. Immunization protocols and techniques for isolation of immunized splenocytes for fusion are known in the art. Fusion partners (e.g., murine myeloma cells) and fusion procedures are also known.

[0280] Chimeric or humanized antibodies described herein can be prepared based on the sequence of a murine monoclonal antibody prepared as described above. DNA encoding the heavy and light chain immunoglobulins can be obtained from the murine hybridoma of interest and engineered to contain non-murine (e.g., human) immunoglobulin sequences using standard molecular biology techniques. For example, to create a chimeric antibody, the murine variable regions can be linked to human constant regions using methods known in the art (see e.g., U.S. Patent No. 4,816,567 to Cabilly et al.). To create a humanized antibody, the murine CDR regions can be inserted into a human framework using methods known in the art (see e.g., U.S. Patent No. 5,225,539 to Winter, and U.S. Patent Nos. 5,530,101; 5,585,089; 5,693,762 and 6,180,370 to Queen et al.).

[0281] In one embodiment, the antibodies described herein are human monoclonal antibodies. Such human monoclonal antibodies directed against OX40 can be generated using transgenic or transchromosomal mice carrying parts of the human immune system rather than the mouse system. These transgenic and transchromosomal mice include mice referred to herein as HuMAb mice and KM mice, respectively, and are collectively referred to herein as "human Ig mice."

[0282] The HuMAb mouse[®] (Medarex, Inc.) contains human immunoglobulin gene miniloci that encode unrearranged human heavy (μ and γ) and κ light chain immunoglobulin sequences, together with targeted mutations that inactivate the endogenous μ and κ chain loci (see e.g., Lonberg, et al. (1994) *Nature* 368(6474): 856-859). Accordingly, the mice exhibit reduced expression of mouse IgM or κ , and in response to immunization, the introduced human heavy and light chain transgenes undergo class switching and somatic mutation to generate high affinity human IgGk monoclonal (Lonberg, N. *et al.* (1994), *supra*; reviewed in Lonberg, N. (1994) *Handbook of Experimental Pharmacology* 113:49-101; Lonberg, N. and Huszar, D. (1995) *Intern. Rev. Immunol.* 13: 65-93, and Harding, F. and Lonberg, N. (1995) *Ann. N.Y. Acad. Sci.* 764:536-546). The preparation and use of HuMAb mice, and the genomic modifications carried by such mice, is further described in Taylor, L. et al. (1992) *Nucleic Acids Research* 20:6287-6295; Chen, J. et al. (1993) *International Immunology* 5: 647-656; Tuailon et al. (1993) *Proc. Natl. Acad. Sci. USA* 90:3720-3724; Choi et al. (1993) *Nature Genetics* 4:117-123; Chen, J. et al. (1993) *EMBO J.* 12: 821-830; Tuailon et al. (1994) *J. Immunol.* 152:2912-2920; Taylor, L. et al. (1994) *International Immunology* 6: 579-591; and Fishwild, D. et al. (1996) *Nature Biotechnology* 14: 845-851. See further, U.S. Patent Nos. 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,789,650; 5,877,397; 5,661,016; 5,814,318; 5,874,299; and 5,770,429; all to Lonberg and Kay; U.S. Patent No. 5,545,807 to Surani et al.; PCT Publication Nos. WO 92/03918, WO 93/12227, WO 94/25585, WO 97/13852, WO 98/24884 and WO 99/45962, all to Lonberg and Kay; and PCT Publication No. WO 01/14424 to Korman et al.

[0283] In certain embodiments, antibodies described herein are raised using a mouse that carries human immunoglobulin sequences on transgenes and transchromosomes, such as a mouse that carries a human heavy chain transgene and a human light chain transchromosome. Such mice, referred to herein as "KM mice", are described in

detail in PCT Publication WO 02/43478 to Ishida et al.

[0284] Still further, alternative transgenic animal systems expressing human immunoglobulin genes are available in the art and can be used to raise anti-OX40 antibodies described herein. For example, an alternative transgenic system referred to as the Xenomouse (Abgenix, Inc.) can be used; such mice are described in, for example, U.S. Patent Nos. 5,939,598; 6,075,181; 6,114,598; 6,150,584 and 6,162,963 to Kucherlapati et al.

[0285] Moreover, alternative transchromosomal animal systems expressing human immunoglobulin genes are available in the art and can be used to raise anti-OX40 antibodies described herein. For example, mice carrying both a human heavy chain transchromosome and a human light chain transchromosome, referred to as "TC mice" can be used; such mice are described in Tomizuka et al. (2000) Proc. Natl. Acad. Sci. USA 97:722-727. Furthermore, cows carrying human heavy and light chain transchromosomes have been described in the art (Kuroiwa et al. (2002) Nature Biotechnology 20:889-894) and can be used to raise anti-OX40 antibodies described herein.

[0286] Additional mouse systems described in the art for raising human antibodies, e.g., human anti-OX40 antibodies, include (i) the VelocImmune[®] mouse (Regeneron Pharmaceuticals, Inc.), in which the endogenous mouse heavy and light chain variable regions have been replaced, via homologous recombination, with human heavy and light chain variable regions, operatively linked to the endogenous mouse constant regions, such that chimeric antibodies (human V/mouse C) are raised in the mice, and then subsequently converted to fully human antibodies using standard recombinant DNA techniques; and (ii) the MeMo[®] mouse (Merus Biopharmaceuticals, Inc.), in which the mouse contains unrearranged human heavy chain variable regions but a single rearranged human common light chain variable region. Such mice, and use thereof to raise antibodies, are described in, for example, WO 2009/15777, US 2010/0069614, WO 2011/072204, WO 2011/097603, WO 2011/163311, WO 2011/163314, WO 2012/148873, US 2012/0070861 and US 2012/0073004.

[0287] Human monoclonal antibodies described herein can also be prepared using phage display methods for screening libraries of human immunoglobulin genes. Such phage display methods for isolating human antibodies are established in the art. See for example: U.S. Patent Nos. 5,223,409; 5,403,484; and 5,571,698 to Ladner et al.; U.S. Patent Nos. 5,427,908 and 5,580,717 to Dower et al.; U.S. Patent Nos. 5,969,108 and 6,172,197 to McCafferty et al.; and U.S. Patent Nos. 5,885,793; 6,521,404; 6,544,731; 6,555,313; 6,582,915 and 6,593,081 to Griffiths et al.

[0288] Human monoclonal antibodies described herein can also be prepared using SCID mice into which human immune cells have been reconstituted such that a human antibody response can be generated upon immunization. Such mice are described in, for example, U.S. Patent Nos. 5,476,996 and 5,698,767 to Wilson et al.

Immunizations

[0289] To generate fully human antibodies to OX40, transgenic or transchromosomal mice containing human immunoglobulin genes (e.g., HCo12, HCo7 or KM mice) can be immunized with a purified or enriched preparation of the OX40 antigen and/or cells expressing OX40 or fragment thereof, as described for other antigens, for example, by Lonberg et al. (1994) Nature 368(6474): 856-859; Fishwild et al. (1996) Nature Biotechnology 14: 845-851 and WO 98/24884. Alternatively, mice can be immunized with DNA encoding human OX40 or fragment thereof. Preferably, the mice will be 6-16 weeks of age upon the first infusion. For example, a purified or enriched preparation (5-50 µg) of the recombinant OX40 antigen can be used to immunize the HuMAb mice intraperitoneally. In the event that immunizations using a purified or enriched preparation of the OX40 antigen do not result in antibodies, mice can also be immunized with cells expressing OX40, e.g., a cell line, to promote immune responses. Exemplary cell lines include OX40-overexpressing stable CHO and Raji cell lines.

[0290] Cumulative experience with various antigens has shown that the HuMAb transgenic mice respond best when initially immunized intraperitoneally (IP) or subcutaneously (SC) with antigen in Ribi's adjuvant, followed by every other week IP/SC immunizations (up to a total of 10) with antigen in Ribi's adjuvant. The immune response can be monitored over the course of the immunization protocol with plasma samples being obtained by retroorbital bleeds. The plasma can be screened by ELISA and FACS (as described below), and mice with sufficient titers of anti-OX40 human immunoglobulin can be used for fusions. Mice can be boosted intravenously with antigen 3 days before sacrifice and

removal of the spleen and lymph nodes. It is expected that 2-3 fusions for each immunization may need to be performed. Between 6 and 24 mice are typically immunized for each antigen. Usually, HCo7, HCo12, and KM strains are used. In addition, both HCo7 and HCo12 transgene can be bred together into a single mouse having two different human heavy chain transgenes (HCo7/HCo12).

Generation of Hybridomas Producing Monoclonal Antibodies to OX40

[0291] To generate hybridomas producing the antibodies described herein, splenocytes and/or lymph node cells from immunized mice can be isolated and fused to an appropriate immortalized cell line, such as a mouse myeloma cell line. The resulting hybridomas can be screened for the production of antigen-specific antibodies. For example, single cell suspensions of splenic lymphocytes from immunized mice can be fused to Sp2/0 nonsecreting mouse myeloma cells (ATCC, CRL 1581) with 50% PEG. Cells are plated at approximately 2×10^5 in flat bottom microtiter plate, followed by a two week incubation in selective medium containing 10% fetal Clone Serum, 18% "653" conditioned media, 5% origen (IGEN), 4 mM L-glutamine, 1 mM sodium pyruvate, 5mM HEPES, 0.055 mM 2-mercaptoethanol, 50 units/ml penicillin, 50 mg/ml streptomycin, 50 mg/ml gentamycin and 1X HAT (Sigma). After approximately two weeks, cells can be cultured in medium in which the HAT is replaced with HT. Individual wells can then be screened by ELISA for human monoclonal IgM and IgG antibodies. Once extensive hybridoma growth occurs, medium can be observed usually after 10-14 days. The antibody secreting hybridomas can be replated, screened again, and if still positive for human IgG, the monoclonal antibodies can be subcloned at least twice by limiting dilution. The stable subclones can then be cultured *in vitro* to generate small amounts of antibody in tissue culture medium for characterization.

[0292] To purify the antibodies, selected hybridomas can be grown in two-liter spinner-flasks for monoclonal antibody purification. Supernatants can be filtered and concentrated before affinity chromatography with protein A-sepharose (Pharmacia, Piscataway, N.J.). Eluted IgG can be checked by gel electrophoresis and high performance liquid chromatography to ensure purity. The buffer solution can be exchanged into PBS, and the concentration can be determined by OD280 using 1.43 extinction coefficient. The antibodies can then be aliquoted and stored at -80° C.

Generation of Transfectomas Producing Monoclonal Antibodies to OX40

[0293] Antibodies can be produced in a host cell transfectoma using, for example, a combination of recombinant DNA techniques and gene transfection methods as is well known in the art (Morrison, S. (1985) Science 229:1202).

[0294] For example, to express antibodies, or antibody fragments thereof, DNAs encoding partial or full-length light and heavy chains, can be obtained by standard molecular biology techniques (e.g., PCR amplification or cDNA cloning using a hybridoma that expresses the antibody of interest) and the DNAs can be inserted into expression vectors such that the genes are operatively linked to transcriptional and translational control sequences. In this context, the term "operatively linked" is intended to mean that an antibody gene is ligated into a vector such that transcriptional and translational control sequences within the vector serve their intended function of regulating the transcription and translation of the antibody gene. The expression vector and expression control sequences are chosen to be compatible with the expression host cell used. The antibody light chain gene and the antibody heavy chain gene can be inserted into separate vector or both genes are inserted into the same expression vector. The antibody genes are inserted into the expression vector(s) by standard methods (e.g., ligation of complementary restriction sites on the antibody gene fragment and vector, or blunt end ligation if no restriction sites are present). The light and heavy chain variable regions of the antibodies described herein can be used to create full-length antibody genes of any antibody isotype by inserting them into expression vectors already encoding heavy chain constant and light chain constant regions of the desired isotype such that the V_H segment is operatively linked to the C_H segment(s) within the vector and the V_L segment is operatively linked to the C_L segment within the vector.

[0295] Additionally or alternatively, the recombinant expression vector can encode a signal peptide that facilitates secretion of the antibody chain from a host cell. The antibody chain gene can be cloned into the vector such that the signal peptide is linked in-frame to the amino terminus of the antibody chain gene. The signal peptide can be an immunoglobulin signal peptide or a heterologous signal peptide (*i.e.*, a signal peptide from a non-immunoglobulin

protein). Exemplary signal sequences for use in antibody heavy and light chains include the signal sequences originally found in the anti-OX40 antibodies described herein.

[0296] In addition to the antibody chain genes, recombinant expression vectors may carry regulatory sequences that control the expression of the antibody chain genes in a host cell. The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (e.g., polyadenylation signals) that control the transcription or translation of 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)). It will be appreciated by those skilled in the art that 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, the level of expression of protein desired, etc. Preferred 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), Simian Virus 40 (SV40), adenovirus, (e.g., the adenovirus major late promoter (AdMLP) and polyoma. Alternatively, nonviral regulatory sequences may be used, such as the ubiquitin promoter or β -globin promoter. Still further, regulatory elements composed of sequences from different sources, such as the SR α promoter system, which contains sequences from the SV40 early promoter and the long terminal repeat of human T cell leukemia virus type 1 (Takebe, Y. et al. (1988) Mol. Cell. Biol. 8:466-472).

[0297] In addition to the antibody chain genes and regulatory sequences, recombinant expression vectors may carry additional sequences, such as sequences that regulate replication of the vector in host cells (e.g., origins of replication) and selectable marker genes. The selectable marker gene facilitates selection of host cells into which the vector has been introduced (see, e.g., U.S. Pat. Nos. 4,399,216, 4,634,665 and 5,179,017, all by Axel et al.). For example, typically the selectable marker gene confers resistance to drugs, such as G418, hygromycin or methotrexate, on a host cell into which the vector has been introduced. Preferred selectable marker genes include the dihydrofolate reductase (DHFR) gene (for use in dhfr- host cells with methotrexate selection/amplification) and the neo gene (for G418 selection).

[0298] For expression of the light and heavy chains, the expression vector(s) encoding the heavy and light chains is transfected into a host cell by standard techniques. The various forms of the term "transfection" are intended to encompass a wide variety of techniques commonly used for the introduction of exogenous DNA into a prokaryotic or eukaryotic host cell, e.g., electroporation, calcium-phosphate precipitation, DEAE-dextran transfection and the like. Although it is theoretically possible to express the antibodies described herein in either prokaryotic or eukaryotic host cells, expression of antibodies in eukaryotic cells, and most preferably mammalian host cells, is the most preferred because such eukaryotic cells, and in particular mammalian cells, are more likely than prokaryotic cells to assemble and secrete a properly folded and immunologically active antibody. Prokaryotic expression of antibody genes has been reported to be ineffective for production of high yields of active antibody (Boss, M. A. and Wood, C. R. (1985) Immunology Today 6:12-13). The antibodies disclosed herein can also be produced in glycoengineered strains of the yeast *Pichia pastoris*. Li et al. (2006) Nat. Biotechnol. 24:210.

[0299] Preferred mammalian host cells for expressing the recombinant antibodies described herein 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 R. J. Kaufman and P. A. Sharp (1982) Mol. Biol. 159:601-621), NSO myeloma cells, COS cells and SP2 cells. In particular, for use with NSO myeloma cells, another preferred expression system is the GS gene expression system disclosed in WO 87/04462, WO 89/01036 and EP 338,841. 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, more preferably, secretion of the antibody into the culture medium in which the host cells are grown. Antibodies can be recovered from the culture medium using standard protein purification methods.

[0300] The N- and C-termini of antibody polypeptide chains of the present invention may differ from the expected sequence due to commonly observed post-translational modifications. For example, C-terminal lysine residues are often missing from antibody heavy chains. Dick et al. (2008) Biotechnol. Bioeng. 100:1132. N-terminal glutamine residues, and to a lesser extent glutamate residues, are frequently converted to pyroglutamate residues on both light and heavy chains of therapeutic antibodies. Dick et al. (2007) Biotechnol. Bioeng. 97:544; Liu et al. (2011) JBC 286:11211; Liu et al. (2011) J. Biol. Chem. 286:11211.

XII. Assays

[0301] Anti-OX40 antibodies described herein can be tested for binding to OX40 by, for example, standard ELISA. Briefly, microtiter plates are coated with purified OX40 at 1-2 µg/ml in PBS, and then blocked with 5% bovine serum albumin in PBS. Dilutions of antibody (e.g., dilutions of plasma from OX40-immunized mice) are added to each well and incubated for 1-2 hours at 37°C. The plates are washed with PBS/Tween and then incubated with secondary reagent (e.g., for human antibodies, a goat-anti-human IgG Fc-specific polyclonal reagent) conjugated to horseradish peroxidase (HRP) for 1 hour at 37°C. After washing, the plates are developed with ABTS substrate (Moss Inc, product: ABTS-1000) and analyzed by a spectrophotometer at OD 415-495. Sera from immunized mice are then further screened by flow cytometry for binding to a cell line expressing human OX40, but not to a control cell line that does not express OX40. Briefly, the binding of anti-OX40 antibodies is assessed by incubating OX40 expressing CHO cells with the anti-OX40 antibody at 1:20 dilution. The cells are washed and binding is detected with a PE-labeled anti-human IgG Ab. Flow cytometric analyses are performed using a FACScan flow cytometry (Becton Dickinson, San Jose, CA). Preferably, mice which develop the highest titers will be used for fusions.

[0302] An ELISA assay as described above can be used to screen for antibodies and, thus, hybridomas that produce antibodies that show positive reactivity with the OX40 immunogen. Hybridomas that produce antibodies that bind, preferably with high affinity, to OX40 can then be subcloned and further characterized. One clone from each hybridoma, which retains the reactivity of the parent cells (by ELISA), can then be chosen for making a cell bank, and for antibody purification.

[0303] To purify anti-OX40 antibodies, selected hybridomas can be grown in two-liter spinner-flasks for monoclonal antibody purification. Supernatants can be filtered and concentrated before affinity chromatography with protein A-sepharose (Pharmacia, Piscataway, NJ). Eluted IgG can be checked by gel electrophoresis and high performance liquid chromatography to ensure purity. The buffer solution can be exchanged into PBS, and the concentration can be determined by OD₂₈₀ using 1.43 extinction coefficient. The monoclonal antibodies can be aliquoted and stored at -80 °C.

[0304] To determine if the selected anti-OX40 antibodies bind to unique epitopes, each antibody can be biotinylated using commercially available reagents (Pierce, Rockford, IL). Biotinylated MAb binding can be detected with a streptavidin labeled probe. Competition studies using unlabeled monoclonal antibodies and biotinylated monoclonal antibodies can be performed using OX40 coated-ELISA plates as described above.

[0305] To determine the isotype of purified antibodies, isotype ELISAs can be performed using reagents specific for antibodies of a particular isotype. For example, to determine the isotype of a human monoclonal antibody, wells of microtiter plates can be coated with 1 µg/ml of anti-human immunoglobulin overnight at 4° C. After blocking with 1% BSA, the plates are reacted with 1 µg/ml or less of test monoclonal antibodies or purified isotype controls, at ambient temperature for one to two hours. The wells can then be reacted with either human IgG1 or human IgM-specific alkaline phosphatase-conjugated probes. Plates are developed and analyzed as described above.

[0306] To test the binding of antibodies to live cells expressing OX40, flow cytometry can be used, as described in the Examples. Briefly, cell lines expressing membrane-bound OX40 (grown under standard growth conditions) are mixed with various concentrations of monoclonal antibodies in PBS containing 0.1% BSA at 4°C for 1 hour. After washing, the cells are reacted with Fluorescein-labeled anti- IgG antibody under the same conditions as the primary antibody staining. The samples can be analyzed by FACScan instrument using light and side scatter properties to gate on single cells and binding of the labeled antibodies is determined. An alternative assay using fluorescence microscopy may be used (in addition to or instead of) the flow cytometry assay. Cells can be stained exactly as described above and examined by fluorescence microscopy. This method allows visualization of individual cells, but may have diminished sensitivity depending on the density of the antigen.

[0307] Anti-OX40 antibodies can be further tested for reactivity with the OX40 antigen by Western blotting. Briefly, cell extracts from cells expressing OX40 can be prepared and subjected to sodium dodecyl sulfate polyacrylamide gel electrophoresis. After electrophoresis, the separated antigens will be transferred to nitrocellulose membranes, blocked with 20% mouse serum, and probed with the monoclonal antibodies to be tested. IgG binding can be detected using

anti-IgG alkaline phosphatase and developed with BCIP/NBT substrate tablets (Sigma Chem. Co., St. Louis, MO).

[0308] Methods for analyzing binding affinity, cross-reactivity, and binding kinetics include standard assays known in the art, for example, BIACORE[®] SPR analysis using a BIACORE[®] 2000 SPR instrument (Biacore AB, Uppsala, Sweden).

[0309] In certain embodiments, the anti-OX40 antibody specifically binds to the extracellular region of human OX40. For example, the antibody may specifically bind to a particular domain (e.g., a functional domain) within the extracellular domain of OX40. In a particular embodiment, the antibody specifically binds to the site on OX40 to which OX40-L binds. In other embodiments, the antibody specifically binds to the extracellular region of human OX40 and the extracellular region of cynomolgus OX40.

XIII. Immunoconjugates, Antibody Derivatives and Diagnostics

[0310] Anti-OX40 antibodies described herein can be used for diagnostic purposes, including sample testing and *in vivo* imaging, and for this purpose the antibody (or binding fragment thereof) can be conjugated to an appropriate detectable agent, to form an immunoconjugate. For diagnostic purposes, appropriate agents are detectable labels that include radioisotopes, for whole body imaging, and radioisotopes, enzymes, fluorescent labels and other suitable antibody tags for sample testing.

[0311] The detectable labels can be any of the various types used currently in the field of *in vitro* diagnostics, including particulate labels including metal sols such as colloidal gold, isotopes such as ¹²⁵I or ⁹⁹Tc presented for instance with a peptidic chelating agent of the N₂S₂, N₃S or N₄ type, chromophores including fluorescent markers, biotin, luminescent markers, phosphorescent markers and the like, as well as enzyme labels that convert a given substrate to a detectable marker, and polynucleotide tags that are revealed following amplification such as by polymerase chain reaction. A biotinylated antibody would then be detectable by avidin or streptavidin binding. Suitable enzyme labels include horseradish peroxidase, alkaline phosphatase and the like. For instance, the label can be the enzyme alkaline phosphatase, detected by measuring the presence or formation of chemiluminescence following conversion of 1,2 dioxetane substrates such as adamantyl methoxy phosphoryloxy phenyl dioxetane (AMPPD), disodium 3-(4-(methoxyspiro{1,2-dioxetane-3,2'-(5'-chloro)tricyclo{3.3.1.1^{3,7}}decan}-4-yl) phenyl phosphate (CSPD), as well as CDP and CDP-star[®] or other luminescent substrates well-known to those in the art, for example the chelates of suitable lanthanides such as Terbium(III) and Europium(III). The detection means is determined by the chosen label. Appearance of the label or its reaction products can be achieved using the naked eye, in the case where the label is particulate and accumulates at appropriate levels, or using instruments such as a spectrophotometer, a luminometer, a fluorimeter, and the like, all in accordance with standard practice.

[0312] Preferably, conjugation methods result in linkages which are substantially (or nearly) non-immunogenic, e.g., peptide- (i.e. amide-), sulfide-, (sterically hindered), disulfide-, hydrazone-, and ether linkages. These linkages are nearly non-immunogenic and show reasonable stability within serum (see e.g. Senter, P. D., Curr. Opin. Chem. Biol. 13 (2009) 235-244; WO 2009/059278; WO 95/17886).

[0313] Depending on the biochemical nature of the moiety and the antibody, different conjugation strategies can be employed. In case the moiety is naturally occurring or recombinant polypeptide of between 50 to 500 amino acids, there are standard procedures in text books describing the chemistry for synthesis of protein conjugates, which can be easily followed by the skilled artisan (see e.g. Hackenberger, C. P. R., and Schwarzer, D., Angew. Chem. Int. Ed. Engl. 47 (2008) 10030-10074). In one embodiment the reaction of a maleinimido moiety with a cysteine residue within the antibody or the moiety is used. This is an especially suited coupling chemistry in case e.g. a Fab or Fab'-fragment of an antibody is used. Alternatively in one embodiment coupling to the C-terminal end of the antibody or moiety is performed. C-terminal modification of a protein, e.g. of a Fab-fragment can e.g. be performed as described (Sunbul, M. and Yin, J., Org. Biomol. Chem. 7 (2009) 3361-3371).

[0314] In general, site specific reaction and covalent coupling is based on transforming a natural amino acid into an amino acid with a reactivity which is orthogonal to the reactivity of the other functional groups present. For example, a specific cysteine within a rare sequence context can be enzymatically converted in an aldehyde (see Frese, M. A., and

Dierks, T., ChemBioChem. 10 (2009) 425-427). It is also possible to obtain a desired amino acid modification by utilizing the specific enzymatic reactivity of certain enzymes with a natural amino acid in a given sequence context (see, e.g., Taki, M. et al., Prot. Eng. Des. Sel. 17 (2004) 119-126; Gautier, A. et al. Chem. Biol. 15 (2008) 128-136; and Protease-catalyzed formation of C--N bonds is described in Bordusa, F., Highlights in Bioorganic Chemistry (2004) 389-403).

[0315] Site specific reaction and covalent coupling can also be achieved by the selective reaction of terminal amino acids with appropriate modifying reagents.

[0316] The reactivity of an N-terminal cysteine with benzonitrils (see Ren et al., Angew. Chem. Int. Ed. Engl. 48 (2009) 9658-9662) can be used to achieve a site-specific covalent coupling.

[0317] Native chemical ligation can also rely on C-terminal cysteine residues (Taylor, E. Vogel; Imperiali, B, Nucleic Acids and Molecular Biology (2009), 22 (Protein Engineering), 65-96).

[0318] EP 1 074 563 describes a conjugation method which is based on the faster reaction of a cysteine within a stretch of negatively charged amino acids than a cysteine located in a stretch of positively charged amino acids.

[0319] The moiety may also be a synthetic peptide or peptide mimic. In case a polypeptide is chemically synthesized, amino acids with orthogonal chemical reactivity can be incorporated during such synthesis (see e.g. de Graaf et al., Bioconjug. Chem. 20 (2009) 1281-1295). Since a great variety of orthogonal functional groups is at stake and can be introduced into a synthetic peptide, conjugation of such peptide to a linker is standard chemistry.

[0320] In order to obtain a mono-labeled polypeptide, the conjugate with 1:1 stoichiometry may be separated by chromatography from other conjugation side-products. This procedure can be facilitated by using a dye labeled binding pair member and a charged linker. By using this kind of labeled and highly negatively charged binding pair member, mono conjugated polypeptides are easily separated from non-labeled polypeptides and polypeptides which carry more than one linker, since the difference in charge and molecular weight can be used for separation. The fluorescent dye can be useful for purifying the complex from un-bound components, like a labeled monovalent binder.

[0321] In one embodiment, the moiety attached to the anti-OX40 antibody is selected from the group consisting of a binding moiety, a labeling moiety, and a biologically active moiety.

[0322] Anti-OX40 antibodies described herein also may be conjugated to a therapeutic agent to form an immunoconjugate such as an antibody-drug conjugate (ADC). Suitable therapeutic agents include antimetabolites, alkylating agents, DNA minor groove binders, DNA intercalators, DNA crosslinkers, histone deacetylase inhibitors, nuclear export inhibitors, proteasome inhibitors, topoisomerase I or II inhibitors, heat shock protein inhibitors, tyrosine kinase inhibitors, antibiotics, and anti-mitotic agents. In the ADC, the antibody and therapeutic agent preferably are conjugated via a linker cleavable such as a peptidyl, disulfide, or hydrazone linker. More preferably, the linker is a peptidyl linker such as Val-Cit, Ala-Val, Val-Ala-Val, Lys-Lys, Pro-Val-Gly-Val-Val (SEQ ID NO: 180), Ala-Asn-Val, Val-Leu-Lys, Ala-Ala-Asn, Cit-Cit, Val-Lys, Lys, Cit, Ser, or Glu. The ADCs can be prepared as described in U.S. Pat. Nos. 7,087,600; 6,989,452; and 7,129,261; PCT Publications WO 02/096910; WO 07/038658; WO 07/051081; WO 07/059404; WO 08/083312; and WO 08/103693; U.S. Patent Publications 20060024317; 20060004081; and 20060247295.

[0323] More specifically, in an ADC, the antibody is conjugated to a drug, with the antibody functioning as a targeting agent for directing the ADC to a target cell expressing its antigen, such as a cancer cell. Preferably, the antigen is a tumor associated antigen, *i.e.*, one that is uniquely expressed or overexpressed by the cancer cell. Once there, the drug is released, either inside the target cell or in its vicinity, to act as a therapeutic agent. For a review on the mechanism of action and use of ADCs in cancer therapy, see Schrama et al., Nature Rev. Drug Disc. 2006, 5, 147.

[0324] For cancer treatment, the drug preferably is a cytotoxic drug that causes death of the targeted cancer cell. Cytotoxic drugs that can be used in ADCs include the following types of compounds and their analogs and derivatives:

1. (a) enediynes such as calicheamicin (see, e.g., Lee et al., J. Am. Chem. Soc. 1987, 109, 3464 and 3466) and unciamycin (see, e.g., Davies et al., WO 2007/038868 A2 (2007) and Chowdari et al., US 8,709,431 B2

(2012));

2. (b) tubulysins (see, e.g., Domling et al., US 7,778,814 B2 (2010); Cheng et al., US 8,394,922 B2 (2013); and Cong et al., US Ser. No. 14/177376, filed Feb. 11, 2014));
3. (c) CC-1065 and duocarmycin (see, e.g., Boger, US 6,545,530 B1 (2003); Sufi et al., US 8,461,117 B2 (2013); and Zhang et al., US 2012/0301490 A1 (2012));
4. (d) epothilones (see, e.g., Vite et al., US 2007/0275904 A1 (2007) and US RE42930 E (2011));
5. (e) auristatins (see, e.g., Senter et al., US 6,844,869 B2 (2005) and Doronina et al., US 7,498,298 B2 (2009));
6. (f) pyrrolobenzodiazepine (PBD) dimers (see, e.g., Howard et al., US 2013/0059800 A1 (2013); US 2013/0028919 A1 (2013); and WO 2013/041606 A1 (2013)); and
7. (g) maytansinoids such as DM1 and DM4 (see, e.g., Chari et al., US 5,208,020 (1993) and Amphlett et al., US 7,374,762 B2 (2008)).

[0325] In an ADC, a linker covalently connects the antibody and the drug. Typically, there is one drug molecule attached to each linker, but the linker can be branched, allowing the attachment of plural drug molecules to increase the drug payload delivered per ADC. Further, each antibody may have more than one linker attached. The number drug molecules carried on an ADC is referred to as the drug-antibody ratio (DAR). For instance, if each heavy chain of the antibody has attached to it one linker that in turn has one drug molecule attached, the DAR is 2. Preferably, the DAR is between 1 and 5, more preferably between 2 and 4. Those skilled in the art will also appreciate that, while in each individual ADC the antibody is conjugated to an integer number of drug molecules, as a whole, a preparation of the ADC may analyze for a non-integer DAR, reflecting a statistical average. In summary, the architecture of an ADC may be represented by the following formula:

$$[\text{Antibody}]-[\text{Linker}-(\text{Drug})_n]_m$$

where typically m is 1, 2, 3, 4, 5, or 6 (preferably 2, 3, or 4) and n is 1, 2, or 3.

[0326] In some embodiments, the linker contains a cleavable group that is cleaved inside or in the vicinity of the target cell, to release the drug. In other embodiments, the linker does not contain a cleavable group but, rather, the ADC relies on catabolism of the antibody to release the drug.

[0327] One type of cleavable group is a pH sensitive group. The pH in blood plasma is slightly above neutral, while the pH inside a lysosome - where most ADCs end up after internalization inside a target cell - is acidic, circa 5. Thus, a cleavable group whose cleavage is acid catalyzed will cleave at a rate several orders of magnitude faster inside a lysosome than in the blood plasma. Examples of acid-sensitive groups include cis-aconityl amides and hydrazones, as described in Shen et al., US 4,631,190 (1986); Shen et al., US 5,144,011 (1992); Shen et al., Biochem. Biophys. Res. Commun. 1981, 102, 1048; and Yang et al., Proc. Nat'l Acad. Sci (USA), 1988, 85, 1189.

[0328] In another embodiment, the cleavable group is a disulfide. Disulfides can be cleaved by a thiol-disulfide exchange mechanism, at a rate dependent on the ambient thiol concentration. As the intracellular concentration of glutathione and other thiols is higher than their serum concentrations, the cleavage rate of a disulfide will be higher intracellularly, i.e., after internalization of the ADC. Further, the rate of thiol-disulfide exchange can be modulated by adjustment of the steric and electronic characteristics of the disulfide (e.g., an alkyl-aryl disulfide versus an alkyl-alkyl disulfide; substitution on the aryl ring, etc.), enabling the design of disulfide linkages that have enhanced serum stability or a particular cleavage rate. For additional disclosures relating to disulfide cleavable groups in conjugates, see, e.g., Thorpe et al., Cancer Res. 1988, 48, 6396; Santi et al., US 7,541,530 B2 (2009); Ng et al., US 6,989,452 B2 (2006); Ng et al., WO 2002/096910 A1 (2002); Boyd et al., US 7,691,962 B2 (2010); and Sufi et al., US 2010/0145036 A1 (2010).

[0329] A preferred cleavable group is a peptide that is cleaved selectively by a protease inside the target cell, as opposed to by a protease in the serum. Typically, a cleavable peptide group comprises from 1 to 20 amino acids, preferably from 1 to 6 amino acids, more preferably from 1 to 3 amino acids. The amino acid(s) can be natural and/or non-natural α -amino acids. Natural amino acids are those encoded by the genetic code, as well as amino acids derived therefrom, e.g., hydroxyproline, γ -carboxyglutamate, citrulline, and O-phosphoserine. In this context, the term "amino acid" also includes amino acid analogs and mimetics. Analogs are compounds having the same general $\text{H}_2\text{N(R)CHCO}_2\text{H}$ structure of a natural amino acid, except that the R group is not one found among the natural amino acids. Examples of analogs include homoserine, norleucine, methionine-sulfoxide, and methionine methyl sulfonium. An amino acid mimetic is a compound that has a structure different from the general chemical structure of an α -amino acid

but functions in a manner similar to one. The amino acid can be of the "L" stereochemistry of the genetically encoded amino acids, as well as of the enantiomeric "D" stereochemistry.

[0330] Preferably, a cleavable peptide group contains an amino acid sequence that is a cleavage recognition sequence for a protease. Many cleavage recognition sequences are known in the art. See, e.g., Matayoshi et al. *Science* 247: 954 (1990); Dunn et al. *Meth. Enzymol.* 241: 254 (1994); Seidah et al. *Meth. Enzymol.* 244: 175 (1994); Thornberry, *Meth. Enzymol.* 244: 615 (1994); Weber et al. *Meth. Enzymol.* 244: 595 (1994); Smith et al. *Meth. Enzymol.* 244: 412 (1994); and Bouvier et al. *Meth. Enzymol.* 248: 614 (1995).

[0331] More preferably, a cleavable peptide group comprises an amino acid sequence selected for cleavage by an endosomal or lysosomal protease, especially the latter. Examples of such proteases include cathepsins B, C, D, H, L and S, especially cathepsin B. Cathepsin B preferentially cleaves peptides at a sequence -AA²-AA¹- where AA¹ is a basic or strongly hydrogen bonding amino acid (such as lysine, arginine, or citrulline) and AA² is a hydrophobic amino acid (such as phenylalanine, valine, alanine, leucine, or isoleucine), for example Val-Cit (where Cit denotes citrulline) or Val-Lys, written in the N-to-C direction. For additional information regarding cathepsin-cleavable groups, see Dubowchik et al., *Biorg. Med. Chem. Lett.* 1998, 8, 3341; Dubowchik et al., *Bioorg. Med. Chem. Lett.*, 1998, 8, 3347; and Dubowchik et al., *Bioconjugate Chem.* 2002, 13, 855. Another enzyme that can be utilized for cleaving peptidyl linkers is legumain, a lysosomal cysteine protease that preferentially cleaves at Ala-Ala-Asn.

[0332] In a preferred embodiment, the linker in ADCs comprises a di- or tripeptide that is preferentially cleaved by a protease located inside the target cell. Preferably, the di- or tripeptide is cleavable by cathepsin B, more preferably a Val-Cit or Val-Lys dipeptide.

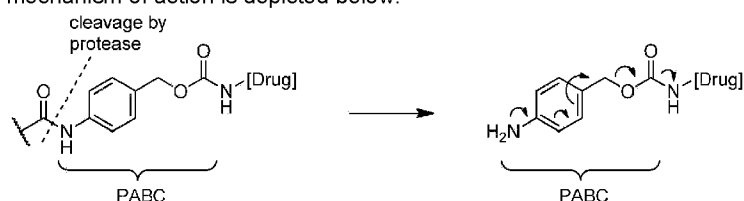
[0333] Single amino acid cleavable peptide groups also can be used, as disclosed in Chen et al., US 2010/0113476 A1 (2010).

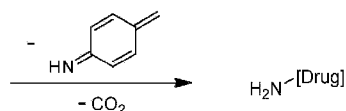
[0334] For conjugates that are not intended to be internalized by a cell, the cleavable group can be chosen such that it is cleaved by a protease present in the extracellular matrix in the vicinity of the target cell, e.g., a protease released by nearby dying cells or a tumor-associated protease. Exemplary extracellular tumor-associated proteases are matrix metalloproteases (MMP), plasmin, thimet oligopeptidase (TOP) and CD10. See, e.g., Trouet et al., US 5,962,216 (1999) and US 7,402,556 B2 (2008); Dubois et al., US 7,425,541 B2 (2008); and Bebbington et al., US 6,897,034 B2 (2005).

[0335] The linker can perform other functions in addition to covalently linking the antibody and the drug. For instance, the linker can contain poly(ethylene glycol) (PEG) groups, which enhance solubility either during the performance the conjugation chemistry or in the final ADC product.

[0336] The linker can further include a self-immolating moiety located adjacent to a cleavable peptide group. The self-immolating group serves as a spacer that prevents the antibody and/or the drug moiety from sterically interfering with the cleavage of the peptide group by a protease but thereafter spontaneously releases itself (*i.e.*, self-immolates) so as to not interfere with the action of the drug. See Carl et al., *J. Med. Chem.* 1981, 24 (3), 479; Carl et al., WO 81/01145 (1981); Dubowchik et al., *Pharmacology & Therapeutics* 1999, 83, 67; Firestone et al., US 6,214,345 B1 (2001); Toki et al., *J. Org. Chem.* 2002, 67, 1866; Doronina et al., *Nature Biotechnology* 2003, 21 (7), 778 (*erratum*, p. 941); de Groot et al., *Org. Chem.* 2001, 66, 8815; Boyd et al., US 7,691,962 B2 (2010); Boyd et al., US 2008/0279868 A1 (2008); Sufi et al., WO 2008/083312 A2 (2008); Feng, US 7,375,078 B2 (2008); Jeffrey, US 8,039,273 B2 (2011); and Senter et al., US 2003/0096743 A1 (2003).

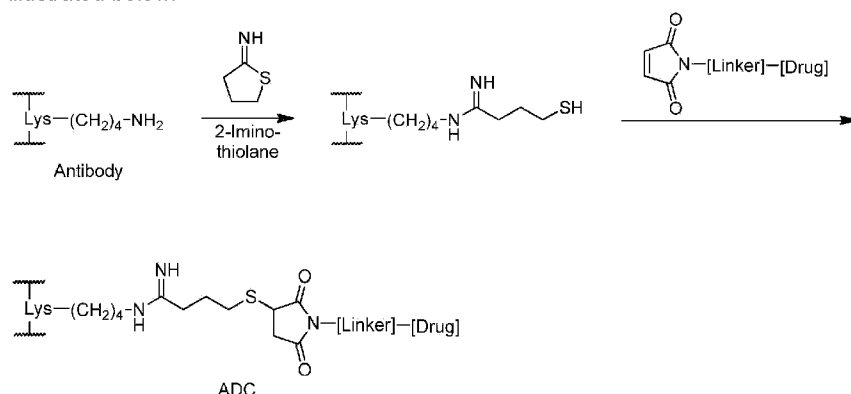
[0337] A preferred self-immolating group is a p-aminobenzyl oxycarbonyl (PABC) group, whose structure and mechanism of action is depicted below:





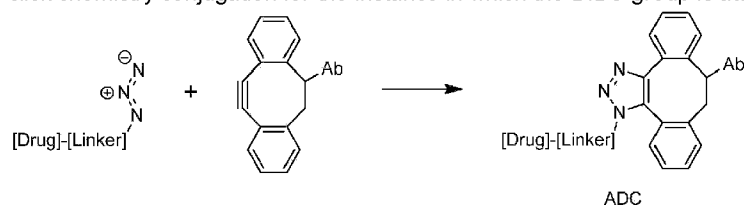
[0338] Thus, in a preferred embodiment, an ADC has a linker comprising a di- or tripeptide that is preferentially cleaved by a protease located inside the target cell and, adjacent to the di- or tripeptide, a self-immolating group. Preferably, the di- or tripeptide is cleavable by cathepsin B. Preferably, the self-immolating group is a PABC group.

[0339] Numerous techniques can be used for conjugating the antibody and the drug. In a preferred one, an ϵ -amino group in the side chain of a lysine residue in the antibody is reacted with 2-iminothiolane to introduce a free thiol (-SH) group. The thiol group can react with a maleimide or other nucleophile acceptor group to effect conjugation, as illustrated below:



[0340] Typically, a thiolation level of two to three thiols per antibody is achieved. For a representative procedure, see Chowdari et al., US 8,709,431 B2 (2014). Thus, in one embodiment, an antibody of this invention has one or more lysine residues (preferably two or three) modified by reaction with iminothiolane.

[0341] An alternative conjugation technique employs copper-free "click chemistry," in which an azide group adds across the strained alkyne bond of a cyclooctyne to form an 1,2,3-triazole ring. See, *e.g.*, Agard et al., J. Amer. Chem. Soc. 2004, 126, 15046; Best, Biochemistry 2009, 48, 6571. The azide can be located on the antibody and the cyclooctyne on the drug moiety, or vice-versa. A preferred cyclooctyne group is dibenzocyclooctyne (DIBO). Various reagents having a DIBO group are available from Invitrogen/Molecular Probes, Eugene, Oregon. The reaction below illustrates click chemistry conjugation for the instance in which the DIBO group is attached to the antibody:

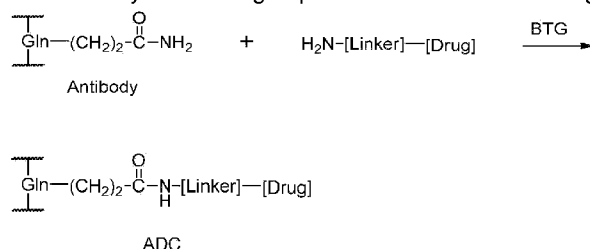


In an ADC made by this technique, the linker comprises a 1,2,3-triazole ring.

[0342] Yet another conjugation technique involves introducing a non-natural amino acid into an antibody, with the non-natural amino acid providing a functionality for conjugation with a reactive functional group in the drug moiety. For instance, the non-natural amino acid p-acetylphenylalanine can be incorporated into an antibody or other polypeptide, as taught in Tian et al., WO 2008/030612 A2 (2008). The ketone group in p-acetylphenylalanine can be a conjugation site by the formation of an oxime with a hydroxylamino group on the linker-drug moiety. Alternatively, the non-natural amino acid p-azidophenylalanine can be incorporated into an antibody to provide an azide functional group for conjugation via click chemistry, as discussed above. Non-natural amino acids can also be incorporated into an antibody or other polypeptide using cell-free methods, as taught in Goerke et al., US 2010/0093024 A1 (2010) and Goerke et al., Biotechnol. Bioeng. 2009, 102 (2), 400-416. Thus, in one embodiment, the antibody has one or more amino acids replaced by a non-natural amino acid, which preferably is p-acetylphenylalanine or p-azidophenylalanine, more

preferably p-acetylphenylalanine.

[0343] Still another conjugation technique uses the enzyme transglutaminase (preferably bacterial transglutaminase or BTG), as taught in Jeger et al., *Angew. Chem. Int. Ed.* 2010, 49, 9995. BTG forms an amide bond between the side chain carboxamide of a glutamine and an alkyleneamino group, which can be, for example, the ϵ -amino group of a lysine or a 5-amino-n-pentyl group. In a typical conjugation reaction, the glutamine residue is located on the antibody, while the alkyleneamino group is located on the linker-drug moiety, as shown below:



[0344] The positioning of a glutamine residue on a polypeptide chain has a large effect on its susceptibility to BTG mediated transamidation. None of the glutamine residues on an antibody are normally BTG substrates. However, if the antibody is deglycosylated - the glycosylation site being asparagine 297 (N297) - nearby glutamine 295 (Q295) is rendered BTG susceptible. Alternatively, an antibody can be synthesized glycoside free by introducing an N297A mutation in the constant region, to eliminate the N297 glycosylation site. Further, it has been shown that an N297Q substitution in an antibody not only eliminates glycosylation, but also introduces a second glutamine residue (at position 297) that too is susceptible BTG-mediated transamidation. Thus, in one embodiment, the anti-OX40 antibody is deglycosylated. In another embodiment, the anti-OX40 antibody has an N297Q substitution. Those skilled in the art will appreciate that deglycosylation by post-synthesis modification or by introducing an N297A mutation generates two BTG-reactive glutamine residues per antibody (one per heavy chain, at position 295), while an antibody with an N297Q substitution will have four BTG-reactive glutamine residues (two per heavy chain, at positions 295 and 297).

[0345] Further, another conjugation technique uses the enzyme Sortase A, as taught in Levary et al., *PLoS One* 2011, 6(4), e18342; Proft, *Biotechnol. Lett.* 2010, 32, 1-10; Ploegh et al., WO 2010/087994 A2 (2010); and Mao et al., WO 2005/051976 A2 (2005). The Sortase A recognition motif (typically LPXTG (SEQ ID NO: 181), where X is any natural amino acid) may be attached to the antibody and the nucleophilic acceptor motif (typically GGG) may be located on the drug moiety, or vice-versa.

[0346] Anti-OX40 antibodies described herein also can be used for detecting OX40, such as human OX40, e.g., human OX40 in tissues or tissue samples. The antibodies may be used, e.g., in an ELISA assay or in flow cytometry. In certain embodiments, the anti-OX40 antibody is contacted with cells, e.g., cells in a tissue, for a time appropriate for specific binding to occur, and then a reagent, e.g., an antibody that detects the anti-OX40 antibody, is added. Exemplary assays are provided in the Examples. The anti-OX40 antibody may be a fully human antibody, or it may be a chimeric antibody, such as an antibody having human variable regions and murine constant regions or a portion thereof. Exemplary methods for detecting OX40, e.g., human OX40, in a sample (cell or tissue sample) comprise (i) contacting a sample with an anti-OX40 antibody, for a time sufficient for allowing specific binding of the anti-OX40 antibody to OX40 in the sample, and (2) contacting the sample with a detection reagent, e.g., an antibody, that specifically binds to the anti-OX40 antibody, such as to the Fc region of the anti-OX40 antibody, to thereby detect OX40 bound by the anti-OX40 antibody. Wash steps may be included after the incubation with the antibody and/or detection reagent. Anti-OX40 antibodies for use in these methods do not have to be linked to a label or detection agents, as a separate detection agent can be used.

XIV. Bispecific Molecules

[0347] Anti-OX40 antibodies described herein may be used for forming bispecific molecules. For example, the antibody, or antigen-binding portions thereof, can be derivatized or linked to another functional molecule, e.g., another peptide or protein (e.g., another antibody or ligand for a receptor) to generate a bispecific molecule that binds to at least two different binding sites or target molecules. In one embodiment, the anti-OX40 antibody may be linked to an antibody or

scFv that binds specifically to any protein that may be used as potential targets for combination treatments, such as the proteins described herein (e.g., antibodies to PD-1, PD-L1, or LAG-3). Alternatively, the antibody may be derivatized or linked to more than one other functional molecule to generate multispecific molecules that bind to more than two different binding sites and/or target molecules. Such multispecific molecules are also intended to be encompassed by the term "bispecific molecule" as used herein. To create a bispecific molecule described herein, the anti-OX40 antibody can be functionally linked (e.g., by chemical coupling, genetic fusion, noncovalent association or otherwise) to one or more other binding molecules, such as another antibody, antibody fragment, peptide or binding mimetic, such that a bispecific molecule results.

[0348] Accordingly, provided herein are bispecific molecules comprising at least one first binding specificity for OX40 and a second binding specificity for a second target epitope. In one embodiment, the bispecific molecule is multispecific, e.g., the molecule further includes a third binding specificity.

[0349] In certain embodiments, the bispecific molecules comprises as a binding specificity at least one antibody, or an antibody fragment thereof, including, e.g., an Fab, Fab', F(ab')₂, Fv, or a single chain Fv (scFv). The antibody may also be a light chain or heavy chain dimer, or any minimal fragment thereof such as a Fv or a single chain construct as described in Ladner et al. U.S. Patent No. 4,946,778.

[0350] While human monoclonal antibodies are preferred, other antibodies can be employed in the bispecific molecules described herein, including, e.g., murine, chimeric and humanized antibodies.

[0351] Bispecific molecules provided herein can be prepared by conjugating the constituent binding specificities using methods known in the art. For example, each binding specificity of the bispecific molecule can be generated separately and then conjugated to one another. When the binding specificities are proteins or peptides, a variety of coupling or cross-linking agents can be used for covalent conjugation. Examples of cross-linking agents include protein A, carbodiimide, N-succinimidyl-S-acetyl-thioacetate (SATA), 5,5'-dithiobis(2-nitrobenzoic acid) (DTNB), o-phenylenedimaleimide (oPDM), N-succinimidyl-3-(2-pyridyldithio)propionate (SPDP), and sulfosuccinimidyl 4-(N-maleimidomethyl) cyclohexane-1-carboxylate (sulfo-SMCC) (see e.g., Karpovsky et al. (1984) J. Exp. Med. 160:1686; Liu, MA et al. (1985) Proc. Natl. Acad. Sci. USA 82:8648). Other methods include those described in Paulus (1985) Behring Ins. Mitt. No. 78, 118-132; Brennan et al. (1985) Science 229:81-83), and Glennie et al. (1987) J. Immunol. 139: 2367-2375). Preferred conjugating agents are SATA and sulfo-SMCC, both available from Pierce Chemical Co. (Rockford, IL).

[0352] When the binding specificities are antibodies, they can be conjugated via sulfhydryl bonding of the C-terminus hinge regions of the two heavy chains. In a particularly preferred embodiment, the hinge region is modified to contain an odd number of sulfhydryl residues, preferably one, prior to conjugation.

[0353] Alternatively, both binding specificities can be encoded in the same vector and expressed and assembled in the same host cell. This method is particularly useful where the bispecific molecule is a mAb x mAb, mAb x Fab, mAb x (scFv)₂, Fab x F(ab')₂ or ligand x Fab fusion protein. A bispecific antibody may comprise an antibody comprising an scFv at the C-terminus of each heavy chain. A bispecific molecule described herein can be a single chain molecule comprising one single chain antibody and a binding determinant, or a single chain bispecific molecule comprising two binding determinants. Bispecific molecules may comprise at least two single chain molecules. Methods for preparing bispecific molecules are described for example in U.S. Patent Number 5,260,203; U.S. Patent Number 5,455,030; U.S. Patent Number 4,881,175; U.S. Patent Number 5,132,405; U.S. Patent Number 5,091,513; U.S. Patent Number 5,476,786; U.S. Patent Number 5,013,653; U.S. Patent Number 5,258,498; and U.S. Patent Number 5,482,858.

[0354] Binding of the bispecific molecules to their specific targets can be confirmed using art-recognized methods, such as enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), FACS analysis, bioassay (e.g., growth inhibition), or Western Blot assay. Each of these assays generally detects the presence of protein-antibody complexes of particular interest by employing a labeled reagent (e.g., an antibody) specific for the complex of interest.

XV. Compositions

[0355] Further provided are compositions, e.g., a pharmaceutical compositions, containing one or more anti-OX40 antibodies, alone or in combination with antibodies to other targets, formulated together with a pharmaceutically acceptable carrier. Such compositions may include one or a combination of (e.g., two or more different) antibodies, or immunoconjugates or bispecific molecules described herein. For example, the composition can comprise a combination of antibodies (or immunoconjugates or bispecifics) described herein that bind to different epitopes on OX40 or that have complementary activities.

[0356] In certain embodiments, the composition comprises an anti-OX40 antibody at a concentration of at least 1 mg/ml, 5 mg/ml, 10 mg/ml, 50 mg/ml, 100 mg/ml, 150 mg/ml, 200 mg/ml, 1-300 mg/ml, or 100-300 mg/ml.

[0357] Pharmaceutical compositions described herein also can be administered in combination therapies, i.e., combined with other agents. For example, the combination therapy can include administration of an anti-OX40 antibody described herein combined with at least one other anticancer and/or T-cell stimulating (e.g., activating) agent. Examples of therapeutic agents that can be used in combination therapy are described in greater detail below in the section on uses of the antibodies described herein.

[0358] In certain embodiments, therapeutic compositions disclosed herein include other compounds, drugs, and/or agents used for the treatment of cancer. Such compounds, drugs, and/or agents can include, for example, chemotherapy drugs, small molecule drugs or antibodies that stimulate the immune response to a given cancer. In some instances, therapeutic compositions can include, for example, one or more of an anti-CTLA-4 antibody, an anti-PD-1 antibody, an anti-PDL-1 antibody, an anti-GITR antibody, an anti-CD137 antibody, or an anti-LAG-3 antibody.

[0359] As used herein, "pharmaceutically acceptable carriers" include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like that are physiologically compatible. Preferably, the carrier is suitable for intravenous, intramuscular, subcutaneous, parenteral, spinal or epidermal administration (e.g., by injection or infusion). Depending on the route of administration, the active compound, i.e., antibody, immunoconjugate, or bispecific molecule, may be coated in a material to protect the compound from the action of acids and other natural conditions that may inactivate the compound.

[0360] The pharmaceutical compositions described herein may include one or more pharmaceutically acceptable salts. A "pharmaceutically acceptable salt" refers to a salt that retains the desired biological activity of the parent compound and does not impart any undesired toxicological effects (see e.g., Berge, S.M., et al. (1977) J. Pharm. Sci. 66:1-19). Examples of such salts include acid addition salts and base addition salts. Acid addition salts include those derived from nontoxic inorganic acids, such as hydrochloric, nitric, phosphoric, sulfuric, hydrobromic, hydroiodic, phosphorous and the like, as well as from nontoxic organic acids such as aliphatic mono- and dicarboxylic acids, phenyl-substituted alkanic acids, hydroxy alkanic acids, aromatic acids, aliphatic and aromatic sulfonic acids and the like. Base addition salts include those derived from alkaline earth metals, such as sodium, potassium, magnesium, calcium and the like, as well as from nontoxic organic amines, such as N,N'-dibenzylethylenediamine, N-methylglucamine, chlorprocaine, choline, diethanolamine, ethylenediamine, procaine and the like.

[0361] The pharmaceutical compositions described herein also may include a pharmaceutically acceptable anti-oxidant. Examples of pharmaceutically acceptable antioxidants include: (1) water soluble antioxidants, such as ascorbic acid, cysteine hydrochloride, sodium bisulfate, sodium metabisulfite, sodium sulfite and the like; (2) oil-soluble antioxidants, such as ascorbyl palmitate, butylated hydroxyanisole (BHA), butylated hydroxytoluene (BHT), lecithin, propyl gallate, alpha-tocopherol, and the like; and (3) metal chelating agents, such as citric acid, ethylenediamine tetraacetic acid (EDTA), sorbitol, tartaric acid, phosphoric acid, and the like.

[0362] Examples of suitable aqueous and nonaqueous carriers that may be employed in the pharmaceutical compositions described herein include water, ethanol, polyols (such as glycerol, propylene glycol, polyethylene glycol, and the like), and suitable mixtures thereof, vegetable oils, such as olive oil, and injectable organic esters, such as ethyl oleate. Proper fluidity can be maintained, for example, by the use of coating materials, such as lecithin, by the maintenance of the required particle size in the case of dispersions, and by the use of surfactants.

[0363] These compositions may also contain adjuvants such as preservatives, wetting agents, emulsifying agents and dispersing agents. Prevention of presence of microorganisms may be ensured both by sterilization procedures, *supra*,

and by the inclusion of various antibacterial and antifungal agents, for example, paraben, chlorobutanol, phenol sorbic acid, and the like. It may also be desirable to include isotonic agents, such as sugars, sodium chloride, and the like into the compositions. In addition, prolonged absorption of the injectable pharmaceutical form may be brought about by the inclusion of agents which delay absorption such as aluminum monostearate and gelatin.

[0364] Pharmaceutically acceptable carriers include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. The use of such media and agents for pharmaceutically active substances is known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the pharmaceutical compositions described herein is contemplated. A pharmaceutical composition may comprise a preservative or may be devoid of a preservative. Supplementary active compounds can be incorporated into the compositions.

[0365] Therapeutic compositions typically must be sterile and stable under the conditions of manufacture and storage. The composition can be formulated as a solution, microemulsion, liposome, or other ordered structure suitable to high drug concentration. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as mannitol, sorbitol, or sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent that delays absorption, for example, monostearate salts and gelatin.

[0366] Sterile injectable solutions can be prepared by incorporating the active compound in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by sterilization microfiltration. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated herein. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze-drying (lyophilization) that yield a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

[0367] The amount of active ingredient which can be combined with a carrier material to produce a single dosage form will vary depending upon the subject being treated, and the particular mode of administration. The amount of active ingredient which can be combined with a carrier material to produce a single dosage form will generally be that amount of the composition which produces a therapeutic effect. Generally, out of one hundred per cent, this amount will range from about 0.01 per cent to about ninety-nine percent of active ingredient, preferably from about 0.1 per cent to about 70 per cent, most preferably from about 1 per cent to about 30 per cent of active ingredient in combination with a pharmaceutically acceptable carrier.

[0368] Dosage regimens are adjusted to provide the optimum desired response (e.g., a therapeutic response). For example, a single bolus may be administered, several divided doses may be administered over time or the dose may be proportionally reduced or increased as indicated by the exigencies of the therapeutic situation. It is especially advantageous to formulate parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subjects to be treated; each unit contains a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms described herein are dictated by and directly dependent on (a) the unique characteristics of the active compound and the particular therapeutic effect to be achieved, and (b) the limitations inherent in the art of compounding such an active compound for the treatment of sensitivity in individuals.

[0369] For administration of the anti-OX40 antibody, the dosage ranges from about 0.0001 to 100 mg/kg, about 0.01 to 5 mg/kg, about 0.01 to 10 mg/kg, about 0.1 to 1 mg/kg, about 0.1 to 0.5 mg/kg, or about 0.5 to 0.8 mg/kg of the host body weight. For example, dosages can be 0.2 mg/kg body weight, 0.3 mg/kg body weight, 0.5 mg/kg body weight, 1 mg/kg body weight, 3 mg/kg body weight, 5 mg/kg body weight or 10 mg/kg body weight or within the range of 1-10 mg/kg. In certain embodiments, the dosage is 0.2 mg/kg. In some embodiments, the dosage is 0.25 mg/kg. In other embodiments, the dosage is 0.5 mg/kg. An exemplary treatment regime entails administration once per week, once

every two weeks, once every three weeks, once every four weeks, once a month, once every 3 months or once every three to 6 months. Exemplary dosage regimens for the antibodies described herein include 1 mg/kg body weight or 3 mg/kg body weight via intravenous administration, with the antibody being given using one of the following dosing schedules: (i) every four weeks for six dosages, then every three months; (ii) every three weeks; (iii) 3 mg/kg body weight once followed by 1 mg/kg body weight every three weeks.

[0370] In certain embodiments, for combination treatment with an anti-OX40 antibody and anti-PD-1 or anti-CTLA-4 antibody, the antibodies are administered at a fixed dose. Accordingly, in some embodiments, the anti-OX40 antibody is administered at a fixed dose of about 25 to about 320 mg, for example, about 25 to about 160 mg, about 25 to about 80 mg, about 25 to about 40 mg, about 40 to about 320 mg, about 40 to about 160 mg, about 40 to about 80 mg, about 80 to about 320 mg, about 30 to about 160 mg, or about 160 to about 320 mg. In one embodiment, the anti-OX40 antibody is administered at a dose of 20 mg or about 20 mg. In another embodiment, the anti-OX40 antibody is administered at a dose of 40 mg or about 40 mg. In another embodiment, the anti-OX40 antibody is administered at a dose of 80 mg or about 80 mg. In another embodiment, the anti-OX40 antibody is administered at a dose of 160 mg or about 160 mg. In another embodiment, the anti-OX40 antibody is administered at a dose of 320 mg or about 320 mg.

[0371] In some embodiments, the anti-PD-1 antibody is administered at a fixed dose of about 100 to 300 mg, For example, the dosage of the immuno-oncology agent can be 240 mg or about 240 mg, 360 mg or about 360 mg, or 480 mg or about 480 mg. In certain embodiments, the dose of the anti-PD1 antibody ranges from about 0.0001 to 100 mg/kg, and more usually 0.01 to 5 mg/kg, of the host body weight. For example dosages can be 0.3 mg/kg body weight or about 0.3 mg/kg body weight, 1 mg/kg body weight or about 1 mg/kg body weight, 3 mg/kg body weight or about 3 mg/kg body weight, 5 mg/kg body weight or about 5 mg/kg body weight, or 10 mg/kg body weight or about 10 mg/kg body weight, or within the range of 1-10 mg/kg. In some embodiments, the dosage of the anti-PD-1 antibody is 240 mg or about 240 mg administered once every 2 weeks (Q2W). This dosage can be adjusted proportionately (at 120 mg per week) for longer or shorter periods, e.g., 360 mg administered once every 3 weeks (Q3W) or 480 mg administered once every 4 weeks (Q4W).

[0372] In some embodiments, the anti-CTLA-4 antibody is administered at a dose of about 0.1 mg/kg to about 10 mg/kg. For example, dosages can be 1 mg/kg or about 1 mg/kg or 3 mg/kg or about 3 mg/kg, of the host body weight.

[0373] Exemplary dosage regimens for combination treatment with an anti-OX40 and anti-PD-1 or anti-CTLA-4 antibody are provided *infra* under the section titled "Uses and Methods."

[0374] In certain embodiments, the anti-OX40 antibody is administered to a patient with an infusion duration of about 15 minutes to about 60 minutes, for example, about 30 minutes.

[0375] In certain embodiments, the anti-PD-1 antibody (e.g., nivolumab) is administered to a patient with an infusion duration of about 15 minutes to about 60 minutes, for example, about 30 minutes, when administered at a dose of 3 mg/kg (0.1 mg/kg/min). In certain embodiments, the anti-PD-1 antibody is administered to a patient with an infusion duration of about 45 minutes to 75 minutes, for example, about 60 minutes, when administered at a dose of 10 mg/kg.

[0376] In certain embodiments, the anti-CTLA-4 antibody (e.g., ipilimumab) is administered to a patient with an infusion duration of about 15 minutes to 120 minutes, for example, about 30 minutes when administered at a dose of 3 mg/kg. In certain embodiments, the anti-CTLA-4 antibody is administered to a patient with an infusion duration of about 15 minutes to 120 minutes, for example, 90 minutes, when administered at a dose of 10 mg/kg.

[0377] In certain embodiments, when administered on the same day, the anti-OX40 antibody is administered before the anti-PD-1 or anti-CTLA-4 antibody. In certain embodiments, when administered on the same day, the anti-OX40 antibody is administered after the anti-PD-1 or anti-CTLA-4 antibody. In certain embodiments, when administered on the same day, the anti-OX40 antibody is administered simultaneously with the anti-PD-1 or anti-CTLA-4 antibody.

[0378] In certain embodiments, when administered on the same day, the anti-OX40 antibody is administered about 15 to 45 minutes (e.g., about 30 minutes) before the anti-PD-1 or anti-CTLA-4 antibody. In certain embodiments, when administered on the same day, the anti-OX40 antibody is administered about 15 to 45 minutes (e.g., about 30 minutes) after the anti-PD-1 or anti-CTLA-4 antibody.

[0379] Alternatively, anti-OX40 antibodies provided herein can be administered at a flat dose (flat dose regimen).

[0380] In some cases, two or more monoclonal antibodies with different binding specificities are administered simultaneously, such that the dosage of each antibody administered falls within the ranges above. In addition, the antibodies usually are administered on multiple occasions. Intervals between single dosages can be, for example, weekly, monthly, every three months or yearly. Intervals can also be irregular as indicated by measuring blood levels of antibody to the target antigen in the patient. In some methods, dosage is adjusted to achieve a plasma antibody concentration of about 1-1000 µg/ml and in some methods about 25-300 µg/ml.

[0381] Anti-OX40 antibodies described herein may be administered with another antibody at the dosage regimen of the other antibody. For example, the anti-OX40 antibody may be administered with an anti-PD-1 antibody, such as nivolumab (OPDIVO), every two weeks as an i.v. infusion over 60 minutes until disease progression or unacceptable toxicity occurs. Alternatively, the anti-OX40 antibody may be administered with pembrolizumab (KEYTRUDA) every 3 weeks as an i.v. infusion over 30 minutes until disease progression or unacceptable toxicity occurs.

[0382] Antibodies can be administered as a sustained release formulation, in which case less frequent administration is required. Dosage and frequency vary depending on the half-life of the antibody in the patient. In general, human antibodies show the longest half-life, followed by humanized antibodies, chimeric antibodies, and nonhuman antibodies. The dosage and frequency of administration can vary depending on whether the treatment is prophylactic or therapeutic. In prophylactic applications, a relatively low dosage is administered at relatively infrequent intervals over a long period of time. Some patients continue to receive treatment for the rest of their lives. In therapeutic applications, a relatively high dosage at relatively short intervals is sometimes required until progression of the disease is reduced or terminated, and preferably until the patient shows partial or complete amelioration of symptoms of disease. Thereafter, the patient can be administered a prophylactic regime.

[0383] Actual dosage levels of the active ingredients in the pharmaceutical compositions described herein may be varied so as to obtain an amount of the active ingredient which is effective to achieve the desired therapeutic response for a particular patient, composition, and mode of administration, without being toxic to the patient. The selected dosage level will depend upon a variety of pharmacokinetic factors including the activity of the particular compositions described herein employed, or the ester, salt or amide thereof, the route of administration, the time of administration, the rate of excretion of the particular compound being employed, the duration of the treatment, other drugs, compounds and/or materials used in combination with the particular compositions employed, the age, sex, weight, condition, general health and prior medical history of the patient being treated, and like factors well known in the medical arts.

[0384] "Therapeutically effective dosages" of the antibodies described herein preferably results in a decrease in severity of disease symptoms, an increase in frequency and duration of disease symptom-free periods, or a prevention of impairment or disability due to the disease affliction. In the context of cancer, a therapeutically effective dose preferably results in increased survival, and/or prevention of further deterioration of physical symptoms associated with cancer. Symptoms of cancer are well-known in the art and include, for example, unusual mole features, a change in the appearance of a mole, including asymmetry, border, color and/or diameter, a newly pigmented skin area, an abnormal mole, darkened area under nail, breast lumps, nipple changes, breast cysts, breast pain, death, weight loss, weakness, excessive fatigue, difficulty eating, loss of appetite, chronic cough, worsening breathlessness, coughing up blood, blood in the urine, blood in stool, nausea, vomiting, liver metastases, lung metastases, bone metastases, abdominal fullness, bloating, fluid in peritoneal cavity, vaginal bleeding, constipation, abdominal distension, perforation of colon, acute peritonitis (infection, fever, pain), pain, vomiting blood, heavy sweating, fever, high blood pressure, anemia, diarrhea, jaundice, dizziness, chills, muscle spasms, colon metastases, lung metastases, bladder metastases, liver metastases, bone metastases, kidney metastases, and pancreatic metastases, difficulty swallowing, and the like.

[0385] A therapeutically effective dose may prevent or delay onset of cancer, such as may be desired when early or preliminary signs of the disease are present. Laboratory tests utilized in the diagnosis of cancer include chemistries (including the measurement of OX40 levels), hematology, serology and radiology. Accordingly, any clinical or biochemical assay that monitors any of the foregoing may be used to determine whether a particular treatment is a therapeutically effective dose for treating cancer. One of ordinary skill in the art would be able to determine such amounts based on such factors as the subject's size, the severity of the subject's symptoms, and the particular

composition or route of administration selected.

[0386] Antibodies and compositions described herein can be administered via one or more routes of administration using one or more of a variety of methods known in the art. As will be appreciated by the skilled artisan, the route and/or mode of administration will vary depending upon the desired results. Preferred routes of administration for antibodies described herein include intravenous, intramuscular, intradermal, intraperitoneal, subcutaneous, spinal or other parenteral routes of administration, for example by injection or infusion. The phrase "parenteral administration" as used herein means modes of administration other than enteral and topical administration, usually by injection, and includes, without limitation, intravenous, intramuscular, intraarterial, intrathecal, intracapsular, intraorbital, intracardiac, intradermal, intraperitoneal, transtracheal, subcutaneous, subcuticular, intraarticular, subcapsular, subarachnoid, intraspinal, epidural and intrasternal injection and infusion.

[0387] Alternatively, the antibody can be administered via a non-parenteral route, such as a topical, epidermal or mucosal route of administration, for example, intranasally, orally, vaginally, rectally, sublingually or topically.

[0388] The active compounds can be prepared with carriers that will protect the compound against rapid release, such as a controlled release formulation, including implants, transdermal patches, and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Many methods for the preparation of such formulations are patented or generally known to those skilled in the art. See, e.g., Sustained and Controlled Release Drug Delivery Systems, J.R. Robinson, ed., Marcel Dekker, Inc., New York, 1978.

[0389] Antibody compositions can be administered with medical devices known in the art. For example, in one embodiment, the composition is administered with a needleless hypodermic injection device, such as the devices disclosed in U.S. Patent 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 for use in administering the antibodies include: U.S. Patent No. 4,487,603, which discloses an implantable micro-infusion pump for dispensing medication at a controlled rate; U.S. Patent No. 4,486,194, which discloses a therapeutic device for administering medicants through the skin; U.S. Patent No. 4,447,233, which discloses a medication infusion pump for delivering medication at a precise infusion rate; U.S. Patent No. 4,447,224, which discloses a variable flow implantable infusion apparatus for continuous drug delivery; U.S. Patent No. 4,439,196, which discloses an osmotic drug delivery system having multi-chamber compartments; and U.S. Patent No. 4,475,196, which discloses an osmotic drug delivery system. Many other such implants, delivery systems, and modules are known to those skilled in the art.

[0390] In certain embodiments, the anti-OX40 antibodies are formulated to ensure proper distribution *in vivo*. For example, the blood-brain barrier (BBB) excludes many highly hydrophilic compounds. To ensure the antibodies cross the BBB (if desired, e.g., for brain cancers), they can be formulated, for example, in liposomes. For methods of manufacturing liposomes, see, e.g., U.S. Patents 4,522,811; 5,374,548; and 5,399,331. The liposomes may comprise one or more moieties which are selectively transported into specific cells or organs, thus enhance targeted drug delivery (see, e.g., V.V. Ranade (1989) J. Clin. Pharmacol. 29:685). Exemplary targeting moieties include folate or biotin (see, e.g., U.S. Patent 5,416,016 to Low et al.); mannosides (Umezawa et al., (1988) Biochem. Biophys. Res. Commun. 153:1038); antibodies (P.G. Bloeman et al. (1995) FEBS Lett. 357:140; M. Owais et al. (1995) Antimicrob. Agents Chemother. 39:180); surfactant protein A receptor (Briscoe et al. (1995) Am. J. Physiol. 1233:134); p120 (Schreier et al. (1994) J. Biol. Chem. 269:9090); see also K. Keinänen; M.L. Laukkanen (1994) FEBS Lett. 346:123; J.J. Killian; I.J. Fidler (1994) Immunomethods 4:273.

XVI. Uses and Methods

[0391] Anti-OX40 antibodies and compositions described herein have numerous *in vitro* and *in vivo* applications involving, for example, enhancement of immune response by activating OX40 signaling, or detection of OX40. In a preferred embodiment, the antibodies are human antibodies. For example, anti-OX40 antibodies described herein can be contacted with cells in culture, *in vitro* or *ex vivo*, or administered to human subjects, e.g., *in vivo*, to enhance immunity in a variety of diseases. Accordingly, provided herein are the antibodies for use in methods of modifying an immune response in a subject comprising administering to the subject an antibody, or antigen-binding portion thereof,

described herein such that the immune response in the subject is modified. Preferably, the response is enhanced, stimulated or up-regulated.

[0392] Preferred subjects include human patients in whom enhancement of an immune response would be desirable. The methods are particularly suitable for treating human patients having a disorder that can be treated by augmenting an immune response (e.g., a T-cell mediated immune response, e.g., an antigen specific T cell response). In a particular embodiment, the antibodies are for use in methods for treatment of cancer *in vivo*. To achieve antigen-specific enhancement of immunity, anti-OX40 antibodies described herein can be administered together with an antigen of interest or the antigen may already be present in the subject to be treated (e.g., a tumor-bearing or virus-bearing subject). When anti-OX40 antibodies are administered together with another agent, the two can be administered separately or simultaneously.

[0393] Also encompassed are methods for detecting the presence of human OX40 antigen in a sample, or measuring the amount of human OX40 antigen, comprising contacting the sample, and a control sample, with anti-OX40 antibodies (or antigen binding portions thereof) described herein, under conditions that allow for formation of a complex between the antibody and human OX40. The formation of a complex is then detected, wherein a difference complex formation between the sample compared to the control sample is indicative the presence of human OX40 antigen in the sample. The anti-OX40 antibodies described herein also can be used to purify human OX40 via immunoaffinity purification.

[0394] Given the ability of anti-OX40 antibodies described herein to stimulate or co-stimulate T cell responses, e.g., antigen-specific T cell responses, also provided herein are *in vitro* and *in vivo* methods of using the antibodies to stimulate, enhance or upregulate antigen-specific T cell responses, e.g., anti-tumor T cell responses. In certain embodiments, CD3 stimulation is also included (e.g., by coinubation with a cell expressing membrane CD3), which stimulation can be provided at the same time, before, or after stimulation with an anti-OX40 antibody. In one embodiment, the method comprises contacting T cells with an anti-OX40 antibody described herein, and optionally with an anti-CD3 antibody, such that an antigen-specific T cell response is stimulated. Any suitable indicator of an antigen-specific T cell response can be used to measure the antigen-specific T cell response. Non-limiting examples of such suitable indicators include increased T cell proliferation in the presence of the antibody and/or increase cytokine production in the presence of the antibody. In a preferred embodiment, interleukin-2 and/or interferon- γ production by the antigen-specific T cell is stimulated.

[0395] T cells that can be enhanced or co-stimulated with anti-OX40 antibodies include CD4⁺ T cells and CD8⁺ T cells. The T cells can be T_{eff} cells, e.g., CD4⁺ T_{eff} cells, CD8⁺ T_{eff} cells, Thelper (T_h) cells and T cytotoxic (T_c) cells.

[0396] Also provided are the antibodies for use in methods of stimulating an immune response (e.g., an antigen-specific T cell response) in a subject comprising administering a therapeutically effective amount of an anti-OX40 antibody described herein to the subject such that an immune response (e.g., an antigen-specific T cell response) in the subject is stimulated. In a preferred embodiment, the subject is a tumor-bearing subject and an immune response against the tumor is stimulated. A tumor may be a solid tumor or a liquid tumor, e.g., a hematological malignancy. In certain embodiments, a tumor is an immunogenic tumor. In certain embodiments, a tumor is non-immunogenic. In certain embodiments, a tumor is PD-L1 positive. In certain embodiments a tumor is PD-L1 negative. A subject may also be a virus-bearing subject and an immune response against the virus is stimulated.

[0397] Further provided are the antibodies for use in methods for inhibiting growth of tumor cells in a subject comprising administering to the subject a therapeutically effective amount of an anti-OX40 antibody described herein such that growth of the tumor is inhibited in the subject. Also provided are the antibodies for use in methods of treating viral infection in a subject comprising administering to the subject an anti-OX40 antibody described herein such that the viral infection is treated in the subject.

[0398] Also encompassed herein are the claimed antibodies for use in methods for depleting Treg cells from the tumor microenvironment of a subject having a tumor, e.g., cancerous tumor, comprising administering to the subject a therapeutically effective amount of an anti-OX40 antibody described herein that comprises an Fc that stimulates depletion of T_{reg} cells in the tumor microenvironment. An Fc may, e.g., be an Fc with effector function or enhanced effector function, such as binding or having enhanced binding to one or more activating Fc receptors. In a preferred

embodiment, T_{reg} depletion occurs without significant depletion or inhibition of T_{eff} in the tumor microenvironment, and without significant depletion or inhibition of T_{eff} cells and T_{reg} cells outside of the tumor microenvironment, e.g., in the periphery. In certain embodiments, the subject has higher levels of OX40 on T_{reg} cells than on T_{eff} cells, e.g., in the tumor microenvironment.

[0399] In certain embodiments, the subject is treated with an anti-OX40 antibody having an Fc that enhances agonism, e.g., binds to or has enhanced binding to the inhibitory FcRIIb. Anti-OX40 antibodies may deplete Tregs in tumors and/or Tregs in tumor infiltrating lymphocytes (TILs).

[0400] In certain embodiments, the anti-OX40 antibody is given to a subject as an adjunctive therapy. Treatments of subjects having cancer with the anti-OX40 antibody may lead to prolonged survival, e.g., long-term durable response relative to the current standard of care; long term survival of at least 3 months, 6 months, 9 months, 1, 2, 3, 4, 5, 10 or more years, or recurrence-free survival of at least 3 months, 6 months, 9 months, 1, 2, 3, 4, 5, or 10 or more years. In certain embodiments, treatment of a subject having cancer with the anti-OX40 antibody prevents recurrence of cancer or delays recurrence of cancer by, e.g., 3 months, 6 months, 9 months, 1, 2, 3, 4, 5, or 10 or more years. The anti-OX40 antibody treatment can be used as a first-, second-, or third-line treatment.

[0401] In preferred embodiments, the anti-OX40 antibody is not significantly toxic. For example, the antibody is not significantly toxic to an organ of a human, e.g., one or more of the liver, kidney, brain, lungs, and heart, as determined, e.g., in clinical trials. In certain embodiments, the antibody does not significantly trigger an undesirable immune response, e.g., autoimmunity or inflammation.

[0402] In certain embodiments, treatment of a subject with the anti-OX40 antibody does not result in overstimulation of the immune system to the extent that the subject's immune system then attacks the subject itself (e.g., autoimmune response) or results in, e.g., anaphylaxis. Thus, the antibodies preferably do not cause anaphylaxis.

[0403] In certain embodiments, treatment of a subject with the anti-OX40 antibody does not cause significant inflammatory reactions, e.g., immune-mediated pneumonitis, immune-mediated colitis, immune mediated hepatitis, immune-mediated nephritis or renal dysfunction, immune-mediated hypophysitis, immune-mediated hypothyroidism and hyperthyroidism, or other immune-mediated adverse reactions.

[0404] In certain embodiments, the anti-OX40 antibody provides synergistic anti-tumor effects in combination with another cancer therapy, such as a compound that stimulates the immune system (e.g., an immune-oncology agent), e.g., a compound described herein or a compound modulating a target described herein.

[0405] These and other methods described herein are discussed in further detail below.

Cancer

[0406] Activation of OX40 by anti-OX40 antibodies can enhance the immune response to cancerous cells in the patient. Accordingly, provided herein are the antibodies for use in methods for treating a subject having cancer, comprising administering to the subject the anti-OX40 antibodies described herein, such that the subject is treated, e.g., such that growth of cancerous tumors is inhibited or reduced and/or that the tumors regress and/or that prolonged survival is achieved. The anti-OX40 antibody can be used alone to inhibit the growth of cancerous tumors. Alternatively, the anti-OX40 antibody can be used in conjunction with another agent, e.g., another immunogenic agent, a standard cancer treatment, or another antibody, as described below.

[0407] Accordingly, provided herein are the antibodies for use in methods of treating cancer, e.g., by inhibiting growth of tumor cells, in a subject, comprising administering to the subject a therapeutically effective amount of anti-OX40 antibodies described herein. The antibody may be a human antibody. Additionally or alternatively, the antibody can be a chimeric or humanized antibody.

[0408] Also provided herein are the antibodies for use in combination therapies comprising administration of an anti-OX40 antibody and an anti-PD-1 or anti-CTLA-4 antibody to treat subjects having tumors (e.g., advanced solid tumors).

[0409] In certain embodiments, provided herein are the antibodies for use in methods of treating cancer wherein an anti-OX40 antibody and an anti-PD-1 antibody or anti-CTLA-4 antibody are administered to a patient with a tumor (e.g., advanced solid tumor) according to a defined clinical dosage regimen. In certain embodiments, the anti-OX40 antibody is OX40.21. In certain embodiments, the anti-PD-1 antibody is BMS-936558 (nivolumab). In certain embodiments, the anti-CTLA-4 antibody is ipilimumab (Yervoy®). In certain embodiments, dosage regimens are adjusted to provide the optimum desired response (e.g., an effective response).

[0410] As used herein, adjunctive or combined administration (coadministration) includes simultaneous administration of the compounds in the same or different dosage form, or separate administration of the compounds (e.g., sequential administration). Thus, the anti-OX40 and anti-PD-1 antibody or anti-CTLA-4 antibody can be simultaneously administered in a single formulation. Alternatively, the anti-OX40 and anti-PD-1 antibody or anti-CTLA-4 antibody can be formulated for separate administration and are administered concurrently or sequentially (e.g., one antibody is administered within about 30 minutes prior to administration of the second antibody).

[0411] For example, the anti-PD-1 antibody or anti-CTLA-4 antibody can be administered first and followed by (e.g., immediately followed by) the administration of the anti-OX40 antibody, or vice versa. In certain embodiments, the anti-PD-1 antibody or anti-CTLA-4 antibody is administered prior to administration of the anti-OX40 antibody. In another embodiment, the anti-PD-1 antibody or anti-CTLA-4 antibody is administered after administration of the anti-OX40 antibody. In another embodiment, the anti-OX40 antibody and anti-PD-1 antibody or anti-CTLA-4 antibody are administered concurrently. Such concurrent or sequential administration preferably results in both antibodies being simultaneously present in treated patients.

[0412] Cancers whose growth may be inhibited with anti-OX40 antibodies, or combination therapy with an anti-OX40 and an anti-PD-1 or anti-CTLA-4 antibody, include cancers typically responsive to immunotherapy and those that are not typically responsive to immunotherapy. Cancers may be cancers with solid tumors or blood malignancies (liquid tumors). Non-limiting examples of cancers for treatment include squamous cell carcinoma, small-cell lung cancer, non-small cell lung cancer, squamous non-small cell lung cancer (NSCLC), non squamous NSCLC, glioma, gastrointestinal cancer, renal cancer (e.g. clear cell carcinoma), ovarian cancer, liver cancer, colorectal cancer, endometrial cancer, kidney cancer (e.g., renal cell carcinoma (RCC)), prostate cancer (e.g. hormone refractory prostate adenocarcinoma), thyroid cancer, neuroblastoma, pancreatic cancer, glioblastoma (glioblastoma multiforme), cervical cancer, stomach cancer, bladder cancer, hepatoma, breast cancer, colon carcinoma, and head and neck cancer (or carcinoma), gastric cancer, germ cell tumor, pediatric sarcoma, sinonasal natural killer, melanoma (e.g., metastatic malignant melanoma, such as cutaneous or intraocular malignant melanoma), bone cancer, skin cancer, uterine cancer, cancer of the anal region, testicular cancer, carcinoma of the fallopian tubes, carcinoma of the endometrium, carcinoma of the cervix, carcinoma of the vagina, carcinoma of the vulva, cancer of the esophagus, cancer of the small intestine, cancer of the endocrine system, cancer of the parathyroid gland, cancer of the adrenal gland, sarcoma of soft tissue, cancer of the urethra, cancer of the penis, solid tumors of childhood, cancer of the ureter, carcinoma of the renal pelvis, neoplasm of the central nervous system (CNS), primary CNS lymphoma, tumor angiogenesis, spinal axis tumor, brain cancer, brain stem glioma, pituitary adenoma, Kaposi's sarcoma, epidermoid cancer, squamous cell cancer, T-cell lymphoma, environmentally-induced cancers including those induced by asbestos, virus-related cancers or cancers of viral origin (e.g., human papilloma virus (HPV)-related or -originating tumors)), and hematologic malignancies derived from either of the two major blood cell lineages, i.e., the myeloid cell line (which produces granulocytes, erythrocytes, thrombocytes, macrophages and mast cells) or lymphoid cell line (which produces B, T, NK and plasma cells), such as all types of leukemias, lymphomas, and myelomas, e.g., acute, chronic, lymphocytic and/or myelogenous leukemias, such as acute leukemia (ALL), acute myelogenous leukemia (AML), chronic lymphocytic leukemia (CLL), and chronic myelogenous leukemia (CML), undifferentiated AML (M0), myeloblastic leukemia (M1), myeloblastic leukemia (M2; with cell maturation), promyelocytic leukemia (M3 or M3 variant [M3V]), myelomonocytic leukemia (M4 or M4 variant with eosinophilia [M4E]), monocytic leukemia (M5), erythroleukemia (M6), megakaryoblastic leukemia (M7), isolated granulocytic sarcoma, and chloroma; lymphomas, such as Hodgkin's lymphoma (HL), non-Hodgkin's lymphoma (NHL), B cell hematologic malignancy, e.g., B-cell lymphomas, T-cell lymphomas, lymphoplasmacytoid lymphoma, monocytoid B-cell lymphoma, mucosa-associated lymphoid tissue (MALT) lymphoma, anaplastic (e.g., Ki 1+) large-cell lymphoma, adult T-cell lymphoma/leukemia, mantle cell lymphoma, angio immunoblastic T-cell lymphoma, angiocentric lymphoma, intestinal T-cell lymphoma, primary mediastinal B-cell lymphoma, precursor T-lymphoblastic lymphoma, T-lymphoblastic; and lymphoma/leukaemia (T-Lbly/T-ALL), peripheral T- cell lymphoma, lymphoblastic lymphoma, post-

transplantation lymphoproliferative disorder, true histiocytic lymphoma, primary central nervous system lymphoma, primary effusion lymphoma, B cell lymphoma, lymphoblastic lymphoma (LBL), hematopoietic tumors of lymphoid lineage, acute lymphoblastic leukemia, diffuse large B-cell lymphoma, Burkitt's lymphoma, follicular lymphoma, diffuse histiocytic lymphoma (DHL), immunoblastic large cell lymphoma, precursor B-lymphoblastic lymphoma, cutaneous T-cell lymphoma (CTLC) (also called mycosis fungoides or Sezary syndrome), and lymphoplasmacytoid lymphoma (LPL) with Waldenstrom's macroglobulinemia; myelomas, such as IgG myeloma, light chain myeloma, nonsecretory myeloma, smoldering myeloma (also called indolent myeloma), solitary plasmocytoma, and multiple myelomas, chronic lymphocytic leukemia (CLL), hairy cell lymphoma; hematopoietic tumors of myeloid lineage, tumors of mesenchymal origin, including fibrosarcoma and rhabdomyosarcoma; seminoma, teratocarcinoma, tumors of the central and peripheral nervous, including astrocytoma, schwannomas; tumors of mesenchymal origin, including fibrosarcoma, rhabdomyosarcoma, and osteosarcoma; and other tumors, including melanoma, xeroderma pigmentosum, keratoacanthoma, seminoma, thyroid follicular cancer and teratocarcinoma, hematopoietic tumors of lymphoid lineage, for example T-cell and B-cell tumors, including but not limited to T-cell disorders such as T-prolymphocytic leukemia (T-PLL), including of the small cell and cerebriform cell type; large granular lymphocyte leukemia (LGL) preferably of the T-cell type; a/d T-NHL hepatosplenic lymphoma; peripheral/post-thymic T cell lymphoma (pleomorphic and immunoblastic subtypes); angiocentric (nasal) T-cell lymphoma; cancer of the head or neck, renal cancer, rectal cancer, cancer of the thyroid gland; acute myeloid lymphoma, as well as any combinations of said cancers. The methods described herein may also be used for treatment of metastatic cancers, unresectable and/or refractory cancers (e.g., cancers refractory to previous immunotherapy, e.g., with a blocking CTLA-4 or PD-1 antibody), and recurrent cancers.

[0413] In certain embodiments, the patient being treated with the anti-OX40 antibody, or combination of anti-OX40 antibody and anti-PD-1 or anti-CTLA-4 antibody, has an advanced solid tumor. For example, in one embodiment, the patient to be treated has cervical cancer. In another embodiment, the patient to be treated has colorectal (CRC) cancer. In another embodiment, the patient to be treated has bladder cancer (e.g., unresectable locally advanced or metastatic bladder cancer). In another embodiment, the patient to be treated has ovarian cancer (e.g., unresectable locally advanced or metastatic ovarian cancer).

[0414] In one embodiment, the patient being treated with the anti-OX40 antibody, or combination of anti-OX40 antibody and anti-PD-1 or anti-CTLA-4 antibody, has non-small cell lung cancer (NSCLC). In another embodiment, the patient to be treated has squamous cell carcinoma of the head and neck (SCCHN). In another embodiment, the patient to be treated has B-cell non-Hodgkin's lymphoma (B-NHL). In another embodiment, the patient to be treated has myeloma. In another embodiment, the patient has melanoma. In another embodiment, the patient to be treated has diffuse large B-cell lymphoma (DLBCL).

[0415] In certain embodiments, the anti-OX40 antibody is administered to patients having a cancer that exhibited an inadequate response to a prior treatment, e.g., a prior treatment with an immuno-oncology drug, or patients having a cancer that is refractory or resistant, either intrinsically refractory or resistant (e.g., refractory to a PD-1 pathway antagonist), or a wherein the resistance or refractory state is acquired. For example, subjects who are not responsive or not sufficiently responsive to a first therapy or who see disease progression following treatment, e.g., anti-PD-1 treatment, may be treated by administration of the anti-OX40 antibody alone or in combination with another therapy (e.g., with an anti-PD-1 therapy).

[0416] In certain embodiments, the anti-OX40 antibody is administered to patients who have not previously received (i.e., been treated with) an immuno-oncology agent, e.g., a PD-1 pathway antagonist.

[0417] In certain embodiments, the anti-OX40 antibody may be administered with a standard of care treatment (e.g., surgery, radiation, and chemotherapy). In other embodiments, the anti-OX40 antibody may be administered as a maintenance therapy, e.g., a therapy that is intended to prevent the occurrence or recurrence of tumors.

[0418] In certain embodiments, the anti-OX40 antibody may be administered with another treatment, e.g., radiation, surgery, or chemotherapy. For example, anti-OX40 antibody adjunctive therapy may be administered when there is a risk that micrometastases may be present and/or in order to reduce the risk of a relapse.

[0419] In certain embodiments, the anti-OX40 antibody can be administered as a monotherapy, or as the only immunostimulating therapy. In other embodiments, the anti-OX40 antibody can also be combined with an immunogenic

agent, such as cancerous cells, purified tumor antigens (including recombinant proteins, peptides, and carbohydrate molecules), cells, and cells transfected with genes encoding immune stimulating cytokines (He et al (2004) J. Immunol. 173:4919-28). Non-limiting examples of tumor vaccines that can be used include peptides of melanoma antigens, such as peptides of gp100, MAGE antigens, Trp-2, MART1 and/or tyrosinase, or tumor cells transfected to express the cytokine GM-CSF (discussed further below).

[0420] In humans, some tumors have been shown to be immunogenic such as melanomas. By lowering the threshold of T cell activation via OX40 activation, the tumor responses in the host can be activated, allowing treatment of non-immunogenic tumors or those having limited immunogenicity.

[0421] In some embodiments, the anti-OX40 antibody can be used in conjunction with a vaccination protocol. Many experimental strategies for vaccination against tumors have been devised (see Rosenberg, S., 2000, Development of Cancer Vaccines, ASCO Educational Book Spring: 60-62; Logothetis, C., 2000, ASCO Educational Book Spring: 300-302; Khayat, D. 2000, ASCO Educational Book Spring: 414-428; Foon, K. 2000, ASCO Educational Book Spring: 730-738; see also Restifo, N. and Sznol, M., Cancer Vaccines, Ch. 61, pp. 3023-3043 in DeVita et al. (eds.), 1997, Cancer: Principles and Practice of Oncology, Fifth Edition). In one such strategy, of these strategies, a vaccine is prepared using autologous or allogeneic tumor cells. These cellular vaccines have been shown to be most effective when the tumor cells are transduced to express GM-CSF. GM-CSF has been shown to be a potent activator of antigen presentation for tumor vaccination (Dranoff et al. (1993) Proc. Natl. Acad. Sci U.S.A. 90: 3539-43).

[0422] The study of gene expression and large scale gene expression patterns in various tumors has led to the definition of so called tumor specific antigens (Rosenberg, S A (1999) Immunity 10: 281-7). In many cases, these tumor specific antigens are differentiation antigens expressed in the tumors and in the cell from which the tumor arose, for example melanocyte antigens gp100, MAGE antigens, and Trp-2. More importantly, many of these antigens can be shown to be the targets of tumor specific T cells found in the host. OX40 activation can be used in conjunction with a collection of recombinant proteins and/or peptides expressed in a tumor in order to generate an immune response to these proteins. These proteins are normally viewed by the immune system as self antigens and are therefore tolerant to them. The tumor antigen can include the protein telomerase, which is required for the synthesis of telomeres of chromosomes and which is expressed in more than 85% of human cancers and in only a limited number of somatic tissues (Kim et al. (1994) Science 266: 2011-2013). Tumor antigen can also be "neo-antigens" expressed in cancer cells because of somatic mutations that alter protein sequence or create fusion proteins between two unrelated sequences (i.e., bcr-abl in the Philadelphia chromosome), or idiotype from B cell tumors.

[0423] Other tumor vaccines can include the proteins from viruses implicated in human cancers such a Human Papilloma Viruses (HPV), Hepatitis Viruses (HBV and HCV) and Kaposi's Herpes Sarcoma Virus (KHSV). Another form of tumor specific antigen which can be used in conjunction with OX40 activation is purified heat shock proteins (HSP) isolated from the tumor tissue itself. These heat shock proteins contain fragments of proteins from the tumor cells and these HSPs are highly efficient at delivery to antigen presenting cells for eliciting tumor immunity (Suot & Srivastava (1995) Science 269:1585-1588; Tamura et al. (1997) Science 278:117-120).

[0424] Dendritic cells (DC) are potent antigen presenting cells that can be used to prime antigen-specific responses. DC's can be produced *ex vivo* and loaded with various protein and peptide antigens as well as tumor cell extracts (Nestle et al. (1998) Nature Medicine 4: 328-332). DCs can also be transduced by genetic means to express these tumor antigens as well. DCs have also been fused directly to tumor cells for the purposes of immunization (Kugler et al. (2000) Nature Medicine 6:332-336). As a method of vaccination, DC immunization can be effectively combined with OX40 activation to activate more potent anti-tumor responses.

[0425] Anti-OX40 antibodies described herein can also be combined with chemotherapeutic regimes. In these instances, it may be possible to reduce the dose of chemotherapeutic reagent administered (Mokyr et al. (1998) Cancer Research 58: 5301-5304). For example, the anti-OX40 antibody can be used in combination with decarbazine to treat melanoma. In another example, the anti-OX40 antibody can be used in combination with interleukin-2 (IL-2) to treat melanoma. The scientific rationale behind the combined use of anti-OX40 antibodies and chemotherapy is that cell death, a consequence of the cytotoxic action of most chemotherapeutic compounds, should result in increased levels of tumor antigen in the antigen presentation pathway. Other combination therapies that may result in synergy with anti-OX40 antibodies through cell death are radiation, surgery, and hormone deprivation. Each of these protocols

creates a source of tumor antigen in the host. Angiogenesis inhibitors can also be used in combination with the anti-OX40 antibody. Inhibition of angiogenesis leads to tumor cell death which may feed tumor antigen into host antigen presentation pathways.

[0426] Anti-OX40 antibodies described herein can also be used in combination with bispecific antibodies that target Fc α or Fc γ receptor-expressing effector cells to tumor cells (see, e.g., U.S. Pat. Nos. 5,922,845 and 5,837,243). Bispecific antibodies can be used to target two separate antigens. For example anti-Fc receptor/anti tumor antigen (e.g., Her-2/neu) bispecific antibodies have been used to target macrophages to sites of tumor. This targeting may more effectively activate tumor specific responses. The T cell arm of these responses would be augmented by the activation of OX40. Alternatively, antigen may be delivered directly to DCs by the use of bispecific antibodies which bind to tumor antigen and a dendritic cell specific cell surface marker.

[0427] Tumors evade host immune surveillance by a large variety of mechanisms. Many of these mechanisms may be overcome by the inactivation of proteins which are expressed by the tumors and which are immunosuppressive. These include among others TGF- β (Kehrl et al. (1986) J. Exp. Med. 163: 1037-1050), IL-10 (Howard & O'Garra (1992) Immunology Today 13: 198-200), and Fas ligand (Hahne et al. (1996) Science 274: 1363-1365). Antibodies to each of these entities can be used in combination with anti-OX40 antibodies to counteract the effects of the immunosuppressive agent and favor tumor immune responses by the host.

[0428] Other antibodies which activate host immune responsiveness can be used in combination with the anti-OX40 antibodies described herein. These include molecules on the surface of dendritic cells which activate DC function and antigen presentation. Anti-CD40 antibodies are able to substitute effectively for T cell helper activity (Ridge et al. (1998) Nature 393: 474-478) and can be used in conjunction with anti-OX40 antibodies. Activating antibodies to T cell costimulatory molecules such as CTLA-4 (e.g., U.S. Pat. No. 5,811,097), OX-40 (Weinberg et al. (2000) Immunol 164: 2160-2169), 4-1BB (Melero et al. (1997) Nature Medicine 3: 682-685 (1997), and ICOS (Hutloff et al. (1999) Nature 397: 262-266) may also provide for increased levels of T cell activation. Inhibitors of PD1 or PD-L1 may also be used in conjunction with anti-OX40 antibodies.

[0429] Bone marrow transplantation is currently being used to treat a variety of tumors of hematopoietic origin. While graft versus host disease is a consequence of this treatment, therapeutic benefit may be obtained from graft vs. tumor responses. Anti-OX40 antibodies can be used to increase the effectiveness of the donor engrafted tumor specific T cells.

[0430] There are also several experimental treatment protocols that involve *ex vivo* activation and expansion of antigen specific T cells and adoptive transfer of these cells into recipients in order to stimulate antigen-specific T cells against tumor (Greenberg & Riddell (1999) Science 285: 546-51). These methods can also be used to activate T cell responses to infectious agents such as CMV. *Ex vivo* activation in the presence of anti-OX40 antibodies can increase the frequency and activity of the adoptively transferred T cells.

Infectious Diseases

[0431] Also provided herein are the claimed antibodies for use in methods to treat patients who have been exposed to particular toxins or pathogens. Accordingly, provided herein are methods of treating an infectious disease in a subject comprising administering to the subject anti-OX40 antibodies described herein, such that the subject is treated for the infectious disease.

[0432] Similar to its application to tumors as discussed above, anti-OX40 antibodies can be used alone, or as an adjuvant, in combination with vaccines, to stimulate the immune response to pathogens, toxins, and self-antigens. Examples of pathogens for which this therapeutic approach can be particularly useful, include pathogens for which there is currently no effective vaccine, or pathogens for which conventional vaccines are less than completely effective. These include, but are not limited to HIV, Hepatitis (A, B, & C), Influenza, Herpes, Giardia, Malaria, Leishmania, *Staphylococcus aureus*, *Pseudomonas aeruginosa*. Anti-OX40 antibodies may be useful against established infections by agents such as HIV that present altered antigens over the course of the infections. These novel epitopes are recognized as foreign at the time of anti-OX40 antibody administration, thus provoking a strong T cell response.

[0433] Some examples of pathogenic viruses causing infections treatable by the methods described herein include HIV, hepatitis (A, B, or C), herpes virus (e.g., VZV, HSV-1, HAV-6, HSV-II, and CMV, Epstein Barr virus), adenovirus, influenza virus, flaviviruses, echovirus, rhinovirus, coxsackie virus, coronavirus, respiratory syncytial virus, mumps virus, rotavirus, measles virus, rubella virus, parvovirus, vaccinia virus, HTLV virus, dengue virus, papillomavirus, molluscum virus, poliovirus, rabies virus, JC virus and arboviral encephalitis virus.

[0434] Some examples of pathogenic bacteria causing infections treatable by the methods described herein include chlamydia, rickettsial bacteria, mycobacteria, staphylococci, streptococci, pneumonococci, meningococci and gonococci, klebsiella, proteus, serratia, pseudomonas, legionella, diphtheria, salmonella, bacilli, cholera, tetanus, botulism, anthrax, plague, leptospirosis, and Lymes disease bacteria.

[0435] Some examples of pathogenic fungi causing infections treatable by the methods described herein include *Candida* (albicans, krusei, glabrata, tropicalis, etc.), *Cryptococcus neoformans*, *Aspergillus* (fumigatus, niger, etc.), Genus *Mucorales* (mucor, absidia, rhizopus), *Sporothrix schenckii*, *Blastomyces dermatitidis*, *Paracoccidioides brasiliensis*, *Coccidioides immitis* and *Histoplasma capsulatum*.

[0436] Some examples of pathogenic parasites causing infections treatable by the methods described herein include *Entamoeba histolytica*, *Balantidium coli*, *Naegleria fowleri*, *Acanthamoeba* sp., *Giardia lamblia*, *Cryptosporidium* sp., *Pneumocystis carinii*, *Plasmodium vivax*, *Babesia microti*, *Trypanosoma brucei*, *Trypanosoma cruzi*, *Leishmania donovani*, *Toxoplasma gondii*, *Nippostrongylus brasiliensis*.

[0437] In all of the above methods, anti-OX40 antibodies can be combined with other forms of immunotherapy such as cytokine treatment (e.g., interferons, GM-CSF, G-CSF, IL-2), or bispecific antibody therapy, which provides for enhanced presentation of tumor antigens (see, e.g., Holliger (1993) Proc. Natl. Acad. Sci. USA 90:6444-6448; Poljak (1994) Structure 2:1121-1123).

Autoimmune Reactions

[0438] Anti-OX40 antibodies may provoke and amplify autoimmune responses. Indeed, induction of anti-tumor responses using tumor cell and peptide vaccines reveals that many anti-tumor responses involve anti-self reactivities (van Elsas et al. (2001) J. Exp. Med. 194:481-489; Overwijk, et al. (1999) Proc. Natl. Acad. Sci. U.S.A. 96: 2982-2987; Hurwitz, (2000) supra; Rosenberg & White (1996) J. Immunother Emphasis Tumor Immunol 19 (1): 81-4). Therefore, anti-OX40 antibodies can be used in conjunction with various self proteins in order to devise vaccination protocols to efficiently generate immune responses against these self proteins for disease treatment. For example, Alzheimer's disease involves inappropriate accumulation of A β peptide in amyloid deposits in the brain; antibody responses against amyloid are able to clear these amyloid deposits (Schenk et al., (1999) Nature 400: 173-177).

[0439] Other self proteins can also be used as targets such as IgE for the treatment of allergy and asthma, and TNF α for rheumatoid arthritis. Finally, antibody responses to various hormones may be induced by the use of anti-OX40 antibodies. Neutralizing antibody responses to reproductive hormones can be used for contraception. Neutralizing antibody response to hormones and other soluble factors that are required for the growth of particular tumors can also be considered as possible vaccination targets.

[0440] Analogous methods as described above for the use of anti-OX40 antibodies can be used for induction of therapeutic autoimmune responses to treat patients having an inappropriate accumulation of other self-antigens, such as amyloid deposits, including A β in Alzheimer's disease, cytokines such as TNF α , and IgE.

Vaccines

[0441] The claimed anti-OX40 antibodies can be used to stimulate antigen-specific immune responses by coadministration of the antibodies with an antigen of interest (e.g., a vaccine). Accordingly, provided herein are the claimed antibodies for use in methods of enhancing an immune response to an antigen in a subject, comprising

administering to the subject: (i) the antigen; and (ii) an anti-OX40 antibody such that an immune response to the antigen in the subject is enhanced. The antibody may be a human anti-OX40 antibody (such as any of the human anti-OX40 antibodies described herein). The antigen can be, for example, a tumor antigen, a viral antigen, a bacterial antigen or an antigen from a pathogen. Non-limiting examples of such antigens include those discussed in the sections above, such as the tumor antigens (or tumor vaccines) discussed above, or antigens from the viruses, bacteria or other pathogens described above.

[0442] Suitable routes of administering the antibody compositions (e.g., human monoclonal antibodies, multispecific and bispecific molecules and immunoconjugates) described herein *in vivo* and *in vitro* are well known in the art and can be selected by those of ordinary skill. For example, the antibody compositions can be administered by injection (e.g., intravenous or subcutaneous). Suitable dosages of the molecules used will depend on the age and weight of the subject and the concentration and/or formulation of the antibody composition.

[0443] As previously described, anti-OX40 antibodies described herein can be co-administered with one or other more therapeutic agents, e.g., a cytotoxic agent, a radiotoxic agent or an immunosuppressive agent. The antibody can be linked to the agent (as an immuno-complex) or can be administered separate from the agent. In the latter case (separate administration), the antibody can be administered before, after or concurrently with the agent or can be co-administered with other known therapies, e.g., an anti-cancer therapy, e.g., radiation. Such therapeutic agents include, among others, anti-neoplastic agents such as doxorubicin (adriamycin), cisplatin bleomycin sulfate, carmustine, chlorambucil, dacarbazine and cyclophosphamide hydroxyurea which, by themselves, are only effective at levels which are toxic or subtoxic to a patient. Cisplatin is intravenously administered as a 100 mg/ml dose once every four weeks and adriamycin is intravenously administered as a 60-75 mg/ml dose once every 21 days. Co-administration of anti-OX40 antibodies, or antigen binding fragments thereof, described herein with chemotherapeutic agents provides two anti-cancer agents which operate via different mechanisms which yield a cytotoxic effect to human tumor cells. Such co-administration can address problems related to the development of resistance to drugs or a change in the antigenicity of the tumor cells which would render them unreactive with the antibody.

[0444] Also provided herein are non-claimed kits comprising the anti-OX40 antibody compositions described herein (e.g., human antibodies, bispecific or multispecific molecules, or immunoconjugates) and instructions for use. The kit can further contain at least one additional reagent, or one or more additional human antibodies described herein (e.g., a human antibody having a complementary activity which binds to an epitope in OX40 distinct from the first human antibody). Kits typically include a label indicating the intended use of the contents of the kit. The term label includes any writing, or recorded material supplied on or with the kit, or which otherwise accompanies the kit.

Treatment protocols

[0445] Suitable but non-claimed protocols for treating a solid tumor (e.g., an advanced solid tumor) in a human patient include, for example, administering to the patient an effective amount of an anti-OX40 antibody comprising CDR1, CDR2 and CDR3 domains of the heavy chain variable region having the sequence set forth in SEQ ID NO: 318, and CDR1, CDR2 and CDR3 domains of the light chain variable region having the sequence set forth in SEQ ID NO: 94, wherein the method comprises at least one administration cycle, wherein the cycle is a period of two weeks (Q2W), wherein for each of the at least one cycles, at least one dose of the anti-OX40 antibody is administered at a dose of 1 mg/kg body weight; a fixed dose of 20, 40, 80, 160, or 320 mg; a dose of about 1 mg/kg body weight; or a fixed dose of about 20, 40, 80, 160, or 320 mg.

[0446] Another suitable protocol for treating a solid tumor in a human patient includes, for example, administering to the patient an effective amount of each of:

1. (a) an anti-OX40 antibody comprising CDR1, CDR2 and CDR3 domains of the heavy chain variable region having the sequence set forth in SEQ ID NO: 318, and CDR1, CDR2 and CDR3 domains of the light chain variable region having the sequence set forth in SEQ ID NO: 94, and
2. (b) an anti-PD-1 antibody comprising CDR1, CDR2 and CDR3 domains of the heavy chain variable region having the sequence set forth in SEQ ID NO: 301, and CDR1, CDR2 and CDR3 domains of the light chain variable region having the sequence set forth in SEQ ID NO: 302,

wherein the method comprises at least one administration cycle, wherein the cycle is a period of two weeks, wherein for each of the at least one cycles, at least one dose of the anti-OX40 antibody is administered at a dose of 1 mg/kg body weight; a fixed dose of 20, 40, 80, 160, or 320 mg; a dose of about 1 mg/kg body weight; or a fixed dose of about 20, 40, 80, 160, or 320 mg, and at least one dose of the anti-PD-1 antibody is administered at flat dose of 240 mg or a flat dose of about 240 mg. In some embodiments, the anti-PD-1 antibody is administered once every three weeks (q3w) at a fixed dose of 360 mg, or once every four weeks (q4w) at a dose of 480 mg.

[0447] Another suitable protocol for treating a solid tumor in a human patient includes, for example, administering to the patient an effective amount of each of:

1. (a) an anti-OX40 antibody comprising CDR1, CDR2 and CDR3 domains of the heavy chain variable region having the sequence set forth in SEQ ID NO: 318, and CDR1, CDR2 and CDR3 domains of the light chain variable region having the sequence set forth in SEQ ID NO: 94, and
2. (b) an anti-CTLA-4 antibody comprising CDR1, CDR2 and CDR3 domains of the heavy chain variable region having the sequence set forth in SEQ ID NO: 309, and CDR1, CDR2 and CDR3 domains of the light chain variable region having the sequence set forth in SEQ ID NO: 310,

wherein the method comprises at least one administration cycle, wherein the cycle is a period of three weeks (q3w), wherein for each of the at least one cycles, at least one dose of the anti-OX40 antibody is administered at a dose of 1 mg/kg body weight; a fixed dose of 20, 40, 80, 160, or 320 mg; a dose of about 1 mg/kg body weight; or a fixed dose of about 20, 40, 80, 160, or 320 mg, and at least one dose of the anti-CTLA-4 antibody is administered at flat dose of 1 mg/kg body weight or a flat dose of about 1 mg/kg body weight. In one embodiment, the anti-OX40 antibody is administered together with the anti-CTLA-4 antibody for at least one cycle, followed by anti-OX40 antibody monotherapy for at least one cycle. In certain embodiments, the anti-OX40 antibody is administered together with ipilimumab for the initial four cycles, followed by anti-OX40 antibody monotherapy for subsequent cycles.

[0448] In some embodiments, the anti-OX40 antibody and anti-PD-1 antibody are administered at the following doses:

1. (a) 1 mg/kg anti-OX40 antibody and 240 mg, 360 mg, or 480 mg of anti-PD-1 antibody;
2. (b) 20 mg anti-OX40 antibody and 240 mg, 360 mg, or 480 mg of anti-PD-1 antibody;
3. (c) 40 mg anti-OX40 antibody and 240 mg, 360 mg, or 480 mg of anti-PD-1 antibody;
4. (d) 80 mg anti-OX40 antibody and 240 mg, 360 mg, or 480 mg of anti-PD-1 antibody;
5. (e) 160 mg anti-OX40 antibody and 240 mg, 360 mg, or 480 mg of anti-PD-1 antibody; or
6. (f) 320 mg anti-OX40 antibody and 240 mg, 360 mg, or 480 mg of anti-PD-1 antibody.

[0449] In some embodiments, the anti-OX40 antibody and anti-CTLA-4 antibody are administered at the following doses:

1. (a) 1 mg/kg anti-OX40 antibody and 1 mg/kg anti-CTLA-4 antibody;
2. (b) 20 mg anti-OX40 antibody and 1 mg/kg anti-CTLA-4 antibody;
3. (c) 40 mg anti-OX40 antibody and 1 mg/kg anti-CTLA-4 antibody;
4. (d) 80 mg anti-OX40 antibody and 1 mg/kg anti-CTLA-4 antibody;
5. (e) 160 mg anti-OX40 antibody and 1 mg/kg anti-CTLA-4 antibody; or
6. (f) 320 mg anti-OX40 antibody and 1 mg/kg anti-CTLA-4 antibody.

[0450] In one embodiment, the dose of the anti-OX40 and/or anti-PD-1 or anti-CTLA-4 antibody is calculated per body weight, e.g., mg/kg body weight. In another embodiment, the dose of the anti-OX40 and/or anti-PD-1 or anti-CTLA-4 antibody is a flat-fixed dose. In another embodiment, the dose of the anti-OX40 and/or anti-PD-1 or anti-CTLA-4 antibody is varied over time. For example, the anti-OX40 and/or anti-PD-1 or anti-CTLA-4 antibody may be initially administered at a high dose and may be lowered over time. In another embodiment, the anti-OX40 and/or anti-PD-1 or anti-CTLA-4 antibody is initially administered at a low dose and increased over time.

[0451] In another embodiment, the amount of the anti-OX40 and/or anti-PD-1 or anti-CTLA-4 antibody administered is

constant for each dose. In another embodiment, the amount of antibody administered varies with each dose. For example, the maintenance (or follow-on) dose of the antibody can be higher or the same as the loading dose which is first administered. In another embodiment, the maintenance dose of the antibody can be lower or the same as the loading dose.

[0452] In some embodiments, the anti-OX40 and/or anti-PD-1 or anti-CTLA-4 antibody are formulated for intravenous administration. In some embodiments, the anti-OX40 antibody, or anti-OX40 antibody and anti-PD-1 or CTLA-4 antibody, are administered on Day 1 of each cycle.

[0453] In some embodiments, the anti-OX40 and/or anti-PD-1 or anti-CTLA-4 antibody are administered once per week, once every two weeks, once every three weeks, or once every four weeks, or as long as a clinical benefit is observed or until there is a complete response, confirmed progressive disease or unmanageable toxicity.

[0454] In one embodiment, a cycle of administration is two weeks, which can be repeated, as necessary. In another embodiment, the cycle is three weeks. In some embodiments, the treatment consists of up to eight cycles. In other embodiments, the treatment consists of up to 12 cycles.

[0455] In one embodiment, one dose each of an anti-OX40 antibody and an anti-PD-1 antibody is administered per two week cycle. In another embodiment, one dose each of the anti-PD-1 antibody and anti-OX40 antibody is administered per three week cycle. In another embodiment, one dose each of the anti-PD-1 antibody and anti-OX40 antibody is administered per four week cycle.

[0456] In one embodiment, one dose each of the anti-OX40 antibody and anti-CTLA-4 antibody is administered per three week cycle. In some embodiments, one dose each of the anti-OX40 antibody and anti-CTLA-4 antibody is administered per three week cycle for the first four cycles, followed by anti-OX40 antibody monotherapy for the fifth through eighth cycles.

[0457] In another embodiment, the anti-OX40 antibody and anti-PD-1 or anti-CTLA-4 antibody are administered as a first line of treatment (e.g., the initial or first treatment). In another embodiment, the anti-OX40 antibody and anti-PD-1 or anti-CTLA-4 antibody are administered as a second line of treatment (e.g., after the initial or first treatment, including after relapse and/or where the first treatment has failed).

[0458] In another aspect, the invention features any of the aforementioned embodiments, wherein the anti-PD-1 antibody is replaced by, or combined with, an anti-PD-L1 or anti-PD-L2 antibody.

[0459] In some embodiments, the human patient has a cancer selected from the group consisting of cervical cancer, bladder cancer, colorectal cancer, and ovarian cancer.

[0460] The anti-OX40 antibody comprises heavy and light chain variable regions comprising the sequences set forth in SEQ ID NOs: 318 and 94, respectively. In certain embodiments, the anti-OX40 antibody comprises heavy and light chain sequences comprising the sequences set forth in SEQ ID NOs: 124 and 116, respectively.

[0461] In certain embodiments, the anti-PD-1 antibody comprises a heavy chain variable region CDR1, CDR2, and CDR3 comprising the sequences set forth in SEQ ID NOs: 303-305, respectively, and light chain variable region CDR1, CDR2, and CDR3 comprising the sequences set forth in SEQ ID NOs: 306-308, respectively. In certain embodiments, the anti-PD-1 antibody comprises heavy and light chain variable regions sequences set forth in SEQ ID NOs: 301 and 302, respectively. In certain embodiments, the anti-PD-1 antibody comprises heavy and light chain sequences set forth in SEQ ID NOs: 299 and 300, respectively.

[0462] In certain embodiments, the anti-CTLA-4 antibody comprises a heavy chain variable region CDR1, CDR2, and CDR3 comprising the sequences set forth in SEQ ID NOs: 311-313, respectively, and light chain variable region CDR1, CDR2, and CDR3 comprising the sequences set forth in SEQ ID NOs: 314-316, respectively. In certain embodiments, the anti-CTLA-4 antibody comprises heavy and light chain variable regions sequences set forth in SEQ ID NOs: 309 and 310, respectively.

Outcomes

[0463] With respect to target lesions, responses to therapy may include:

Complete Response (CR) (RECIST V1.1)	Disappearance of all target lesions. Any pathological lymph nodes (whether target or non-target) must have reduction in short axis to < 10 mm.
Partial Response (PR) (RECIST V1.1)	At least a 30% decrease in the sum of the diameters of target lesions, taking as reference the baseline sum diameters.
Progressive Disease (PD) (RECIST V1.1)	At least a 20% increase in the sum of the diameters of target lesions, taking as reference the smallest sum on study (this includes the baseline sum if that is the smallest on study). In addition to the relative increase of 20%, the sum must also demonstrate an absolute increase of at least 5 mm. (Note: the appearance of one or more new lesions is also considered progression).
Stable Disease (SD) (RECIST V1.1)	Neither sufficient shrinkage to qualify for PR nor sufficient increase to qualify for PD, taking as reference the smallest sum diameters while on study.
Immune-related Complete Response (irCR) (irRECIST)	Disappearance of all target lesions. Any pathological lymph nodes (whether target or non-target) must have reduction in short axis to < 10 mm.
Immune-related Partial Response (irPR) (irRECIST)	At least a 30% decrease in the sum of diameters of target lesions and all new measurable lesions (ie Percentage Change in Tumor Burden), taking as reference the baseline sum diameters. Note: the appearance of new measurable lesions is factored into the overall Tumor Burden, but does not automatically qualify as progressive disease until the sum of the diameters increases by $\geq 20\%$ when compared to nadir.
Immune-related Progressive Disease (irPD) (irRECIST)	At least a 20% increase in Tumor Burden (ie the sum of diameters of target lesions, and any new measurable lesions) taking as reference the smallest sum on study (this includes the baseline sum if that is the smallest on study). In addition to the relative increase of 20%, the sum must also demonstrate an absolute increase of at least 5 mm. Tumor assessments using immune-related criteria for progressive disease incorporates the contribution of new measurable lesions. Each net percentage change in tumor burden per assessment accounts for the size and growth kinetics of both old and new lesions as they appear.
Immune-related Stable Disease (irSD) (irRECIST)	Neither sufficient shrinkage to qualify for irPR nor sufficient increase to qualify for irPD, taking as reference the smallest sum diameters while on study.

[0464] With respect to non-target lesions, responses to therapy may include:

Complete Response (CR) (RECIST V1.1)	Disappearance of all non-target lesions. All lymph nodes must be non-pathological in size (<10 mm short axis).
Non-CR/Non-PD (RECIST V1.1)	Persistence of one or more non-target lesion(s).
Progressive Disease (PD) (RECIST V1.1)	<i>Unequivocal progression</i> of existing non-target lesions. The appearance of one or more new lesions is also considered progression.
Immune-related Complete Response (irCR) (irRECIST)	Disappearance of all non-target lesions. All lymph nodes must be non-pathological in size (< 10 mm short axis).
Immune-related Progressive Disease (irPD) (irRECIST)	Increases in number or size of non-target lesion(s) does not constitute progressive disease unless/until Tumor Burden

increases by 20% (ie the sum of the diameters at nadir of target lesions and any new measurable lesions increases by the required amount). Non-target lesions are not considered in the definition of Stable Disease and Partial Response.

[0465] Patients treated according to the methods disclosed herein preferably experience improvement in at least one sign of cancer. In one embodiment, improvement is measured by a reduction in the quantity and/or size of measurable tumor lesions. In another embodiment, lesions can be measured on chest x-rays or CT or MRI films. In another embodiment, cytology or histology can be used to evaluate responsiveness to a therapy.

[0466] In one embodiment, the patient treated exhibits a complete response (CR), a partial response (PR), stable disease (SD), immune-related complete disease (irCR), immune-related partial response (irPR), or immune-related stable disease (irSD). In another embodiment, the patient treated experiences tumor shrinkage and/or decrease in growth rate, *i.e.*, suppression of tumor growth. In another embodiment, unwanted cell proliferation is reduced or inhibited. In yet another embodiment, one or more of the following can occur: the number of cancer cells can be reduced; tumor size can be reduced; cancer cell infiltration into peripheral organs can be inhibited, retarded, slowed, or stopped; tumor metastasis can be slowed or inhibited; tumor growth can be inhibited; recurrence of tumor can be prevented or delayed; one or more of the symptoms associated with cancer can be relieved to some extent.

[0467] In other embodiments, administration of effective amounts of the anti-OX40 antibody and anti-PD-1 or anti-CTLA-4 antibody according to any of the methods disclosed herein produces at least one therapeutic effect selected from the group consisting of reduction in size of a tumor, reduction in number of metastatic lesions appearing over time, complete remission, partial remission, or stable disease. In still other embodiments, the methods of treatment produce a comparable clinical benefit rate ($\text{CBR} = \text{CR} + \text{PR} + \text{SD} \geq 6 \text{ months}$) better than that achieved by an anti-OX40 antibody or anti-PD-1 or anti-CTLA-4 antibody alone. In other embodiments, the improvement of clinical benefit rate is about 20%, 30%, 40%, 50%, 60%, 70%, 80% or more compared to an anti-OX40 antibody or anti-PD-1 or anti-CTLA-4 antibody alone.

Combination Therapies

[0468] In addition to the combinations therapies disclosed above, anti-OX40 antibodies described herein can be used in combination therapy, as described below.

[0469] Methods of combination therapy include those in which an anti-OX40 antibody, or a combination of anti-OX40 antibody and anti-PD-1 or anti-CTLA-4 antibody, is coadministered with one or more additional agents, *e.g.*, small molecule drugs, antibodies or antigen binding portions thereof, and which are effective in stimulating immune responses to thereby further enhance, stimulate or upregulate immune responses in a subject. For instance, as shown in the Examples, the administration of an anti-OX40 antibody and an antagonist anti-PD-1 antibody to mice can result in a synergic effect in inhibiting tumor growth.

[0470] The anti-OX40 antibody can be combined with (i) an agonist of a stimulatory (*e.g.*, co-stimulatory) molecule (*e.g.*, receptor or ligand) and/or (ii) an antagonist of an inhibitory signal or molecule (*e.g.*, receptor or ligand) on immune cells, such as T cells, both of which result in amplifying immune responses, such as antigen-specific T cell responses. In certain aspects, an immuno-oncology agent is (i) an agonist of a stimulatory (including a co-stimulatory) molecule (*e.g.*, receptor or ligand) or (ii) an antagonist of an inhibitory (including a co-inhibitory) molecule (*e.g.*, receptor or ligand) on cells involved in innate immunity, *e.g.*, NK cells, and wherein the immuno-oncology agent enhances innate immunity. Such immuno-oncology agents are often referred to as immune checkpoint regulators, *e.g.*, immune checkpoint inhibitor or immune checkpoint stimulator.

[0471] In certain embodiments, the anti-OX40 antibody is administered with an agent that targets a stimulatory or inhibitory molecule that is a member of the immunoglobulin super family (IgSF). For example, the anti-OX40 antibody may be administered to a subject with an agent that targets a member of the IgSF family to increase an immune response. In other embodiments, the anti-OX40 antibody may be administered with an agent that targets (or binds specifically to) a member of the B7 family of membrane-bound ligands that includes B7-1, B7-2, B7-H1 (PD-L1), B7-DC

(PD-L2), B7-H2 (ICOS-L), B7-H3, B7-H4, B7-H5 (VISTA), and B7-H6 or a co-stimulatory or co-inhibitory receptor binding specifically to a B7 family member.

[0472] The anti-OX40 antibody may also be administered with an agent that targets a member of the TNF and TNFR family of molecules (ligands or receptors), such as CD40 and CD40L, GITR, GITR-L, CD70, CD27L, CD30, CD30L, 4-1BBL, CD137, TRAIL/Apo2-L, TRAILR1/DR4, TRAILR2/DR5, TRAILR3, TRAILR4, OPG, RANK, RANKL, TWEAKR/Fn14, TWEAK, BAFFR, EDAR, XEDAR, TACI, APRIL, BCMA, LT β R, LIGHT, DcR3, HVEM, VEGI/TL1A, TRAMP/DR3, EDA1, EDA2, TNFR1, Lymphotoxin α /TNF β , TNFR2, TNF α , LT β R, Lymphotoxin α 1 β 2, FAS, FASL, RELT, DR6, TROY, and NGFR (see, e.g., Tansey (2009) Drug Discovery Today 00:1).

[0473] T cell responses can be stimulated by a combination of anti-OX40 antibodies and one or more of the following agents:

1. (1) An antagonist (inhibitor or blocking agent) of a protein that inhibits T cell activation (e.g., immune checkpoint inhibitors), such as CTLA-4, PD-1, PD-L1, PD-L2, and LAG-3, as described above, and any of the following proteins: TIM-3, Galectin 9, CEACAM-1, BTLA, CD69, Galectin-1, TIGIT, CD113, GPR56, VISTA, B7-H3, B7-H4, 2B4, CD48, GARP, PD1H, LAIR1, TIM-1, and TIM-4; and/or
2. (2) An agonist of a protein that stimulates T cell activation, such as B7-1, B7-2, CD28, 4-1BB (CD137), 4-1BBL, ICOS, ICOS-L, GITR, GITR-L, CD70, CD27, CD40, DR3 and CD28H.

[0474] Exemplary agents that modulate one of the above proteins and may be combined with the anti-OX40 antibody for treating cancer, include: Yervoy[™] (ipilimumab) or Tremelimumab (to CTLA-4), galiximab (to B7.1), BMS-936558 (to PD-1), MK-3475 (to PD-1), AMP224 (to B7DC), BMS-936559 (to B7-H1), MPDL3280A (to B7-H1), MEDI-570 (to ICOS), AMG557 (to B7H2), MGA271 (to B7H3), IMP321 (to LAG-3), BMS-663513 (to CD137), PF-05082566 (to CD137), CDX-1127 (to CD27), Atacicept (to TACI), CP-870893 (to CD40), Lucatumumab (to CD40), Dacetuzumab (to CD40), Muromonab-CD3 (to CD3), Ipilimumab (to CTLA-4).

[0475] Anti-OX40 antibodies may also be administered with pidilizumab (CT-011).

[0476] Other molecules that can be combined with the anti-OX40 antibody for the treatment of cancer include antagonists of inhibitory receptors on NK cells or agonists of activating receptors on NK cells. For example, the anti-OX40 antibody can be combined with antagonists of KIR (e.g., lirilumab).

[0477] T cell activation is also regulated by soluble cytokines, and anti-OX40 antibodies may be administered to a subject, e.g., having cancer, with antagonists of cytokines that inhibit T cell activation or agonists of cytokines that stimulate T cell activation.

[0478] In certain embodiments, anti-OX40 antibodies can be used in combination with (i) antagonists (or inhibitors or blocking agents) of proteins of the IgSF family or B7 family or the TNF family that inhibit T cell activation or antagonists of cytokines that inhibit T cell activation (e.g., IL-6, IL-10, TGF- β , VEGF; "immunosuppressive cytokines") and/or (ii) agonists of stimulatory receptors of the IgSF family, B7 family or the TNF family or of cytokines that stimulate T cell activation, for stimulating an immune response, e.g., for treating proliferative diseases, such as cancer.

[0479] Yet other agents for combination therapies include agents that inhibit or deplete macrophages or monocytes, including but not limited to CSF-1R antagonists such as CSF-1R antagonist antibodies including RG7155 (WO11/70024, WO11/107553, WO11/131407, WO13/87699, WO13/119716, WO13/132044) or FPA-008 (WO11/140249; WO13169264; WO14/036357).

[0480] The anti-OX40 antibodies may also be administered with agents that inhibit TGF- β signaling.

[0481] Additional agents that may be combined with the anti-OX40 antibodies described herein include agents that enhance tumor antigen presentation, e.g., dendritic cell vaccines, GM-CSF secreting cellular vaccines, CpG oligonucleotides, and imiquimod, or therapies that enhance the immunogenicity of tumor cells (e.g., anthracyclines).

[0482] Yet other therapies that may be combined with the anti-OX40 antibodies include therapies that deplete or block Treg cells, e.g., an agent that specifically binds to CD25.

[0483] Another therapy that may be combined with the anti-OX40 antibodies is a therapy that inhibits a metabolic enzyme such as indoleamine dioxigenase (IDO), dioxigenase, arginase, or nitric oxide synthetase.

[0484] Another class of agents that may be used with the anti-OX40 antibodies includes agents that inhibit the formation of adenosine or inhibit the adenosine A2A receptor.

[0485] Other therapies that may be combined with anti-OX40 antibodies for treating cancer include therapies that reverse/prevent T cell anergy or exhaustion and therapies that trigger an innate immune activation and/or inflammation at a tumor site.

[0486] The anti-OX40 antibody may be combined with more than one immuno-oncology agent, and may be, e.g., combined with a combinatorial approach that targets multiple elements of the immune pathway, such as one or more of the following: a therapy that enhances tumor antigen presentation (e.g., dendritic cell vaccine, GM-CSF secreting cellular vaccines, CpG oligonucleotides, imiquimod); a therapy that inhibits negative immune regulation e.g., by inhibiting CTLA-4 and/or PD1/PD-L1/PD-L2 pathway and/or depleting or blocking Tregs or other immune suppressing cells; a therapy that stimulates positive immune regulation, e.g., with agonists that stimulate the CD-137 and/or GITR pathway and/or stimulate T cell effector function; a therapy that increases systemically the frequency of anti-tumor T cells; a therapy that depletes or inhibits Tregs, such as Tregs in the tumor, e.g., using an antagonist of CD25 (e.g., daclizumab) or by ex vivo anti-CD25 bead depletion; a therapy that impacts the function of suppressor myeloid cells in the tumor; a therapy that enhances immunogenicity of tumor cells (e.g., anthracyclines); adoptive T cell or NK cell transfer including genetically modified cells, e.g., cells modified by chimeric antigen receptors (CAR-T therapy); a therapy that inhibits a metabolic enzyme such as indoleamine dioxigenase (IDO), dioxigenase, arginase, or nitric oxide synthetase; a therapy that reverses/prevents T cell anergy or exhaustion; a therapy that triggers an innate immune activation and/or inflammation at a tumor site; administration of immune stimulatory cytokines; or blocking of immuno repressive cytokines.

[0487] Anti-OX40 antibodies can be used together with one or more of agonistic agents that ligate positive costimulatory receptors, blocking agents that attenuate signaling through inhibitory receptors, antagonists, and one or more agents that increase systemically the frequency of anti-tumor T cells, agents that overcome distinct immune suppressive pathways within the tumor microenvironment (e.g., block inhibitory receptor engagement (e.g., PD-L1/PD-1 interactions), deplete or inhibit Tregs (e.g., using an anti-CD25 monoclonal antibody (e.g., daclizumab) or by ex vivo anti-CD25 bead depletion), inhibit metabolic enzymes such as IDO, or reverse/prevent T cell anergy or exhaustion) and agents that trigger innate immune activation and/or inflammation at tumor sites.

[0488] In certain embodiments, the anti-OX40 antibody is administered to a subject together with a BRAF inhibitor if the subject is BRAF V600 mutation positive.

[0489] In certain embodiments, the anti-OX40 antibody is administered together with another immunostimulatory antibody.

[0490] Provided herein are the claimed antibodies for use in methods for stimulating an immune response in a subject comprising administering to the subject the anti-OX40 antibody, and one or more additional immunostimulatory antibodies, such as an anti-PD-1 antagonist, e.g., antagonist antibody, an anti-PD-L1 antagonist, e.g., antagonist antibody, an antagonist anti-CTLA-4 antagonist, e.g., antagonist antibody and/or an anti-LAG3 antagonist, e.g., an antagonist antibody, such that an immune response is stimulated in the subject, for example to inhibit tumor growth or to stimulate an anti-viral response. In one embodiment, the subject is administered the anti-OX40 antibody and an antagonist anti-PD-1 antibody. In one embodiment, the subject is administered the anti-OX40 antibody and an antagonist anti-PD-L1 antibody. In one embodiment, the subject is administered the anti-OX40 antibody and an antagonist anti-CTLA-4 antibody. In one embodiment, the anti-OX40 antibody is a human antibody. Alternatively, the anti-OX40 antibody can be, for example, a chimeric or humanized antibody. In one embodiment, the at least one additional immunostimulatory antibody (e.g., an antagonist anti-PD-1, an antagonist anti-PD-L1, an antagonist anti-CTLA-4 and/or an antagonist anti-LAG3 antibody) is a human antibody. Alternatively, the at least one additional

immunostimulatory antibody can be, for example, a chimeric or humanized antibody (e.g., prepared from a mouse anti-PD-1, anti-PD-L1, anti-CTLA-4 and/or anti-LAG3 antibody).

[0491] Provided herein are the claimed antibodies for use in methods for treating a hyperproliferative disease (e.g., cancer), comprising administering the anti-OX40 antibody with an antagonist PD-1 antibody, an antagonist PD-L1 antibody, an anti-CTLA-4 antibody, or an anti-LAG3 antibody to a subject. In certain embodiments, one or both antibodies are administered at a subtherapeutic dose. Also provided herein are the antibodies for use in methods for altering an adverse event associated with treatment of a hyperproliferative disease with an immunostimulatory agent, comprising administering the anti-OX40 antibody and a subtherapeutic dose of an anti-PD-1, anti-PD-L1, anti-CTLA-4, or anti-LAG3 antibody to a subject (e.g., a human). In certain embodiments, the anti-OX40 antibody comprises the CDRs or variable regions of 3F4, 14B6-1, 14B6-2, 23H3, 6E1-1, 6E1-2, 18E9, 8B11, 20B3, 14A2-1, 14A2-2, and 20C1, or is another agonist anti-OX40 antibody described herein.

[0492] Suitable PD-1 antagonists for use in the methods described herein, include, without limitation, ligands, antibodies (e.g., monoclonal antibodies and bispecific antibodies), and multivalent agents. In one embodiment, the PD-1 antagonist is a fusion protein, e.g., an Fc fusion protein, such as AMP-244. In one embodiment, the PD-1 antagonist is an anti-PD-1 or anti-PD-L1 antibody.

[0493] An exemplary anti-PD-1 antibody is nivolumab (BMS-936558) or an antibody that comprises the CDRs or variable regions of one of antibodies 17D8, 2D3, 4H1, 5C4, 7D3, 5F4 and 4A11 described in WO 2006/121168. In certain embodiments, an anti-PD1 antibody is MK-3475 (Lambrolizumab) described in WO2012/145493; and AMP-514 described in WO 2012/145493. Further known PD-1 antibodies and other PD-1 inhibitors include those described in WO 2009/014708, WO 03/099196, WO 2009/114335, WO 2011/066389, WO 2011/161699, WO 2012/145493, U.S. Patent Nos. 7,635,757 and 8,217,149, and U.S. Patent Publication No. 2009/0317368. Any of the anti-PD-1 antibodies disclosed in WO2013/173223 may also be used. An anti-PD-1 antibody that competes for binding with, and/or binds to the same epitope on PD-1 as, as one of these antibodies may also be used in combination treatments. Another approach to target the PD-1 receptor is the recombinant protein composed of the extracellular domain of PD-L2 (B7-DC) fused to the Fc portion of IgG1, called AMP-224. In certain embodiments, the antibody has at least about 90% variable region amino acid sequence identity with the above-mentioned antibodies.

[0494] In certain embodiments, the anti-OX40 antibody is used in combination with nivolumab, which comprises heavy and light chains comprising the sequences shown in SEQ ID NOs: 299 and 300, respectively, or antigen binding fragments and variants thereof. In certain embodiments, the antibody has heavy and light chain CDRs or variable regions of nivolumab. Accordingly, in one embodiment, the antibody comprises CDR1, CDR2, and CDR3 domains of the VH of nivolumab having the sequence set forth in SEQ ID NO: 301, and CDR1, CDR2 and CDR3 domains of the VL of nivolumab having the sequence set forth in SEQ ID NO: 302. In certain embodiments, the antibody comprises CDR1, CDR2 and CDR3 domains comprising the sequences set forth in SEQ ID NOs: 303-305, respectively, and CDR1, CDR2 and CDR3 domains comprising the sequences set forth in SEQ ID NOs: 306-308, respectively. In certain embodiments, the antibody comprises VH and/or VL regions comprising the amino acid sequences set forth in SEQ ID NO: 301 and/or SEQ ID NO: 302, respectively. In certain embodiments, the antibody has at least about 90%, e.g., at least about 90%, 95%, or 99% variable region identity with SEQ ID NO: 301 or SEQ ID NO: 302.

[0495] Exemplary anti-PD-L1 antibodies include BMS-936559 (referred to as 12A4 in WO 2007/005874 and US Patent No. 7,943,743), or an antibody that comprises the CDRs or variable regions of 3G10, 12A4, 10A5, 5F8, 10H10, 1B12, 7H1, 11E6, 12B7 and 13G4, which are described in PCT Publication WO 07/005874 and US Patent No. 7,943,743. In certain embodiments, the anti-PD-L1 antibody is MEDI4736 (also known as Anti-B7-H1), MPDL3280A (also known as RG7446), MSB0010718C (WO2013/79174), or rHigM12B7. Any of the anti-PD-L1 antibodies disclosed in WO2013/173223, WO2011/066389, WO2012/145493, U.S. Patent Nos. 7,635,757 and 8,217,149 and U.S. Publication No. 2009/145493 may also be used.

[0496] Exemplary anti-CTLA-4 antibodies include Yervoy[™] (ipilimumab or antibody 10D1, described in PCT Publication WO 01/14424), tremelimumab (formerly ticilimumab, CP-675,206), or an anti-CTLA-4 antibody described in any of the following publications: WO 98/42752; WO 00/37504; U.S. Pat. No. 6,207,156; Hurwitz et al. (1998) Proc. Natl. Acad. Sci. USA 95(17):10067-10071; Camacho et al. (2004) J. Clin. Oncology 22(145): Abstract No. 2505 (antibody CP-675206); and Mokyr et al. (1998) Cancer Res. 58:5301-5304. Any of the anti-CTLA-4 antibodies disclosed in

WO2013/173223 may also be used.

[0497] Exemplary anti-LAG3 antibodies include antibodies comprising the CDRs or variable regions of antibodies 25F7, 26H10, 25E3, 8B7, 11F2 or 17E5, which are described in U.S. Patent Publication No. US2011/0150892, WO10/19570 and WO2014/008218. In one embodiment, an anti-LAG-3 antibody is BMS-986016. Other art recognized anti-LAG-3 antibodies that can be used include IMP731 and IMP-321, described in US 2011/007023, WO08/132601, and WO09/44273.

[0498] In certain embodiments, the anti-OX40 antibody is used in combination with ipilimumab. In certain embodiments, the antibody has heavy and light chain CDRs or variable regions of ipilimumab. Accordingly, in one embodiment, the antibody comprises CDR1, CDR2, and CDR3 domains of the VH of ipilimumab having the sequence set forth in SEQ ID NO: 309, and CDR1, CDR2 and CDR3 domains of the VL of ipilimumab having the sequence set forth in SEQ ID NO: 310. In certain embodiments, the antibody comprises CDR1, CDR2 and CDR3 domains comprising the sequences set forth in SEQ ID NOs: 311-313, respectively, and CDR1, CDR2 and CDR3 domains comprising the sequences set forth in SEQ ID NOs: 314-316, respectively. In certain embodiments, the antibody comprises VH and/or VL regions comprising the amino acid sequences set forth in SEQ ID NO: 309 and/or SEQ ID NO: 310, respectively. In certain embodiments, the antibody has at least about 90%, e.g., at least about 90%, 95%, or 99% variable region identity with SEQ ID NO: 309 or SEQ ID NO: 310.

[0499] Administration anti-OX40 antibodies and antagonists, e.g., antagonist antibodies, to one or more second target antigens such as LAG-3 and/or CTLA-4 and/or PD-1 and/or PD-L1 can enhance the immune response to cancerous cells in the patient. Cancers whose growth may be inhibited using anti-OX40 antibodies include cancers typically responsive to immunotherapy and those that are not typically responsive to immunotherapy. Representative examples of cancers for treatment with the combination therapy of the instant disclosure include those cancers listed herein.

[0500] In certain embodiments, the combination of therapeutic antibodies discussed herein can be administered concurrently as a single composition in a pharmaceutically acceptable carrier, or concurrently as separate compositions with each antibody in a pharmaceutically acceptable carrier. In another embodiment, the combination of therapeutic antibodies can be administered sequentially. Furthermore, if more than one dose of the combination therapy is administered sequentially, the order of the sequential administration can be reversed or kept in the same order at each time point of administration, and sequential administrations can be combined with concurrent administrations, or any combination thereof. For example, the first administration of a combination of anti-OX40 antibody and anti-PDL antibody (and/or anti-CTLA-4 antibody and/or anti-PD-L1 antibody and/or anti-LAG-3 antibody) can be concurrent, the second administration can be sequential with anti-PD1 antibody first and the anti-OX40 antibody second, and the third administration can be sequential with the anti-OX40 antibody first and anti-PDL antibody second, etc. Another representative dosing scheme involves a first administration that is sequential with the anti-OX40 first and anti-PDL antibody (and/or anti-CTLA-4 antibody and/or anti-PD-L1 antibody and/or anti-LAG-3 antibody) second, and subsequent administrations may be concurrent.

[0501] In certain embodiment, a subject having a disease that may benefit from stimulation of the immune system, e.g., cancer or an infectious disease, is treated by administration to the subject of the anti-OX40 antibody and an immuno-oncology agent. Exemplary immune-oncology agents include CD137 (4-1BB) agonists (e.g., an agonistic CD137 antibody such as urelumab or PF-05082566 (WO12/32433)); GITR agonists (e.g., an agonistic anti-GITR antibody); CD40 agonists (e.g., an agonistic CD40 antibody); CD40 antagonists (e.g., an antagonistic CD40 antibody such as lucatumumab (HCD122), dacetuzumab (SGN-40), CP-870,893 or Chi Lob 7/4); CD27 agonists (e.g., an agonistic CD27 antibody such as varlilumab (CDX-1127)), MGA271 (to B7H3) (WO11/109400)); KIR antagonists (e.g., lirilumab); IDO antagonists (e.g., INCB-024360 (WO2006/122150, WO07/75598, WO08/36653, WO08/36642), indoximod, NLG-919 (WO09/73620, WO09/1156652, WO11/56652, WO12/142237) or F001287); Toll-like receptor agonists (e.g., TLR2/4 agonists (e.g., Bacillus Calmette-Guerin); TLR7 agonists (e.g., Hiltonol or Imiquimod); TLR7/8 agonists (e.g., Resiquimod); or TLR9 agonists (e.g., CpG7909)); and TGF- β inhibitors (e.g., GC1008, LY2157299, TEW7197, or IMC-TR1).

[0502] In one embodiment, the anti-OX40 antibody is administered prior to administration of a second agent, e.g., an immuno-oncology agent. In another embodiment, the anti-OX40 antibody is administered concurrently with the second agent, e.g., an immunology-oncology agent. In yet another embodiment, the anti-OX40 antibody is administered after

administration of the second agent. The administration of the two agents may start at times that are, e.g., 30 minutes, 60 minutes, 90 minutes, 120 minutes, 3 hours, 6 hours, 12 hours, 24 hours, 36 hours, 48 hours, 3 days, 5 days, 7 days, or one or more weeks apart, or administration of the second agent may start, e.g., 30 minutes, 60 minutes, 90 minutes, 120 minutes, 3 hours, 6 hours, 12 hours, 24 hours, 36 hours, 48 hours, 3 days, 5 days, 7 days, or one or more weeks after the first agent has been administered.

[0503] In certain embodiments, the anti-OX40 antibody and a second agent, e.g., an immuno-oncology agent, are administered simultaneously, e.g., are infused simultaneously, e.g., over a period of 30 or 60 minutes, to a patient. The anti-OX40 antibody may be co-formulated with the second agent, e.g., an immuno-oncology agent.

[0504] Optionally, the anti-OX40 antibody as sole immunotherapeutic agent, or a combination of the anti-OX40 antibody and one or more additional immunotherapeutic antibodies (e.g., anti-CTLA-4 and/or anti-PD-1 and/or anti-PD-L1 and/or anti-LAG-3 blockade), can be further combined with an immunogenic agent, such as cancerous cells, purified tumor antigens (including recombinant proteins, peptides, and carbohydrate molecules), cells, and cells transfected with genes encoding immune stimulating cytokines (He et al. (2004) J. Immunol. 173:4919-28). Non-limiting examples of tumor vaccines that can be used include peptides of melanoma antigens, such as peptides of gp100, MAGE antigens, Trp-2, MART1 and/or tyrosinase, or tumor cells transfected to express the cytokine GM-CSF (discussed further below). A combination of the anti-OX40 antibody and one or more additional antibodies (e.g., CTLA-4 and/or PD-1 and/or PD-L1 and/or LAG-3 blockade) can also be further combined with standard cancer treatments. For example, a combination of the anti-OX40 antibody and one or more additional antibodies (e.g., CTLA-4 and/or PD-1 and/or PD-L1 and/or LAG-3 blockade) can be effectively combined with chemotherapeutic regimes. In these instances, the dose of other chemotherapeutic reagent administered with the combination can be reduced (Mokyr et al. (1998) Cancer Research 58: 5301-5304). For example, such a combination may include the anti-OX40 antibody with or without and an additional antibody (e.g., anti-CTLA-4 antibodies and/or anti-PD-1 antibodies and/or anti-PD-L1 antibodies and/or anti-LAG-3 antibodies), further in combination with decarbazine or interleukin-2 (IL-2) for the treatment of melanoma. The scientific rationale behind combining an agonistic anti-OX40 antibody with CTLA-4 and/or PD-1 and/or PD-L1 and/or LAG-3 blockade with chemotherapy is that cell death, which is a consequence of the cytotoxic action of most chemotherapeutic compounds, should result in increased levels of tumor antigen in the antigen presentation pathway. Other combination therapies that may result in synergy with a combination of the anti-OX40 antibody with or without and CTLA-4 and/or PD-1 and/or PD-L1 and/or LAG-3 blockade through cell death include radiation, surgery, or hormone deprivation. Each of these protocols creates a source of tumor antigen in the host. Angiogenesis inhibitors can also be combined with a combination of the anti-OX40 antibody and CTLA-4 and/or PD-1 and/or PD-L1 and/or LAG-3 blockade. Inhibition of angiogenesis leads to tumor cell death, which can be a source of tumor antigen fed into host antigen presentation pathways.

[0505] In certain embodiments, the anti-OX40 antibody can be used as the sole immunotherapeutic agent, or a combination of the anti-OX40 antibody and CTLA-4 and/or PD-1 and/or PD-L1 and/or LAG-3 blocking antibodies, can also be used in combination with bispecific antibodies that target Fc α or Fc γ receptor-expressing effector cells to tumor cells (see, e.g., U.S. Pat. Nos. 5,922,845 and 5,837,243). Bispecific antibodies can be used to target two separate antigens. The T cell arm of these responses would be augmented by the use of a combination of the anti-OX40 antibody and CTLA-4 and/or PD-1 and/or PD-L1 and/or LAG-3 blockade.

[0506] In another example, the anti-OX40 antibody can be used as the sole immunotherapeutic agent, or a combination of the anti-OX40 antibody and additional immunostimulating agent, e.g., anti-CTLA-4 antibody and/or anti-PD-1 antibody and/or anti-PD-L1 antibody and/or LAG-3 agent (e.g., antibody) can be used in conjunction with an anti-neoplastic antibody, such as Rituxan[®] (rituximab), Herceptin[®] (trastuzumab), Bexxar[®] (tositumomab), Zevalin[®] (ibritumomab), Campath[®] (alemtuzumab), Lymphocide[®] (eptuzumab), Avastin[®] (bevacizumab), and Tarceva[®] (erlotinib), and the like. By way of example and not wishing to be bound by theory, treatment with an anti-cancer antibody or an anti-cancer antibody conjugated to a toxin can lead to cancer cell death (e.g., tumor cells) which would potentiate an immune response mediated by the immunostimulating agent (e.g., OX40, CTLA-4, PD-1, PD-L1 or LAG-3 agent, e.g., antibody). In an exemplary embodiment, a treatment of a hyperproliferative disease (e.g., a cancer tumor) can include an anti-cancer agent (e.g., antibody) in combination with the anti-OX40 antibody and optionally an additional immunostimulating agent, e.g., anti-CTLA-4 and/or anti-PD-1 and/or anti-PD-L1 and/or anti-LAG-3 agent (e.g., antibody), concurrently or sequentially or any combination thereof, which can potentiate an anti-tumor immune responses by the host.

[0507] Tumors evade host immune surveillance by a large variety of mechanisms. Many of these mechanisms may be overcome by the inactivation of proteins, which are expressed by the tumors and which are immunosuppressive. These include, among others, TGF- β (Kehrl et al. (1986) J. Exp. Med. 163: 1037-1050), IL-10 (Howard & O'Garra (1992) Immunology Today 13: 198-200), and Fas ligand (Hahne et al. (1996) Science 274: 1363-1365). Antibodies to each of these entities can be further combined with the anti-OX40 antibody with or without an additional immunostimulating agent, e.g., an anti-CTLA-4 and/or anti-PD-1 and/or anti-PD-L1 and/or anti-LAG-3 agent, such as antibody, to counteract the effects of immunosuppressive agents and favor anti-tumor immune responses by the host.

[0508] Other agents (e.g., antibodies) that can be used to activate host immune responsiveness can be further used in combination with the anti-OX40 antibody with or without an additional immunostimulating agent, such as anti-CTLA-4 and/or anti-PD-1 and/or anti-PD-L1 and/or anti-LAG-3 antibody. These include molecules on the surface of dendritic cells that activate DC function and antigen presentation. Anti-CD40 antibodies (Ridge et al., *supra*) can be used in conjunction with the anti-OX40 antibody and optionally an additional immunostimulating agent, e.g., an anti-CTLA-4 and/or anti-PD-1 and/or anti-PD-L1 and/or anti-LAG-3 agent, e.g., antibody. Other activating antibodies to T cell costimulatory molecules Weinberg et al., *supra*, Melero et al. *supra*, Hutloff et al., *supra*, may also provide for increased levels of T cell activation.

[0509] As discussed above, bone marrow transplantation is currently being used to treat a variety of tumors of hematopoietic origin. Anti-OX40 immunotherapy alone or combined with CTLA-4 and/or PD-1 and/or PD-L1 and/or LAG-3 blockade can be used to increase the effectiveness of the donor engrafted tumor specific T cells.

[0510] Several experimental treatment protocols involve *ex vivo* activation and expansion of antigen specific T cells and adoptive transfer of these cells into recipients in order to antigen-specific T cells against tumor (Greenberg & Riddell, *supra*). These methods can also be used to activate T cell responses to infectious agents such as CMV. *Ex vivo* activation in the presence of the anti-OX40 antibody with or without an additional immunostimulating therapy, e.g., anti-CTLA-4 and/or anti-PD-1 and/or anti-PD-L1 and/or anti-LAG-3 antibodies can be expected to increase the frequency and activity of the adoptively transferred T cells.

[0511] Provided herein are the antibodies for use in methods for altering an adverse event associated with the treatment of a hyperproliferative disease (e.g., cancer) with an immunostimulatory agent, comprising administering the anti-OX40 antibody with or without an anti-CTLA-4 and/or anti-PD-1 and/or anti-PD-L1 and/or anti-LAG-3 agent (e.g., antibody), to a subject. For example, the methods described herein provide for a method of reducing the incidence of immunostimulatory therapeutic antibody-induced colitis or diarrhea by administering a non-absorbable steroid to the patient. As used herein, a "non-absorbable steroid" is a glucocorticoid that exhibits extensive first pass metabolism such that, following metabolism in the liver, the bioavailability of the steroid is low, i.e., less than about 20%. In one embodiment, the non-absorbable steroid is budesonide. Budesonide is a locally-acting glucocorticosteroid, which is extensively metabolized, primarily by the liver, following oral administration. ENTOCORT EC[®] (Astra-Zeneca) is a pH- and time-dependent oral formulation of budesonide developed to optimize drug delivery to the ileum and throughout the colon. ENTOCORT EC[®] is approved in the U.S. for the treatment of mild to moderate Crohn's disease involving the ileum and/or ascending colon. The usual oral dosage of ENTOCORT EC[®] for the treatment of Crohn's disease is 6 to 9 mg/day. ENTOCORT EC[®] is released in the intestines before being absorbed and retained in the gut mucosa. Once it passes through the gut mucosa target tissue, ENTOCORT EC[®] is extensively metabolized by the cytochrome P450 system in the liver to metabolites with negligible glucocorticoid activity. Therefore, the bioavailability is low (about 10%). The low bioavailability of budesonide results in an improved therapeutic ratio compared to other glucocorticoids with less extensive first-pass metabolism. Budesonide results in fewer adverse effects, including less hypothalamic-pituitary suppression, than systemically-acting corticosteroids. However, chronic administration of ENTOCORT EC[®] can result in systemic glucocorticoid effects such as hypercorticism and adrenal suppression. See PDR 58th ed. 2004; 608-610.

[0512] In still further embodiments, the anti-OX40 antibody with or without CTLA-4 and/or PD-1 and/or PD-L1 and/or LAG-3 blockade (i.e., anti-CTLA-4 and/or anti-PD-1 and/or anti-PD-L1 and/or anti-LAG-3 antibodies) in conjunction with a non-absorbable steroid can be further combined with a salicylate. Salicylates include 5-ASA agents such as, for example:

sulfasalazine (AZULFIDINE[®], Pharmacia & UpJohn); olsalazine (DIPENTUM[®], Pharmacia & UpJohn); balsalazide

(COLAZAL[®], Salix Pharmaceuticals, Inc.); and mesalamine (ASACOL[®], Procter & Gamble Pharmaceuticals; PENTASA[®], Shire US; CANASA[®], Axcan Scandipharm, Inc.; ROWASA[®], Solvay).

[0513] In accordance with the methods described herein, a salicylate administered in combination with the anti-OX40 antibody with or without anti-CTLA-4 and/or anti-PD-1 and/or anti-PD-L1 and/or LAG-3 antibodies and a non-absorbable steroid can include any overlapping or sequential administration of the salicylate and the non-absorbable steroid for the purpose of decreasing the incidence of colitis induced by the immunostimulatory antibodies. Thus, for example, methods for reducing the incidence of colitis induced by the immunostimulatory antibodies described herein encompass administering a salicylate and a non-absorbable concurrently or sequentially (e.g., a salicylate is administered 6 hours after a non-absorbable steroid), or any combination thereof. Further, a salicylate and a non-absorbable steroid can be administered by the same route (e.g., both are administered orally) or by different routes (e.g., a salicylate is administered orally and a non-absorbable steroid is administered rectally), which may differ from the route(s) used to administer the anti-OX40 antibody and anti-CTLA-4 and/or anti-PD-1 and/or anti-PD-L1 and/or anti-LAG-3 antibodies.

[0514] Anti-OX40 antibodies and combination antibody therapies described herein may also be used in conjunction with other well-known therapies that are selected for their particular usefulness against the indication being treated (e.g., cancer). Combinations with anti-OX40 antibodies may be used sequentially with known pharmaceutically acceptable agent(s).

[0515] For example, anti-OX40 antibodies and combination antibody therapies described herein can be used in combination (e.g., simultaneously or separately) with an additional treatment, such as irradiation, chemotherapy (e.g., using camptothecin (CPT-11), 5-fluorouracil (5-FU), cisplatin, doxorubicin, irinotecan, paclitaxel, gemcitabine, cisplatin, paclitaxel, carboplatin-paclitaxel (Taxol), doxorubicin, 5-fu, or camptothecin + apo21/TRAIL (a 6X combo)), one or more proteasome inhibitors (e.g., bortezomib or MG132), one or more Bcl-2 inhibitors (e.g., BH3l-2' (bcl-xl inhibitor), indoleamine dioxygenase-1 inhibitor (e.g., INCB24360, indoximod, NLG-919, or F001287), AT-101 (R-(-)-gossypol derivative), ABT-263 (small molecule), GX-15-070 (obatoclax), or MCL-1 (myeloid leukemia cell differentiation protein-1) antagonists), IAP (inhibitor of apoptosis protein) antagonists (e.g., smac7, smac4, small molecule smac mimetic, synthetic smac peptides (see Fulda et al., Nat Med 2002;8:808-15), ISIS23722 (LY2181308), or AEG-35156 (GEM-640)), HDAC (histone deacetylase) inhibitors, anti-CD20 antibodies (e.g., rituximab), angiogenesis inhibitors (e.g., bevacizumab), anti-angiogenic agents targeting VEGF and VEGFR (e.g., Avastin), synthetic triterpenoids (see Hyer et al., Cancer Research 2005;65:4799-808), c-FLIP (cellular FLICE-inhibitory protein) modulators (e.g., natural and synthetic ligands of PPAR γ (peroxisome proliferator-activated receptor γ), 5809354 or 5569100), kinase inhibitors (e.g., Sorafenib), Trastuzumab, Cetuximab, Temsirolimus, mTOR inhibitors such as rapamycin and temsirolimus, Bortezomib, JAK2 inhibitors, HSP90 inhibitors, PI3K-AKT inhibitors, Lenalidomide, GSK3 β inhibitors, IAP inhibitors and/or genotoxic drugs.

[0516] Anti-OX40 antibodies and combination antibody therapies described herein can further be used in combination with one or more anti-proliferative cytotoxic agents. Classes of compounds that may be used as anti-proliferative cytotoxic agents include, but are not limited to, the following:

Alkylating agents (including, without limitation, nitrogen mustards, ethylenimine derivatives, alkyl sulfonates, nitrosoureas and triazenes): Uracil mustard, Chloromethine, Cyclophosphamide (CYTOXAN[™]) fosfamide, Melphalan, Chlorambucil, Pipobroman, Triethylenemelamine, Triethylenethiophosphoramine, Busulfan, Carmustine, Lomustine, Streptozocin, Dacarbazine, and Temozolomide.

[0517] Antimetabolites (including, without limitation, folic acid antagonists, pyrimidine analogs, purine analogs and adenosine deaminase inhibitors): Methotrexate, 5-Fluorouracil, Floxuridine, Cytarabine, 6-Mercaptopurine, 6-Thioguanine, Fludarabine phosphate, Pentostatine, and Gemcitabine.

[0518] Suitable anti-proliferative agents for combining with anti-OX40 antibodies, without limitation, taxanes, paclitaxel (paclitaxel is commercially available as TAXOL[™]), docetaxel, discodermolide (DDM), dictyostatin (DCT), Peloruside A, epothilones, epothilone A, epothilone B, epothilone C, epothilone D, epothilone E, epothilone F, furanopothilone D, desoxyepothilone B, [17]-dehydrodesoxyepothilone B, [18]dehydrodesoxyepothilones B, C12,13-cyclopropyl-epothilone A, C6-C8 bridged epothilone A, trans-9,10-dehydroepothilone D, cis-9,10-dehydroepothilone D, 16-desmethylepothilone B, epothilone B10, discoderomolide, patupilone (EPO-906), KOS-862, KOS-1584, ZK-EPO, ABJ-789, XAA296A (Discodermolide), TZT-1027 (soblidotin), ILX-651 (tasidotin hydrochloride), Halichondrin B, Eribulin

mesylate (E-7389), Hemiasterlin (HTI-286), E-7974, Cryptophycins, LY-355703, Maytansinoid immunoconjugates (DM-1), MKC-1, ABT-751, T1-38067, T-900607, SB-715992 (ispinesib), SB-743921, MK-0731, STA-5312, eleutherobin, 17 β -acetoxy-2-ethoxy-6-oxo-B-homo-estra-1,3,5(10)-trien-3-ol, cyclostreptin, isolaulimalide, laulimalide, 4-epi-7-dehydroxy-14,16-didemethyl-(+)-discodermolides, and cryptothilone 1, in addition to other microtubuline stabilizing agents known in the art.

[0519] In cases where it is desirable to render aberrantly proliferative cells quiescent in conjunction with or prior to treatment with the anti-OX40 antibody, hormones and steroids (including synthetic analogs), such as 17 α -Ethinylestradiol, Diethylstilbestrol, Testosterone, Prednisone, Fluoxymesterone, Dromostanolone propionate, Testolactone, Megestrolacetate, Methylprednisolone, Methyl-testosterone, Prednisolone, Triamcinolone, Chlorotrianisene, Hydroxyprogesterone, Aminoglutethimide, Estramustine, Medroxyprogesteroneacetate, Leuprolide, Flutamide, Toremifene, ZOLADEX[™], can also be administered to the patient. When employing the methods or compositions described herein, other agents used in the modulation of tumor growth or metastasis in a clinical setting, such as antimetotics, can also be administered as desired.

[0520] In certain embodiments, the anti-OX40 antibody is administered in combination (concurrently or separately) with nivolumab to treat a patient with cancer, for example, colorectal or bladder cancer.

[0521] In certain embodiments, the anti-OX40 antibody is administered in combination (concurrently or separately) with ipilimumab to treat a patient with cancer, for example, ovarian, bladder, or prostate cancer.

[0522] Methods for the safe and effective administration of chemotherapeutic agents are known to those skilled in the art. In addition, their administration is described in the standard literature. For example, the administration of many of the chemotherapeutic agents is described in the Physicians' Desk Reference (PDR), e.g., 1996 edition (Medical Economics Company, Montvale, N.J. 07645-1742, USA).

The chemotherapeutic agent(s) and/or radiation therapy can be administered according to therapeutic protocols well known in the art. It will be apparent to those skilled in the art that the administration of the chemotherapeutic agent(s) and/or radiation therapy can be varied depending on the disease being treated and the known effects of the chemotherapeutic agent(s) and/or radiation therapy on that disease. Also, in accordance with the knowledge of the skilled clinician, the therapeutic protocols (e.g., dosage amounts and times of administration) can be varied in view of the observed effects of the administered therapeutic agents on the patient, and in view of the observed responses of the disease to the administered therapeutic agents.

[0523] The present disclosure is further illustrated by the following examples, which should not be construed as further limiting.

XVII. Kits and Unit Dosage Forms

[0524] Also provided herein but not claimed are kits which include a pharmaceutical composition containing an anti-OX40 antibody and an anti-PD-1 (e.g., nivolumab) or anti-CTLA-4 (ipilimumab) antibody, and a pharmaceutically-acceptable carrier, in a therapeutically effective amount adapted for use in the preceding methods. The kits optionally also can include instructions, e.g., comprising administration schedules, to allow a practitioner (e.g., a physician, nurse, or patient) to administer the composition contained therein to administer the composition to a patient having cancer (e.g., a solid tumor). The kit also can include a syringe.

[0525] Optionally, the kits include multiple packages of the single-dose pharmaceutical compositions each containing an effective amount of the anti-OX40 antibody or anti-PD-1 or anti-CTLA-4 antibody for a single administration in accordance with the methods provided above. Instruments or devices necessary for administering the pharmaceutical composition(s) also may be included in the kits. For instance, a kit may provide one or more pre-filled syringes containing an amount of the anti-OX40 antibody or anti-PD-1 or anti-CTLA-4 antibody.

[0526] In one case, the present disclosure provides a kit for treating a solid tumor in a human patient, the kit comprising a dose of an anti-OX40 antibody comprising CDR1, CDR2 and CDR3 domains of the heavy chain variable region having the sequence set forth in SEQ ID NO: 318, and CDR1, CDR2 and CDR3 domains of the light chain variable

region having the sequence set forth in SEQ ID NO: 94, and instructions for use in the methods described herein. In certain embodiments, the kit further comprises (a) a dose of an anti-PD-1 antibody comprising CDR1, CDR2 and CDR3 domains of the heavy chain variable region having the sequence set forth in SEQ ID NO: 301, and CDR1, CDR2 and CDR3 domains of the light chain variable region having the sequence set forth in SEQ ID NO: 302, or (b) a dose of an anti-CTLA-4 antibody comprising CDR1, CDR2 and CDR3 domains of the heavy chain variable region having the sequence set forth in SEQ ID NO: 309, and CDR1, CDR2 and CDR3 domains of the light chain variable region having the sequence set forth in SEQ ID NO: 310.

EXAMPLES

[0527] The antibodies of the claimed invention are designated "OX40.21" in the following description of the figures. Antibodies other than those claimed are disclosed below for reference purposes and to fully understand the invention

Example 1: Generation of anti-OX40 Antibodies

[0528] Human anti-OX40 monoclonal antibodies were generated in Hco7, Hco12, Hco17, and Hco38 strains of HuMAb[®] transgenic mice ("HuMAb" is a Trade Mark of Medarex, Inc., Princeton, New Jersey) and KM mice (the KM Mouse[®] strain contains the SC20 transchromosome as described in PCT Publication WO 02/43478) using recombinant hexahistidine-OX40 antigen.

[0529] A total of 52 mice, including 5 genotypes of transgenic mice (KM, Hco7, Hco12, Hco17, and Hco38), were immunized with different immunization strategies. The immunogen was huOX40-6xhis prepared in-house and used at 2.0 mg/mL for a total dose of 20 µg per mouse. Routes of administration included: base of tail injection, Hock immunization, intraperitoneal (ip) and subcutaneous (sc) injection, and adjuvant (Ribi, Cat# S6322, Sigma). 27 fusions from 30 mice were performed and screened. 541 ELISA antigen positive antibodies were identified from these 27 fusions, and further characterization led to the isolation of antibodies of particular interest, including the antibodies designated as 3F4, 14B6-1, 14B6-2, 23H3, 6E1-1, 6E1-2, 18E9, 8B11, 20B3 (also referred to as OX40.17), 14A2-1, 14A2-2, and 20C1. Their variable region amino acid sequences and isotype are set forth in Figures 1-9. The heavy and light chain variable regions of 3F4 consist of amino acid sequences SEQ ID NOs: 17 and 18. The heavy and light chain variable regions of 14B6-1 consist of amino acid sequences SEQ ID NOs: 28 and 29. The heavy and light chain variable regions of 14B6-2 consist of amino acid sequences SEQ ID NOs: 28 and 30. The heavy and light chain variable regions of 23H3 consist of amino acid sequences SEQ ID NOs: 37 and 38. The heavy and light chain variable regions of 6E1-1 consist of amino acid sequences SEQ ID NOs: 48 and 49. The heavy and light chain variable regions of 6E1-2 consist of amino acid sequences SEQ ID NOs: 48 and 50. The heavy and light chain variable regions of 18E9 consist of amino acid sequences SEQ ID NOs: 57 and 58. The heavy and light chain variable regions of 8B11 consist of amino acid sequences SEQ ID NOs: 65 and 66. The heavy and light chain variable regions of 20B3 consist of amino acid sequences SEQ ID NOs: 73 and 74. The heavy and light chain variable regions of 14A2-1 consist of amino acid sequences SEQ ID NOs: 84 and 85. The heavy and light chain variable regions of 14A2-2 consist of amino acid sequences SEQ ID NOs: 84 and 86. The heavy and light chain variable regions of 20C1 consist of amino acid sequences SEQ ID NOs: 93 and 94.

[0530] cDNA sequencing identified one heavy and one light chain for each of the antibodies 3F4, 23H3, 18E9, 8B11, 20B3 (also referred to as OX40.17) and 20C1, and one heavy chain and two light chains (light chain 1 or "L1" and light chain 2 or "L2") for each of the antibodies 14B6, 14A2 and 6E1. By protein analysis, a single light chain was identified for antibodies 14B6, 6E1 and 14A2, and N-terminal sequencing and molecular weight determination indicated that it was light chain L1 for 14B6 and 14A2 and light chain L2 for 6E1. Antibodies 14B6-1 and 14B6-2 correspond to antibody 14B6 with a light chain L1 and L2, respectively. Antibodies 14A2-1 and 14A2-2 correspond to antibody 14A2 with a light chain L1 and L2, respectively. Antibodies 6E1-1 and 6E1-2 correspond to antibody 6E1 with a light chain L1 and L2, respectively. The amino acid and nucleotide sequences of each of the light chains of the 3 antibodies are provided in Table 23.

[0531] For some of the antibodies above, substitutions in the parental antibody were made in HCDR2 in order to

remove the presence of an isomerization site (DG), and framework substitutions (due to derivation from the DP44 germline) were introduced to make the framework more like a commonly expressed antibody. For 20C1-based antibodies, three additional unusual framework residues were reverted to germline (A2V, D24G, and G82bS). The G82bS framework reversion also eliminates a deamidation site (NG). A summary of the various substitutions introduced into the parental hybrid clone sequences is provided in Table 6.

Table 6.

Name	Parental hybridoma clone	Isotype	Variable region substitutions
OX40.6	23H3	glf	Anti-OX40 23H3 with VH-H13Q/M87T
OX40.7	23H3	glf	Anti-OX40 23H3 with VH-M87T/M95Y
OX40.8	14A2	glf	Anti-OX40 14A2 with VH-G103W
OX40.9	14A2	glf	Anti-OX40 14A2 with VH-M97Y/G103W
OX40.10	14A2	glf	Anti-OX40 14A2 with VH-D53S
OX40.11	14A2	glf	Anti-OX40 14A2 with VH-G54S
OX40.12	14A2	glf	Anti-OX40 14A2 with VH-D53S/G103W
OX40.13	14A2	glf	Anti-OX40 14A2 with VH-G54S/G103W
OX40.14	14A2	glf	Anti-OX40 14A2 with VH-D53S/M97Y/G103W
OX40.15	14A2	glf	Anti-OX40 14A2 with VH-G54S/M97Y/G103W
OX40.16	20C1	glf	Anti-OX40 20C1 with VH-A2V/H13Q/D24G/M87T/G82bS
OX40.17	20B3	glf	Anti-OX40 20B3 (no substitutions)
OX40.18	3F4	glf	Anti-OX40 3F4 with VH-N27Y/N72D/P102Y
OX40.19	14A2	glf	Anti-OX40 14A2 with VH-M97L/G103W
OX40.20	20C1	glf	Anti-OX40 20C1 with VH-A2V/H13Q/D24G/D54S/M87T/G82bS
OX40.21	20C1	glf	Anti-OX40 20C1 with VH-A2V/H13Q/D24G/G55A/M87T/G82bS
OX40.22	20C1	glf	Anti-OX40 20C1 with VH-A2V/H13Q/D24G/D54S/G55T/M87T/G82bS
*Depending on the germline, there may be a D53 and G54 or a D54 and G55 present, as a potential isomerization site			

Example 2: Binding of anti-OX40 antibodies to activated primary human T cells

[0532] The human monoclonal anti-OX40 antibodies generated in Example 1 were tested for the ability to bind to activated primary human T cells.

[0533] Cells were activated for several days before the binding assay in order to induce OX40 expression. Briefly, PBMCs were cultured for three or four days with magnetic beads coated with anti-human CD3 plus anti-human CD28, in the presence of recombinant human IL-2. On the day of the assay, the beads were removed and the cells stained with a titration of each anti-OX40 antibody. Bound antibodies were detected with a fluorescently conjugated anti-human IgG polyclonal secondary antibody, and the cells were co-stained for CD4 and CD25 to detect activated CD4 T cells. The fluorescence intensity of the staining was measured using a FACSCanto II flow cytometer (Becton Dickinson). The geometric mean fluorescence intensity (GMFI) or median fluorescence intensity (MedFI) of anti-OX40 antibody staining was calculated for the CD4+CD25+ population (FACSDiva software). EC₅₀s for antibody binding were calculated using GraphPad Prism software.

[0534] As shown in Figure 11A, the anti-OX40 antibodies bound to activated primary human T cells with subnanomolar EC₅₀s. Notably, OX40.5 showed lowest binding of the anti-OX40 antibodies tested. The same experiment was performed with anti-OX40 antibodies with variable region substitutions. Initial experiments were carried out using

antibodies in the form of supernatants from cultures of host cells transfected with recombinant antibody expression vectors. As shown in Figure 11B, certain substitutions caused a significant loss of binding, namely for antibodies OX40.7, OX40.9, OX40.14 and OX40.15. A set of antibodies with variable region substitutions was analyzed further using purified antibody material.

[0535] As shown in Figures 11C and 11D, all tested antibodies bound with subnanomolar EC₅₀s to OX40, except for OX40.18, which showed lower binding than the 3F4 hybridoma parent clone. OX40.5 showed the lowest binding among the panel of antibodies tested in Figure 11B, whereas OX40.1 showed the lowest binding among the panel of antibodies tested in Figure 11C. A summary of the EC₅₀ values is presented in Table 7 below.

Table 7: EC₅₀s for binding of OX40 antibodies to activated human primary T cells.

Name	Human T Cell Binding EC ₅₀ (nM) (mean ± SD)	n
3F4	0.19 ± 0.15	3
8B11	0.14 ± 0.07	2
18E9	0.22 ± 0.12	2
20B3	0.34 ± 0.23	3
20C1	0.10 ± 0.06	3
23H3	0.15 ± 0.09	3
6E1	0.97 ± 0.05	2
14A2	0.33 ± 0.30	3
14B6	0.18 ± 0.16	2
OX40.6	0.13 ± 0.06	7
OX40.8	0.14 ± 0.07	7
OX40.16	0.06 ± 0.03	5
OX40.17	0.26 ± 0.17	3
OX40.18	3.15 ± 3.9	2
OX40.21	0.07 ± 0.02	5
OX40.1	0.35 ± 0.09	2
OX40.4	0.36 ± 0.06	2
OX40.5	3.20 ± 0.00	2

Example 3: Binding of anti-OX-40 antibodies to activated primary cynomolgus macaque T cells

[0536] The human monoclonal anti-OX-40 antibodies that were tested for binding to activated primary human T cells in Example 1 were tested for the ability to bind activated primary cynomolgus macaque T cells.

[0537] Briefly, cells were activated for several days before the binding assay in order to induce OX40 expression. Total leukocytes were isolated from cynomolgus macaque peripheral blood by lysis of red blood cells using an ammonium chloride buffer. The leukocytes were then cultured for four to five days with in flasks pre-coated with anti-human CD3 plus anti-human CD28 antibodies that cross-react with cynomolgus macaque, in the presence of recombinant human IL-2, in order to expand and activate T cells. On the day of the assay, the cells were harvested and stained with a titration of each anti-OX40 antibody. Bound antibodies were detected with a fluorescently conjugated anti-human IgG polyclonal secondary antibody, and the cells were co-stained for CD4 and CD25 to detect activated CD4 T cells. The fluorescence intensity of the staining was measured using a FACSCanto II flow cytometer (Becton Dickinson). The geometric mean fluorescence intensity (GMFI) or median fluorescence intensity (MedFI) of anti-OX40 antibody staining was calculated for the CD4+CD25+ population (FACSDiva software). Dose-response curves were generated and EC₅₀s for antibody binding were calculated using GraphPad Prism software.

[0538] As shown in Figures 12A and 12B, the anti-OX40 antibodies tested bound with high potency to activated

cynomolgus macaque CD4 T cells, with EC₅₀s ranging from 0.068 nM (20C1) to 1.4 nM (20B3). 18E9 and 20B3 bound with EC₅₀s between 1 and 1.5 nM, while the remaining antibodies bound with EC₅₀s below 1 nM. OX40.1 showed the lowest binding among the anti-OX40 antibodies tested in Figure 12A, and OX40.5 showed the lowest binding among the anti-OX40 antibodies tested in Figure 12B. The same experiment was performed with anti-OX40 antibodies with variable region substitutions. As shown in Figure 12C, OX40.6, OX40.8 and OX40.21 antibodies showed the highest potency of binding, with EC₅₀s of 0.12 nM or lower. OX40.1 showed much lower binding to cynomolgus macaque CD4 T cells. No binding of the OX40.21 antibody was detected on activated mouse or rat CD4+ T cells. A summary of the EC₅₀ values is presented in Table 8 below.

Table 8:

Name	Cyno T Cell Binding EC ₅₀ (nM) (mean ± SD)	n
3F4	0.37 ± 0.13	4
8B11	0.20 ± 0.08	4
18E9	41.70 ± 37.78	4
20B3	1.18 ± 0.27	4
20C1 *	0.17 ± 0.07	4
23H3	0.18 ± 0.10	4
6E1	0.77 ± 0.14	4
14A2	0.27 ± 0.02	4
14B6	0.31	1
OX40.6	0.11 ± 0.01	5
OX40.8	0.10 ± 0.02	4
OX40.16	0.06 ± 0.01	3
OX40.17	0.52 ± 0.12	3
OX40.18		
OX40.21	0.07 ± 0.01	5
OX40.1	23.40 ± 37.75	4
OX40.4	1.3	1
OX40.5	~ 2.2e+012	1

Example 4: Scatchard analysis of binding of anti-OX40 antibodies to activated primary T cells and cells overexpressing human and cynomolgus monkey OX40

[0539] The binding of OX40.21 (IgG1 isotype) to activated human T cells was further assessed using Scatchard analysis. Briefly, OX40.21 was radioiodinated with ¹²⁵I-Na (1mCi; PerkinElmer Catalog NEZ033H001 MC) using IODO-GEN® solid phase iodination reagent (1,3,4,6-tetrachloro-3a-6a-diphenylglycouril; Pierce Catalog 28601). Activated human CD4+ T cells were isolated from peripheral blood mononuclear cells (PBMC), Donor W-326470, purchased from the Stanford Blood Bank. CD4+ T cells were isolated by negative selection (RosetteSep™ Human CD4+ T cell enrichment cocktail, StemCell Technologies Catalog 15062) and frozen. The isolated CD4+ T cells were activated for four days before the binding assay in order to induce OX40 expression, as follows. Thawed cells were cultured for four days with magnetic beads coated with anti-human CD3 plus anti-human CD28 (human T-Expander CD3/CD28 Dynabeads, Invitrogen Catalog 111.41D), at a 1:1 bead cell ratio, in the presence of 200 IU/mL recombinant human IL-2 (Peprotech Catalog 200-02).

[0540] Radioiodinated OX40.21 IgG1 binding to activated human T cells was demonstrated by incubating activated human T cells with a titration of ¹²⁵I_OX40.21 IgG1. Nonspecific binding was determined by binding in the presence of a titration of a 100 fold molar excess of unlabeled antibody and was subtracted from total CPM to calculate specific

binding. A linear standard curve of ^{125}I _OX40.21 IgG1 concentration versus CPM was used to extrapolate specific activity, maximal nM bound ^{125}I _OX40.21 IgG1 and thereby calculate receptor number per cell.

[0541] As shown in Table 9 and Figure 13A, saturable binding of OX40.21 IgG1 was observed on activated human T cells endogenously expressing OX40, with a K_D of 0.05 nM for each of two T cell donors.

Table 9. Binding of ^{125}I -OX40.21 to Activated Human T Cells

Ab Cone. (nM)	Total Binding ^{125}I - labeled Antibody (nM)		Non-Specific Binding ^{125}I - labeled Antibody (nM)		Specific Binding ^{125}I - labeled Antibody (nM)	
10	0.0317	0.0292	0.0120	0.0117	0.0197	0.0175
	0.0283	0.0275	0.0073	0.0072	0.0210	0.0204
5	0.0230	0.0256	0.0036	0.0030	0.0195	0.0226
2.5	0.0205	0.0221	0.0029	0.0025	0.0176	0.0196
1.25	0.0197	0.0223	0.0014	0.0017	0.0183	0.0207
0.625	0.0197	0.0229	0.0013	0.0012	0.0184	0.0217
0.3125	0.0177	0.0201	0.0012	0.0011	0.0165	0.0190
0.15625	0.0140	0.0152	0.0010	0.0011	0.0129	0.0141
0.078125	0.0083	0.0091	0.0007	0.0010	0.0076	0.0081
0.039063	0.0057	0.0057	0.0009	0.0010	0.0049	0.0047
0.019531	0.0024	0.0030	0.0007	0.0008	0.0017	0.0022
0.009766						

[0542] The same assay was performed using HEK293 cells overexpressing human OX40 ("hOX40-293"). Briefly, radioiodinated OX40.21 binding to overexpressed human OX40 was demonstrated by incubating hOX40-293 cells with a titration of ^{125}I _OX40.21. Nonspecific binding was determined by binding in the presence of a titration of a 100 fold molar excess of unlabeled antibody and was subtracted from total CPM to calculate specific binding. A linear standard curve of ^{125}I _OX40.21 concentration versus CPM was used to extrapolate maximal nM bound ^{125}I _OX40.21 and thereby calculate receptor numbers per cell. As shown in Figure 13B and Table 10, saturable binding of OX40.21 IgG1 was observed for binding to OX40 expressed on hOX40-293 cells. The average K_D for binding from two test conditions using different numbers of hOX40-293 cells per sample was 0.22 nM.

Table 10: OX40.21 Binding to hOX40-293 Cells

Ab Cone. (nM)	Total Binding ^{125}I - labeled Antibody (nM)		Non-Specific Binding ^{125}I - labeled Antibody (nM)		Specific Binding ^{125}I - labeled Antibody (nM)	
10	0.1866	0.1712	0.0129	0.0137	0.1737	0.1575
	0.1800	0.1710	0.0080	0.0099	0.1720	0.1611
5	0.1799	0.1643	0.0065	0.0065	0.1734	0.1578
2.5	0.1722	0.1628	0.0057	0.0054	0.1665	0.1574
1.25	0.1583	0.1436	0.0067	0.0048	0.1515	0.1388
0.625	0.0986	0.0936	0.0038	0.0044	0.0948	0.0891
0.3125	0.0624	0.0501	0.0035	0.0048	0.0589	0.0453
0.15625	0.0351	0.0289	0.0035	0.0033	0.0316	0.0255
0.078125	0.0211	0.0162	0.0038	0.0027	0.0173	0.0136
0.039063	0.0117	0.0091	0.0029	0.0028	0.0088	0.0063
0.019531	0.0075	0.0056	0.0027	0.0028	0.0048	0.0028
0.009766						

[0543] The same assay was performed using CHO cells overexpressing cynomolgus monkey OX40 ("cynoOX40-

CHO"). Briefly, radioiodinated OX40.21 binding to cynomolgus OX40 was demonstrated by incubating cynoOX40-CHO cells with a titration of ^{125}I -OX40.21. Nonspecific binding was determined by binding in the presence of a titration of a 100 fold molar excess of unlabeled antibody and was subtracted from total CPM to calculate specific binding. A linear standard curve of ^{125}I -OX40.21 concentration versus CPM was used to extrapolate maximal nM bound ^{125}I -OX40.21 and thereby calculate receptor numbers per cell. As shown in Figure 13C and Table 11, saturable binding of OX40.21 IgG1 was observed for binding to cynomolgus OX40 expressed on cynoOX40-CHO cells. The average K_D for binding from two test conditions using different numbers of cells per sample was 0.63 nM.

Table 11: OX40.21 Binding to cynoOX40-CHO Cells

Ab Cone. (nM)	Total Binding ^{125}I -labeled antibody (nM)		Non-Specific Binding ^{125}I -labeled antibody (nM)		Specific Binding ^{125}I -labeled antibody (nM)	
20	0.1781	0.1814	0.0266	0.0414	0.1515	0.1400
	0.1768	0.1651	0.0161	0.0197	0.1607	0.1454
10	0.1629	0.1820	0.0109	0.0171	0.1520	0.1649
5	0.1665	0.1659	0.0080	0.0092	0.1586	0.1567
2.5	0.1197	0.1839	0.0079	0.0084	0.1117	0.1755
1.25	0.0892	0.1197	0.0060	0.0074	0.0832	0.1123
0.625	0.0630	0.0754	0.0057	0.0053	0.0573	0.0701
0.3125	0.0318	0.0437	0.0049	0.0050	0.0269	0.0386
0.15625	0.0158	0.0212	0.0030	0.0034	0.0128	0.0179
0.078125	0.0082	0.0110	0.0027	0.0029	0.0055	0.0082
0.039063	0.0058	0.0058	0.0026	0.0023	0.0032	0.0035
0.019531	0.0030	0.0032	0.0022	0.0021	0.0009	0.0011
0.009766						

Example 5: Specific binding of anti-OX40 antibodies to lymphocytes

[0544] The specificity of various OX40 antibodies was tested on a panel of 22 normal human tissue types, including spleen, tonsil, thymus, cerebrum, cerebellum, heart, liver, lung, kidney, pancreas, pituitary, peripheral nerves, stomach, colon, small intestine, thyroid, skin, skeletal muscle, prostate, uterus, testes, and placenta by immunohistochemistry.

[0545] Fresh, frozen and/or OCT-embedded human tissues were purchased from multiple commercial tissue networks/vendors (Asterand Inc. Detroit, MI; Cooperative Human Tissue Network, Philadelphia, PA; ProteoGenex Inc, Culver City, CA). To detect tissue binding, a series of anti-OX40 antibodies (OX40.6-FITC, OX40.8-FITC, 6E1-FITC, OX40.16-FITC, OX40.17-FITC, OX40.20-FITC, and OX40.21-FITC) were fluoresceinated and applied to acetone fixed cryostat sections, followed by an anti-FITC bridging antibody and visualization by the EnVision+ System. A nonspecific fluoresceinated human IgG1 was used as isotype control antibody. HT1080 cells stably expressing human OX40 (HT1080/huOX40) and hyperplastic human tonsil tissue sections were used as positive control cells and tissues. To determine if FITC conjugation has any impact on binding properties, both FITC-conjugated and unconjugated anti-OX40 antibodies were compared in HT1080/huOX40 cells using anti-huIgG as bridging antibody. Stained slides were evaluated under a light microscope.

[0546] Initial tests revealed that both un-conjugated and FITC-conjugated anti-OX40 antibodies specifically stained the cytoplasm and membrane of human OX40 transfected cells but not parent HT1080 cells. There was no difference between unconjugated and FITC-conjugated anti-OX40 antibodies. These results suggest that the antibodies were suitable for immunohistochemistry analyses, and that FITC conjugation has no impact on tissue binding properties.

[0547] All anti-OX40 antibodies tested exhibited positive staining in a small subset, either as scattered or small clusters, of mononuclear cells (MNC) in lymphoid tissues (tonsil, spleen, and thymus) and lymphoid-rich tissues (colon, stomach, and small intestine), as well as a few scattered MNC in multiple tissues (lung, skin, and thyroid). Based on morphology,

these positive cells are primarily lymphocytes.

[0548] In addition to staining a subset of lymphocytes, the OX40.6 antibody, a ligand blocker, displayed strong staining in subsets of endothelium/subendothelial matrix and interstitial elements, more often associated with small arteries and adventitia of vessel and its surrounding connective tissues, in virtually all tissues examined (Figure 14A), as well as specialized interstitial tissue elements such as sheath-like interstitium surrounding the seminiferous tubule in the testis. The OX40.8 antibody, a ligand non-blocker, positively labeled myofilament-like structures in cardiac muscles of the heart (Figure 14A) and mesangial-like cells in glomerulus of the kidney. Staining with another ligand non-blocker, i.e., the 6E1 antibody, also revealed staining in cardiac muscle cells, as well as in neurons and neuropils of cerebrum and cerebellum and a subset of tubule epithelial cells in kidney. In general, the staining of non-lymphocytes was detected only when the antibodies were used at relatively high concentrations (3 or 5 µg/ml), but not at lower concentrations (1 µg/ml), suggesting low affinity binding or potential off-target binding.

[0549] Further testing of other ligand blocking antibodies, OX40.16 (Figure 14A) and OX40.17, revealed clean staining of a subset of lymphocyte, with no specific staining of other tissue elements for all tissues examined. The OX40.21 antibody, a variant of the OX40.16 antibody, had a similar binding pattern as the OX40.16 antibody (Figure 14B). Immunohistochemistry in a similar panel of normal cynomolgus tissues revealed very similar staining pattern to human, demonstrating the utility of cynomolgus monkey as a relevant preclinical species.

Example 6: Expression of OX40 in cancers

[0550] FFPE (formalin fixed paraffin embedded) tumor tissue samples were purchased from commercial tissue vendors (n=12-20 for each tumor type). To detect binding to tissues, an automated IHC assay with a commercial anti-human OX40 antibody was developed using the Leica BondRX platform. Briefly, heat-induced antigen retrieval (HIER) was performed in pH9 ER2 buffer (Leica) for 20 min at 95°C. The mouse anti-human OX40 monoclonal antibody clone ACT35 (BD Pharmingen) was incubated at 5 µg/ml for 60 minutes, followed by Novolink Max polymer (Leica) for 30 minutes. Finally, slides were reacted with DAB substrate-chromogen solution for 6 minutes, counterstained with Mayer's hematoxylin, dehydrated, cleared, and coverslipped with Permount. Dako protein block was used as diluent for the primary antibody.

[0551] To profile TILs, commercially available anti-CD3 (T cell marker) and anti-FoxP3 (Treg marker) monoclonal antibodies were used to stain adjacent sections. Commercial mouse IgG1 was used as a negative control and hyperplastic human tonsil tissue was used as a positive control. After immunostaining, slides were manually evaluated and scored under a light microscope.

[0552] In the four tumor types examined, CD3+ TILs were present in all samples examined, with the amount of TILs varying across samples and the distribution within the same tissue heterogeneous. In some cases, TILs were more heavily distributed in the tumor and host interface, as expected. Most TILs were localized in the tumor stroma in the vast majority tissue samples. However, they were readily found in intratumoral nests in many cases. Positive OX40 staining was observed in a small fraction of TILs and primarily distributed in the tumor stroma. In general, the abundance of OX40+ TILs was in proportion to that of CD3+ TILs. Among the four tumor types examined, OX40+ TILs were more abundant in HCC and CRC (Figures 15A-15C).

Example 7: Human monoclonal anti-OX40 antibodies that block the binding of OX-40L to OX-40

[0553] Several anti-OX40 antibodies were tested for their ability to block the binding of recombinant soluble OX40L to human OX40-transfected 293 cells. Briefly, 293 cells stably transfected with human OX40 were first pre-incubated with varying concentrations of anti-OX40 antibodies. A fixed concentration (0.2 µg/mL) of recombinant soluble his-tagged human OX40L (OX40L-His, R & D Systems) was then added and the samples incubated further. After washing the cells, bound OX40L-His was detected using an in-house APC-labeled anti-His tag antibody. The fluorescence intensity of the staining was measured using a FACSCanto II flow cytometer (Becton Dickinson). The geometric mean fluorescence intensity (GMFI) of APC-anti-His tag antibody/OX40L-His staining for the cell population was calculated (FACSDiva software). Dose-response curves were generated and EC50s for antibody blocking of OX40L binding were

calculated using GraphPad Prism software; the EC50s are shown in Table 12.

Table 12. EC50 values for blocking of OX40L/OX40 interaction as measured by FACS.

Antibody Clone	EC50 (nM)
14B6.C5.C8	1.0
3F4.G11.D2	0.54
8B11.H9.C1	0.45
18E9.G5.H4	0.48
20B3.G12.A2	0.93
20C1.F2.D1	0.34
6E1.A12.A2	<i>no blocking</i>
23H3.C6	0.38
OX40.4	<i>no blocking</i>
OX40.5	~ 1.2e+013

[0554] As shown in Figure 16, most of the anti-OX40 antibodies tested fully blocked the binding of soluble human OX40L to human OX40 on the surface of transfected cells, with the exception of 6E1, OX40.4, and OX40.5. The incomplete blocking by OX40.5 may be due to a lower potency of binding to human OX40 than the other antibodies tested or binding to an overlapping but different epitope. In contrast, 6E1 and OX40.4 did not block the binding of human OX-40L to OX40. This lack of blocking is likely due to binding to a different epitope than the remaining antibodies.

Example 8: Antibody competition/binning

[0555] Antibody binning experiments were carried out as follows. One or more anti-OX40 antibodies were coated directly onto a Biacore CM5 chip using amine coupling chemistry. Anti-OX40 antibodies, serially diluted (1:3) from a starting concentration of 60 µg/mL, were incubated with 20 nM of OX40-6X-His antigen for at least 1 hour. The incubated complex was flowed over the antibody coupled surfaces and observed for cross-blocking. The exercise was repeated with several antibodies on the surface to create the epitope map based on mutual cross-blocking of all the antibodies. OX40L was also coated on the surface to identify and bin the antibodies that were able block OX40-OX40L interaction. Experiments were carried out on Biacore T200 or Biacore 3000 SPR instruments.

[0556] As summarized in Figure 17, antibodies 20C1, 20B3, 8B11, 23H3, 18E9, 14B6, OX40.1, and OX40.2 were ligand blockers; antibody 3F4 was a partial ligand blocker; and 14A2, 6E1, and OX40.5 were ligand non-blockers.

Example 9: Biophysical properties of OX40 antibodies

[0557] The affinity of several OX40 antibodies for soluble human OX40 was tested by SPR analysis. Briefly, affinity measurements were carried out by capturing 1-10 µg/mL of the respective antibody on a CM5 chip coated with anti-human-CH1. Human-OX40-6XHIS antigen in either a single concentration of 400 nM or a 1:2 serial dilution from 400 nM was used. Experiments were carried out on BIACORE® T200 or BIACORE® 3000 SPR instruments. Data was fit to a 1:1 model.

[0558] As shown in Table 13, the anti-OX40 antibodies tested had dissociation constants (K_D s) in the range of 10^{-8} M to 10^{-9} M.

Table 13: K_D values for OX-40 antibodies

Clone	K_D (M)	k-on (1/Ms)	k-off (1/s)
3F4	7.13 e-9	5.31 e4	3.79 e-4

Clone	K_D (M)	k-on (1/Ms)	k-off (1/s)
8B11	1.05 e-8	4.8 e4	5.1 e-4
14B6	8.84 e-9	7.4E4	6.54 e-4
6E1	1.1 e-8	1.28 e5	1.41 e-3
14A2	1.51 e-9	1.46 e5	2.2 e-4
18E9	2.04 e-9	6.83 E4	1.39 e-4
20B3	3.71 e-9	5.42 e4	2.01 e-4
23H3	3.6 e-9	1.1 E5	3.95 e-4
20C1	3.22 e-9	6.48 E4	2.09 e-4
OX40.21	1.49 e-9	9.41e+5	0.0014

[0559] The thermal stability of the OX40.21 antibody was also tested, with results summarized in Table 14. Thermal stabilities were determined using GE Healthcare CAP-DSC. Samples were run at 250 µg/mL concentration in PBS. The scan rate was 60 °C/hr. Data was fit to a non-2-state model. The OX40.21 antibody was determined to be one of the more stable antibodies tested when considered together with other attributes (e.g., low off-target effects, immunogenicity, etc).

Table 14:

Clone	Tm1	Tm2	Tm3	% reversibility
3F4		68	83	
8B11		72.7	82.9	
14B6		66.3	70.5	
18E9		65.8	71.2	
23H3		72.3	82.7	
20C1		68.0	83.0	
OX40.21	72.2		79.5	48% at 80°C

[0560] The pharmacokinetics of the OX40.21 antibody after single intravenous dosing to cynomolgus monkeys also was tested. The OX40.21 antibody exhibited acceptable pharmacokinetic (PK) properties after single intravenous (IV) dosing to cynomolgus monkeys with linear PK (0.4 to 4 mg/kg) and a long terminal half-life (6 days).

Table 15: Pharmacokinetic parameters of OX40.1 after intravenous administration in cynomolgus monkeys (N=3)

Dose (mg/kg)	AUC(INF)* (µg/mL×day)	$t_{1/2}$ (day)	CLT (mL/h/kg)	Vss (mL/kg)
0.4	86 ± 5	5.6 ± 0.5	0.20 ± 0.01	36 ± 2
4	785 ± 138	6.2 ± 0.6	0.22 ± 0.04	49 ± 12

PK parameters were calculated by a non-compartmental method. Values are mean ± SD.

* PK parameters were calculated using plasma conc. up to 10 days, except monkey 2 at 0.4 mg/kg up to 7 days

* % AUCextra ranged between 24% and 42%

[0561] The human PK parameters of OX40.21 were projected from cynomolgus monkey PK data using allometric scaling (assuming power exponent = 0.85 for CLT and 1 for Vss). The projected human $t_{1/2}$ was 10 days (Table 16). PK parameters were calculated by a two-compartment method.

Table 16: Projected Human Pharmacokinetic Parameters of OX40.21

Ab	Dose (mg/kg)	AUC(INF) (µg/mL×day)	$t_{1/2}$ (day)	CLT (mL/h/kg)	Vss (mL/kg)
OX40.21	1	303	10	0.14	47

Example 10: FACS cross-blocking of PE-labeled anti-OX40 antibody clone L106 by a panel of unlabeled anti-OX40 antibodies

[0562] Several anti-OX40 antibodies were tested for their ability to block the binding of PE-labeled anti-OX40 antibody clone L106 to human OX40-transfected 293 cells. Briefly, 293 cells stably transfected with human OX40 were first incubated with varying concentrations of unlabeled anti-OX40 antibodies. The cells were then washed and incubated with a fixed concentration of 2.5 µg/mL of PE-labeled L106 antibody (BD Biosciences). The fluorescence intensity of the staining was measured using a FACSCanto II flow cytometer (Becton Dickinson). The geometric mean fluorescence intensity (GMFI) of PE-L106 antibody staining for the cell population was calculated (FACSDiva software). Dose-response curves for blocking of L106 binding were generated using GraphPad Prism software.

[0563] As shown in Figure 18, the 18E9 and OX40.1 antibodies fully blocked L106 binding to human OX40-transfected cells, while 20B3 showed partial blocking. The remaining antibodies showed little or no blocking, indicating that 18E9 and OX40.1 bind to a different epitope on OX40 than the other antibodies tested.

Example 11: Cross-block analysis of anti-OX40 antibodies

[0564] This experiment was performed to test the cross-blocking properties of various anti-OX40 antibodies to assess binding specificities. In brief, the OX40 antibody OX40.1 was conjugated to allophycocyanin (APC), and human OX40 antibodies OX40.4 and OX40.5 were biotinylated. A panel of unconjugated human OX40 antibodies were applied in dose to engineered 293 or HT1080 cell lines that over-express human OX40 protein on their surface and were permitted to bind at 4°C for 30 min. Without washout of the unconjugated Ab, APC-OX40.1 (1 µg/mL), biotin-OX40.4 (0.4 µg/mL), or biotin-OX40.5 (0.4 µg/mL) was applied to the assay wells and allowed to bind at 4°C for 30 min. Cells were washed and if necessary further incubated in the presence of streptavidin-APC conjugate under the same conditions. After the final wash, cells were analyzed on a FACSCanto flow cytometer (BD Bioscience, San Jose, CA). Mean fluorescence intensity (MFI) signal was proportional to bound conjugated antibody.

[0565] As shown in Figures 19A-19C, binding of APC-OX40.1 to cells overexpressing human OX-40 protein was blocked by OX40.2 and OX40.5, but only modestly, if at all, by OX40.4. Binding of APC-OX40.1 was blocked by 8B11.H9, 3F4.G11, 20B3.G2, and 14B6.C5, but not by 6E1.A12 and 14A2.B9. A diagram of the observed binding relationships between the antibodies evaluated in Figures 19A-19C is shown in Figure 19H.

[0566] Figures 19D-19E show that binding of biotin-OX40.4 was strongly blocked by 20B3.G2, moderately blocked by 20C1.F2, weakly blocked, if at all, by 3F4.G11 and 23H3.C6, and was not blocked by 14A2.B9. Binding of biotin-OX40.5 was strongly blocked by 20B3.G2, 23H3.C6, and 20C1.F2, moderately blocked by 3F4.G11, and weakly blocked by 14A2.B9.

[0567] Figures 19F-19G show that binding of biotin-OX40.4 was not blocked by OX40.1 or OX40.8, and was only weakly blocked, if at all, by OX40.5 or OX40.6. Binding of biotin-OX40.5 was blocked by OX40.1, moderately blocked by OX40.6, and was only very weakly blocked, if at all, by OX40.4 or OX40.6.

[0568] A diagram of the observed binding relationships between the Abs evaluated in Figures 19D-19G is shown in Figure 19I.

Example 12: Anti-OX40 antibodies bind to a conformation epitope/epitope mapping

[0569] This example shows that OX40.21 binds to non-denatured human OX40, but not to denatured human OX40, and that binding is not affected by N-glycosylation.

[0570] Binding of OX40.21 to native or denatured OX40 that has N-linked glycosylation or not was determined as follows. Samples of native (i.e., non-denatured) and denatured human OX40 were incubated with or without the

enzyme N-glycanase PNGase F to remove N-glycosylation. Samples of native human OX40 with or without N-linked glycosylation were subjected to SDS gel electrophoresis, and samples of denatured human OX40 with or without N-linked glycosylation were subjected to denaturing SDS gel electrophoresis.

[0571] As shown in Figure 20A, OX40.21 binds only to native OX40, and not to the denatured form, and the presence or absence of glycosylation does not affect binding to OX40. Figures 20B and 20C show that two N-glycopeptides were identified by peptide mapping after deglycosylation (60% occupancy for both AspN1 18 and AspN12).

[0572] These data suggest that OX40.21 binds to an epitope that is conformational and independent of N-linked glycosylation.

[0573] Epitope mapping studies were also conducted using mass spectrometry. Peptide fragments of his-tagged human OX40 ("hOX40") were generated by enzymatic digestion with endoproteases. LC-MS was performed using AB Sciex 5600 Triple-TOF.

[0574] As shown in Figures 20D and 20E, binding experiments from native hOX40 by limited proteolysis revealed that OX40.16 and OX40.21 bound predominantly to the peptide DVVSSKPKPCTWCNLR (SEQ ID NO: 178), which corresponds to amino acids 46-62 of the extracellular portion of mature human OX-40 (SEQ ID NO: 2). OX40.8 bound to the peptide DSYKPGVDCAPCPGPHFSPGDNQACKPWTNCTLAGK (SEQ ID NO: 179), which corresponds to amino acids 89-124 of the extracellular portion of mature human OX40 (SEQ ID NO: 2). The location of the epitope bound by OX40.21 overlaps part of the binding site of OX40 ligand as determined by crystal structure of the human OX40/OX40L complex (Protein Data Bank (PDB) ID code 2HEV). Additional peptides identified by mass spectrometry for OX40.21 are shown in the upper panel of Figure 20E, and include QLCTATQDTVCR (SEQ ID NO: 184), SQNTVCRPCGPGFYN (SEQ ID NO: 185),

[0575] SQNTVCRPCGPGFYNDVVSSKPKPCTWCNLR (SEQ ID NO: 182), and PCKPCTWCNLR (SEQ ID NO: 183).

Example 13: Anti-OX-40 antibodies promote T cell proliferation and induce IFA- γ and IL-2 secretion from T cells

[0576] Anti-OX-40 antibodies were tested for their ability to induce T cell activity *in vitro* by measuring the proliferation of and amount of IL-2 and IFN- γ secreted by T cells incubated with the antibodies.

[0577] A transfected CHO cell line was generated for use as artificial antigen-presenting cells in a primary T cell activation assay. The CHO-CD3-CD32A cell line expresses anti-human CD3 antibody in a single-chain Fv format, along with the human Fc receptor CD32A to present anti-OX40 antibodies on the CHO cell surface. Briefly, human primary CD4 T cells were isolated by negative selection (RosetteSep™, StemCell Technologies) and co-cultured with irradiated CHO-CD3-CD32A cells at an 8:1 T:CHO ratio, in the presence of graded doses of anti-OX40 antibodies or isotype control antibody. After 3 to 4 days in culture at 37 °C, supernatants were harvested for assessment of T cell activation by means of measurement of secreted human IFN γ either by ELISA (BD Biosciences) or HTRF assay (Cisbio), following the manufacturers' recommendations. Afterwards, tritiated thymidine was added for the final approximately 18 hours of culture to measure T proliferation by tritiated thymidine incorporation, as an additional assessment of T cell activation.

[0578] As shown in Figures 21A-21D and 22A-22D (and summarized in Table 17 below), most tested anti-OX40 antibodies strongly potentiated human CD4 T cell activation stimulated by CHO-CD3-CD32 cells, in a dose-dependent manner, as measured by proliferation and IFN γ secretion. The panel of antibodies tested in this assay co-stimulated T cell activation at least as well as, or better than, OX40.1, OX40.4, and OX40.5.

Table 17.

Name	Proliferation EC ₅₀ (nM) (mean $\pm$ SD)	n	IFN γ EC ₅₀ (nM) (mean $\pm$ SD)	n
3F4	0.016 $\pm$ 0.008	5		
8B11	0.022 $\pm$ 0.027	3		
18E9	0.010 $\pm$ 0.005	3		

Name	Proliferation EC ₅₀ (nM) (mean ± SD)	n	IPNy EC ₅₀ (nM) (mean ± SD)	n
20B3	0.008 ± 0.003	3		
20C1	0.008 ± 0.006	4		
23H3	0.028 ± 0.017	3		
6E1	0.014 ± 0.008	2		
14A2	0.037 ± 0.044	4		
14B6	0.012 ± 0.008	3		
OX40.6	0.032 ± 0.028	2	0.033 ± 0.004	2
OX40.8	0.043 ± 0.037	2	0.024	1
OX40.16	0.017	1	0.044	1
OX40.17	0.009 ±	1	0.044	1
OX40.18	0.230 ±	1	0.490	1
OX40.21	0.011 ± 0.006	9	0.043 ± 0.023	9
OX40.1	0.024 ± 0.012	4		
OX40.4	0.094	1	~ 2.3 e+009	1
OX40.5	1.900	1	~ 37	1

[0579] The anti-human OX40 antibodies were also tested for their effects on stimulating primary T cells in cultures of staphylococcus enterotoxin B (SEB)-activated human peripheral blood mononuclear cells (PBMCs). Human whole blood was obtained from AllCells, Inc. (Berkeley, CA) or from donors at Bristol-Myers Squibb, Redwood City, CA under the auspices of an in-house phlebotomy program. PBMCs were isolated by gradient purification on a Ficoll-Hypaque cushion and cultured for 3 days in culture medium supplemented with fixed, suboptimal (85 ng/mL) of superantigen staphylococcus enterotoxin B (SEB; Toxin Technologies, Sarasota, FL) in the presence of graded doses of OX40 antibodies or isotype control antibody together with 2 - 5 µg/mL of soluble cross-linking antibody, F(ab')₂ goat anti-human Fcγ. After culturing for 3 days at 37 °C, supernatants were harvested for assessment of T cell activation by means of ELISA measurement of secreted human IL-2. Briefly, culture supernatants were diluted 1:10 in sample diluent and tested for the presence of human IL-2 by ELISA (BD Bioscience) per the manufacturer's recommended protocol. Following the addition of TMB substrate, assay plates were read on a Spectramax 340PC reader using Softmax operating software at a wavelength of 650 nm. Measured optical densities of the chromogenic substrate were proportional to bound detecting antibody.

[0580] Data from PBMCs isolated from different donors are shown in Figures 23A-23F. In general, solubly-crosslinked clone 20C1.F2 elicited a more robust cytokine response (EC50 of 1.3 - 2.0 nM) compared to solubly-crosslinked clones 23H3.C6, 8B11.H9, 3F4.G11, 18E9.G5, 6E1.A12, and 20B3.G2 (Figures 23A-23C). With respect to antibodies with variable region mutations, OX-40.21, in general, elicited a more robust cytokine response compared to solubly-crosslinked antibodies OX-40.17, OX40.18, OX40.6, and OX40.8 (Figures 23D-23F). Data from these donors together with data from 8 additional donors, in which additional anti-OX40 antibodies were tested, collectively demonstrate that on average, OX40.21 exhibited superior potency in enhancing T cell responses compared to OX40.1, OX40.2, OX40.4, OX40.5, OX40.17, and OX40.18. These results further demonstrate that OX40.21 elicits responses that are comparable to those elicited by OX40.6 and OX40.8 (Table 18).

Table 18:

[illegible]

Donor#		OX40.21	OX40.17	OX40.18	OX40.6	OX40.8				
Donor#		OX40.21	OX40.17	OX40.18	OX40.6	OX40.8	OX40.1	OX40.2	OX40.4	OX40.5
WB10024	EC50(nM)	0.82	1.06	~ 3.17	~ 0.42	~ 0.44	~ 1.87	2.53	1.25	~ 1.83
WB10025	EC50 (nM)	1.31	1.35	~ 1.14	~0.85	0.79	2.08	~ 3.26	1.08	3.07
WB10026	EC50 (nM)	0.79	1.68	3.02	0.28	0.63	2.24	3.16	1.14	2.59
WB10027	EC50 (nM)	1.08	1.15	~ 3.27 ~ 3.27	~ 0.45	~ 0.46	1.26	2.26	0.93	~ 3.09
Donor#		OX40.21	OX40.17	OX40.18	OX40.6	OX40.8	OX40.1	OX40.2	OX40.4	OX40.5
WB10137	EC50 (nM)	0.56	0.92	>100	0.56	0.42	~ 1.824	>100	1.37	>100
BMS-001	EC50 (nM)	0.41	0.41	~ 84.76	0.49	~ 0.42	0.64	4.95	~ 089	~ 0.43
BMS-004	EC50 (nM)	~ 0.84	1.03	2.43	0.48	0.55	2.52	13.89	0.84	1.94
	BMS-015 EC50 (nM)	0.76	1.16	>100	~ 0.46	~ 0.42	2.41	>100	0.91	1.92
	Mean EC50(nM)	0.64	1.17	2.89	0.46	0.44	1.86	5.36	1.07	2.38
*Each set of experiments was performed on different days.										

Example 14: Anti-OX40 Antibody Promotion of NK92-mediated Cell Lysis Using Cell Lines

[0581] Several anti-human OX40 antibodies were tested for their ability to promote NK92 cell-mediated lysis of activated CD4⁺ T cells using calcein release as a read-out. Briefly, CD4⁺ T cells for use as target cells were separated by negative selection using magnetic beads and activated for 72 hours with beads coated with anti-CD3 and anti-CD28. After three days, NK92 cells were plated with calcein AM-labeled activated CD4⁺ cells at a ratio of 5 to 1. A titration of each anti-OX40 antibody was added and cells were incubated for two hours. Calcein release was measured by reading the fluorescence intensity of the media using an Envision plate reader (Perkin Elmer). The percentage of antibody-dependent cell lysis was calculated based on mean fluorescence intensity (MFI) with the following formula: [(test MFI - mean background)/(mean maximum - mean background)] × 100.

[0582] As shown in Figure 24, OX40.8 and OX40.16 induced the highest amount of specific lysis of target cells (60% and 30%, respectively). The EC₅₀ of OX40.8 was 16 ng/mL and that for OX40.16 was 4 ng/mL. All other antibodies tested induced ADCC at levels too low for accurate quantitation.

Example 15: Anti-OX40 antibody promotion of NK-mediated cell lysis of primary human CD4⁺ T cells

[0583] Several anti-human OX40 antibodies were tested for their ability to promote primary NK cell-mediated lysis of activated CD4⁺ T cells. Briefly, CD4⁺ T cells for use as target cells were separated from PBMCs from two donors by magnetic selection and activated for 72 hours with beads coated with anti-CD3 and anti-CD28. NK cells, for use as effectors, were separated from a separate donor by negative selection using magnetic beads and activated with IL-2 for 24 hrs. Following the activation period, NK effector cells were mixed with calcein-labeled target T cells at 20:1, 10:1, or

5:1 ratios in the presence of antibody at 1 µg/ml for 2 hours. The level of calcein released by lysed target cells was measured by reading the fluorescence intensity of the media using an Envision plate reader (Perkin Elmer). The percentage of antibody-dependent cell lysis was calculated based on mean fluorescence intensity (MFI) with the following formula:

$$[(\text{test MFI} - \text{mean background})/(\text{mean maximum} - \text{mean background})] \times 100.$$

[0584] As shown in Figures 25A and 25B, activated CD4+ T cell targets from two donors were lysed most effectively by OX40.8. Lower levels of ADCC activity were seen with both OX40.21 and OX40.1.

Example 16: OX40 antibody promotion of macrophage-mediated cell phagocytosis of OX40-expressing HEK293 cells

[0585] To determine the antibody-mediated phagocytic activity of several OX40 antibodies, primary human macrophages were cultured for four hours with CellTrace Violet-labeled HEK293/OX40 cells and a titration of anti-OX40 antibodies. After four hours, cells were harvested, stained with anti-CD64-APC, and run on a flow cytometer. Cells that stained double positive for CD64 and CellTrace Violet were considered to have been phagocytosed. The percentage of target cells phagocytosed was calculated using the formula: $100 \times (\text{Number of double positive cells} / \text{Total number of CellTrace Violet positive cells})$.

[0586] As shown in Figure 26, all tested anti-OX40 antibodies induced the phagocytosis of OX40-expressing target cells in a dose-dependent manner. OX40.8 had the highest overall level of phagocytosis and the lowest EC₅₀ concentration of 6.2 ng/mL. This demonstrates that human IgG1 anti-OX40 antibodies induce FcR-mediated phagocytosis in a dose-dependent manner.

Example 17: Anti-OX40 antibodies bind the C1q component of human complement

[0587] A colorimetric ELISA assay was developed to evaluate whether the C1q component of human serum complement binds to the OX40.21 antibody. All tested antibodies were coated on a high binding immunoassay plate at 10 µg/mL. After blocking unoccupied protein binding sites, graded doses of human C1q (3.125-200 µM) were added to the wells, including blocked empty wells that served as controls for non-specific background C1q binding to the assay plate. Binding of C1q to the immobilized antibodies was detected using a combination of biotinylated mouse anti-C1q antibody and streptavidin-poly-HRP, together with tetramethylbenzidine substrate. The results are reported as the optical density read at 450 nm minus 630 nm.

[0588] As shown in Figure 27, C1q bound to OX40.21 (solid squares) and the human IgG1 isotype control (open circles) in a dose dependent manner. The level of C1q binding to OX40.21 however, was lower than to the human IgG1 isotype control antibody. As expected, there was little background signal (gray circles) and no evident C1q binding to an IgG1.1 isotype control (solid black circles). The IgG1.1 antibody contains five mutations in the Fc portion designed to eliminate C1q binding and FcR interaction. This result demonstrates that the C1q component of human serum complement can bind to OX40.21 and indicates that OX40.21 may induce complement mediated lysis of OX40-expressing cells *in vivo*.

Example 18: OX40 is expressed in tumor infiltrating lymphocytes

[0589] OX-40 is expressed in tumor infiltrating lymphocytes, with a pattern that is generally limited to CD4+ cells (Figure 28A) with minimal expression on CD8+ T cells (Figure 28B) in colorectal, lung, and ovarian cancer (Figure 28C).

[0590] Similarly, OX40 is expressed by CD4+ T cells and Tregs in mouse Sa1N tumors (Figure 28D) and mouse MC38 tumors (Figure 28E). To test expression of mouse OX-40 in tumors, 2×10^6 SA1N sarcoma cells or 2×10^6 MC38 cells were implanted subcutaneously into AJ or B6 mice respectively. On day 15 post-implantation, tumors were harvested,

dissociated into single cell suspensions, and stained for flow cytometry. T cell populations were identified based on their expression of CD8, CD4 and Foxp3. For Sa1N tumors, CD4⁺ Foxp3⁺ cells from the tumor are shown in the red histogram, CD4⁺ Foxp4⁻ cells are in the blue histogram and CD8⁺ cells are in the orange histogram (Figure 28D). Isotype control stained cells are in the green histogram. For MC38 tumors, Tregs are shown in the blue histogram, CD4⁺ cells are shown in the green histogram and CD8⁺ cells in the red histogram (Figure 28E).

Example 19: Anti-OX40 antibody reversal of Treg cell-mediated suppression

[0591] Several anti-human OX40 antibodies were tested for their ability to reverse regulatory T (Treg) cell-mediated suppression of human CD4⁺ T cell proliferation. Briefly, Treg and T responder (Tresp) cells were isolated by enriching PBMCs for CD4⁺ cells by magnetic bead separation and then sorting CD4⁺CD25^{hi}CD127^{lo} Treg and CD4⁺CD25^{lo}CD127^{hi}CD45RO⁺ Tresp cells. Tresp cells were then labeled with proliferation dye and plated with titrating numbers of Treg cells, beginning at a 1:1 ratio. Cultures were stimulated with 3 µg/mL plate-bound anti-CD3, 1 µg/mL soluble anti-CD28, and 2 µg/mL plate-bound anti-OX40 or isotype control. After 96 hours, Tresp cell proliferation was measured by assessing dye dilution using flow cytometry.

[0592] As shown in Figure 29, in both the presence and absence of Treg cells, the anti-OX40 antibodies increased Tresp cell proliferation compared to the isotype control. This suggests that the anti-OX40 antibodies tested reversed the suppressive effects of Treg cells on Tresp cell proliferation.

Example 20: Toxicity studies

[0593] OX40.6 (2 mg/kg) was administered intravenously to monkeys on Days 1 (Figure 30A) and 29 (Figure 30B) to evaluate any associated toxicities. No evidence of tolerability issues or clinical pathology abnormalities was observed. OX40.6 stimulated an enhanced immune response to KLH, as characterized by a trend towards enhanced CD69 expression in CD4⁺ T cells in an ex vivo KLH recall assay. Two of 4 monkeys exhibited accelerated clearance, which correlated with the formation of anti-drug antibodies.

[0594] The concentration of OX40.6 in cynomolgus monkey serum samples for the experiment above was analyzed by a chemiluminescence (CL) immunoassay. OX40.6 antibody was used to prepare calibrators and quality control (QC) samples. Biotinylated-human-OX40-his was immobilized on streptavidin-coated microplates (Greiner Bio-one) as a capture molecule for OX40.6. Samples, standards, and quality control samples brought up to a final matrix of 10% cyno serum were incubated on the plates. Samples were analyzed at 10% minimum required dilution in 1% BSA/PBS/0.05% Tween 20 (PTB) containing 2% mouse serum. The unbound material was washed away and the captured OX40.6 antibody was detected using an HRP-labeled mouse monoclonal anti-human IgG antibody as the detection molecule. Following addition of SuperSignal ELISA Pico Chemiluminescent Substrate (Thermo Scientific), the concentration of OX40.6 in cyno serum samples was calculated from luminescence intensity as measured by a M5 plate reader using a 4-parameter logistic (4-PL) calibration curve generated from OX40.6 antibody calibrators. The range of the OX40.6 antibody calibration curve was from 5 to 5,000 ng/mL in cyno serum. The upper and lower limits of quantification were 5,000 and 10 ng/mL, respectively (i.e., ULOQ 5000 ng/mL, LLOQ 10 ng/mL). Quality control samples were prepared at 3750, 400, and 20 ng/mL in cynomolgus monkey serum and analyzed on each plate to ensure acceptable assay performance. Calibrators, QCs, and samples were diluted 5-fold in PTB containing 2% mouse serum. Four streptavidin plates were used to analyze the samples. Assay performance was within an acceptable range: interplate % CV of standards was below 25%, and QC recovery was within ± 30% nominal values.

[0595] The presence of anti-drug antibodies to OX40.6 in cynomolgus monkey serum in the experiment described above was determined by electrochemiluminescence (ECL) bridging immunoassay. Specifically, mouse monoclonal anti-human IgG Fc antibody was used to prepare the positive control. Biotinylated-anti-OX40: anti-hOX40-his was used at 25 ng/mL as the capture molecule and ruthenylated-anti-OX40:anti-hOX40-his was used at 25 ng/mL as the detection molecule. Samples were analyzed at 100-fold dilution in 1% BSA/PBS/0.05% Tween 20 (PTB) containing capture and detection molecules. After 2 hours of incubation in polypropylene plates, the sample mix was transferred to streptavidin-coated MSD plates. Following a one hour incubation, unbound material was washed away, MSD read

buffer was added, and ECL was measured with the MSD plate reader SI6000. The positive control (Mouse anti-human IgG Fc) was prepared at 1000 (HPC), 100 (MPC), and 10 ng/mL (LPC) in cynomolgus serum. Pooled cynomolgus serum was used as a negative control (NC). The signal ratio for HPC, MPC, and LPC versus NC was 102, 10, and 2, respectively. One streptavidin plate was used to analyze the samples. Assay performance was within the acceptable range: % CV of the PC was below 10%, and the raw signal for the negative control (54 RLU) was comparable to the raw signal for predose samples (48-55 RLU).

Example 21: Immunogenicity risk assessment study

[0596] *In vitro* T cell proliferation assays were conducted for several of the anti-human OX40 antibodies to assess their human immunogenicity potential. Briefly, peripheral blood mononuclear cells (PBMC) from healthy volunteers were isolated by Ficoll (GE Healthcare) and gradient centrifugation, and human lymphocyte antigen (HLA) Class II was characterized by polymerase chain reaction (PCR) amplification and hybridization with oligonucleotide probes (ProImmune).

[0597] A panel of 40 PBMC donors having HLA Class II types closely matching world population frequencies was used for an assay run. PBMCs were labeled with CFSE (Invitrogen) to monitor proliferation and plated on 96 well plates in 6 replicates at 200,000 cells per well in RPMI (Lonzo) containing 10% human AB (Bioreclamation), non essential amino acids (Gibco), and pen-strep (Gibco). Anti-human OX40 antibodies, controls proteins, reference antibodies, and ConA were cultured with PBMCs at 1 μ M for 7 days, after which media was washed away and cells were labeled with an anti-human CD4 APC (BD science) monoclonal antibody. After removal of unbound anti-CD4 antibody with a wash step, cells were fixed with 3.7% formalin (Sigma) in PBS, and analyzed by flow cytometry to determine the percentage of proliferating CD4+ cells.

[0598] The percentage of 40 donors that showed a positive response (defined as a significant increase in proliferating CD4+ T cells relative to media-incubated PBMCs) for the different anti-human OX40 antibodies is shown in Figure 31. All variants of the anti-human OX40 antibodies showed low potential to activate CD4+ cells in this assay, comparable to the low QC protein, with the exception of OX40.16 and OX40.21, which did not show a positive CD4 proliferation response in any of the 40 donors. These results suggest that these anti-human OX40 antibodies have low potential to elicit an anti-drug antibody response in humans.

Example 22: Binding to activated Fc receptors enhances anti-mOX40 activity in a colon carcinoma model

[0599] To test the role of FcR binding in the activity of anti-mouse OX40 antibodies in mouse tumor models, anti-OX40 antibodies of different isotypes were tested. C57BL/6 mice were subcutaneously injected with 2 million MC38 tumor cells. After 7 days, tumor volumes were determined and mice were randomized into treatment groups so as to have comparable mean tumor volumes. Antibodies formulated in PBS were administered intraperitoneally on days 7, 10, and 14 at 200 μ g per dose in a volume of 200 μ l.

[0600] In syngeneic mouse tumor models, anti-murine OX40 antibodies (e.g., OX86, rat IgG1) exhibit anti-tumor activity. Since varying the isotype of many antibodies specific for T cell surface receptors (both co-stimulatory and co-inhibitory) can alter the anti-tumor activity of these antibodies, mouse Fc isotype variants of OX86, an antibody which does not block the OX40/OX40L interaction, were generated. As shown in Figures 32A-32C, OX86 formatted as a mouse IgG2a Fc (Figure 32C) results in superior anti-tumor activity compared to OX86 formatted as a mouse IgG1 (Figure 32B). This is likely due both to depletion of Treg cells at the tumor site and to T effector cell expansion from antibody-mediated agonism of OX40.

[0601] To confirm the effects of different antibody isotypes on tumor infiltrating T cell populations, tumors from MC38 mice that were treated with the different isotypes were assessed by flow cytometry. Selected mice were sacrificed and tumors and spleens were harvested for analysis on day 15 after tumor implantation. Single cell suspensions were prepared by dissociating tumor and lymph node with the back of a syringe in a 24 well plate. Cell suspensions were passed through 70 μ m filters, pelleted, resuspended, and counted. Cells were then plated in 96 well plates with 1×10^6

cells per well for staining. Samples were then analyzed on a FACS Canto flow cytometer (BD). Analysis of the spleens and tumors of tumor bearing mice treated with anti-OX40 antibodies show that the IgG2a isotype can deplete CD4⁺ Tregs in tumors (Figure 33A), and that IgG1 and IgG2a isotypes can activate T cell expansion in the periphery (Figure 33B) and result in increased cell numbers in the spleen (Figure 33C). These results suggest that agonism of OX40 (but not necessarily blocking the OX40/OX40L interaction) and Fc receptor binding of the OX86 antibody promotes anti-tumor activity.

[0602] The role of human Fc and FcRs were tested using mice where mouse FcRs have been knocked out and replaced with the human FcRs. These experiments were performed using a bone marrow chimera system where CD45.1 congenic hosts were irradiated then reconstituted with human FcR transgenic bone marrow cells. These mice were then allowed to reconstitute for 8 weeks before being inoculated with 2×10^6 MC38 tumor cells. After 7 days, tumor volumes were determined and mice were randomized into treatment groups so as to have comparable mean tumor volumes. Antibodies formulated in PBS were administered intraperitoneally on days 7, 10, and 14 at 200 μ g per dose in a volume of 200 μ l. Mice were treated with either a control human IgG1 (Figure 34A), a chimeric OX-86 human G1 hybrid Ab (Figure 34B), or the OX-86 human G1 hybrid with a S267E mutation (Figure 34C). The results were similar to what was observed with the mouse isotypes, i.e., the human IgG1 antibody had a significant anti-tumor effect as it can bind to activating FcRs, while the S267E mutation which increases binding to both CD32B and CD32A had higher activity (Figures 34A-34C). This higher level of activity is likely due to increased agonism on effector T cells as well as increased depletion of Tregs at the tumor site.

[0603] T cell populations at the tumor site and spleens of tumor bearing mice were examined as described earlier. Tregs were less prevalent in mice treated with either the G1 or G1 S267E antibody, with a larger effect seen with the S267E isotype (Figure 35A). Increases in the percentages of CD8⁺ T cells (Figure 35B) and CD4⁺ effector (Figure 35C) and at the tumor site were also evident, and these increases were greater with the G1 S267E antibody. Increased cellularity in the spleens of mice treated with the anti-OX-40 antibodies was also noted (Figure 35D). These results suggest that the OX86-hIgG1 antibody exhibited potent anti-tumor activity (Figures 34A-34C) and measurable Treg depletion (Figures 35A-35D).

Example 23: A blocking anti-OX40 antibody exhibits anti-tumor activity in a mouse tumor model

[0604] The following experiment was conducted to determine whether an antibody which blocks the interaction between OX40/OX40L exhibits potent anti-tumor activity. To this end, a hamster anti-mouse OX40 antibody which blocks the OX40/OX40L interaction (hamster IgG1 8E5 antibody) was generated and tested for its anti-tumor activity in a subcutaneous mouse CT-26 tumor model. CT-26 is a mouse colon adenocarcinoma tumor cell line whose solid tumor growth can be monitored in BALB/c mice when the cells are transplanted subcutaneously.

[0605] Female BALB/c mice (Charles River Laboratories, Hollister, CA) were acclimated for a minimum of three days prior to the start of the studies. Mice were housed 5 animals per cage, and the cages were placed in microisolator ventilated racks. Housing was at 18-26°C and 50 + 20% relative humidity with at least twelve room air changes per hour. A 12h light/dark cycle was maintained. Animals were provided with sanitized laboratory rodent diet and municipal water ad libitum.

[0606] CT-26 cells were maintained in RPMI-1640 medium (Hyclone, Cat. No. SH30096.01) supplemented with 10% fetal bovine serum (FBS; Hyclone, Cat. No. SH30071.03). Approximately twice a week, cells contained in a single T175 flask were divided and expanded to four T175 flasks at a 1:5 dilution until sufficient number of cells were obtained for tumor implantation. The cells were harvested near 80% confluence, washed and resuspended in PBS.

[0607] On Day 0, 1×10^6 CT-26 cells were implanted into the mice using a 1 cc syringe (Becton Dickinson, Franklin Lakes, NJ) and 27 gauge 5/8 inch needle. Tumors were then measured two times weekly in 3 dimensions with an electronic caliper (Mitutoyo, Aurora, Illinois) and recorded. Tumor volumes (mm^3) were calculated using the formula: width $\times$ length $\times$ height $\times$ 0.5. Following tumor volume measurements on Day 6 post implantation, mice were staged according to tumor volume. Mice with a mean tumor volume of 26 mm^3 were randomized into groups and treated as shown in Table 19.

[0608] The hamster isotype control antibody is an inert Armenian hamster IgG monoclonal antibody (mAb) to GST (clone PIP, catalog # BE0260; BioXcell, West Lebanon, NH). It was prepared in PBS immediately prior to administration to provide doses of 10 mg/kg per mouse via intraperitoneal (IP) injection on Days 6, 10 and 14 as shown in Table 19.

[0609] The monoclonal antibody against mouse OX40 (clone 8E5) was prepared in PBS immediately prior to administration to provide doses of 10, 3, 1 or 0.3 mg/kg per mouse via IP injection on Days 6, 10 and 13 as shown in Table 19.

Table 19:

Treatment	Dose	N	Route	Treatment schedule
Hamster IgG Istopype Control mAb	10 mg/kg	12	IP	Days 6, 10, 14
Hamster anti-mouse OX40 (clone 8E5) mAb	10 mg/kg	12	IP	Days 6, 10, 14
Hamster anti-mouse OX40 (clone 8E5) mAb	3 mg/kg	12	IP	Days 6, 10, 14
Hamster anti-mouse OX40 (clone 8E5) mAb	1 mg/kg	12	IP	Days 6, 10, 14
Hamster anti-mouse OX40 (clone 8E5) mAb	0.3 mg/kg	12	IP	Days 6, 10, 14

[0610] Animals were checked daily for postural, grooming, and respiratory changes, as well as lethargy. Animals were weighed two times weekly and euthanized if weight loss was $\geq 20\%$. Mice were checked for the presence and size of tumors twice weekly until death or euthanasia. Tumors were measured in 3 dimensions with an electronic caliper (Mitutoyo, Aurora, Illinois) and recorded. Response to treatment compounds was measured as a function of tumor growth. If the tumor reached a volume of $\geq 1500 \text{ mm}^3$ or appeared ulcerated, animals were euthanized.

[0611] As shown in Figures 36A-36E, the hamster anti-mouse OX40 mAb (clone 8E5; Figures 36B-36E showing treatment with different doses of 8E5) demonstrated potent anti-tumor activity in the subcutaneous CT-26 model as compared to the hamster IgG isotype control group (Figure 36A). The 8E5 antibody was administered at doses ranging from 0.3 to 10 mg/kg, and even at the lowest dose evaluated (0.3 mg/kg), 10 of 12 mice were tumor-free (TF) at the end of the study period (Day 72). Although the number of tumor-free mice did not differ significantly amongst each dose group, with each group having 9 or 10 tumor-free mice by the end of the study period, mice treated with either of the two highest doses (3 or 10 mg/kg) showed more tumor growth delays as compared to mice treated with the two lowest doses (0.3 or 1 mg/kg). There were no tumor-free mice in the isotype control-treated group; all mice in that group had been sacrificed by Day 39 as a result of ulceration or tumor burden ($>1500 \text{ mm}^3$).

[0612] These data indicate that an anti-OX40 antibody that blocks the interaction between OX40 and OX40-L demonstrates potent anti-tumor activity in a subcutaneous mouse CT-26 tumor model when administered to mice with established tumors.

Example 24: OX40 agonism synergizes with PD-1 blockage in a murine MC38 colon carcinoma model

[0613] To test for synergy between anti-OX-40 antibody and anti-PD-1 antibody treatments, combinations of these antibodies were tested in the MC38 mouse tumor model. C57BL/6 mice were subcutaneously injected with 2 million MC38 tumor cells. After 7 days, tumor volumes were determined and mice were randomized into treatment groups so as to have comparable mean tumor volumes. Antibodies formulated in PBS were administered intraperitoneally on days 7, 10, and 14 at 200 μg per dose in a volume of 200 μl .

[0614] As shown in Figures 37A-37D, both the anti-PD-1 antibody (Figure 37B) and anti-OX40 antibody (Figure 37C) showed minimal activity when used alone, but had significant anti-tumor activity when combined (Figure 37D), with 5 of 8 mice rendered tumor free.

Example 25: OX40 agonism enhances the response to vaccines in cynomolgus monkey

[0615] Enhancement of immune responses to vaccines was measured to evaluate the ability of the OX40.6 antibody to stimulate immune responses in cynomolgus monkeys. This approach was selected because the desired effect, i.e., enhancement of immune responses to tumors, cannot be evaluated in healthy non-human primates, as they lack tumors.

[0616] Monkeys were immunized with keyhole limpet hemocyanin (KLH) on Day 1 (10 mg, intramuscularly) and with hepatitis B virus surface antigen (HBsAg) (ENGERIX-B) (20 µg intramuscularly on Days 1 and 29). Following administration of the vaccines, the monkeys were dosed intravenously with 0 or 2 mg/kg of OX40.6 antibody on Days 1 and 29. Immune responses were measured on Days 22 and 41 by *ex vivo* T cell response to KLH and by T-cell-dependent antibody responses to KLH and HBsAg. As shown in Figures 38A and 38B, OX40.6-related findings at 2 mg/kg at Days 22 (Figure 38A) and 41 (Figure 38B) included an increase in the *ex vivo* recall response to KLH, characterized by increases in the mean percent of CD69+, IFN-gamma+, and TNF-alpha+ expressing CD4+CD8- T cells.

Example 26: Fc Receptor binding for antibodies with engineered constant domains

[0617] This Example demonstrates that antibodies having modified heavy chain constant regions comprising the CH1 and hinge of IgG2 bind to FcγRs when they contain CH2 and CH3 domains of IgG1.

[0618] In addition to antigen binding by the variable domains, antibodies can engage Fc-gamma receptors (FcγRs) through interaction with the constant domains. These interactions mediate effector functions such as antibody-dependent cellular cytotoxicity (ADCC) and antibody-dependent cellular phagocytosis (ADCP). Effector function activity is high for the IgG1 isotype, but very low or absent for IgG2 and IgG4 due to these isotypes having lower affinity for FcγRs. In addition, the effector function of IgG1 can be modified through mutation of amino acid residues within the constant regions to alter FcγR affinity and selectivity.

[0619] The binding of antibodies to Fc gamma receptors (FcγRs or FcγRs) was studied using biosensor technologies including Biacore surface plasmon resonance (SPR) and ForteBio Biolayer Interferometry (BLI). SPR studies were performed on a Biacore T100 instrument (GE Healthcare) at 25°C. The Fab fragment from a murine anti-6xHis antibody was immobilized on a CM5 sensor chip using EDC/NHS to a density of ~3000 RU. Various his-tagged FcγRs (7 µg/ml) were captured via the C-terminal his-tag using a contact time of 30 s at 10 µl/min, and the binding of 1.0 µM antibody was evaluated in a running buffer of 10 mM NaPO₄, 130 mM NaCl, 0.05% p20 (PBS-T) pH 7.1. FcγRs used for these experiments included CD64 (FcγRI), CD32a-H131 (FcγRIIa-H131), CD32a-R131 (FcγRIIa-R131), CD32b (FcγRIIb), CD16a-V158 (FcγRIIIa-V158), CD16b-NA1 (FcγRIIIb-NA1), and CD16B-NA2 (FcγRIIIb-NA2). BLI experiments were performed on a ForteBio Octet RED instrument (Pall, ForteBio) at 25°C in 10 mM NaPO₄, 130 mM NaCl, 0.05% p20 (PBS-T) pH 7.1. Antibodies were captured out of undiluted expression supernatants on protein A coated sensors, followed by the binding of 1 µM hCD32a-H131, hCD32a-R131, hCD32b, hCD16a-V158, or 0.1 µM hCD64 analytes.

[0620] First, antibodies were made that contain modified IgG1 Fc domains including the substitutions S267E (SE) and S267E/L328F (SELF), as well as various combinations of the mutations P238D, P271G, H268D, A330R, G237D, E233D, referred to as V4, V7, V8, V9 and V12. The binding of these antibodies was studied by Biacore SPR with comparison to IgG1f, IgG2.3 (IgG2-C219S) and IgG4.1 (IgG4-S228P) antibodies, as well as an IgG1.1f antibody which has been engineered to reduce binding to all FcγRs. The results, which are shown in Figure 70, demonstrate the expected FcγR binding properties for IgG1f, IgG2.3 and IgG4.1 and the mutated IgG1 antibodies, including increased CD32a-H131, CD32a-R131 and CD32b binding for SE and SELF, as well as increased selectivity of the V4, V7, V8, V9 and V12 mutants for CD32b over CD32a-H131 and CD32a-R131 (Figure 39).

[0621] The next set of constructs was used to engineer effector function into the otherwise effector function negative IgG2 isotype. For this study, the mutations described above were introduced in the context of IgG2.3 constant region, or an IgG2.3/IgG1f hybrid termed IgG2.3G1-AY (Table 20). Antibodies were expressed at small scale as supernatants, and tested for binding to FcγRs using ForteBio Octet BioLayer Interferometry biosensor technology. Since the antibodies were present at low concentration in the supernatants, the experiment was performed by capturing antibodies out of the supernatants using protein A coated sensors, followed by binding of FcγR analytes in solution.

Purified and supernatant control IgGf including wild type IgG1, SE, P238D, V4 and V12 antibodies were also included for comparison, and each of these control antibodies demonstrated expected FcγR binding properties (Figure 40). The IgG2.3 antibody also demonstrated the expected binding profile, with appreciable binding to only CD32a-H131. However, all mutations to introduce S267E, L328F, P238D, P271G, H268D, A330R, G237D, or E233D mutations into IgG2.3 failed to recapitulate the FcγR affinity of the corresponding engineered IgG1 mAbs (Figure 40). In contrast, the IgG2.3G1-AY construct was able to fully preserve the FcγR binding properties of wild type IgG1, while retaining the CH1 and hinge regions of IgG2.3. In addition, all IgG2.3G1-AY mutants containing S267E, L328F, P238D, P271G, H268D, A330R, G237D, and E233D demonstrated FcγR binding properties comparable to the IgG1 version mAbs containing the same mutations (Figure 40). This demonstrates the successful engineering of antibodies with CH1 and hinge regions of IgG2 combined with effector function of wild type or mutant IgG1.

Table 20: Engineered IgG2 constructs

Set	ID	Construct	Seq ID#
1	IgG2.3	hHC-IgG2-C219S	258
	IgG2.3-V13	hHC-IgG2-C219S - P238D	267
	IgG2.3-V14	hHC-IgG2-C219S - P238D,P271G	268
	IgG2.3-V15	hHC-IgG2-C219S - P238D,H268D,P271G	269
	IgG2.3-V16	hHC-IgG2-C219S - P238D,P271G,A330R	270
	IgG2.3-V17	hHC-IgG2-C219S - P238D,H268D,P271G,A330R	271
	IgG2.3-V18	hHC-IgG2-C219S - S267E	272
	IgG2.3-V19	hHC-IgG2-C219S - S267E,L328F	273
2	IgG2.3G1	hHC-IgG2-C219S/hHC-IgG1f	262
	IgG2.3GI-AY-V20	hHC-IgG2-C219S/hHC-IgG1f - P238D	274
	IgG2.3GI-AY-V21	hHC-IgG2-C219S/hHC-IgG1f - P238D,P271G	275
	IgG2.3G1-AY-V22	hHC-IgG2-C219S/hHC-IgG1f - P238D,H268D,P271G	276
	IgG2.3GI-AY-V23	hHC-IgG2-C219S/hHC-IgG1f - P238D,P271G,A330R	277
	IgG2.3GI-AY-V24	hHC-IgG2-C219S/hHC-IgG1f - P238D,H268D,P271G,A330R	278
	IgG2.3G1-AY-V25	hHC-IgG2-C219S/hHC-IgG1f - G237D,P238D,H268D,P271G,A330R	279
	IgG2.3G1-AY-V26	hHC-IgG2-C219S/hHC-IgG1f - E233D,G237D,P238D,H268D,P271G,A330R	280
	IgG2.3G1-AY-V27	hHC-IgG2-C219S/hHC-IgG1f - S267E	266
	IgG2.3G1-AY-V28	hHC-IgG2-C219S/hHC-IgG1f-S267E,L328F	281

[0622] This engineering strategy was further explored by producing other antibodies formatted with IgG2.3G1-AY, IgG2.3G1-AY-S267E (IgG2.3G1-AY-V27), as well as IgG2-B-form variants (IgG2.5G1-AY and IgG2.5G1-AY-V27), and other hybrid antibodies containing different combinations of IgG1 and IgG2 constant domains, and testing the binding of these antibodies to anti-his Fab captured his-tagged FcγRs using Biacore SPR technology. In agreement with the Octet supernatant data, the SPR data showed that the IgG2.3G1-AY and IgG2.3G1-AY-V27 antibodies had comparable FcγR binding properties to IgGf and IgG1f-S267E respectively, despite containing the CH1 and hinge regions of an A-form IgG2 antibody (IgG2.3) (Table 21). Similar data was also obtained using IgG2.5G1-AY and IgG2.5G1-AY-V27 antibodies, demonstrating the successful engineering of B-form IgG2 antibodies (containing C131S mutation termed IgG2.5) having IgGf or modified IgGf like effector functions. Data for several other antibodies with IgG2.3G1-AY, IgG2.3G1-AY-V27, IgG2.5G1-AY, or IgG2.5G1-AY-V27 constant regions but different variable regions shows that this engineering strategy is broadly applicable to other antibodies independent of the variable domains (Table 21).

Table 21: %Rmax values for 1 uM antibodies binding to anti-his Fab captured FcγR-his proteins

mAb	hCD64	hCD32aH131	hCD32a-R131	hCD32b	hCD16a-V158	hCD16B-NA2
mAb8-IgG1f	80%	82%	51%	27%	51%	21%
mAb9-IgG1f	70%	33%	19%	4%	28%	10%

mAb	hCD64	hCD32aH131	hCD32a-R131	hCD32b	hCD16a-V158	hCD16B-NA2
mAb11-IgG2.3	2%	44%	17%	5%	1%	0%
mAb6-IgG2.3	3%	66%	14%	3%	1%	0%
mAb4-IgG2.3	1%	39%	6%	1%	1%	0%
mAb5-IgG2.3	6%	100%	30%	4%	3%	0%
mAb12-IgG2.3	2%	39%	7%	1%	1%	0%
mAb13-IgG2.3	2%	40%	7%	1%	1%	0%
mAb11-IgG2.5	0%	40%	13%	3%	0%	-1%
mAb7-IgG2.5	4%	72%	19%	2%	2%	0%
mAb8-IgG2.5	3%	59%	14%	3%	2%	0%
mAb10-IgG2.5	1%	29%	5%	1%	1%	0%
mAb6-IgG2.5	3%	75%	17%	4%	2%	0%
mAb4-IgG2.5	2%	46%	8%	1%	1%	0%
mAb5-IgG2.5	6%	89%	26%	5%	4%	1%
mAb12-IgG2.5	1%	36%	6%	1%	1%	0%
mAb13-IgG2.5	-2%	39%	4%	-2%	0%	-2%
mAb8-IgG2.3G1-AY	77%	61%	38%	10%	38%	13%
mAb10-IgG2.3G1-AY	67%	23%	14%	4%	24%	8%
mAb7-IgG2.5G1-AY	80%	73%	45%	12%	47%	19%
mAb8-IgG2.5G1-AY	77%	70%	45%	17%	48%	22%
mAb7-IgG2.3G1-AY-V27	84%	68%	92%	76%	26%	7%
mAb8-IgG2.3G1-AY-V27	78%	67%	80%	67%	24%	7%
mAb10-IgG2.3G1-AY-V27	69%	24%	57%	40%	12%	3%
mAb7-IgG2.5G1-AY-V27	81%	74%	89%	84%	32%	9%
mAb8-IgG2.5G1-AY-V27	77%	76%	79%	77%	33%	10%

Example 27: Effects of anti-OX40 antibodies with modified heavy chain constant regions on T cell proliferation and IFN- γ and IL-2 secretion from T cells with or without cross-linking.

[0623] Anti-OX40 antibodies with modified IgG2 CH1/hinge regions may have the ability to promote T cell activation in the absence of cross-linking, and thus may be able to promote T cell activation *in vivo* in the absence or low expression of cell types expressing Fc γ R_s, and possibly to promote anti-tumor activity in a wider range of tumor types than IgG1 isotype antibodies.

[0624] Alternatively, modified CH1/hinge region antibodies may still require cross-linking in order to promote T cell activation, but may have increased agonist activity when bound to Fc γ R_s compared to IgG1 isotype antibodies, and

thus be more potent in promoting T cell activation and anti-tumor activity.

[0625] Anti-OX40 antibodies having modified heavy chain constant regions comprising the sequences shown in Table 22 are generated and tested for their effects on T cell proliferation and IFN- γ and IL-2 secretion from T cells with or without cross-linking using the assays described below. The light chain sequences for antibodies OX40.6, 40.8, 40.16, and 40.21 correspond to SEQ ID NOs: 96, 110, and 116 (for both OX40.16 and 40.21), respectively.

Table 22.

Constructs	SEQ ID NO
OX40.6-Vh-hHC-IgG2.3	282
OX40.8-Vh-hHC-IgG2.3	283
OX40.16-Vh-hHC-IgG2.3	284
OX40.6-Vh-hHC-IgG2.3G1	285
OX40.8-Vh-hHC-IgG2.3G1	286
OX40.16-Vh-hHC-IgG2.3G1	287
OX40.6-Vh-hHC-IgG2.3G1-V27	288
OX40.8-Vh-hHC-IgG2.3G1-V27	289
OX40.16-Vh-hHC-IgG2.3G1-V27	290
OX40.6-Vh-hHC-IgG2.5	291
OX40.8-Vh-hHC-IgG2.5	292
OX40.16-Vh-hHC-IgG2.5	293
OX40.21-Vh-hHC-IgG2.5	294
OX40.21-Vh-hHC-IgG2.5G1	295
OX40.21-Vh-hHC-IgG2.5G1-V27	296

CHO-CD3 +/- CD32 assay

[0626] Anti-OX-40 antibodies with the sequences shown in Table 22 are tested for their ability to induce T cell activity *in vitro* by measuring the proliferation of and amount of IL-2 and IFN- γ secreted by T cells incubated with the antibodies.

[0627] Transfected CHO cell lines are generated for use as artificial antigen-presenting cells in a primary T cell activation assay. The CHO-CD3-CD32A cell line expresses anti-human CD3 antibody in a single-chain Fv format, along with the human Fc receptor (FcR) CD32A to present anti-OX40 antibodies on the CHO cell surface. The CHO-CD3 cell line expresses anti-human CD3 antibody in a single-chain Fv format without FcR.

[0628] Briefly, human primary CD4 T cells are isolated by negative selection (RosetteSep™, StemCell Technologies) and co-cultured with either irradiated CHO-CD3-CD32A cells, or irradiated CHO-CD3 cells, at an 8:1 T:CHO ratio, in the presence of graded doses of anti-OX40 antibodies or isotype control antibody. After 3 to 4 days in culture at 37 °C, supernatants are harvested for assessment of T cell activation by means of measurement of secreted human IFN- γ either by ELISA (BD Biosciences) or HTRF assay (Cisbio), following the manufacturers' recommendations. Afterwards, tritiated thymidine is added for the final approximately 18 hours of culture to measure T proliferation by tritiated thymidine incorporation, as an additional assessment of T cell activation.

SEB PBMC assay

[0629] Anti-OX-40 antibodies with the sequences shown in Table 22 are tested for their effects on stimulating primary T cells in cultures of staphylococcus enterotoxin B (SEB)-activated human peripheral blood mononuclear cells (PBMCs). Human whole blood samples are obtained from AllCells, Inc. (Berkeley, CA) or from donors at Bristol-Myers Squibb, Redwood City, CA under the auspices of an in-house phlebotomy program. PBMCs are isolated by gradient purification

on a Ficoll-Hypaque cushion and cultured for 3 days in culture medium supplemented with fixed, suboptimal (85 ng/mL) of superantigen staphylococcus enterotoxin B (SEB; Toxin Technologies, Sarasota, FL) in the presence of graded doses of OX40 antibodies or isotype control antibody. In some cases, 2 - 5 µg/mL of soluble cross-linking antibody, F(ab')₂ goat anti-human Fcγ, is also added to the cultures. After culturing for 3 days at 37 °C, supernatants are harvested for assessment of T cell activation by means of ELISA measurement of secreted human IL-2. Briefly, culture supernatants are diluted 1:10 in sample diluent and tested for the presence of human IL-2 by ELISA (BD Bioscience) per the manufacturer's recommended protocol. Following the addition of TMB substrate, assay plates are read on a Spectramax 340PC reader using Softmax operating software at a wavelength of 650 nm. Measured optical densities of the chromogenic substrate were proportional to bound detecting antibody.

MLR assay

[0630] Anti-OX-40 antibodies with the sequences shown in Table 22 tested for their ability to potentiate primary human T cell proliferation and IFN-γ secretion in a T cell: Dendritic Cell Allogeneic Mixed Lymphocyte Reaction (T:DC AlloMLR). Total T cells are isolated from peripheral blood from healthy human donors by negative selection (RosetteSep, Stemcell Technologies). Monocytes are isolated from peripheral blood from healthy human donors using CD14 microbeads (Miltenyi), and cultured for six days in the presence of GM-CSF and IL-4 to derive immature dendritic cells (DCs). DCs and T cells are co-cultured in the presence of graded doses of OX40 antibodies or isotype control antibody. In some cases, 2 - 5 µg/mL of soluble cross-linking antibody, such as F(ab')₂ goat anti-human Fcγ, is also added to the cultures. Supernatant from each sample is harvested between Day 4 and Day 7 for measurement of secreted IFN-γ by ELISA (BD Biosciences) or HTRF assay (Cisbio), following the manufacturers' recommendations. After supernatant harvest, the cell cultures are pulsed with 1 µCi/well of ³[H]-thymidine for the last 16-18 hours of the culture. The cells are harvested onto filter plates, and ³[H] counts per minute of cell-incorporated ³[H]-thymidine are read as a measure of T cell proliferation.

Example 28: Anti-tumor Activity of OX40 Agonist mAb with CTLA-4 Blockade in a CT26 model

[0631] To test for synergy between anti-OX-40 antibody and anti-CTLA-4 antibody treatments, combinations of these antibodies were tested in the CT26 mouse tumor model. Mice were inoculated with CT26 tumors and mAb dosing was initiated at Day +3 following inoculation (dosed on Days 3, 7, and 10) with 200 µg/mouse of the antibodies indicated in Figures 41A-41D.

[0632] As shown in Figures 41A-41D, both the anti-CTLA-4 antibody (Figure 41B) and anti-OX40 antibody (Figure 41C) showed minimal activity when used alone (1 of 8 mice tumor free for both treatments), but had significant anti-tumor activity when combined (Figure 41D), with 4 of 8 mice rendered tumor free.

Example 29: Phase 1/2a Trial in Subject Having Solid Tumors

[0633] A Phase 1/2a study of OX40.21 administered alone or in combination with nivolumab or ipilimumab is conducted in subjects having advanced solid tumors to demonstrate the efficacy of administering OX40.21 alone or in combination with nivolumab or ipilimumab.

1. Objective

[0634] The primary objective of the study is to assess the safety, tolerability, dose-limiting toxicities (DLTs), and maximum tolerated dose (MTD)/recommended phase 2 dose (RP2D) of OX40.21 administered alone or in combination with nivolumab or ipilimumab in subjects with advanced malignant tumors.

[0635] Secondary objectives include investigating the preliminary anti-tumor activity of OX40.21 administered alone or in combination with nivolumab or ipilimumab in subjects with advanced malignant tumors; characterizing the PK of

OX40.21 administered alone and in combination with nivolumab or ipilimumab; and characterizing the immunogenicity of OX40.21 administered alone or in combination with nivolumab or ipilimumab and the immunogenicity of nivolumab or ipilimumab administered with OX40.21. Additional exploratory objectives include exploring potential associations between anti-tumor activity and select biomarker measures in tumor biopsy specimens and peripheral blood prior to treatment and following administration of OX40.21 alone or in combination with nivolumab or ipilimumab; assessing the potential effect of OX40.21 monotherapy and combination therapy on QTc interval; characterizing nivolumab PK in subjects receiving the combination of nivolumab and OX40.21; characterizing ipilimumab PK in subjects receiving the combination of ipilimumab and OX40.21; assessing the overall survival (OS) in subjects treated with OX40.21 alone and in combination with nivolumab or ipilimumab; and exploring potential relationships between dose/exposure and anti-tumor activity, pharmacodynamic (PD) effects (selected biomarkers in the peripheral blood and tumor biopsy specimens), and key safety measures in subjects treated with OX40.21 alone and in combination with nivolumab or ipilimumab.

2. Study Design and Duration

[0636] This is a Phase 1/2a, open label study of OX40.21 in subjects with advanced solid tumors that integrates initial OX40.21 monotherapy with subsequent nivolumab or ipilimumab combination therapy.

[0637] Study sections (dose escalation and dose expansion) proceed in a phased approach based on study-emergent safety, PK, and PD data. The first section of the study begins with OX40.21 monotherapy dose escalation cohorts. Clinical data from the first 3 monotherapy dose cohorts serve as a foundation for initiating dose escalation of OX40.21 in combination with nivolumab. Clinical data from the first 3 monotherapy dose cohorts in addition to the clinical data from the first cohort of OX40.21 in combination with nivolumab serve as a foundation for initiating dose escalation of OX40.21 in combination with ipilimumab. After establishment of a tolerable and pharmacologically active RP2D of OX40.21 in the dose escalation section, dose expansion in specific tumor cohorts is initiated.

3. Dose Escalation

[0638] A schematic of the study design for Part 1A is shown in Figure 42.

[0639] The dose escalation phase of the study evaluates the safety and tolerability of OX40.21, alone or in combination with nivolumab or ipilimumab, in subjects with advanced solid tumors.

[0640] The initial dose level of OX40.21 is 20 mg. Dose escalation decisions for subsequent doses are based on DLTs using a BLRM model (for OX40.21 monotherapy) or a BLRM (-Copula) model (for OX40.21 in combination with nivolumab or ipilimumab). The DLT period is 28 days for both monotherapy and combination therapy dose escalation parts. The DLT rate is determined based on the incidence, severity, and duration of AEs that occur within the DLT period and for which no alternative cause can be identified. Dose selection for the next monotherapy cohort/dose level takes into account the BLRM (-Copula) recommendation in conjunction with all available PK, PD, and clinical and laboratory safety data from all treated subjects. Starting dose selection of OX40.21 for Part 2A is determined using data available from Part 1A, including clinical and laboratory safety assessments, PK/PD data, and modeling recommendation within Bayesian hierarchical modeling framework by incorporating single-agent toxicity profiles of both OX40.21 (Part 1A) and nivolumab (CA209-003). Starting dose selection of OX40.21 for Part 3A is determined using data available from Parts 1A and 2A, including clinical and laboratory safety assessments, PK/PD data, and modeling recommendation within Bayesian modeling framework by incorporating single-agent toxicity profiles of both OX40.21 (Part 1A) and ipilimumab (CA184-022). Actual doses can be modified per the BLRM (-Copula), but do not exceed doubling of the previously tested dose.

[0641] During dose escalation for all dose cohorts, the initial subject (sentinel subject) is observed for 5 days before additional subjects in that cohort are treated with study drug.

[0642] Approximately 30 subjects are enrolled in each dose escalation part. The number of subjects in each dose escalation cohort varies depending on BLRM (-Copula) recommendations. Initially, approximately 3 subjects are treated

at the starting dose levels of OX40.21 or OX40.21 in combination with nivolumab or ipilimumab. Additional cohorts of approximately 3 evaluable subjects are treated at recommended dose levels per BLRM (-Copula) during the dose escalation phase. At least 6 DLT-evaluable subjects are treated at the MTD.

[0643] Part 1A: Enrollment begins in Part 1A, OX40.21 monotherapy dose escalation. The initial dose of OX40.21 for Part 1A is 20 mg, with expected subsequent doses of 40, 80, 160, and 320 mg. Actual doses can be modified per the BLRM but do not exceed doubling of the previously tested dose.

[0644] Part 2A: Part 2A is the combination arm of OX40.21 with nivolumab that is initiated after at least 3 dose levels in the monotherapy dose escalation are found to be tolerated or an MTD has been determined in the monotherapy dose escalation (Part 1A). The starting dose of OX40.21 in Part 2A is at least 1 dose level below a dose demonstrated to be tolerated in Part 1A to ensure further safety of the combination. At no time does the dose for OX40.21 in Part 2A exceed the highest tolerated dose in Part 1A. Nivolumab is administered at a flat dose of 240 mg. Each treatment cycle is 2 weeks in length and study drugs are administered every 2 weeks starting on Day 1 of each cycle for up to 12 cycles.

[0645] Part 3A: Part 3A is the combination arm of OX40.21 with ipilimumab that is initiated only after at least 3 dose levels in the monotherapy dose escalation are found to be tolerated or an MTD is determined in the monotherapy dose escalation (Part 1A) and at least 1 dose cohort is found to be tolerated in the OX40.21 with nivolumab dose escalation part. The starting dose of OX40.21 in Part 3A is at least 1 dose level below a dose demonstrated to be tolerated in Part 1A. At no time does the dose for OX40.21 in Part 3A exceed the highest tolerated dose in Part 1A to further ensure safety of the combination doses in treated subjects. Ipilimumab is administered at a dose of 1 mg/kg. Each treatment cycle is 3 weeks in length. OX40.21 is administered every 3 weeks starting on Cycle 1 Day 1, up to and including 8 cycles, and ipilimumab is administered every 3 weeks starting on Day 1 for 4 cycles. Only OX40.21 is administered in the last 4 cycles.

Dose Expansion:

[0646] Treatment in the dose expansion cohorts is initiated when the MTD/RP2D has been determined based on the evaluation of totality of available clinical safety (DLTs, significant AEs occurring after the DLT period), PK, PD, and modeling data from the dose escalation (Parts 1A, 2A, and 3A). Approximately 110 subjects are treated in all dose expansion cohorts.

[0647] Part 1B is the OX40.21 monotherapy dose expansion cohort in subjects with cervical cancer at the MTD/RP2D determined in Part 1A. Dosing of OX40.21 begins on Day 1 of each cycle and is administered every 2 weeks for up to 12 cycles. Approximately 12 subjects are treated in this expansion cohort.

[0648] Parts 2B is the combination therapy (OX40.21 with nivolumab) dose expansion part in subjects with CRC at the MTD/RP2D determined in Part 2A. Nivolumab is administered at a flat dose of 240 mg. Each treatment cycle is 2 weeks in length and study drugs are administered every 2 weeks starting on Day 1 of each cycle for up to 12 cycles. Approximately 35 subjects are treated in this expansion cohort.

[0649] Part 2C is the combination therapy (OX40.21 with nivolumab) dose expansion part in subjects with BC at the MTD/RP2D determined in Part 2A. Each treatment cycle is 2 weeks in length and study drugs are administered every 2 weeks starting on Day 1 of each cycle for up to 12 cycles. Approximately 27 subjects are treated in this expansion cohort.

[0650] Part 3B is the combination therapy (OX40.21 with ipilimumab) dose expansion part in subjects with OC at the MTD/RP2D determined in Part 3A. Each treatment cycle is 3 weeks in length. Ipilimumab is administered in the initial 4 cycles in combination with OX40.21. Then the subject continues on OX40.21 monotherapy for up to an additional 4 cycles for a total of up to 24 weeks (8 cycles) of treatment. Approximately 35 subjects with OC are treated in this expansion cohort.

Summary of Study Periods:

[0651] Subjects complete up to 5 periods in the study: Screening (up to 28 days), Treatment (up to 24 weeks), Safety Follow-up (minimum 100 days), Response Follow-up, and Survival Long-term Follow-up (up to approximately 2 years from the first dose) as described below. The study visit schematic is presented in Figure 43.

Screening Period:

[0652] The Screening period lasts for up to 28 days. The screening period begins by establishing the subject's initial eligibility and signing of the informed consent form. Subjects are enrolled using an Interactive Response Technology (IRT).

Treatment Period:

[0653] The Treatment period consists of up to 24 weeks of dosing. Following each treatment cycle, the decision to treat a subject with the next cycle of study therapy, up to 24 weeks of treatment, is based on risk/benefit and tumor assessments. Tumor assessments are performed every 8 weeks for every 2-week (q2w) dosing regimen and every 9 weeks for every 3-week (q3w) dosing regimen. Assessments of partial response (PR) and complete response (CR) are confirmed at least 4 weeks following initial assessment. Tumor progression or response endpoints are assessed using Response Evaluation Criteria In Solid Tumors (RECIST) v1.1.

[0654] Subjects with a response of stable disease (SD), PR, or CR at the end of a given cycle continue to the next treatment cycle. Subjects are generally allowed to continue study therapy until the first occurrence of one of the following: 1) completion of the maximum number of cycles; 2) progressive disease; 3) clinical deterioration suggesting that no further benefit from treatment is likely; 4) intolerability to therapy; or 5) meeting the criteria for discontinuation of study therapy.

Safety Follow-up:

[0655] Upon completion of study therapy, subjects enter the Safety Follow-up period. After the end of treatment (EOT) visit, subjects are evaluated for any new adverse events (AEs) for at least 100 days after the last dose of therapy. Follow-up visits occur at Days 30, 60 and 100 after the last dose or the date of discontinuation. Subjects (except those who withdraw consent for study participation) complete 3 clinical Safety Follow-up visits regardless of whether they start new anti-cancer therapy.

Survival Follow-up:

[0656] After completion of the Safety Follow-up period, subjects enter the Survival Follow-up period. Subjects are followed approximately every 3 months (12 weeks) until death, lost to follow-up, withdrawal of consent, or conclusion of the study, whichever comes first. The duration of this phase is up to 2 years following the first dose of study drug.

Response Follow-up:

[0657] After completion of the Safety Follow-up period, all subjects with ongoing SD, PR, or CR at the EOT visit enter the Response Follow-up period, which occurs simultaneously with the Survival Follow-up period. These subjects continue to have radiological and clinical tumor assessments every 3 months (12 weeks) during the Response Follow-up period or until disease progression or withdrawal of study consent. Radiological tumor assessments for subjects who have ongoing clinical benefit continue to be collected after subjects complete the survival phase of the study. Subjects who have disease progression following initial course of study therapy are not evaluated for response beyond the EOT

visit and are allowed to receive other tumor directed therapy as required.

Duration of Study:

[0658] The total duration of study time for any individual subject is approximately 2 years. The study ends when the last subject completes their last study visit, which is approximately 4 years after the start of the study.

Number of Subjects:

[0659] Approximately 225 subjects will be enrolled, and approximately 200 subjects will be treated in the study.

Study Population:

[0660] Subjects are at least 18 years old and have histologic or cytologic confirmation of a malignancy that is advanced (metastatic, recurrent, refractory and/or unresectable) with measurable disease per RECIST v1.1.

Dose Escalation and Stopping Rules

[0661] In Parts 1A, 2A, and 3A, the BLRM and BLRM (-Copula) models are utilized for dose escalation recommendations after DLT information becomes available for each cohort of subjects. OX40.21 dose selection for the next cohort/dose level takes into account the BLRM (-Copula) recommendation in conjunction with clinical recommendation and all available PK, PD, and clinical and laboratory safety data from all treated subjects.

Dose-limiting Toxicities

[0662] To guide dose escalation, DLTs are defined based on the incidence, intensity, and duration of AEs for which no clear alternative cause is identified. The DLT period is 28 days of initiation of the study drug(s). For subject management, an AE that meets DLT criteria, regardless of the cycle in which it occurs, leads to discontinuation of study drug. Subjects who withdraw from the study during the DLT evaluation interval for reasons other than a DLT may be replaced with a new subject at the same dose level. The incidence of DLT(s) during the DLT evaluation period is used in dose escalation decisions and to define the MTD. AEs occurring after the DLT period are considered for the purposes of defining the MTD, if they are determined to have no clear alternative cause and are not related to disease progression. Subjects experiencing a DLT are not retreated with study drug and enter the safety follow-up period of the study. AEs are graded according to the National Cancer Institute (NCI) Common Terminology Criteria for Adverse Events (CTCAE) v4.03.

Non-Hematologic DLT:

[0663]

1. A. Hepatic DLT

- Any $\geq$ Grade 3 elevation of AST, ALT, or total bilirubin
- AST, ALT, or total bilirubin,
- Grade 2 AST or ALT with symptomatic liver inflammation (e.g., right upper quadrant tenderness, jaundice, pruritis)
- AST or ALT $> 3 \times$ ULN and concurrent total bilirubin $> 2 \times$ ULN without initial findings of cholestasis (elevated serum alkaline phosphatase [ALP]) (e.g., findings consistent with Hy's law or FDA definition of potential drug-induced liver injury or pDILI)

2. B. Non-hepatic DLT

- Grade 2 or greater uveitis, episcleritis, or iritis
- Any other Grade 2 eye pain or blurred vision that does not respond to topical therapy and does not improve to Grade 1 severity within 2 weeks OR requires systemic treatment
- Grade 3 or greater pneumonitis, bronchospasm, neurologic toxicity, hypersensitivity reaction, or infusion reaction
- Any Grade 3 or greater non-dermatologic, non-hepatic toxicity will be considered a DLT with the following specific exceptions:
 - Grade 3 or Grade 4 electrolyte abnormalities that are not complicated by associated clinical adverse experiences, last less than 72 hours, and either resolve spontaneously or respond to conventional medical intervention
 - Grade 3 nausea, vomiting, or diarrhea that lasts less than 72 hours, and either resolves spontaneously or responds to conventional medical intervention
 - Grade 3 or 4 elevation of amylase or lipase not associated with clinical or radiographic evidence of pancreatitis
 - Isolated Grade 3 fever not associated with hemodynamic compromise (e.g., hypotension, clinical, or laboratory evidence of impaired end-organ perfusion)
 - Grade 3 endocrinopathy that is well controlled by hormone replacement
 - Grade 3 tumor flare (defined as pain, irritation, or rash that localizes to sites of known or suspected tumor)
 - Grade 3 fatigue for less than 7 days
 - Grade 3 infusion reaction that returns to Grade 1 in less than 6 hours

Dermatologic DLT**[0664]**

- Grade 4 rash
- Grade 3 rash if no improvement (i.e., resolution to $\leq$ Grade 1) after a 1- to 2-week infusion delay. Subjects who have not experienced a Grade 3 skin AE may resume treatment in the presence of Grade 2 skin toxicity.

Hematologic DLT**[0665]**

- Grade 4 neutropenia $\geq$ 5 days in duration
- Grade 4 thrombocytopenia or Grade 3 thrombocytopenia with clinically significant bleeding, or any requirement for platelet transfusion
- Grade 4 anemia not explained by underlying disease
- Grade 4 febrile neutropenia
- Grade 3 febrile neutropenia that lasts $>$ 48 hours
- Grade $\geq$ 3 hemolysis (i.e., requiring transfusion or medical intervention such as steroids)

Treatment with Additional Cycles Beyond 24 Weeks

[0666] Subjects are treated for 24 weeks unless criteria for study drug discontinuation are met earlier. Subjects completing approximately 24 weeks of treatment with ongoing disease control (CR, PR, or SD) are eligible for an additional 24 weeks of study therapy in monotherapy (Part 1) and combination therapy (Parts 2 and 3) beyond the

initial 24 weeks when the risk/benefit assessment favors continued administration of study therapy. Upon completion of the additional 24 weeks of study therapy, subjects enter the Safety Follow-up period.

Treatment Beyond Progression

[0667] Treatment beyond progression is allowed in select subjects with initial RECIST v1.1-defined progressive disease after determining that the benefit/risk assessment favors continued administration of study therapy (e.g., subjects are continuing to experience clinical benefit, tolerating treatment, and meeting other criteria).

Retreatment

[0668] Retreatment is allowed if confirmed disease progression occurs during the response follow-up period. Subjects completing approximately 24 weeks (or additional cycles of treatment, if appropriate) of therapy who enter the response follow-up period with ongoing disease control (CR, PR, or SD) without any significant toxicity are eligible for retreatment. Such subjects are eligible for retreatment on a case-by-case basis after evaluation and determining whether the risk/benefit ratio supports administration of further study therapy, and the subject continues to meet eligibility criteria for treatment with study therapy. Subjects meeting criteria for retreatment are treated with the originally assigned monotherapy or combination therapy regimen (e.g., the same dose and dose schedule as administered during the first 24 weeks), unless that dose and schedule were subsequently found to exceed the MTD, in which case the subject is treated at the next lower dose deemed tolerable/safe.

Inclusion criteria

[0669]

1. 1) Signed Written Informed Consent

1. a) The subject must sign the informed consent form prior to the performance of any study-related procedures that are not considered part of SOC.
2. b) Consent for tumor biopsy samples (mandatory pre- and on-treatment biopsies are required for the dose expansion cohorts, and for additional subjects added to any of the previously completed dose escalation cohorts and optional for dose escalation cohorts).

2. 2) Target Population

Subjects must be at least 18 years old and have histologic or cytologic confirmation of a malignancy that is advanced (metastatic, recurrent, refractory, and/or unresectable) with measurable disease per RECIST v1.1.

1. A. Dose Escalation:

Subjects must have received, and then progressed, or have been refractory or intolerant to, at least 1 standard treatment regimen in the advanced or metastatic setting, if such a therapy exists. Subjects who are ineligible for any standard therapy are allowed to enroll provided their ineligibility is documented in medical records. The following tumor histologies are permitted except for subjects with primary central nervous system (CNS) tumors, or with CNS metastases as the only site of active disease.

1. (i) Melanoma: BRAF mutation status must be documented if known.
2. (ii) NSCLC: EGFR, ALK, KRAS, and ROS1 mutational status must be documented if known
3. (iii) Head and neck cancer restricted to squamous cell carcinoma. HPV status must be documented if known
4. (iv) Transitional cell carcinoma of the genitourinary tract
5. (v) Renal cell carcinoma
6. (vi) Pancreatic adenocarcinoma
7. (vii) CRC: MSI, KRAS, and BRAF status must be documented if known.
8. (viii) Cervical cancer: HPV status must be documented if known.
9. (ix) Triple negative breast cancer HER2, ER and PR status must be documented
10. (x) Adenocarcinoma of the endometrium
11. (xi) Ovarian cancer

12. (xii) Prostate adenocarcinoma
13. (xiii) Hepatocellular cancer-Child Pugh A only
14. (xiv) Small cell lung cancer
15. (xv) Gastric and gastric esophageal junction cancer: HER2 Status must be documented if known.

2. B. Dose Expansion: Parts 1B, 2B, 2C, and 3B

The following tumor types will be permitted:

1. (a) Cervical Cancer - Part 1B

1. (i) Histologically confirmed cervical cancer that is unresectable, metastatic, or recurrent with documented disease progression
2. (ii) Document tumor HPV status if known. If unknown, subjects must consent to allow their submitted archived tumor tissue sample (block or unstained slides) to be tested.
3. (iii) Prior therapy requirement:
 1. 1. Must have received and then progressed or have been intolerant or refractory to at least 1 standard systemic therapy, for metastatic and/or unresectable disease (e.g., paclitaxel/cisplatin, paclitaxel/cisplatin/bevacizumab). Concurrent chemotherapy administered with primary radiation and adjuvant chemotherapy given following completion of radiation therapy do not count as systemic chemotherapy regimens.

2. (b) Colorectal Cancer - Part 2B

1. (i) Histologically confirmed CRC that is metastatic or recurrent with documented disease progression
2. (ii) Document MSI, MMR, KRAS, and BRAF status if known. If unknown, subjects must consent to allow their submitted archived tumor tissue sample (block or unstained slides) to be tested.
3. (iii) Prior therapy requirement:

Subjects must have received and then progressed or have been intolerant or refractory to at least 1 standard systemic therapy, for metastatic and/or unresectable disease (or have progressed within 6 months of adjuvant therapy).

3. (c) Bladder Cancer - Part 2C

1. (i) Histologically or cytologically confirmed urothelial carcinoma (including mixed histologies of urothelial carcinoma with elements of other subtypes) of the renal pelvis, ureter, bladder, or urethra with progression or refractory disease
2. (ii) Prior therapy requirement:

Subjects must have received and then progressed or have been intolerant or refractory to at least 1 standard systemic therapy (e.g., platinum based chemotherapy) regimen for the treatment of metastatic (Stage IV) or locally advanced unresectable disease.

4. (d) Ovarian - Part 3B

1. (i) Histologically or cytologically confirmed ovarian carcinoma (including epithelial OC, primary peritoneal, or fallopian tube carcinoma) with documented disease progression
2. (ii) Documented germline BRCA mutation status, if known. If unknown, subjects must consent to allow their submitted archived tumor tissue sample (block or unstained slides) to be tested.
3. (iii) Prior therapy requirement:

Subjects must have received and then progressed or have been intolerant or refractory to at least 1 standard systemic therapy (e.g., platinum-based chemotherapy), for metastatic and/or unresectable disease.

3. 3) Eastern Cooperative Oncology Group (ECOG) performance status of ≤ 1 .

4. 4) Presence of at least 1 lesion with measurable disease as defined by RECIST v1.1 for response assessment. Subjects with lesions in a previously irradiated field as the sole site of measurable disease are permitted to enroll provided the lesion(s) have demonstrated clear progression and can be measured accurately.

5. 5) For subjects requiring fresh tumor biopsy, subjects must have at least one lesion accessible for pre- and on-treatment biopsy, in addition to the minimum one RECIST v1.1 measureable lesion required for response assessment. This lesion needs to be distinct from index lesion(s) being evaluated for radiological response.

6. 6) Subjects with prior exposure to therapy with any agent specifically targeting checkpoint pathway inhibition (such as anti-PD-1, anti-PD-L1, anti-PD-L2, anti-LAG-3, and anti-CTLA-4 antibody) are permitted after a washout period of any time greater than 4 weeks from the last treatment

Note: (i) Subjects who experienced prior Grade 1 to 2 checkpoint therapy-related immune-mediated AEs must

have confirmed recovery from these events at the time of study entry, **other than endocrinopathies treated with supplementation**, as documented by resolution of all related clinical symptoms, abnormal findings on physical examination, and/or associated laboratory abnormalities. Where applicable, these subjects must also have completed steroid tapers for treatment of these AEs by a minimum of 14 days prior to commencing treatment with study therapy. (ii) Eligibility of subjects with prior $\geq$ Grade 3 checkpoint therapy-related immune AEs, will be considered on a case-by-case basis after discussion with the Medical Monitor (e.g., asymptomatic isolated Grade 3 lipase elevations without clinical or radiological features of pancreatitis are permitted to enroll).

7. 7) Subjects with prior therapy with any agent specifically targeting T-cell co-stimulation pathways **except** anti-OX40 antibody, anti-CD137, anti-GITR antibody, and anti-CD27 are permitted after a washout period of any time greater than 4 weeks from the last treatment.
8. 8) Prior palliative radiotherapy must have been completed at least 2 weeks prior to first dose of study drug. Subjects with symptomatic tumor lesions at baseline that may require palliative radiotherapy within 4 weeks of first dose of study drug are strongly encouraged to receive palliative radiotherapy prior to enrollment.
9. 9) Subjects enrolled into dose escalation and expansion cohorts must consent to the acquisition of existing formalin-fixed, paraffin-embedded (FFPE) tumor tissue, either a block or a minimum of 15 unstained slides (25 slides preferred), for performance of correlative studies. If an archived sample is not available, subject must consent to a pre-treatment tumor biopsy. Subjects unable to provide an archived tumor sample and who either do not consent to a pre-treatment tumor biopsy or do not have accessible lesions are not eligible. (However, subjects whose pre-treatment biopsy yields inadequate tissue quantity or quality will not be ineligible on this basis alone). For any additional subjects added to any of the previously completed dose escalation cohorts, mandatory pre- and on-treatment biopsies are required.
10. 10) Subjects enrolled into dose expansion, or added to any previously completed dose escalation cohort, are required to undergo mandatory pre- and on-treatment biopsies at acceptable clinical risk. (a) The solid tumor tissue specimen must be a core needle, excisional, or incisional biopsy. Fine needle biopsies, drainage of pleural effusions with cytospins, or punch biopsies are not considered adequate for biomarker review. Biopsies of bone lesions that do not have a soft tissue component or decalcified bone tumor samples are also not acceptable. (b) Biopsied lesions should be distinct from index lesion(s) being evaluated for radiological response
11. 11) Adequate organ function for subjects as defined by the following:
 1. (a) Neutrophils $\geq 1500/\mu\text{L}$ (stable off any growth factor within 4 weeks of first study drug administration)
 2. (b) Platelets $\geq 80 \times 10^3/\mu\text{L}$ (transfusion to achieve this level is not permitted within 2 weeks of first study drug administration)
 3. (c) Hemoglobin $\geq 8 \text{ g/dL}$ (transfusion to achieve this level is not permitted within 2 weeks of first study drug administration)
 4. (d) ALT and AST $\leq 3 \times$ upper limit of normal (ULN)
 5. (e) Total bilirubin $\leq 1.5 \times$ ULN (except subjects with Gilbert's Syndrome who must have normal direct bilirubin)
 6. (f) Normal thyroid function or stable on hormone supplementation per investigator assessment
 7. (g) Albumin $\geq 2 \text{ mg/dl}$
 8. (h) Serum creatinine $\leq 1.5 \times$ ULN or creatinine clearance (CrCl) $\geq 40 \text{ ml/min}$ (measured using the Cockcroft-Gault formula below):

$$\text{Female CrCl} = (140 - \text{age in years}) \times \text{weight in kg} \times 0.85$$

$$72 \times \text{serum creatinine in mg/dL}$$

$$\text{Male CrCl} = (140 - \text{age in years}) \times \text{weight in kg} \times 1.00$$

$$72 \times \text{serum creatinine in mg/dL}$$
12. 12) Ability to comply with treatment, PK and PD sample collection, and required study follow-up

Age and Reproductive Status

[0670]

1. a) Men and women, ages ≥ 18 years at the time of informed consent.
2. b) Women of childbearing potential (WOCBP) must have a negative serum or urine pregnancy test (minimum

sensitivity 25

IU/L or equivalent units of human chorionic gonadotrophin [hCG]) within 24 hours prior to the start of study drug.

3. c) Women must not be breastfeeding.
4. d) WOCBP must agree to follow instructions for method(s) of contraception for the duration of treatment with study drug OX40.21 plus 5 half-lives of study drug plus 30 days. This duration should be 12 weeks for Parts 1 and 3 subjects (50 days plus 30 days) or 23 weeks for Part 2 subjects (130 days plus 30 days [duration of ovulatory cycle]), for a total of up to 160 days post-treatment completion.
5. e) Men who are sexually active with WOCBP must agree to follow instructions for method(s) of contraception for the duration of treatment with study drug OX40.21 plus 5 half-lives of the study drug plus 90 days. The duration should be 20 weeks for Parts 1 and 3 subjects (50 days plus 90 days) or 31 weeks for Part 2 subjects (130 days completion. In addition, male subjects must be willing to refrain from sperm donation during this time.
6. f) Azoospermic males are exempt from contraceptive requirements. WOCBP who are continuously not heterosexually active are also exempt from contraceptive requirements, but still undergo pregnancy testing.

Exclusion Criteria

[0671]

1. 1) Target Disease Exceptions

1. a) Subjects with known or suspected CNS metastases or untreated CNS metastases, or with the CNS as the only site of disease, are excluded. However, subjects with controlled brain metastases are allowed to enroll. Controlled brain metastases are defined as no radiographic progression for at least 4 weeks following radiation and/or surgical treatment (or 4 weeks of observation if no intervention is clinically indicated), and off of steroids for at least 2 weeks, and no new or progressive neurological signs and symptoms.
2. b) Subjects with carcinomatous meningitis
3. c) For ovarian cancer:
 1. i) ovarian cancer subjects with history of bowel obstruction in the prior 6 months or with Tenckhoff catheter are excluded.
 2. ii) up to 4 prior anti-cancer treatments are permitted (i.e, chemotherapy, radiotherapy, hormonal, or immunotherapy). Restarting the same regimen after a drug holiday may be considered one regimen; however it would be counted as two regimens if there was any other regimen used in between.

2. 2) Medical History and Concurrent Diseases

1. a) Subjects with a prior malignancy, different from the one used for enrollment in this study, diagnosed within less than 2 years prior to study entry are excluded (except non-melanoma skin cancers and in situ cancers such as bladder, colon, cervical/dysplasia, melanoma, or breast). In addition, subjects with other second malignancies diagnosed more than 2 years ago who have received therapy with curative intent with no evidence of disease during the interval who are considered to present a low risk for recurrence are eligible.
2. b) Other active malignancy requiring concurrent intervention
3. c) Prior organ allograft
4. d) Previous treatment:
 1. i) Prior anti-cancer treatments are permitted (i.e, chemotherapy, radiotherapy, hormonal, or immunotherapy)
 2. ii) Toxicity (except for alopecia) related to prior anti-cancer therapy and/or surgery must either have resolved, returned to baseline or Grade 1 or have been deemed irreversible
 3. iii) For cytotoxic agents at least 4 weeks must have elapsed between the last dose of prior to anti-cancer therapy and initiation of study therapy
 4. iv) For non-cytotoxic agents at least 4 weeks or 5 half-lives (whichever is shorter) must have elapsed from last dose of prior anti-cancer therapy and the initiation of study therapy.
5. e) Prior therapy with anti-OX40 antibody
6. f) Subjects with active, known, or suspected autoimmune disease are excluded. Subjects with vitiligo, type 1 diabetes mellitus, residual hypothyroidism due to autoimmune condition only requiring hormone

replacement, euthyroid subjects with a history of Grave's disease (subjects with suspected autoimmune thyroid disorders must be negative for thyroglobulin and thyroid peroxidase antibodies and thyroid stimulating immunoglobulin prior to first dose of study drug), psoriasis not requiring systemic treatment, or conditions not expected to recur in the absence of an external trigger are permitted to enroll. Subjects with well controlled asthma and/or mild allergic rhinitis (seasonal allergies) are eligible.

7. g) Subjects with history of life-threatening toxicity related to prior immune therapy (e.g., anti-CTLA-4 or anti-PD-1/PD-L1 treatment or any other antibody or drug specifically targeting T-cell co-stimulation or immune checkpoint pathways) except those that are unlikely to re-occur with standard countermeasures (e.g., hormone replacement after adrenal crisis)
 8. h) Subjects with interstitial lung disease that is symptomatic or that may interfere with the detection or management of suspected drug-related pulmonary toxicity
 9. i) Chronic obstructive pulmonary disease requiring recurrent steroid bursts or chronic steroids at doses greater than 10 mg/day of prednisone or the equivalent
 10. j) Subjects with a condition requiring systemic treatment with either corticosteroids (> 10 mg daily prednisone equivalents) or other immunosuppressive medications within 14 days of study drug administration except for adrenal replacement steroid doses > 10 mg daily prednisone equivalent in the absence of active autoimmune disease. Note: Treatment with a short course of steroids (< 5 days) up to 7 days prior to initiating study drug is permitted.
 11. k) Uncontrolled or significant cardiovascular disease, including but not limited to any of the following:
 1. i) Myocardial infarction or stroke/transient ischemic attack within the past 6 months
 2. ii) Uncontrolled angina within the past 3 months
 3. iii) Any history of clinically significant arrhythmias (such as ventricular tachycardia, ventricular fibrillation, or torsades de pointes)
 4. iv) History of other clinically significant heart disease (e.g., cardiomyopathy, congestive heart failure with New York Heart Association functional classification III-IV, pericarditis, significant pericardial effusion)
 5. v) Cardiovascular disease-related requirement for daily supplemental oxygen therapy
 6. vi) QT interval corrected for heart rate using Fridericia's formula (QTcF) prolongation >480 msec
 12. l) History of any chronic hepatitis as evidenced by the following:
 1. i) Positive test for hepatitis B surface antigen
 2. ii) Positive test for qualitative hepatitis C viral load (by PCR)

Note: Subjects with positive hepatitis C antibody and negative quantitative hepatitis C by PCR are eligible. History of resolved hepatitis A virus infection is not an exclusion criterion. Additional testing or substitute testing per institutional guidelines to rule out infection is permitted.
 13. m) Evidence of active infection that requires systemic antibacterial, antiviral, or antifungal therapy ≤ 7 days prior to initiation of study drug therapy (does not apply to viral infections that are presumed to be associated with the underlying tumor type required for study entry)
 14. n) Known history of testing positive for HIV or known acquired immunodeficiency syndrome.
 15. o) Evidence or history of active or latent tuberculosis infection including PPD recently converted to positive; chest x-ray with evidence of infectious infiltrate; recent unexplained changes in fever/chill patterns.
 16. p) Any major surgery within 4 weeks of study drug administration. Subjects must have recovered from the effects of major surgery or significant traumatic injury at least 14 days before the first dose of study drug.
 17. q) Use of non-oncology vaccines containing live virus for prevention of infectious diseases within 4 weeks prior to study drug. The use of inactivated seasonal influenza vaccines, e.g., Fluzone®, is permitted.
 18. r) Use of pRBC or platelet transfusion within 2 weeks prior to the first dose of study drug
 19. s) A known or underlying medical or psychiatric condition and/or social reason that could make the administration of study drug hazardous to the subjects or could adversely affect the ability of the subject to comply with or tolerate the study.
3. 3) Allergies and Adverse Drug Reaction
1. a) History of allergy to nivolumab or ipilimumab (Parts 2 and 3 only, respectively)
 2. b) History of any significant drug allergy (such as anaphylaxis or hepatotoxicity) to prior anti-cancer immune modulating therapies (e.g., checkpoint inhibitors, T-cell co-stimulatory antibodies)

Study Assessments:

[0672] Physical examinations, vital sign measurements, 12-lead electrocardiograms (ECGs), and clinical laboratory evaluations are performed at selected times throughout the dosing interval. Subjects are closely monitored for AEs throughout the study.

- **Safety Assessments:** AEs are assessed during the study and for 100 days after the last treatment. AEs are evaluated according to NCI CTCAE v4.03. Subjects are followed until all treatment-related AEs have recovered to baseline or are deemed irreversible.
- **Efficacy Assessments:** Disease assessment with CT and/or MRI as appropriate are performed at baseline and every 8 weeks (± 1 week) for q2w dosing regimens and every 9 weeks (± 1 week) for q3w dosing regimens, then every 12 weeks during the treatment and response follow-up phases until discontinuation of treatment or withdrawal from study. Tumor assessments at other time points are performed if there are concerns about tumor progression. Assessment of tumor response is made according to RECIST v1.1 for subjects with malignant tumors.
- **Pharmacokinetic and Immunogenicity Assessments:** Samples for PK and immunogenicity assessments are collected for subjects receiving OX40.21 alone or in combination with nivolumab or ipilimumab. The PK of OX40.21 is characterized by non-compartmental analysis (NCA) method. Immunogenicity samples are analyzed for anti-OX40.21 antibodies and/or anti-nivolumab antibodies and/or anti-ipilimumab antibodies by validated immunoassays.
- **Exploratory Biomarker Assessments:** To explore potential predictive markers for clinical response to OX40.21 in relation to dose and PK, 3 types of specimens are obtained from all subjects for biomarker testing: (i) whole blood, (ii) serum/plasma, and (iii) tumor tissue.

Statistical Considerations

Sample Size Determination

Dose Escalation:

[0673] As a Phase 1 dose escalation trial, the sample size for each dose escalation cohort depends on observed toxicity and posterior inference. Approximately 30 subjects are treated during each dose escalation part (OX40.21 monotherapy [Part 1A], OX40.21 in combination with nivolumab [Part 2A], and OX40.21 in combination with ipilimumab [Part 3A]) for a combined total of about 90 subjects in Parts 1A, 2A, and 3A. Initially, approximately 3 subjects are treated at the starting dose levels of OX40.21 or OX40.21 in combination with nivolumab or ipilimumab. Additional cohorts of approximately 3 evaluable subjects are treated at recommended dose levels per BLRM (-Copula) recommendations during the dose escalation phase. At least 6 DLT-evaluable subjects are treated at the MTD.

Dose Expansion:

[0674] In general terms, the expansion phase sizing is based on target response rates (target overall response rate) and the ability to identify a signal for such clinical response that is above the standard of care (historical overall response rate).

[0675] Approximately 12 subjects are treated in the Part 1B dose expansion cohort. Approximately 35 subjects are treated in the Part 2B dose expansion cohort. Approximately 27 subjects are treated in the Part 2C dose expansion cohort. Approximately 35 subjects are treated in the Part 3B dose expansion cohort.

Endpoints

Primary Endpoints

[0676] The assessment of safety is based on the incidence of AEs, serious AEs, AEs leading to discontinuation, and deaths. In addition, clinical laboratory test abnormalities are examined.

Secondary Endpoints

[0677] Efficacy: The anti-tumor activity of OX40.21 alone and OX40.21 in combination with nivolumab or ipilimumab is measured by ORR, duration of response, and progression free survival rate (PFSR) at 24 weeks based on RECIST v1.1. The above are determined based on tumor measurements occurring at baseline, every 8 weeks (± 1 week) for q2w dosing regimens and every 9 weeks (± 1 week) for q3w dosing regimens during the treatment period, and every 3 months (12 weeks) during the survival follow-up period.

- Best overall response (BOR) is assessed per RECIST 1.1 criteria.
- ORR is the proportion of all treated subjects whose BOR is either CR or PR.
- Duration of response, computed for all treated subjects with a BOR of CR or PR, is the time between the date of first response and the date of disease progression or death, whichever occurs first.
- PFSR at 24 weeks is defined as the proportion of treated subjects remaining progression free and surviving at 24 weeks. The proportion is calculated by the Kaplan-Meier estimate, which takes into account censored data.

Pharmacokinetics

[0678] Selected parameters, such as C_{max}, T_{max}, AUC(0-t), and AUC(TAU), are assessed in 2 cycles depending on the schedule for monotherapy or in combination with nivolumab or ipilimumab. Parameters such as C_{tau}, CLT, C_{ss}-avg, accumulation index (AI), and effective elimination half-life (T-HALFeff) are assessed in the second cycle when intensive PK is collected.

Immunogenicity

[0679] The secondary objective of immunogenicity is assessed by the frequency of positive ADA to OX40.21 or nivolumab or ipilimumab.

Exploratory endpoints

[0680] Exploratory objectives related to OS are assessed by OS rate at a certain time point (e.g., 2 years). OS rate is the proportion of subjects alive at that time point. OS for a subject is defined the time from the date of first dose of study medication to the date of death from any cause. Exploratory objectives related to biomarkers are assessed by the change from baseline or baseline level biomarker measurements in peripheral blood (e.g., soluble factors including, but not limited to, cytokine and chemokines) or tumor tissue (e.g., tumor-infiltrating lymphocytes).

[0681] For subjects with multiple ECG measurements, the following parameters are optionally assessed: changes in the ECG intervals QT, QTc, QRS, and P-R interval from baseline.

Analyses

[0682] Safety analyses: All recorded AEs are listed and tabulated by system organ class, preferred term, and treatment. Vital signs and clinical laboratory test results are listed and summarized by treatment. Any significant physical examination findings and clinical laboratory results are also noted. ECG readings are evaluated, and abnormalities, if present, are noted.

[0683] Efficacy analyses: Listing of tumor measurements are provided by subject and study day in each arm and dose level. Individual subject's BOR is listed based on RECIST 1.1. To describe the anti-tumor activity of OX40.21 alone or in combination with nivolumab or ipilimumab, ORR is calculated. ORR and corresponding 2-sided 95% CI by the Clopper-Pearson method are provided by treatment and/or dose level and tumor type. Median duration of response and corresponding 2-sided 95% CI are reported by treatment and/or dose level and tumor type. Duration of response is analyzed using the Kaplan-Meier method. In addition, PFSR, the probability of a subject remaining progression free or surviving to 24 weeks, is estimated by the Kaplan-Meier methodology by treatment, tumor type, and dose level. The corresponding 95% CI is derived based on Greenwood formula. OS is plotted using the Kaplan-Meier method. Median OS and corresponding 2-sided 95% CI are reported.

[0684] Pharmacokinetic analyses: All individual PK parameters are listed for each analyte, including any exclusions and reasons for exclusion from summaries. Summary statistics are tabulated for each PK parameter by treatment. Geometric means and coefficients of variation are presented for C_{max}, AUC(0-t), AUC(TAU), C_{tau}, CLT, C_{ss}avg, and A_l. Medians and ranges are presented for T_{max}. Means and standard deviations are presented for all other PK parameters (e.g., T-HALFeff).

[0685] OX40.21 dose dependency is assessed in dose escalation monotherapy. To describe the dependency on dose of OX40.21, scatter plots of C_{max}, AUC(0-t), and AUC(TAU) versus dose are provided for each day measured. An exploratory assessment of dose proportionality based on a power model and a CI around the power coefficient is performed. Nivolumab and ipilimumab end of infusion and trough (C_{trough}) concentrations and OX40.21 trough concentration are tabulated by treatment and study day using summary statistics. These data may also be pooled with other datasets for population PK analysis.

[0686] Immunogenicity analysis: All available immunogenicity data are provided by treatment, dose, and immunogenicity status. The frequency of subjects with positive ADA assessment of OX40.21, nivolumab, and ipilimumab are determined.

[0687] Exploratory biomarker analyses: Summary statistics for biomarkers and their corresponding changes (or percent changes) from baseline are tabulated by planned study day and dose in each arm. The time course of biomarker measures are represented graphically. If there is indication of meaningful pattern over time, further analysis (e.g., by linear mixed model) is performed to characterize the relationship. Methods such as, but not limited to, logistic regression are used to explore possible associations between biomarker measures from peripheral blood or tumor biopsy and clinical outcomes.

TABLE 23: SUMMARY OF SEQUENCES

SEQ ID	Description	Sequence
1	Human OX40 precursor	MCVGARRLGRGPCAALLLLGLGLSLTVGLHCVGDTYPSNDRCCHECRPGNGMVS RCRSQNTVCRPCGPGFYNDVVSSKPKFCTWNLRSRGSERKQLCTATQDTVCR CRAGTQPLDSYKPGVDCAPCPGHFSPGDNQACKFWTNCTLAGKHTLQFASNSS DAICEDRDPPATQPGTQGPAPRPTTVQPTTAMPRTSQGPSTRFVSVPGGRAVA AILGLGLVLLGLPLAILLALYLLRRDQRLPPDAHKPFGGGSFRTPIQEEQADA ASTLAKI
2	Extracellular domain of mature human OX40	LHCVGDTYPSNDRCCHECRPGNGMVSRCRSQNTVCRPCGPGFYNDVVSSKPKF CTWNLRSRGSERKQLCTATQDTVCRCRAGTQPLDSYKPGVDCAPCPGHFSPG DNQACKFWTNCTLAGKHTLQFASNSSDAICEDRDPPATQPGTQGPAPRPTTVQ PTTAMPRTSQGPSTRFVSVPGGRAVA
3	Cynomolgus OX40	MCVGARRLGRGPCAALLLLGLGLSLTAKLHCVGDTYPSNDRCCQECRPGNGMVS RCRSQNTVCRPCGPGFYNDVVSAAKPKACFWNLRSRGSERKQPLCTATQDTVCR CRAGTQPLDSYKPGVDCAPCPGHFSPGDNQACKFWTNCTLAGKHTLQFASNSS DAICEDRDPTTPTQPGTQGPAPRPTTVQPTTAMPRTSQGPSTRFVSVPGGRAVA STLGLGLVLLGLPLAILLALYLLRRDQRLPPDAHKPFGGGSFRTPIQEEQADA

SEQ ID	Description	Sequence
		ATGCGCCAGCCTGGCPDAMDLAAGLGGFARDQKLPPLAPKAPGCCGFRTPTIQEYADAA ASALAKI
4	Human OX40-L	MERVQPLEEN VGNAAARPEFE RNEILLVASV IQGLSLLLCF TYICLMFSTL QVSHRYPRIQ SIKVQPTFYK KKEGFILTSQ KEDEIMKVQN NSVIINCDGF YLISLKGYFS QEVNISLIHQ KDEELFLQLK KVRSVNSLMV ASLTWKDKVY LNVTTDTNTSL DDFRVNGGEL ILIRQNPGEF CVL*
5	human IgG1 constant domain	ASTKGPSVFFLAPSSKSTSGGTAAAGCLVKDYFPEPVTWNSGAL TSGVHTFPAYLVQSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNT KVDKRVEPKSCDKTHITCPPCPAPELLGGPSVFLFPPKPKDITLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR VVSVELTLHQQDWLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQ VYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWEESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALTHNHYTQK SLSLSPG
6	human IgG1 constant domain (allotypic variant)	ASTKGPSVFFLAPSSKSTSGGTAAAGCLVKDYFPEPVTWNSGAL TSGVHTFPAYLVQSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHITCPPCPAPELLGGPSVFLFPPKPKDITLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR VVSVELTLHQQDWLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPQ VYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWEESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALTHNHYTQK SLSLSPG
7	human IgG1 kappa light chain	RTVAAPSVPFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDSITYLSSTLLLSKADYEKHKKVYACEVTHQ GLSSPVTKSFNRGEC
8	heavy chain constant region alternative C-terminus	LSPGK
9	heavy chain constant region alternative C-terminus	LSPG
10	Human IgG1 kappa light chain constant region (CL)	RTVAAPSVPFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKDSITYLSSTLLLSKADYEKHKKVYACEVTHQGGLSSPV TKSFNRGEC
11	3F4 VH CDR1	SYDVN
12	3F4 VH CDR2	WMNPNSGNTGYAPKFQG
13	3F4 VH CDR3	IYSSSYNWFDPI
14	3F4 VL CDR1	RASQSVSSYLA
15	3F4 VL CDR2	DASNRAT
16	3F4 VL CDR3	QQRSNWPLT
17	3F4 VH	QVQLVQSGAEVKKPGASVKVSCKASGNIFTSYDVNHWVRQATGQGLEWMG WMNPNSGNTGYAPKFQGRVTMTRNLSTIAYMEISSLRSEDTAVYYCAR IYSSSYNWFDPIWGQGITLVSS
18	3F4 VL	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIY DASNRAFGIPARFSGSGSGIDFTLTISSELEPEFAVYYCQQRSNWPLTF GGGIKVEIK
19	14B6 VH CDR1	SNWIG
20	14B6 VH CDR2	FIIYPGDS TRYSPSFQG

SEQ ID	Description	Sequence
21	14B6 VH CDR3	YGDDWYFDL
22	14B6 VL1 CDR1	RASQSVSSYLA
23	14B6 VL1 CDR2	DASNRAT
24	14B6 VL1 CDR3	QQRGDWPIT
25	14B6 VL2 CDR1	RASQGISSWLA
26	14B6 VL2 CDR2	AASSLQS
27	14B6 VL2 CDR3	QQYNSYPRIT
28	14B6 VH	EVQLEQSGAEVKKPQGESLKISCKGSGYSFTSNWIGWVRQMPGKGLEWMG FIYPGDSSTRYSFSFQQVTISADKSIISTAYLQWSSLKASDIAMYYCAR YGDDWYFDLWGRGTLVTSS
29	14B6 VL1	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWFQQRPGQAPRLLEY DASNRATGIPARFSGSGGTDFSLTLSSLEPEDFAVYYCQQRGDWPIIF GQGTIRLEIK
30	14B6 VL2	DIQMTQSPSSLSASVGRVITTCRASQGISSWLAWYQQKPEKAPKSLIY AASSLQSGVPSRFSGSGGTDFTLTISLQPEDFATYYCQQYNSYPRIT FQGQIRLEIK
31	23H3 VH CDR1	NYAMY
32	23H3 VH CDR2	AIGIGGDTFYTDSVKG
33	23H3 VH CDR3	MGTGYFFDY
34	23H3 VL CDR1	RASQSVSSYLA
35	23H3 VL CDR2	DASNRAT
36	23H3 VL CDR3	QQRSNWPLT
37	23H3 VH	EVQLVQSGGGLVHPGGSLRLSCAGSGITFSNYAMYWVRQAPGKGLEWVS AIGIGGDTFYTDSVKGRTTISRDNANKSLSLQMNSLRAEDMAVYYCARM GTGYFFDYWGQGITLVTVSS
38	23H3 VL	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPCQAPRLLEY DASNRATGIPARFSGSGGTDFTLTISLQPEDFAVYYCQQRSNWPLTF GPSTKVDIK
39	6E1 VH CDR1	SFAMH
40	6E1 VH CDR2	VISYDGSIKYYTDSVKG
41	6E1 VH CDR3	DGNYGSARYFQH
42	6E1 VL1 CDR1	RASQGISSWLA
43	6E1 VL1 CDR2	AASSLQS
44	6E1 VL1 CDR3	QQYNSYPRT
45	6E1 VL2 CDR1	RASQSVSSYLA
46	6E1 VL2 CDR2	DASNRAT
47	6E1 VL2 CDR3	QQRSNWPYT
48	6E1 VH	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSFAMHWVRQAPGKGLEWVT VISYDGSIKYYTDSVKGRTTISRDNANKNTLYLQMNSLRAEDTAVYYCTR DGNYGSARYFQHWGQGITLVTVSS
49	6E1 VL1	DIQMTQSPSSLSASVGRVITTCRASQGISSWLAWYQQKPEKAPKSLIY AASSLQSGVPSRFSGSGGTDFTLTISLQPEDFATYYCQQYNSYPRIT GQGTIRLEIK

SEQ ID	Description	Sequence
50	6E1 VL2	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIY DASNRATGIPARFSGSGSGTDFTLTISSELPEDFAVYYCQQRSNWPYTF GGGTKLEIK
51	18E9 VH CDR1	SSAMH
52	18E9 VH CDR2	AIGTGGDTYYADSVKG
53	18E9 VH CDR3	DFYDILTGFIDY
54	18E9 VL CDR1	RASQGISSWLA
55	18E9 VL CDR2	AASSLQS
56	18E9 VL CDR3	QQANSFPST
57	18E9 VH	EVQLVQSGGGLVHPGGSRLRLSCAHSQFTFTSSAMHWVRQAPCKGLEWIS A G'GGD'YYADSVKGRFTISRDNAKNSLYLQINSIRAKIDMAVYYCARD PYDILEGIFDYWGQGTILVTVSS
58	18E9 VL	DIQMTQSPSSVSASVGDRTITCRASQGISSWLAWYQHKPGKAPKLLIY AASSLQSCVPSRFSGSGSGTDFTLTISSELPEDFAVYYCQQANSFPSTF GGGTKVEIK
59	8B11 VH CDR1	SDAMY
60	8B11 VH CDR2	AIGIGGDTYYTDSVMG
61	8B11 VH CDR3	LGMGYFDY
62	8B11 VL CDR1	RASQSVSSYLA
63	8B11 VL CDR2	DASNRAT
64	8B11 VL CDR3	QQRSNWPPT
65	8B11 VH	MEFVLSWVFLVAILKCVQCEIQLVQSGGGLVHPGGSRLRLSCAGSCFTFS SDAMYWVRQAPCKGLEWVSAIGIGGDTYYTDSVMGRFTISRDNAKNSLY LQMNSLRADMAVYYCARLGMGYFDYWGQGTILVTVSS
66	8B11 VL	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIY DASNRATGIPARFSGSGSGTDFTLTISSELPEDFAVYYCQQRSNWPPTF GGGTKVEIK
67	20B3 VH CDR1	SYDMH
68	20B3 VH CDR2	VIGTAGDTYYPGSVKG
69	20B3 VH CDR3	GGMGNFYFDY
70	20B3 VL CDR1	RASQSVSSYLA
71	20B3 VL CDR2	DASNRAT
72	20B3 VL CDR3	QQRSNWPLT
73	20B3 VH	EVQLVESGGGLVQPGGSLRLSCAASSFTFSSYDMHWVRQTTGKGLEWVS VIGTAGDTYYPGSVKGRFTISRENKNSLYLQMNSLRAGDTAVYYCARG GGMGNFYFDYWGQGTILVTVSS
74	20B3 VL	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIY DASNRATGIPARFSGSGSGTDFTLTISSELPEDFAVYYCQQRSNWPPTF GGGTKVEIK
75	14A2 VH CDR1	NYALH
76	14A2 VH CDR2	LISYDGSRKHADSVKG

SEQ ID	Description	Sequence
77	14A2 VH CDR3	LTMVREGG
78	14A2 VL1 CDR1	RASQSVSSSYLA
79	14A2 VL1 CDR2	GASSRAT
80	14A2 VL1 CDR3	QQYGSSPFT
81	14A2 VL2 CDR1	RVSQGISSYLN
82	14A2 VL2 CDR2	SASNLQS
83	14A2 VL2 CDR3	QRTYNAPYT
84	14A2 VH	QVQLVESGCCGVVQPGRLRLSCAASCFTFSNYALHWVRQAPGKCLEWVA LISYDGSRKHYADSVKGRFSLSRDNSKNTLYLQMNSLRAEDTAVYYCAS LTMVREGGQGTLVTVSS
85	14A2 VL1	EIVLTQSPGTLISLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLI YGASSRATGIPDRFSGSGSTDFTLTISRLPEPEFAVYYCQQYGSSPFT FGPGTKVDIK
86	14A2 VL2	ELQLTQSPSSLASVCDRVTLCRVSSQGISSYLNWYRQKPKVKPLLIY SASNLQSGVPSRFSGSGSGTDFTLTISLQPEEVATYYGQRTYNAPYTF GGSTKVEIK
87	20C1 VH CDR1	SYAMY
88	20C1 VH CDR2	AIDTDGGTFYADSVRG
89	20C1 VH CDR3	LGEGYFFDY
90	20C1 VL CDR1	RASQSVSSSYLA
91	20C1 VL CDR2	DASNRAT
92	20C1 VL CDR3	QQRSNWPPT
93	20C1 VH	EAQLVQSGGGLVHPGGLRLSCADSGFTFSNYAMYWVRQAPGKGLEWVS AIDTDGGTFYADSVRGRTISRDNAKNSLYLQMNSLRAEDMAVYFCARL GEGYFFDYWGQGTLLVTVSS
94	20C1 VL	EIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIY DASNRATGIPARFSGSGSGTDFTLTISLPEPEFAVYYCQQRSNWPPTF CCCTKVEIK
95	OX40.6 heavy chain	EVQLVQSGGGLVQPGGLRLSCAGSGFTFSNYAMYWVRQAPGKGLE WVSAIGIGGDTFYTDSVKGRFTISRDNAKNSLSLQMNSLRAEDTAV YYCARMGTGYFFDYWGQGTLLVTVSSASTKGPSVFELAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKRVPEKSCDKHTCPCPF APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
96	OX40.6 light chain	EIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYDASNRATGIPARFSGSGSGTDFTLTISLPEPEFAVYYCQQRS NWPLTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNN FYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC
97	OX40.7 heavy chain	EVQLVQSGGGLVHPGGLRLSCAGSGFTFSNYAMYWVRQAPGKGLE WVSAIGIGGDTFYTDSVKGRFTISRDNAKNSLSLQMNSLRAEDTAV YYCARYGTGYFFDYWGQGTLLVTVSSASTKGPSVFELAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKRVPEKSCDKHTCPCPF

SEQ ID	Description	Sequence
		APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
98	OX40.7 light chain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRL LIYDASNRAIGIPARFSGSGSGTDFTLTITSSLEPEDFAVYYCQQR NWPLTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN FYFREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC
99	OX40.8 heavy chain	QVQLVESGGGVVQPGRSRLRSCAASGFTFSNYALHWVRQAPGKGLE WVALISYDGSRKHYADSVKGRFISRDNSKNTLYLQMNSLRAEDTA VYYCASLTMVREWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV TVPSSSLGTQTYICNVNHKFSNTKVDKRVPEPKSCDKTHTCPFCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
100	OX40.8 light chain	EIVLTQSPGTLTLSPGERATLSCRASQSVSSYLAWYQQKPGQAPR LLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQY GSSPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN NFYFREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSK ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
101	OX40.9 heavy chain	QVQLVESGGGVVQPGRSRLRSCAASGFTFSNYALHWVRQAPGKGLE WVALISYDGSRKHYADSVKGRFISRDNSKNTLYLQMNSLRAEDTA VYYCASLTYVREWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV TVPSSSLGTQTYICNVNHKFSNTKVDKRVPEPKSCDKTHTCPFCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
102	OX40.9 light chain	EIVLTQSPGTLTLSPGERATLSCRASQSVSSYLAWYQQKPGQAPR LLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQY GSSPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN NFYFREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSK ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
103	OX40.10 heavy chain	QVQLVESGGGVVQPGRSRLRSCAASGFTFSNYALHWVRQAPGKGLE WVALISYSGSRKHADSVKGRFISRDNSKNTLYLQMNSLRAEDTA VYYCASLTMVREGGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV TVPSSSLGTQTYICNVNHKFSNTKVDKRVPEPKSCDKTHTCPFCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
104	OX40.10 light chain	EIVLTQSPGTLTLSPGERATLSCRASQSVSSYLAWYQQKPGQAPR LLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQY GSSPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN NFYFREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSK ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
105	OX40.11 heavy chain	QVQLVESGGGVVQPGRSRLRSCAASGFTFSNYALHWVRQAPGKGLE WVALISYDSSRKHYADSVKGRFISRDNSKNTLYLQMNSLRAEDTA VYYCASLTMVREGGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTA

SEQ ID	Description	Sequence
		ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV TVPSSSLGTQTYICNVNHKPSNTKVDKRVPEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPGDIWVESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFCSCVMHEALHNYHTQKSLSLSPG
106	OX40.11 light chain	EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPR LLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQY GSSPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVCLLN NFYPREAKVQMKVDNALQSGNSQESVTEQDSKDSSTYLSSTLTLSK ADYEKKHVVACEVTHQGLSSPVTKSFNRGEC
107	OX40.12 heavy chain	QVQLVESGGGVVQPGRSRLRSCAASGFTFSNYALHWVRQAPGKGLE WVALISYSGSRKHADSVKGRFSISRDN SKNTLYLQMNSLRAEDTA VYYCASLTVMREWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV TVPSSSLGTQTYICNVNHKPSNTKVDKRVPEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPGDIWVESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFCSCVMHEALHNYHTQKSLSLSPG
108	OX40.12 light chain	EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPR LLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQY GSSPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVCLLN NFYPREAKVQMKVDNALQSGNSQESVTEQDSKDSSTYLSSTLTLSK ADYEKKHVVACEVTHQGLSSPVTKSFNRGEC
109	OX40.13 heavy chain	QVQLVESGGGVVQPGRSRLRSCAASGFTFSNYALHWVRQAPGKGLE WVALISYDSSRKHYADSVKGRFSISRDN SKNTLYLQMNSLRAEDTA VYYCASLTVMREWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV TVPSSSLGTQTYICNVNHKPSNTKVDKRVPEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPGDIWVESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFCSCVMHEALHNYHTQKSLSLSPG
110	OX40.13 light chain	EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPR LLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQY GSSPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVCLLN NFYPREAKVQMKVDNALQSGNSQESVTEQDSKDSSTYLSSTLTLSK ADYEKKHVVACEVTHQGLSSPVTKSFNRGEC
111	OX40.14 heavy chain	QVQLVESGGGVVQPGRSRLRSCAASGFTFSNYALHWVRQAPGKGLE WVALISYSGSRKHADSVKGRFSISRDN SKNTLYLQMNSLRAEDTA VYYCASLTVMREWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV TVPSSSLGTQTYICNVNHKPSNTKVDKRVPEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV NKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPGDIWVESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFCSCVMHEALHNYHTQKSLSLSPG
112	OX40.14 light chain	EIVLTQSPGTLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPR LLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQY GSSPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVCLLN NFYPREAKVQMKVDNALQSGNSQESVTEQDSKDSSTYLSSTLTLSK ADYEKKHVVACEVTHQGLSSPVTKSFNRGEC
113	OX40.15 heavy	

SEQ ID	Description	Sequence
	chain	QVQLVESGGGVVQPGSRSLRLSCAASGFTFSNYALHWVRQAPGKGLE WVALISYDSSSRKHADSVKGRFISIRDNSKNTLYLQMNSLRAEDTA VYYCASLTYVREWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV TVFSSSLGTQTYICNVNHKFSNTKVDKRVPEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMEALHNHYTQKSLSLSPG
114	OX40.15 light chain	EIVLTQSPGTLRLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPR LLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQY GSSPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSK ADYEKKHVVACEVTHQGLSSPVTKSFNRGEC
115	OX40.16 heavy chain	EVQLVQSGGGLVQPGGSLRLSCAGSGFTFSYAMYVWRQAPGKGLE WVSAIDTDGGTFYADSVRGRFTISRDNANKSLYLQMNSLRAEDTAV YFCARLGEYFFDYWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKFSNTKVDKRVPEPKSCDKTHTCPPCP APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMEALHNHYTQKSLSLSPG
116	OX40.16 light chain (shared by OX40.20, OX40.21, OX40.22)	EIVLTQSPATLRLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYDASNRAITGIPARFSGSGSGTDFTLTISSELEPEDFAVYYCQQR NWPFTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKA DYEKKHVVACEVTHQGLSSPVTKSFNRGEC
117	OX40.17 heavy chain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSYDMHWVRQITGKGLE WVSVIGTAGDTYYPGSVKGRFTISRDNANKSLYLQMNSLRAGDTAV YYCARGGMGNFYDYWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKFSNTKVDKRVPEPKSCDKTHTCPPCP APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSCSVMEALHNHYTQKSLSLSPG
118	OX40.17 light chain	EIVLTQSPATLRLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYDASNRAITGIPARFSGSGSGTDFTLTISSELEPEDFAVYYCQQR NWPFTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKA DYEKKHVVACEVTHQGLSSPVTKSFNRGEC
119	OX40.18 heavy chain	QVQLVQSGAEVKKPGASVKVSCKASGYFTSYDYNWVRQATGQGLE WMGWMNPNNSGNTGYAPKFQGRVTMTRDTSISTAYMELSSLSRSDTA VYYCARIYSSSYNWFYWGQGTTLTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVPEPKSCDKTHTCP PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEV KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPG
120	OX40.18 light chain	EIVLTQSPATLRLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYDASNRAITGIPARFSGSGSGTDFTLTISSELEPEDFAVYYCQQR NWPFTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKA DYEKKHVVACEVTHQGLSSPVTKSFNRGEC

SEQ ID	Description	Sequence
121	OX40.19 heavy chain	QVQLVESGGGVQPGSRSLRLSCAASGFTFSNYALHWVRQAPGKGLE WVALISYDGSRKHYADSVKGRFSISRDNKNTLYLQMNSLRAEDTA VYYCASLTLVREWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSSV TVPSSSLGTQTYICNVNHKFSNTKVDKRVKPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR WQQGNVVFSCSVMEALHNHYTQKSLSLSPG
122	OX40.19 light chain	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPR LLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYQCQY GSSPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLN NFYFPREAKVQMKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
123	OX40.20 heavy chain	EVQLVQSGGGLVQPGGSLRLSCAGSGFTFSYAMYWVRQAPGKGLE WVSAIDTSGGTFYADSVRGRFTISRDNKNSLYLQMNSLRAEDTAV YFCARLGEYGFYDYGQGLTVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKFSNTKVDKRVKPKSCDKTHTCPPCP APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK SRWQQGNVVFSCSVMEALHNHYTQKSLSLSPG
---	OX40.20 light chain	SEQ ID NO: 116
124	OX40.21 heavy chain	EVQLVQSGGGLVQPGGSLRLSCAGSGFTFSYAMYWVRQAPGKGLE WVSAIDTDAGTFYADSVRGRFTISRDNKNSLYLQMNSLRAEDTAV YFCARLGEYGFYDYGQGLTVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKFSNTKVDKRVKPKSCDKTHTCPPCP APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK SRWQQGNVVFSCSVMEALHNHYTQKSLSLSPG
---	OX40.21 light chain	SEQ ID NO: 116
125	OX40.22 heavy chain	EVQLVQSGGGLVQPGGSLRLSCAGSGFTFSYAMYWVRQAPGKGLE WVSAIDTSTGTFYADSVRGRFTISRDNKNSLYLQMNSLRAEDTAV YFCARLGEYGFYDYGQGLTVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTISWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKFSNTKVDKRVKPKSCDKTHTCPPCP APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK SRWQQGNVVFSCSVMEALHNHYTQKSLSLSPG
---	OX40.22 light chain	SEQ ID NO: 116
1263F4 VH (nucleotide sequence)		CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGGCCT CAGTGAAGGTCTCCTGCAAGGCTTCTGGAAACACCTTCACCAGTTATGA TGTCAACTGGGTGCGACAGGCCACTGGACAAGGCTTGAAGGATGGGA TGGATGAACCCIAACAGTGGTAAACACAGGCATGCACCGAAGTCCAGG GCAGATCACCATGACCAGGAACACCTCCATAAGCACAGCCTACATGGA GCTGAGCAGCCTGAGACTTGAAGACACGGCCGTATTAATCTGTGCGAGA ATATAACACCTCCTACAACTGTTCCACCCCTGGGCCCAGCGCAACCC TGGTCAACCGTCTCTCTCA

SEQ ID	Description	Sequence
1273F4 VL		GAAATTGTTTGACACAGTCTCCAGCCACCCTGCTTTGTTCTCCAGGGG AAAGAGCCACCCTCTCTGCGAGGGCCAGTCAGAGTGTAGCAGCTACTT AGCCCTGGTACCAACAGAAACCTGGCCAGGCTCCAGGCTCCTCATCTAT GATGCATCCAAACAGGCCACTGGCATCCAGCCAGGTTCACTGCCACTG GGCTCTGGACAGACTTCTCTCTCACCATCAGCAGCCTAGAGCCTGAAGA TTTTSCAGTTTATTACTCTCAGCAGCGTAGCAACTGGCCTCTCACTTTC GGCGGAGGGACCAAGTGGAGATCAAA
12814B6 VH		GAGGTGCAGCTGGAGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGT CTCTCAAGATCTCTGTAAAGGCTCTGGAACAGCTTTACCAGCAACTG GATCGGCTGGTGGCCAGATGCCCGGAAAGGCTGGAGTGGATGGGG TTCATCTATCCCTGGTACTCTGATACCAGGACAGCCCGTCTCTCCAG GCCAGGTACCATCTCAGCCGACAAGTCCATCAGCAGCCGCTACCTGCA CTGGAGCAGCTCAAGCCCTCCGACATCCCATCTATTACCTCTCCGACA TATGGGATAGATGGTACTTCGATCTCTGGGSCCGTGGCACCCTGGTCA CTCTCTCTCA
12914B6 VL1		GAAATTGTTTGACACAGTCTCCAGCCACCCTGCTTTGTTCTCCAGGGG AAAGAGCCACCCTCTCTGCGAGGGCCAGTCAGAGTGTAGCAGCTACTT AGCCCTGGTTCACACAGAGACCTGGCCAGGCTCCAGGCTCCTCATCTAT GATGCATCCAAACAGGGCCACTGGCATCCAGCCAGGTTCACTGGCAGTG GGCTCTGGACAGACTTCTCTCTCACCATCAGCAGCCTAGAGCCTGAAGA TTTTSCAGTTTATTACTCTCAGCAGCGTGGCCAGTGGCCCATCACCITC GGCCAGGGACACGACTGGAGATTAAA
130	14B6 VL2	GACATCCAGATGACCCAGTCTCCATCTCTACTGCTGCTCATCTGTAGGAG ACAGAGTCACCATCACCTCTCTGGGCGAGTCAGGTAATAGCAGCTGCTT AGCCCTGGTATCAGCAGAAACAGAGAAAGCCCTAAGTCCCTGATCTAT GCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTCAAGCGCAGTG CATCTGGACACATTTCACTCTCACCATCAGCAGCCTCCAGCCTGAAGA TTTTGCAACTTATTACTGCAACAGTATAATAGTTACCCCTCGGATCACC CTCGGCCAAGGGACACGACTGGAGATTAAA
131	23H3 VH	CAGCTTCAGCTGGTCCAGTCTCGGGGAGGCTTGATACATCTCGGGGCT CCCTGAGACTCTCTGTGCAAGGCTCTGGATTACCTTCAGTAACATATGC TATCTACCTGGCTTCGCCACGCTCCAGCAAAAGCTCTCCATCTGGTATCA GCCATTGGTATTGGTGGTGGACATTTCTATACAGACTCCGTGAAGGGCC GATTACCATCTCTCAGAGACAATGCCAAGAACTCCTTGTCTCTTCAAA GAACAGCCTGAGAGCCGAGGACATGGCTGTATTACTGTGCAAGAAATG GGAACCTGGTACTTCTTTGACTACTGGGGCCAGGGAACCTGGTCACCG TCTCTCA
132	23H3 VL	GAAATTGTTTGACACAGTCTCCAGCCACCCTGCTTTGTTCTCCAGGGG AAAGAGCCACCCTCTCTGCGAGGGCCAGTCAGAGTGTAGCAGCTACTT AGCCCTGGTACCAACAGAAACCTGGCCAGGCTCCAGGCTCCTCATCTAT GATGCATCCAAACAGGGCCACTGGCATCCAGCCAGGTTCACTGGCAGTG GGCTCTGGACAGACTTCTCTCTCACCATCAGCAGCCTAGAGCCTGAAGA TTTTSCAGTTTATTACTCTCAGCAGCGTAGCAACTGGCCTCTCACTTTC GGCCCTGGGACCAAGTGGATATCAAA
133	6E1 VH	CAGCTGCAGCTGGTCCAGTCTGGGGGAGGCTGTCTCAGCCTCGGACCT CCCTGAGACTCTCTGTGCAAGCCTCTGGATTACCTTCAGTAGCTTTGC TATGCATCTGGCTCCGCCAGGCTCCAGCAAGCGGCTGGATCTGCTCACA CTTATTTCATATGATGGAAGCATTAATACTACACAGACTCCGTGAAGG GCCGATTACCTTCTCCAGAGACAATCCAAAGAACTCTGTATCTGCA AATGAACAGCCTCAGAGCTCAGGACACCCCTCTGTATTACTGTACCA GATGGAAACTATGGTTCTGGGAGATACCTCCAGCACCTGGGGCCAGGGCA CCCTGCTCAGGCTCTCTCA
134	6E1 VL1	GACATCCAGATGACCCAGTCTCCATCTCTACTGCTGCTCATCTGTAGGAG ACAGAGTCACCATCACCTCTCTGGGCGAGTCAGGTAATAGCAGCTGCTT AGCCCTGGTATCAGCAGAAACAGAGAAAGCCCTAAGTCCCTGATCTAT GCTGCATCCAGTTTGCAAAAGTGGGGTCCCATCAAGGTTCAAGCGCAGTG CATCTGGACACATTTCACTCTCACCATCAGCAGCCTCCAGCCTGAAGA TTTTGCAACTTATTACTGCAACAGTATAATAGTTACCCCTCGGACGTT GGCCAGGGACCAAGTGGAAATCAAA
135	6E1 VL2	GAAATTGTTTGACACAGTCTCCAGCCACCCTGCTTTGTTCTCCAGGGG

SEQ ID	Description	Sequence
		AAAGAGCCACCCTCTCCTGCAGGSCCAGTCAGAGTGTAGCAGCTACTT AGCCCTGGTACCAACAGAAACCTGGCCAGGCTCCAGGCTCCTCAITCAI GATGCATCCAAACAGGGCCACTGGCATCCAGCCAGSTTCAGTGGCAGTG GGTCTGGCAGACACTTCACCTCACCATCACCAGCCTAGAGCCCTGAACA TTTTGCAGTTTATTACCTCAGCAGCGTAGCAACTGGCCGTACACTTTT GGCCAGGGACCAAGCTGGAGATCAAA
136	18E9 VH	GAGGTCAGCTGGTGGAGCTGGGGGAGGCTTGGTTTCATCTGGGGGGT CCCTGAGACTCTCCTGTGCACACTCTGGATTACCTTCAGTAGCTCTGC TATGCATCGGTTCCGCCAGGCTCCAGGAAAGGCTTGAATGGATATCA GCTATTGGTACTGGTGGTGACACATACTATGCAGACTCCGTGAAGGGCC GATTACCATCTCCAGACACAAAGCCAAAGAACTCCTTGATCTTCAAA AAACAGCCTGAGAGCCGAGGACATGGCTGTATATTACTGTGCAAGAGAC TTTTACGATTTTATGACCTGGTATCTTTGACTACCTGGGCGCAGGGAACCC TGGTACCCGTCTCTCA
137	18E9 VL	GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAG ACAGACTCACCATCACCTTCCGGGCCAGTCAGGTAATTACCACTTCCTT AGCCCTGGTATCAGCATAAAACAGGAAAGCCCTTAAGCTCCTGATCTAT GCTGCATCCAGTTTGCAAGTGGGGTCCCATCAAGSTTCAGCGGCAGTG GATCTGGGACAGATTTTCACTCTCACCATCAGCAGCCCTGAGCCCTGAAGA TTTTGCAGTTTACTATTGTCAACAGGCTAATAGTTTCCCTTCGACGTTT GGCCAGGGACCAAGCTGGAAATCAAA
138	8B11 VH	AAGGAGTTTGTGCTGACCTGGGTTTTCCTTCTTGCATATTAAGAGTCT TCCACTGTGAAATTCAGCTGGTGCAGTCTGGGGCAGGCTTGGTACATCC TGGGGGCTCCCTGACACTCTCCTCTGAGGCTCTGCAATTCACCTTCACT AGCGATGCTATGTACTGGGTTCCGCCAGGCTCCAGGAAAGGCTTGGAGT GGGTATCAGCTATTGGTATGGTGGTGACACATACTATACAGACTCCGT GATGGGCGGATTACCATCTCCAGAGACAAAGCCAAAGAACTCCTTGAT CTTCAATGAACAGCCTGAGAGCCGAGGACATGGCTGTGTATTACTGTG CAAGGCTGGGGATGGGGTACTACTTTGACTACCTGGGGCCAGGGAACCCCT GGTACCCGTCTCTCA
139	8B11 VL	GAAATTTGTGTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGG AAAGAGCCACCCTCTCCTGCAGGSCCAGTCAGAGTGTAGCAGCTACTT AGCCCTGGTACCAACAGAAACCTGGCCAGGCTCCAGGCTCCTCATCTAT GATGCATCCAAACAGGGCCACTGGCATCCAGCCAGSTTCAGTGGCAGTG GGCTGGGACAGACTTCACCTCTCACCATCAGCAGCCCTAGAGCCCTGAAGA TTTTGCAGTTTATTACTCTCAGCAGCGTAGCAACTGCCCTCCGACCTTC GGCCAGGGACCAAGCTGGAAATCAAA
140	20B3 VH	GAGGTCAGCTGGTGGAGCTGGGGGAGGCTTGGTACAGCCTGGGGGGT CCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTACGA CATGCATCTGGTCCGCCAAACTACAGGAAAGGCTTGGAGTGGGTCTCA GCTATTGGTACTGCTGGTGACACATACTATCCAGGCTCCGTGAAGGCC GATTCACCATCTCCAGACAAATGCCAAGAACTCCTTGATCTTCAAA GAACAGCCTGAGAGCCGGGGACAGGCTGTGTATTACTGTGCAAGAGGG CCGATGGCAACTACTTTGACTACCTGGGCCAGGCAACCCCTGCTACCC TCTCTCA
141	20B3 VL	GAAATTTGTGTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGGGG AAAGAGCCACCCTCTCCTGCAGGSCCAGTCAGAGTGTAGCAGCTACTT AGCCCTGGTACCAACAGAAACCTGGCCAGGCTCCAGGCTCCTCAITCAI GATGCATCCAAACAGGGCCACTGGCATCCAGCCAGSTTCAGTGGCAGTG GGCTGGCAGACACTTCACCTCACCATCACCAGCCTAGAGCCCTGAACA TTTTGCAGTTTATTACCTCAGCAGCGTAGCAACTGGCCGTCACTTTT GGCGGAGGGACCAAGCTGGAGATCAAA
142	14A2 VH	CAGGTCAGCTGGTGGAGCTGGGGGAGGCTTGGTCCAGCCTGGGAGGT CCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAAGTATGC TCTGCATGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGGCA CTTATATCATATGATGGAGCAGGAAACACTACGCACTCCGTGAAGG CCGGATTCAGTATCTCCAGACACAAATGCCAAGACACACTGTATCTGCA AATGAACAGCCTGAGAGCTGAGGACAGGCTGTGTATTACTGTGCGAGT CTACATATGGTTGGGGAGGGGGCCAGGGAACCCCTGCTACCCGCTCTCT CA
143	14A2 VL1	GAAATTTGTGTGACACAGTCTCCAGGACCCCTGTCTTTGTCTCCAGGGG

SEQ ID	Description	Sequence
		AAAGAGCCACCCCTCTCCTGCAGGGCCAGTCAGAGTGTAGCAGCAGCTA CTTAGCCCTGGTACCCAGCAGAAACCTGGCCAGGCCTCCAGGCTCCTCATC TAAAGGTCATCCAGCAGGGCCACTGGCATCCAGACAGGTTAGTGGCA CTGGTCTCTGGCACACACTTCACTCTCACCATCAGCAGACTGGACCTCA AGATTTGTCAGTGTATTACCTGCAGCAGTATGGTAGCTACCAATTCAT TTGGGCTCTGGCACAAACCTGGATATCAAA
144	14A2 VL2	GACATCCAGTTGACCCAGTCTCCATCCTCCCTGCTGCATCTGTAGGAG ACAGAGTCACCATCACCTGGCGGGTGGTGCAGGCACTAGCAGTTATTT AAATTTGGTATCGGCAGAAACCTAGGGAAGTTCCCTAAGCTCCTGATCTAT AGTGCATCCAAATTTCCAACTCGGAGTCCCATCTCCCTCAGTCCCACTC GATCTGGGACAGATTTTCACTCTCACAATCAGCAGCCCTGAGCCCTGAAGA TGTTCCAACTTATTACGCTCAACGGACTTACAATGCCCTTACACTTTC GGCGSAGGGACCAAGGTCGAGATCAAA
145	20C1 VH	GAGGCTCAGCTGGTGCAGTCTGGGGGAGGCTTGGTTTCATCCTGGGGGGT CCCTGAGACTCTCCTGTGCAGACTCTGGAATTCACCTTCAGTAGCTATGC TACCTACTGGCTTCGCCAGGCTCCAGCAAAAGCTTCGAGTCCCTATCA GCTATTCATCTGATGGTGGCACATCTCTGCAGACTCCGTGCGGGGCC
		GATTCACCATCTCCAGAGACAATGCCAAGAACTCCCTGTATCTTCAAAI GAACGSCCTGAGAGCCGAGGACATGGCTGTGTATTTCTGTGCAAGACTT GGGGAAGGGTACTTCTCTGACTACTGGGGCCAGGGAACCCCTGGTCACCG TCTCCTCA
146	20C1 VL	GAAATTTGTGTGACACAGTCTCCAGCCACCCCTGTCTTTGTCTCCAGGGG AAAGAGCCACCCCTCTCCTGCAGGGCCAGTCAGAGTGTAGCAGCTACTT AGCCCTGGTACCAACAGAAACCTGGCCAGGCTCCAGGCTCCTCATCTAT GATGCATCCAAACAGGGCCACTGGCATCCAGCCAGGTTCACTGGCAGTG GGCTCTGGGACAGACTTCACTCTCACCATCAGCAGCCCTAGAGCCCTGAAGA TTTTCAGTTTATTACTCTCAGCAGCGTAGCAACTGGCTCTCCCACTTTC GGCGSAGGGACCAAGGTCGAGATCAAA
147	OX40.6 heavy chain	GAGGTTTCAGCTGGTGCAGTCTGGGGGAGGCTTGGTACAGCCTGGGG GGTCCCTGAGACTCTCCTGTGCAGGCTCTGGATTCACCTTCAGTAA CTATGCTATGTACTGGGTTCGCCAGGCTCCAGGAAAAGGCTCTGGAG TGGGTATCAGCCATTGGTATTTGGTGGTGCACATTTCTATACAGACT CCGTGAAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACTC CTTGCTCTTCAAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTG TATTACTGTGCAAGAATGGGAACCTGGGTACTTCTTTGACTACTGGG GCCAGGGAACCCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCC ATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGC ACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCGAACCCTGG TGACGGTGTCTGTGGAACCTCAGGCGCCCTGACCAGCGCGCTGCACAC CTTCCCGGCTGTCTTACAGTCTTCAGGACTTACTCCCTCAGCAGC GTGGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACCTACATCT GCAACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAGAGT TGAGCCCAAACTTTGTGACAAAACCTCACACATGCCACCGTGCCCA GCACCTGAACCTCTGGGGGGACCGTCACTCTCTCTTCCCCCAA AAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGGTGGTGGACGTGAGCCACGAAGCCCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGC GGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCTCAC CGTCTGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCTCCAAACAAAGCCCTCCAGCCCATCGAGAAAACCATCTCCA AAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCCTGCCCCC ATCCCGGGAGGAGATGACCAAGAACCAGCTCAGCCTGACCTGCCTG GTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCA ATGGGCAGCCGGAGAACAACTACAAGACCAGCCTCCCGTGTCTGGA CTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCCTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATG AGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCC GGGT
148	OX40.6 light chain	GAAATTTGTGTGACACAGTCTCCAGCCACCCCTGTCTTTGTCTCCAG GGGAAAGAGCCACCCCTCTCCTGCAGGGCCAGTCAGAGTGTAGCAG CTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCAGGCTCT CTCATCTATGATGCATCCAACAGGGCCACTGGCATCCAGCCAGGT TCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAG CCTAGAGCCTGAAGATTTTGCAGTTTATTACTGTGACAGCGTAGC AACTGGCTCTCACTTTCGGCCCTGGGACCAAGTGGATATCAAAC GTACGGTGGCTGCACCATCTGTCTTCACTTCCCGCCATCTGATGA

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		GCAGTTGAAATCTGGAAGTGCCTCTGTGTGTGCCTGCTGAATAAC TTCTATCCCAGAGAGGCCAAAGTACAGTGGAGGTGGATAACGCCC TCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAA
		GGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCA GACTACGAGAAACACAAAGTCTACGCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
149	OX40.7 heavy chain	GAGGTTACAGCTGGTGCAGTCTGGGGGAGGCTTGGTACATCCTGGGG GGTCCCTGAGACTCTCCTGTGCAGGCTCTGGATTACCTTCAGTAA CTATGCTATGTACTGGGTTCGCCAGGCTCCAGGAAAAGGTCTGGAG TGGGTATCAGCCATTGGTATTGGTGGTGACACATTCTATACAGACT CCGTGAAGGGCCGATTCAACATCTCCAGAGACAATGCCAAGAACTC CTTGCTCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTG TATTACTGTGCAAGATATGGAAGTGGGTACTTCTTTGACTACTGGG GCCAGGGAACCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCC ATCGGTCTTCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGC ACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCGAACC GG TGACGGTGTCTGTGGAAGTCAAGCGCCCTGACCAGCGCGTGCACAC CTTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCT GCAACGTGAATCACAAGCCAGCAACCAAGGTGGACAAGAGAGT TGAGCCCAAATCTTGTGACAAAACCTCACACATGCCCACCGTGCCCA GCACCTGAAGTCTGGGGGGACCGTCAGTCTTCTCTTCCCGCCAA AACCAGAGGACACCTCATGATCTCCGGACCCCTGAGGTACATG CGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCCG GGGAGGAGCAGTACAAACAGCAGTACCGTGTGGTCAAGCTCTCAC CGTCTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCTCCAAACAAAGCCCTCCAGCCCGCATCGAGAAAACCATCTCCA AAGCCAAAGGCGAGCCCGAGAACACAGGTGTACACCTTGCCCC ATCCCGGAGGAGATGACCAAGAACAGGTACAGCTGACCTGCGCTG GTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCA ATGGGCAGCCGAGAACAACTACAAGACCACGCTCCCGTGTCTGGA CTCCGACGCTCTTCTTCTCTATAGCAAGCTACCGTGGACAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGTCTCCGTGATGCATG AGGCTCTGCACAACCACTACACGCAGAGAGCTCTCCCTGTCCCC GGGT
150	OX40.7 light chain	GAAATTGTGTTGACACAGTCTCCAGCCACCCCTGTCTTTGTCTCCAG GGGAAAGAGCCACCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAG CTACTTAGCCTGGTACCAACAGAACTTGGCCAGGCTCCAGGCTC CTCATCTATGATGCATCCAACAGGGCCACTGGCATCCAGCCAGGT TCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAG CCTAGAGCCTGAAGATTCTGAGTTTATTACTGTACGACGCTAGC AACTGGCCTCTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAAC GTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCATCTGATGA GCAGTTGAAATCTGGAAGTGCCTCTGTGTGTGCTGTGTAATAAC TTCTATCCCAGAGAGGCCAAAGTACAGTGGAGGTGGATAACGCCC TCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAA GGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCA GACTACGAGAAACACAAAGTCTACGCTGCGAAGTCACCCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
151	OX40.8 heavy chain	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGA GGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAA CTATGCTCTGCACTGGGTCCGCCAGGCTCCA3GCAAGGGGCTGGAG TGGGTGGCACTTATATCATATGATGGAAGCA3GAAACACTACGCAG
		ACTCCGTGAAGGGCCGATTCAATATCTCCAGAGACAATCCAAGAA CACACTGTATCTGCAATGAACAGCCTGAGAGCTGAGGACACGGCT GTGTATTACTGTGCGAGTCTTACTATGGTTCGGGAGTGGGGCCAGG GAACCTTGGTACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGT CTTCCCCCTGGCACCTCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCGAACC GG TGACGG TGCTGTGGAAGTCAAGCGCCCTGACCAGCGCGTGCACACCTTCCC GGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTG ACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACG TGAATCACAAGCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCC CAAATCTTGTGACAAAACCTCACACATGCCCACCGTGCCAGCACCT GAACCTCTGGGGGGACCGTCAGTCTTCTCTTCCCGCCAAACCCA AGGACACCTCATGATCTCCCGACCCCTGAGGTACATGCGTGGT GGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTAC

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		GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCAGTACCGTGTGGTCAAGCGTCCTCACCCTCCT GCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCC AACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAAGCCA AAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCCATCCCG GGAGGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAA GGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGC AGCCGGGAGAACAATAACAAGACCAGCCTCCCGTGGTGGACTCCGA CGGCTCCTTCTTCTCTATAGCAAGCTACCCGTGGACAAGAGCAGG TGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTC TGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGGT
152	OX40.8 light chain	GAAATTGTGTTGACGCAGTCTCCAGGCACCTGTCTTTGTCTCCAG GGGAAAGAGCCACCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAG CAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGG CTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCAGACA GGTTCAAGTGGCAGTGGGTCTGGACAGACTTCACTCTCACCATCAG CAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTGAGCAGTAT GGTAGCTCACCATTCACTTTGGGCCCTGGGACCAAAGTGGATATCA AACGTACGTTGGCTGCACCATCTGTCTTCACTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAAGTGCCTCTGTGTGCTGCTGAAT AACTTCTATCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACG CCCTCCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAA GCAGACTACGAGAAACACAAAGTCTACGCTGCCAAGTCAACCATC AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTG T
153	OX40.9 heavy chain	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGA GGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAA CTATGCTCTGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAG TGGGTGGCACTTATATCATATGATGGAAGCAGGAAACACTACGCAG ACTCCGTGAAGGGCCGATTCACTATCTCCAGAGACAATTCCAAGAA CACACTGTATCTGCAATGAACAGCCTGAGAGCTGAGGACACGGCT GTGTATTACTGTGCGAGTCTTACTTACGTTCCGGAGTGGGGCCAGG GAACCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGGCCATCGGT CTTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACAGG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG TGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCC GGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTG
		ACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACG TGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCC CAAACTCTTGAGACAAACTCACACATGCCACCGTGCCAGCACCT GAATCCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCCA AGGACACCTCATGATCTCCCGACCCCTGAGGTACATGCGTGGT GGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTAC GTGGACGGCGTGGAGTGCATAATGCCAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCAGTACCGTGTGGTCAAGCTCCTCACCCTCCT GCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCC AACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAAGCCA AAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCCATCCCG GGAGGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAA GGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGC AGCCGGGAGAACAATAACAAGACCAGCCTCCCGTGGTGGACTCCGA CGGCTCCTTCTTCTCTATAGCAAGCTACCCGTGGACAAGAGCAGG TGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTC TGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGGT
154	OX40.9 light chain	GAAATTGTGTTGACGCAGTCTCCAGGCACCTGTCTTTGTCTCCAG GGGAAAGAGCCACCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAG CAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGG CTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCAGACA GGTTCAAGTGGCAGTGGGTCTGGACAGACTTCACTCTCACCATCAG CAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTGAGCAGTAT GGTAGCTCACCATTCACTTTGGGCCCTGGGACCAAAGTGGATATCA AACGTACGTTGGCTGCACCATCTGTCTTCACTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAAGTGCCTCTGTGTGCTGCTGAAT AACTTCTATCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACG CCCTCCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAA GCAGACTACGAGAAACACAAAGTCTACGCTGCCAAGTCAACCATC AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTG T

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155	OX40.10 heavy chain	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGA GGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTTCAGTAA CTATGCTCTGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAG TGGGTGGCACTTATATCATATAGTAGGAAAGCACTACGCAG ACTCCGTGAAGGGCCGATTGAGTATCTCCAGAGACAATTCGAAGAA CACACTGTATCTGCAAAATGAACAGCCTGAGAGCTGAGGACACGGCT GTGTATTACTGTGCGAGTCTTACTATGGTTCGGGAGGGGGGCCAGG GAACCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCATCGGT CTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG TGTCGTGGAACCTCAGGCGCCCTGACCAGCGGCTGCACACCTTCCC GGCTGTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTG ACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACG TGAATCACAAGCCCAGCAACACCAAGTGGACAAGAGAGTTGAGCC CAAACTCTTGACAAAACCTCACACATGCCACCGTGCCACGACCT GAACCTCCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCA AGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGT GGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTAC GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGG AGCAGTACAACAGCACGTACCGTGTGGTCAAGCTCTCACCGTCTCT
		GCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCC AACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCA AAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCCATCCCG GGAGGAGATGACCAAGAACCAGGTGACGCTGACCTGCCTGGTCAAA GGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGC AGCCGGAGAACAACCTACAAGACCACGCTCCCGTGTGGACTCCGA CGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGG TGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGATGAGGCTC TGACAACCACTACACGCAGAAGAGCTCTCCCTGTCCCCGGGT
156	OX40.10 light chain	GAAATGTGTGTGACGCAGTCTCCAGGCACCCCTGTCTTTGTCTCCAG GGGAAAGAGCCACCCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAG CAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGG CTCCTCATCTATGGTGCATCCAGCAGGGGCACTGGCATCCAGACA GGTTCACTGGCAGTGGGTCTGGACAGACTTCACTCTCACCATCAG CAGACTGGAGCCTGAAGATTTCAGTGTATTACTGTACAGCAGTAT GGTAGCTCACCATTCACTTTCGGCCCTGGGACCAAAAGTGGATATCA AACGTACGGTGGCTGCACCATCTGTCTTCTTCTTCCCCCATCTGA TGAGCAGTTGAAATCTGGAAGTCCCTCTGTTGTGTGCTGCTGAAT AACTTCTATCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACG CCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAA GCAGACTACGAGAAACACAAAGTCTACGCTGCGAAGTACCCCATC AGGGCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTG T
157	OX40.11 heavy chain	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGA GGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTTCAGTAA CTATGCTCTGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAG TGGGTGGCACTTATATCATATGATAGTAGCAGGAAACACTACGCAG ACTCCGTGAAGGGCCGATTGAGTATCTCCAGAGACAATTCGAAGAA CACACTGTATCTGCAAAATGAACAGCCTGAGAGCTGAGGACACGGCT GTGTATTACTGTGCGAGTCTTACTATGGTTCGGGAGGGGGGCCAGG GAACCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCATCGGT CTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG TGTCGTGGAACCTCAGGCGCCCTGACCAGCGGCTGCACACCTTCCC GGCTGTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTG ACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACG TGAATCACAAGCCCAGCAACACCAAGTGGACAAGAGAGTTGAGCC CAAACTCTTGACAAAACCTCACACATGCCACCGTGCCACGACCT GAACCTCCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCA AGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGT GGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTAC GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGG AGCAGTACAACAGCACGTACCGTGTGGTCAAGCTCTCACCGTCTCT GCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCC AACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCA AAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCCATCCCG GGAGGAGATGACCAAGAACCAGGTGACGCTGACCTGCCTGGTCAAA GGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGC AGCCGGAGAACAACCTACAAGACCACGCTCCCGTGTGGACTCCGA CGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGG TGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGATGAGGCTC

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		TGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGGT
158	OX40.11 light chain	GAAATTGTGTTGACGCAGTCTCCAGGCACCCCTGTCTTTGTCTCCAG GGGAAAGAGCCACCCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAG CAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGG CTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACA GGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAG CAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCTCAGCAGTAT GGTAGCTCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCA AACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACCTGCCTCTGTGTGTGCTGTGAAT AACTTCTATCCCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACG CCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAA GCAGACTACGAGAAACACAAAGTCTACGCCTGCCAAGTCACCCATC AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTG T
159	OX40.12 heavy chain	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGA GGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAA CTATGCTCTGCACTGGGTCCCGCAGGCTCCAGGCAAGGGGCTGGAG TGGGTGGCACTTATACTATATAGTGAAGCAGGAAACACTACGCAG ACTCCGTGAAGGGCCGATTCACTATCTCCAGAGACAATCCAAGAA CACACTGTATCTGCAATGAACAGCCTGAGAGCTGAGGACACGGCT GTGTATTACTGTGCGAGTCTTACTATGGTTCCGGAGTGGGGCCAGG GAACCCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGT CTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG TGTCGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCC GGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTG ACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACG TGAATCACAAGCCAGCAACACCAAGGTGGACAAAGAGAGTTGAGCC CAAATCTTGTGACAAACTCACACATGCCACCGTGCCAGCACCT GAACCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCA AGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGT GGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTAC GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCAGTACCGTGTGGTCAAGCTCCTCACCCTCCT GCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGTCTCC AACAAAGCCCTCCAGCCCTCATCGAGAAAACCATCTCCAAAGCCA AAGGGCAGCCCGAGAACACAGGTGTACACCCCTGCCCCCATCCCG GGAGGAGATGACCAAGAACCAGGTCAAGCTGACCTGCCTGGTCAAA GGCTTCTATCCAGCAGACATCGCCGTGGAGTGGGAGAGCAATGGGC AGCCGGAGAACAACTACAAGACCACGCTTCCCGTGTGGACTCCGA CGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGG TGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTC TGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGGT
160	OX40.12 light chain	GAAATTGTGTTGACGCAGTCTCCAGGCACCCCTGTCTTTGTCTCCAG GGGAAAGAGCCACCCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAG CAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGG CTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACA GGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAG CAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCTCAGCAGTAT
		GGTAGCTCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCA AACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACCTGCCTCTGTGTGTGCTGTGAAT AACTTCTATCCCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACG CCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAA GCAGACTACGAGAAACACAAAGTCTACGCCTGCCAAGTCACCCATC AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTG T
161	OX40.13 heavy chain	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGA GGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAA CTATGCTCTGCACTGGGTCCCGCAGGCTCCAGGCAAGGGGCTGGAG TGGGTGGCACTTATACTATATAGTAGCAGGAAACACTACGCAG ACTCCGTGAAGGGCCGATTCACTATCTCCAGAGACAATCCAAGAA CACACTGTATCTGCAATGAACAGCCTGAGAGCTGAGGACACGGCT GTGTATTACTGTGCGAGTCTTACTATGGTTCCGGAGTGGGGCCAGG

SEQ ID	Description	Sequence
		GAACCCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGT CTTCCCCCTGGCACCCCTCCTCCAGAGCACCTCTGGGGGCGACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG TGTCGTGGAAGTCAAGCGCCCTGACCAGCGGCGTGACACCTTCCC GGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTG ACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACG TGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCC CAAACTCTTGACAAAACCTCACACATGCCACCGTGCCAGCACCT GAACCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCA AGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGT GGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTAC GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCTACCGTCTC GCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCC AACAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCA AAGGGCAGCCCCGAGAACCACAGGTGTACACCCCTGCCCCCATCCC GGAGGAGATGACCAAGAACCAGGTGACCGCTGACCTGCTTGGTCAAA GGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGC AGCCGGAGAACAACCTACAAGACCACGCTCCCGTGTGGACTCCGA CGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGG TGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTC TGCACAACCACTACACGCAGAAGAGCTCTCCCTGTCCCCGGGT
162	OX40.13 light chain	GAAATTGTGTTGACGCAGTCTCCAGGCACCCCTGTCTTTGTCTCCAG GGGAAAGAGCCACCCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAG CAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGG CTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCAGACA GGTTCACTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAG CAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTGACAGTAT GGTAGCTCACCATTCACTTTCGGCCCTGGGACCAAGTGGAATATCA AACGTACGGTGGCTGCACCATCTGTCTTCTATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACCTGCCTCTGTGTGTGCTGCTGAAT AACTTCTATCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACG CCCTCCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAA GCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAAGTCAACCATC AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTG
		T
163	OX40.14 heavy chain	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGA GGTCCCTGAGACTCTCCTGTGCAGCCCTCTGGATTACCTTCAGTAA CTATGCTCTGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAG TGGGTGGCACTTATATCATATAGTGAAGCAGGAAACACTACGCAG ACTCCGTGAAGGGCCGATTCACTATCTCCAGAGACAATTCCAAGAA CACACTGTATCTGCAATGAACAGCCTGAGAGCTGAGGACACGGCT GTGTATTACTGTGCGAGTCTTACTTACGTTCCGGAGTGGGGCCAGG GAACCCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGT CTTCCCCCTGGCACCCCTCCTCCAAGAGCACTCTGGGGGACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG TGTCGTGGAACCTCAGCGCCCTGACCAGCGGCGTGCACACCTTCCC GGCTGTCTTACAGTCTCAGGACTCTACTCCTCAGCAGCGTGGTG ACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACG TGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCC CAAACTCTTGACAAAACCTCACACATGCCACCGTGCCAGCACCT GAACCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCA AGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGT GGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTAC GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCTACCGTCTC GCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCC AACAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCA AAGGGCAGCCCCGAGAACCACAGGTGTACACCCCTGCCCCCATCCC GGAGGAGATGACCAAGAACCAGGTGACCGCTGACCTGCTTGGTCAAA GGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGC AGCCGGAGAACAACCTACAAGACCACGCTCCCGTGTGGACTCCGA CGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGG TGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTC TGCACAACCACTACACGCAGAAGAGCTCTCCCTGTCCCCGGGT
164	OX40.14 light chain	GAAATTGTGTTGACGCAGTCTCCAGGCACCCCTGTCTTTGTCTCCAG GGGAAAGAGCCACCCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAG CAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGG CTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCAGACA GGTTCACTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAG

SEQ ID	Description	Sequence
		CAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTAT GGTAGCTCACCATTCACTTTCCGCCCTGGGACCAAAGTGGATATCA AACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCTGCTGAAT AACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACG CCCTCCAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAA GCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATC AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTG T
165	OX40.15 heavy chain	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGA GGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAA CTATGCTCTGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGTGGAG TGGGTGGCACTTATATCATATGATAGTAGCAGGAAACACTACGCAG ACTCCGTGAAGGGCCGATTCACTATCTCCAGAGACAATTCCAAGAA CACACTGTATCTGCAATGAACAGCCTGAGAGCTGAGGACACGGCT
		GTGTATTACTGTGCGAGTCTTACTTACGTTCCGGAGTGGGGCCAGG GAACCTGTGTACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGT CTTCCCTTGGCACCCTCTCCAGAGCACCTCTGGGGCCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCGAACCGGTGACGG TGTCGTGGAAGTCAAGGCGCCTGACCAGCGGCGTGCACACCTTCCC GGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTG ACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACG TGAATCACAAGCCAGCAACACCAAGTGGACAAAGAGAGTTGAGCC CAAACTTGTGACAAAACCTCACACATGCCACCGTCCCGCAGCACCT GAACCTCCTGGGGGACCGTCACTCTTCTCTTCCCGCCAAACCCA AGGACACCCCTCATGATCTCCCGACCCCTGAGGTACATGCGTGGT GGTGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTAC GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGG AGCAGTACAACAGCACGTACCGTGTGGTCAAGCTCCTCAACGTCCT GCACAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCC AACAAAGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAGGCCA AAGGGCAGCCCCGAGAACCACAGGTGTACACCCCTGCCCCCATCCCG GGAGGAGATGACCAAGAACAGGTACGCTGACCTGCCTGGTCAAA GGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGC AGCCGGAGAACAATAACAAGACCACGCTCCCGTGTGACTCCGA CGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGG TGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTC TGACAACCACTACAGCAGAAAGAGCTCTCCCTGTCCCCGGGT
166	OX40.15 light chain	GAAATGTGTTGACGCAGTCTCCAGGCACCCCTGTCTTTGTCTCCAG GGGAAAGAGCCACCCCTCTCCTGCAGGGCCAGTCAGAGTGTAGCAG CAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCAGG CTCCTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCAGACA GGTTCACTGGCAGTGGGTCTGGACAGACTTACTCTCACCATCAG CAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTAT GGTAGCTCACCATTCACTTTCCGCCCTGGGACCAAAGTGGATATCA AACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCTGCTGAAT AACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACG CCCTCCAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAA GCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATC AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTG T
167	OX40.16 heavy chain	GAGGTTCACTGGTGCAGTCTGGGGGAGGCTTGGTTCAAGCCTGGGG GGTCCCTGAGACTCTCCTGTGCAGGCTCTGGATTCACCTTCAGTAG CTATGCTATGTACTGGGTTCCGCCAGGCTCCAGGAAAAGGTCTGGAG TGGGTATCAGCTATTGATACTGATGGTGGCACATTCTATGCAGACT CCGTGCGGGCCGATTCAACATCTCCAGAGACAATGCCAAGAACTC CTTGATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTG TATTTCTGTGCAAGACTTGGGGAAGGGTACTTCTTTGACTACTGGG GCCAGGGAACCCCTGGTCAACGCTCTCCTCAGCTAGCACCAAGGGCC ATCGGTCTTCCCCIGGCACCTCTCTCCAGAGCACCTCTGGGGG ACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCGAACCGG TGACGGTGTCTGGAAGTCAAGGCGCCTGACCAGCGGCGTGCACAC CTTCCCGGCTGTCTACAGTCTCAGGACTTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCT GCAACGTGAATCACAAGCCAGCAACACCAAGTGGACAAGAGACT

SEQ ID	Description	Sequence
		TGAGCCUCAAATCTTTGTGCAAAATCTCACHCATGCUUCCUGTGCCU GCACCTGAACCTCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAA AACCCAAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGGTGGTGGACGTGAGCCACGAAGCCCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGC GGGAGGAGCAGTACAACAGCACGTACCGTGTGCTCAGCGTCTCTAC CGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCTCCAAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCA AAGCCAAAGGGCAGCCCCGAGAACACAGGTGTACACCCCTGCCCC ATCCCGGGAGGAGATGACCAAGAACCAGGTACGCTGACCTGCCTG GTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCA ATGGGCAGCCGGAGAACAACTACAAGACCACGCCCTCCCGTGTGGA CTCCGACGGCTCCTTCTTCTCTATAGCAAGCTACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATG AGGCTCTGCACAACCCTACACGCAGAAGAGCCTCTCCCTGTCCCC GGTTGA
168	OX40.16 light chain (shared by OX40.20, OX40.21, OX40.22)	GAAATTTGTGTGACACAGTCTCCAGCCACCCCTGCTTTGTCTCCAGGGG AAAGAGCCACCCCTCTCTCGAGGGCCAGTCAGAGTGTAGCAGCTACTT AGCCTGGTACCAACAGAAACCTGGCCAGGCTCCAGSCTCCTCATCTAT GATGCATCCAAACAGGGCCACTGGCATCCAGCCAGGTTCAAGTGGCAGTG GGTCTGGGACAGACTTCACCTCTACCATCAGCAGCCTAGAGCCTGAAGA TTTTGCAGTTTATTACTGTGACGAGCGTAGCACTGGCCTCCCACTTTC GGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTG TCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTC TGTTGTGTGCTGTGAAATAACTTCTATCCAGAGAGGCCAAAGTACAG LGGAAGGTGGATAAACCCCTCCAAATCGCGTAACCCAGCAGACTGTCA CAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGAC GCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCTGCGAAGTC ACCCATCAGGGCCTGAGCTCGCCGTACAAAGAGCTTCAACAGGGGAG AGCTTAG
169	OX40.17 heavy chain	GAGGTGCAGCTGCTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGG GGTCCCTGAGACTCTCTGTGACGCCCTCTGGATTACCTTTCAGTAG CTACGACATGCACCTGGGTCCGCCAAACTACAGGAAAAGGTCTGGAG TGGGTCTCAGTTATTGGTACTGCTGGTGACACATACTATCCAGGCT CCGTGAAGGGCCGATTCACCATCTCCAGAGAAAATGCCAAGAACTC CTTGATCTTCAAATGAACAGCCTGAGAGCCGGGGACACGGCTGTG TATTACTGTGCAAGAGGGGGGATGGGGAACACTTTGACTACTGGG GCCAGGGAACCTGTGTCACCGTCTCCTCAGCTAGCACCAAGGGCCC ATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGG ACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGG TGACGGTGTCTGGAACTCAGGCGCCCTGACCAGCGCGTGCACAC CTTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCT GCAACGTGAATCACAGCCAGCAACACCAAGGTGGACAAGAGAGT TGAGCCCAAACTCTGTGACAAAACCTCACACATGCCACCGTGCCCA GCACCTGAACCTCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAA AACCCAAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGGTGGTGGACGTGAGCCACGAAGCCCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGC GGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCTAC CGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCTCCAAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCA AAGCCAAAGGGCAGCCCCGAGAACACAGGTGTACACCCCTGCCCCC
		ATCCCGGGAGGAGATGACCAAGAACCAGGTACGCTGACCTGCCTG GTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCA ATGGGCAGCCGGAGAACAACTACAAGACCACGCCCTCCCGTGTGGA CTCCGACGGCTCCTTCTTCTCTATAGCAAGCTACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATG AGGCTCTGCACAACCCTACACGCAGAAGAGCCTCTCCCTGTCCCC GGTTGA
170	OX40.17 light chain	GAAATTTGTGTGACACAGTCTCCAGCCACCCCTGCTTTGTCTCCAG GGGAAAGAGCCACCCCTCTCTCGAGGGCCAGTCAGAGTGTAGCAG CTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAAGGCTC CTCATCTATGATGCATCCAAACAGGGCCACTGGCATCCAGCCAGGT TCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAG CCTAGAGCCTGAAGATTTGCAAGTTTATTACTGTACGACGCTAGC AACTGGCCGCTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAAC GTACGGTGGCTGCACCATCTGTCTTCACTTCCCGCCATCTGATGA GCAGTTGAAATCTGGAACCTGCCTCTGTGTGTGCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCC TCCAATCGGGTAACCTCCAGGAGAGTGCACAGAGCAGGACAGCA GGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAGCA

SEQ ID	Description	Sequence
		GAUTTTCGAGCAAAACACAAAGTCTACGCGTTCGCAAGTCTCCCTTCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTA G
171	OX40.18 heavy chain	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGG CCTCAGTGAAGGTCTCCTGCAAGGCTTCTGGATACACCTTCACCAG TTATGATGTCAACTGGGTGCGACAGGCCACTGGACAAGGGCTTGAG TGGATGGGATGGATGAACCTTAACAGTGGTAACACAGGCTATGCAC CGAAGTTCAGGGCAGAGTCAACATGACCAGGGACACCTCCATAAG CACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCC GTTTATTACTGTGCGAGAATATATAGCAGCTCGTACAACCTGGTTTCG ACTACTGGGGCCAGGGAACCTGGTCAACGCTCTCCTCAGCTAGCAC CAAGGGCCCATCGGTCTTCCCGCTGGCACCTCCTCCAAGAGCACCC TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCC CCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCCTGACCAGCGG CGTGACACCTTCCCGGCTGTCTACAGTCTCAGGACTCTACTTCC CTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGA CCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGA CAAGAGAGTTGAGCCCAATCTTGTGACAAACTCACACATGCCCA CCGTGCCCAGCACCTGAACCTCTGGGGGGACCGTCAGTCTTCTCTCT TCCCCCAAAACCCAGGACACCTCATGATCTCCCGACCCCTGA GGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTG AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGA CAAAGCCCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTTCAG CGTCTCACCGTCTGACCCAGGACTGGTGAATGGCAAGGAGTAC AAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAA CCATCTCCAAGCCAAAGGGCAGCCCCGAGAACACAGGTGTACAC CCTGCCCCCATCCCCGGGAGGAGATGACCAAGAACCAGGTGACGCTG ACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGT GGGAGAGCAATGGGACGCCGGAGAACAACTACAAGACACGCTCC CGTGCTGGACTCCGACGGCTCTTCTTCTCTATAGCAAGCTCACC GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAAGAGCTCTC
		CCTGTCCCCGGGTGA
172	OX40.18 light chain	GAAATTGTGTTGACACAGTCTCCAGCCACCTGTCTTTGTCTCCAG GGGAAAGAGCCACCTCTCCTGCAGGGCCAGTCAGAGTGTAGCAG CTACTTAGCCTGGTACCAACAGAACTTGCCAGGCTCCCAGGCTC CTCATCTATGATGCATCCAACAGGGCCACTGGCATCCAGCCAGGT TCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAG CCTAGAGCCTGAAGACTTTGCAAGTTTATTACTGTACGACGCTAGC AACTGGCCCTCTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAAC GTACGGTGGCTGCACCATCTGTCTTCACTCTCCGCCATCTGATGA GCAGTTGAAATCTGGAACCTGCTCTGTTGTGCTGCTGAATAAC TTCTATCCAGAGAGGCCAAAGTACAGTGGGAAGGTGGATAACGCCC TCCAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAA GGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAGCA GACTACGAGAAACACAAAGTCTACGCTGCGAAGTCAACCATCAGG GCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTA G
173	OX40.19 heavy chain	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGA GGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACTTCAGTAA CTATGCTCTGCACTGGGTCCGCCAGGCTCCAGGCAAGGGCTGGAG TGGGTGGCACTTATATCATATGATGGAAGCAGGAAACACTACGCAG ACTCCGTGAAGGGCCGATTCAATATCTCCAGAGACAATCCAAGAA CACACTGTATCTGCAATGAACAGCCTGAGAGCTGAGGACACGGCT GTGTATTACTGTGCGAGTCTTACTCTGGTTCCGGAGTGGGGCCAGG GAACCTTGGTACCGTCTCCTCAGTAGCACCAGGGCCCATCGGT CTTCCCCCTGGCACCTCTCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGG TGTGTTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCC GGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTG ACCGTGCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAAGC TGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCC CAAACTCTTGTGACAAACTCACACATGCCACCGTGCCAGCACCT GAACCTCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCA AGGACACCTCATGATCTCCCGACCCCTGAGGTACATGCGTGGT GGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTAC GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAGCCGCGGGAGG AGCAGTACAACAGCACGTACCGTGTGGTTCAGCGTCTCACCCTCCT GCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCC AACAAAGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAGCCA AAGGGCAGCCCCGAGAACACAGGTGTACACCTGCCCCCATCCCG GGAGGAGATGACCAAGAACCAGGTACGCTGACCTGCCTGGTCAAA

SEQ ID	Description	Sequence
		GGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGC AGCCGGGAGAACAACTACAAGACCAGCCTCCCCGTGGACTCCGA CGGCTCCTTCTTCCCTATAGCAAGCTCACCGTGGACAAGAGTAGG TGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATGCATGAGGCTC TGACAACCACTACACGCAGAAGACCTCTCCCTGTCCCCGGGT
174	OX40.19 light chain	GAAATTTGTTGACGCAGTCTCCAGGCACCCGTGCTTTGTCTCCAG GGGAAAGAGCCACCCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAG CAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGG CTCCTCATCTATGGTGCATCCAGCAGGGGCCACTGGCATCCAGACA GGTTCACTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAG CAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTAT
		GGTAGCTCACCATTCACTTTGGGCCCTGGGACCAAAGTGGATATCA AACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGA TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAAT AACTTCTATCCAGAGAGGCCAAAGTACAGTGGAAAGTGGATAACG CCCTCCAATCGGGTAAGTCCAGGAGAGTGTACAGAGCAGGACAG CAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAA GCAGACTACGAGAAACACAAAGTCTACGCCTGCCAAGTCAACCCATC AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTG T
175	OX40.20 heavy chain	GAGGTTCACTGGTGCAGTCTGGGGGAGGCTTGGTTCAAGCCTGGGG GGTCCCTGAGACTCTCCTGTGCAGGCTCTGGATTACCTTCAGTAG CTATGCTATGTACTGGGTTCCGCCAGGCTCCAGGAAAAGGTCTGGAG TGGGTATCAGCTATTGATACTAGTGGTGACATTCTATGCAGACT CCGTGCGGGGCCGATTACCATCTCCAGAGACAATGCCAAGAACTC CTTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTG TATTTCTGTGCAAGACTTGGGGAAGGGTACTTCTTTGACTACTGGG GCCAGGGAACCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCC ATCGGTCTTCCCGCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGC ACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCGCAACCGG TGACGGTGTCTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACAC CTTCCCGGTGTCTTACAGTCTCAGGACTCTACTCCTCAGCAGC GTGGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACCTACATCT GCAACGTGAATCACAGCCAGCAACACCAAGGTGGACAAGAGAGT TGAGCCCAAATCTTGTGACAAAACCTCACATGCCACCCGTGCCCA GCACCTGAACCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAA AACCACAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGC GGGAGGAGCAGTACACAGCACGTACCGTGTGGTCAAGCTCTCAC CGTCTGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAG GTCTCCAACAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCA AAGCCAAAGGGCAGCCCCGAGAACCAAGGTGTACACCCCTGCCCCC ATCCCGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTG GTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCA ATGGGCAGCCGGAGAACAATAAGACCAGCCTCCCGTGTCTGGA CTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAA AGCAGGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATGCATG AGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCC GGGTTGA
---	OX40.20 light chain	SEQ ID NO: 168
176	OX40.21 heavy chain	GAGGTTCACTGGTGCAGTCTGGGGGAGGCTTGGTTCAAGCCTGGGG GGTCCCTGAGACTCTCCTGTGCAGGCTCTGGATTACCTTCAGTAG CTATGCTATGTACTGGGTTCCGCCAGGCTCCAGGAAAAGGTCTGGAG TGGGTATCAGCTATTGATACTAGTGGTGACATTCTATGCAGACT CCGTGCGGGGCCGATTACCATCTCCAGAGACAATGCCAAGAACTC CTTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTG TATTTCTGTGCAAGACTTGGGGAAGGGTACTTCTTTGACTACTGGG GCCAGGGAACCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCC ATCGGTCTTCCCGCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGC ACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCGCAACCGG TGACGGTGTCTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACAC
		CTTCCCGGTGTCTTACAGTCTCAGGACTCTACTCCTCAGCAGC GTGGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACCTACATCT GCAACGTGAATCACAGCCAGCAACACCAAGGTGGACAAGAGAGT TGAGCCCAAATCTTGTGACAAAACCTCACATGCCACCCGTGCCCA

SEQ ID	Description	Sequence
		GCACCTGAACTCTCTGGGSGGACCTGTAGTCTTCTCTTCCCTCCAA AACCCAAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGC GGGAGGAGCAGTACAACAGCAGTACCGTGTGGTCAGCGTCTCTCAC CGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCA AAGCCAAAGGGCAGCCCCGAGAACACAGGTGTACACCCTGCCCCC ATCCCGGAGGAGATGACCAAGAACCAGGTACAGCTGACCTGCCTG GTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCA ATGGGCAGCCGGAGAACAACTACAAGACCACGCCCTCCCGTGTCTGA CTCCGACGGCTCCTTCTTCTCTATAGCAAGCTACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATGCATG AGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCC GGGTTGA
---	OX40.21 light chain	SEQ ID NO: 168
177	OX40.22 heavy chain	GAGGTTGAGCTGGTGCAGTCTGGGGGAGGCTTGGTTAGCCTGGGG GGTCCCTGAGACTCTCCTGTGCAGGCTCTGGATTACCTTCAGTAG CTATGCTATGTACTGGGTTCCGCCAGGCTCCAGGAAAAGGTCTGGAG TGGGTATCAGCTATTGATACTAGTACTGGCACATTCTATGCAGAT CCGTGGCGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAATC CTTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTG TATTTCTGTCAAGACTTGGGGAAGGTACTTCTTTGACTACTGGG GCCAGGGAACCCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCC ATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGC ACAGCGGCCCTGGGCTGCCGTGGTCAAGGACTACTTCCCGAACCAGG TGACGGTGTCTGGAACTCAGGCGCCCTGACCAGCGCGTGCACAC CTTCCCGGTGTCTTACAGTCTCAGGACTCTACTCCCTCAGCAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCT GCAACGTGAATCACAAGCCAGCAACCAAGGTGGACAAGAGAGT TGAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCCA GCACCTGAATCTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAA AACCCAAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGC GGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCTCAC CGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAG GTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCA AAGCCAAAGGGCAGCCCCGAGAACACAGGTGTACACCCTGCCCCC ATCCCGGAGGAGATGACCAAGAACCAGGTACAGCTGACCTGCCTG GTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCA ATGGGCAGCCGGAGAACAACTACAAGACCACGCCCTCCCGTGTCTGA CTCCGACGGCTCCTTCTTCTCTATAGCAAGCTACCGTGGACAAG AGCAGGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATGCATG AGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCCCC GGGTTGA
-	OX40.22 light chain	SEQ ID NO: 168
178	hOX40 epitope	DWSSKPKCPCTWCNLR
179	hOX40 epitope	DSYKPGVDCAPCPPGHFSPGDNQACKPWTNCTLAGK
180	peptide linker	PVGVV
181	sortase A recognition motif	LPXTG, wherein X is any amino acid
182	hOX40 epitope	QNTVCRPCGPGFYNDVVSCKPKCPCTWCNLR
183	hOX40 epitope	PCKPCTWCNLR
184	hOX40 epitope	QLCTATQDTVCR
185	hOX40 epitope	SQNTVCRPCGPGFYND
186	IgG1 C-terminal C _H 1 (same for IgG3 (17-15-15- 15), IgG3 (17-15- 15), IgG3 (17-15), IgG3 (15-15-15), IgG3 (15), and IgG4	VDKRV

SEQ ID	Description	Sequence
187	IgG2 C-terminal C _H 1	VDKTV
188	IgG1 upper hinge	EPKSCDKTHT
189	IgG3 (17-15-15-15) upper hinge (same for IgG3 (17-15-15) and IgG3 (17-15))	ELKTPLGDTTHT
190	IgG3 (15-15-15) upper hinge (same for IgG3(15))	EPKS
191	IgG4 upper hinge	ESKYGPP
192	IgG1 middle hinge	CPPCP
193	IgG2 middle hinge	CCVECPCP
194	IgG3 (17-15-15-15) middle hinge	CPRCP(EPKSCDTPPPCPRCP) ₃
195	IgG3 (17-15-15) middle hinge	CPRCP(EPKSCDTPPPCPRCP) ₂
196	IgG3 (17-15) middle hinge	CPRCP(EPKSCDTPPPCPRCP) ₁
197	IgG3 (15-15-15) middle hinge	CDTPPPCPRCP(EPKSCDTPPPCPRCP) ₂
198	IgG3 (15) middle hinge	CDTPPPCPRCP
199	IgG4 middle hinge	CPSCP
200	IgG1 lower hinge (same for IgG3 (17-15-15-15), IgG3 (17-15-15), IgG3 (17-15), IgG3 (15-15-15), IgG3 (15), and IgG4)	APELLGG
201	IgG2 lower hinge	APPVAG
202	Wildtype human IgG1 CH1	ASTKQPSVFPLAPSSKSTSCSTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYTCNVNHKPSNTKVKDKV
203	Wildtype human IgG2 CH1	ASTKQPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVTPSSNFGTQTYTCNVDHKPSNTKVKDKV
204	Wildtype human IgG1 CH2	PSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT _SKAK
205	Wildtype human IgG2 CH2	PSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHN AKTKPREEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKT _SKTK
206	Wildtype human IgG1 CH3	GQPREPQVYTLPPSRELMTKNQVSLTCLVKCFYPSD_LAVEWESNCPEN NYKTTTPVLDSDGSFFLYSKLTVDKSRWQQCNVFSQSVMEALHNHYTQ KSLSLSPG

SEQ ID	Description	Sequence
207	Wildtype human IgG2 CH3	GQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTTPMLDSDGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYTQ KSLSLSPGK
208	Alternative hinge	ERKCCVECPPCPAPPVAG
209	Alternative hinge	ERKSCVECPPCPAPPVAG
210	Alternative hinge	ERKCSVECPPCPAPPVAG
211	Alternative hinge	ERKXCVECPPCPAPPVAG
212	Alternative hinge	ERKCXVECPPCPAPPVAG
213	Alternative hinge	ERKCCVECPPCPAPPVAGX
214	Alternative hinge	ERKSCVECPPCPAPPVAGX
215	Alternative hinge	ERKCSVECPPCPAPPVAGX
216	Alternative hinge	ERKXCVECPPCPAPPVAGX
217	Alternative hinge	ERKCXVECPPCPAPPVAGX
218	Alternative hinge	ERKCCVECPPCPAPELLGG
219	Alternative hinge	ERKSCVECPPCPAPELLGG
220	Alternative hinge	ERKCCSVECPPCPAPELLGG
221	Alternative hinge	ERKXCVECPPCPAPELLGG
222	Alternative hinge	ERKCXVECPPCPAPELLGG
223	Alternative hinge	ERKCCVECPPCPAPELLG
224	Alternative hinge	ERKSCVECPPCPAPELLG
225	Alternative hinge	ERKCCSVECPPCPAPELLG
226	Alternative hinge	ERKXCVECPPCPAPELLG
227	Alternative hinge	ERKCXVECPPCPAPELLG
228	Alternative hinge	ERKCCVECPPCPAP
229	Alternative hinge	ERKSCVECPPCPAP
230	Alternative hinge	ERKCSVECPPCPAP
231	Alternative hinge	ERKXCVECPPCPAP
232	Alternative hinge	ERKCXVECPPCPAP
233	Portion of hinge	PVAG
234	Portion of hinge	ELLG
235	Portion of hinge	ELLGG
236	Portion of hinge	SCDKTHT
237	Portion of hinge	CCVE
238	WT human IgG2 hinge	ERKCCVECPPCPAPPVAG
239	Human IgG2 hinge with C219S	ERKSCVECPPCPAPPVAG
240	IgG2/IgG1 hinge	ERKCCVECPPCPAPELLGG
241	IgG2 (C219S)/IgG1 hinge	ERKSCVECPPCPAPELLGG
242	Wild type human IgG1 hinge	EPKSCDKTHTCPPCPAPELLGG
243	Human IgG1 CH2 with A330S/P331S	PSVFLFPPKPKDITLMSRCPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPREEQYNSTYRVVSVLTVLDQDLNKGKEYKCKVSNKALPSSIEKT ISKAK

SEQ ID	Description	Sequence
244	IgG1-IgG2-IgG1f	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKV ERKCCVCECPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVDS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
245	IgG1-IgG2-IgG1f2	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKV ERKCCVCECPPCPAPEFVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
246	IgG1-IgG2CS-IgG1f	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKV ERKCCVCECPPCPAPEFVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
247	IgG 1-IgG2CS-IgG1f2	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKV ERKCCVCECPPCPAPEFVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
248	IgG2-IgG1f	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVTPSSNFGTQTYICNVDHKPSNTKVDKTV ERKCCVCECPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
249	IgG2-IgG1f2	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVTPSSNFGTQTYICNVDHKPSNTKVDKTV ERKCCVCECPPCPAPEFVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
250	IgG2CS-IgG1f	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVTPSSNFGTQTYICNVDHKPSNTKVDKTV ERKCCVCECPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
251	IgG2CS-IgG1f2	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVTPSSNFGTQTYICNVDHKPSNTKVDKTV ERKCCVCECPPCPAPEFVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
252	IgG1-IgG2-IgG1.1f	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKV

SEQ ID	Description	Sequence
		VHTTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRV ERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVHLQDNLNGK EYKCKVSNKALPSSIEKTIISKAKGQPREPQVYTLPPSRREMTKNQVSLT CLVKGFIYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKKS RWQQGNVFSQSVMHREALHNYHTQKSLSLSPG
253	IgG1-IgG2CS-IgG1.1f	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRV ERKSCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVHLQDNLNGK EYKCKVSNKALPSSIEKTIISKAKGQPREPQVYTLPPSRREMTKNQVSLT CLVKGFIYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKKS RWQQGNVFSQSVMHREALHNYHTQKSLSLSPG
254	IgG2-IgG1.1f	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTV ERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVHLQDNLNGK EYKCKVSNKALPSSIEKTIISKAKGQPREPQVYTLPPSRREMTKNQVSLT CLVKGFIYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKKS RWQQGNVFSQSVMHREALHNYHTQKSLSLSPG
255	IgG2CS-IgG1.1f	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTV ERKSCVECPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVHLQDNLNGK KEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRREMTKNQVSL TCLVKGFIYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSQSVMHREALHNYHTQKSLSLSPG
256	IgG1f	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVHLQDNL NGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRREMTKNQ VSLTCLVKGFIYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSQSVMHREALHNYHTQKSLSLSPG
257	IgG1.1f	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRV EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVHLQDNL NGKEYKCKVSNKALPSSIEKTIISKAKGQPREPQVYTLPPSRREMTKNQ VSLTCLVKGFIYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT VDKSRWQQGNVFSQSVMHREALHNYHTQKSLSLSPG
258	IgG2.3	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTV ERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVHLQDNLNGK KEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRREMTKNQVSL TCLVKGFIYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSQSVMHREALHNYHTQKSLSLSPG
259	IgG2.5	ASTKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTV ERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVHLQDNLNGK KEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRREMTKNQVSL TCLVKGFIYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSQSVMHREALHNYHTQKSLSLSPG
260	IgG2.3G1-KH	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTV ERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVHLQDNLNGK KEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRREMTKNQVSL TCLVKGFIYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK SRWQQGNVFSQSVMHREALHNYHTQKSLSLSPG

SEQ ID	Description	Sequence
		LTVLHODWLNKKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSL SPGK
261	IgG2.5G1-KH	ASTKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVPSNFQTQYTCNVDHKPSNT KVDKTVERKCCVECPFCPPAVAGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPREEQYNSTYRVVSV LTVLHODWLNKKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSL SPGK
262	IgG2.3G1-AY	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVPSNFQTQYTCNVDHKPSNT KVDKTVERKSCVECPFCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPREEQYNSTYRVVSV VLTVLHODWLNKKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLSDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSL LSPGK
263	IgG2.5G1-AY	ASTKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVPSNFQTQYTCNVDHKPSNT KVDKTVERKCCVECPFCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPREEQYNSTYRVVSV VLTVLHODWLNKKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLSDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSL LSPGK
264	IgG2.3G1.1f-KH	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVPSNFQTQYTCNVDHKPSNT KVDKTVERKSCVECPFCPPAVAGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPREEQYNSTYRVVSV LTVLHODWLNKKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSL SPGK
265	IgG2.5G1.1f-KH	ASTKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVTVPSNFQTQYTCNVDHKPSNT KVDKTVERKCCVECPFCPPAVAGPSVFLFPPKPKDTLMISRTPEV TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPREEQYNSTYRVVSV LTVLHODWLNKKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSL SPGK
266	IgG2.5G1-V27	ASTKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSNFQTQYTCNVDHKPSNTKVDKTV ERKCCVECPFCPAPELLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPR EEQYNSTYRVVSVLTVLHODWLNKKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN YKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQK SLSLSPGK
267	IgG2.3-V13	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSNFQTQYTCNVDHKPSNTKVDKTV ERKSCVECPFCPPAVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHODWLNK EYKCKVSNKGLPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTPMLDSDGSFFLYSKLTVDKS RWQQGNVSCSVMHEALHNHYTQKSLSLSPGK
268	IgG2.3-V14	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG

SEQ ID	Description	Sequence
		TISTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG VHTEPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTV ERKSCVCECPPCPAPPVAGDSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDGEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGK EYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTTPMLDSGDSFFLYSKLTVDKKS RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
269	IgG2.3-V15	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG VHTEPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTV ERKSCVCECPPCPAPPVAGDSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDGEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGK EYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTTPMLDSGDSFFLYSKLTVDKKS RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
270	IgG2.3-V16	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG VHTEPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTV ERKSCVCECPPCPAPPVAGDSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDGEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGK EYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTTPMLDSGDSFFLYSKLTVDKKS RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
271	IgG2.3-V17	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG VHTEPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTV ERKSCVCECPPCPAPPVAGDSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDGEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGK EYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTTPMLDSGDSFFLYSKLTVDKKS RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
272	IgG2.3-V18	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG VHTEPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTV ERKSCVCECPPCPAPPVAGDSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGK EYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTTPMLDSGDSFFLYSKLTVDKKS RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
273	IgG2.3-V19	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG VHTEPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTV ERKSCVCECPPCPAPPVAGDSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGK EYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLT CLVKGFYPSDIAVEWESNGQPENNYKTTTPMLDSGDSFFLYSKLTVDKKS RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
274	IgG2.3G1-AY-V20	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG VHTEPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTV ERKSCVCECPPCPAPPELLGGDSVFLFPPKPKDTLMISRTPEVTCVVDVSH HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
275	IgG2.3G1-AY-V21	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG VHTEPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTV ERKSCVCECPPCPAPPELLGGDSVFLFPPKPKDTLMISRTPEVTCVVDVSH HEDGEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
276	IgG2.3G1-AY-V22	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG VHTEPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTV ERKSCVCECPPCPAPPELLGGDSVFLFPPKPKDTLMISRTPEVTCVVDVSH HEDGEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDK SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID	Description	Sequence
		TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK SRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
277	IgG2.3G1-AY-V23	ASTKQPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG VHTEPAVLQSSGLYSLSSVTVPSSENGFTQTYTCNVDHKPSNTKVDTV ERKSCVECPGPCPAPELLGGDSVFLFPPKPKDTLMISRTPEVTCVVDVS HEDGEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPKEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK SRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
278	IgG2.3G1-AY-V24	ASTKQPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG VHTEPAVLQSSGLYSLSSVTVPSSENGFTQTYTCNVDHKPSNTKVDTV ERKSCVECPGPCPAPELLGGDSVFLFPPKPKDTLMISRTPEVTCVVDVS HEDGEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPKEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK SRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
279	IgG2.3G1-AY-V25	ASTKQPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG VHTEPAVLQSSGLYSLSSVTVPSSENGFTQTYTCNVDHKPSNTKVDTV ERKSCVECPGPCPAPELLGGDSVFLFPPKPKDTLMISRTPEVTCVVDVS HEDGEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPKEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK SRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
280	IgG2.3G1-AY-V26	ASTKQPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG VHTEPAVLQSSGLYSLSSVTVPSSENGFTQTYTCNVDHKPSNTKVDTV ERKSCVECPGPCPAPELLGGDSVFLFPPKPKDTLMISRTPEVTCVVDVS HEDGEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPKEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK SRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
281	IgG2.3G1-AY-V28	ASTKQPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG VHTEPAVLQSSGLYSLSSVTVPSSENGFTQTYTCNVDHKPSNTKVDTV ERKSCVECPGPCPAPELLGGDSVFLFPPKPKDTLMISRTPEVTCVVDVS HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPKEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK SRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
282	OX40.6-Vh-hHC-IgG2.3	EVQLVQSGGGVLPQGGSLRLSCAGSGFTFSNYAMYWVRQAPGKLEWVS AIGIGSDIFYTDSVKGRTTISRDNKNSLQMNSLRAEDTAVYYCARM GTGYFFDYWQQGTLVTVSSASTKQPSVFPLAPCSRSTSESTAALGCLVK DYFPEPVTVSWNSGALTSGVHTEPAVLQSSGLYSLSSVTVPSSENGFTQ TYTCNVDHKPSNTKVDTVERKSCVECPGPCAPPVAGPSVFLFPPKPKD TLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNS TFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPKEKTIISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP MLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSP GK
283	OX40.8-Vh-hHC-IgG2.3	QVQLVQSGGGVLPQGRSLRLSCAASGFTFSNYALHWVRQAPGKLEWVA LISYDCSRKHAYDSVKGRFSTISRDNKNTLYLQMNSLRAEDTAVYYCAS LTMVREWQGGTLVTVSSASTKQPSVFPLAPCSRSTSESTAALGCLVKD YFPEPVTVSWNSGALTSGVHTEPAVLQSSGLYSLSSVTVPSSENGFTQ TYTCNVDHKPSNTKVDTVERKSCVECPGPCAPPVAGPSVFLFPPKPKD TLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNS TFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPKEKTIISKAKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP MLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSP GK
284	OX40.16-Vh-hHC-IgG2.3	EVQLVQSGGGVLPQGGSLRLSCAGSGFTFSNYAMYWVRQAPGKLEWVS ALDTDGGTIFYADSVRGRTTISRDNKNSLYLQMNSLRAEDTAVYYCARL GEGYFFDYWQQGTLVTVSSASTKQPSVFPLAPCSRSTSESTAALGCLVK DYFPEPVTVSWNSGALTSGVHTEPAVLQSSGLYSLSSVTVPSSENGFTQ TYTCNVDHKPSNTKVDTVERKSCVECPGPCAPPVAGPSVFLFPPKPKD

SEQ ID	Description	Sequence
		LTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQFNSTFRVYVSVLTIVHQDNLNGKEYCKVSNKGLPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPMLDSDCGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK
285	OX40.6-Vh-hHC-IgG2.3G1	EVQLVQSGGGGLVQPGGSLRLSCAAGSFTFSNYAMYWVRQAPGKGLEWVSALIGGSDTFYTDVSVKGRFTISRDNANKNSLSLQMNSLRAEDTAVYYCARMCTCYFFFDYWGQCTILVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSNFGTQTYTCNVDHKPSNTKVDKTVERRKSCVECPPEAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTIVLHQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDCGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK
286	OX40.8-Vh-hHC-IgG2.3G1	QVQLVESGCGGVVQPGKSLRLSCAASGFTFSNYALHWVRQAPGKGLEWVALISYDGSRKHYADSVKGRFISRDNANKNTLYLQMNSLRAEDTAVYYCASLTMVREWQCGCTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSNFGTQTYTCNVDHKPSNTKVDKTVERRKSCVECPPEAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTIVLHQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDCGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK
287	OX40.16-Vh-hHC-IgG2.3G1	EVQLVQSGGGGLVQPGGSLRLSCAAGSFTFSNYAMYWVRQAPGKGLEWVSALDIDGGTFYADSVRGRFTISRDNANKNSLYLQMNSLRAEDTAVYFCARLGEGYFFFDYWGQCTILVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSNFGTQTYTCNVDHKPSNTKVDKTVERRKSCVECPPEAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTIVLHQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDCGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK
288	OX40.6-Vh-hHC-IgG2.3G1-V27	EVQLVQSGCGGLVQPGGSLRLSCAAGSFTFSNYAMYWVRQAPGKGLEWVSALIGGSDTFYTDVSVKGRFTISRDNANKNSLSLQMNSLRAEDTAVYYCARMCTCYFFFDYWGQCTILVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSNFGTQTYTCNVDHKPSNTKVDKTVERRKSCVECPPEAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTIVLHQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDCGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK
289	OX40.8-Vh-hHC-IgG2.3G1-V27	QVQLVESGCGGVVQPGKSLRLSCAASGFTFSNYALHWVRQAPGKGLEWVALISYDGSRKHYADSVKGRFISRDNANKNTLYLQMNSLRAEDTAVYYCASLTMVREWQCGCTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSNFGTQTYTCNVDHKPSNTKVDKTVERRKSCVECPPEAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTIVLHQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDCGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK
290	OX40.16-Vh-hHC-IgG2.3G1-V27	EVQLVQSGCGGLVQPGGSLRLSCAAGSFTFSNYAMYWVRQAPGKGLEWVSALDIDGGTFYADSVRGRFTISRDNANKNSLYLQMNSLRAEDTAVYFCARLGEGYFFFDYWGQCTILVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSNFGTQTYTCNVDHKPSNTKVDKTVERRKSCVECPPEAPPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTIVLHQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDCGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPGK
291	OX40.6-Vh-hHC-	

SEQ ID	Description	Sequence
	IgG2.5	EVQLVQSGGGLVQPCCSLRLSCAGSGFTFSNYAMYWVRQAPGKGLEWVS A ₁ GLGGDIFYTDSVKGRFTISRDNAKNSLSLQMNSLRAEDTAVYYCARM GEGYFFDYWGQGITLVTVSSASTKGPSVFPLAPSSRSTSESTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSNFGTQ TYTCNVDHKPSNTKVDKTVKRCCECPAPCPAPVAGPSVFLFPPKPKD TLMISRTPEVTCVVDVSHEDPEVQFNWYVDCGEVHNAKTKPREEQFNS TFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP MLDSDGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSP GK
292	OX40.8-Vh-hHC-IgG2.5	QVQLVESGGGVVQPGRSRLRLSCAASGFTFSNYALHWVRQAPGKGLEWVA LISYDGSRRKHYSVKGSRFTISRDNASKNTLYLQMNSLRAEDTAVYYCAS LTMVREWCQCTLVTVSSASTKGPSVFPLAPSSRSTSESTAALGCLVKDY FPPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSNFGTQTY TCNVDHKPSNTKVDKTVKRCCECPAPCPAPVAGPSVFLFPPKPKDTL MISRTPEVTCVVDVSHEDPEVQFNWYVDCGEVHNAKTKPREEQFNS TFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQV YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPML DSDGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK
293	OX40.16-Vh-hHC-IgG2.5	EVQLVQSGGGLVQPCCSLRLSCAGSGFTFSNYAMYWVRQAPGKGLEWVS A ₁ DTDGGTIFYADSVRGRTISRDNAKNSLYLQMNSLRAEDTAVYFCARL GEGYFFDYWGQGITLVTVSSASTKGPSVFPLAPSSRSTSESTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSNFGTQ TYTCNVDHKPSNTKVDKTVKRCCECPAPCPAPVAGPSVFLFPPKPKD TLMISRTPEVTCVVDVSHEDPEVQFNWYVDCGEVHNAKTKPREEQFNS TFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP MLDSDGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSP GK
294	OX40.21-Vh-hHC-IgG2.5	EVQLVQSGGGLVQPCCSLRLSCAGSGFTFSNYAMYWVRQAPGKGLEWVS A ₁ DTDAGTIFYADSVRGRTISRDNAKNSLYLQMNSLRAEDTAVYFCARL GEGYFFDYWGQGITLVTVSSASTKGPSVFPLAPSSRSTSESTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSNFGTQ TYTCNVDHKPSNTKVDKTVKRCCECPAPCPAPVAGPSVFLFPPKPKD TLMISRTPEVTCVVDVSHEDPEVQFNWYVDCGEVHNAKTKPREEQFNS TFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQ VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP MLDSDGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSP GK
295	OX40.21-Vh-hHC-IgG2.5G1	EVQLVQSGGGLVQPCCSLRLSCAGSGFTFSNYAMYWVRQAPGKGLEWVS A ₁ DTDAGTIFYADSVRGRTISRDNAKNSLYLQMNSLRAEDTAVYFCARL GEGYFFDYWGQGITLVTVSSASTKGPSVFPLAPSSRSTSESTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSNFGTQ TYTCNVDHKPSNTKVDKTVKRCCECPAPPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVDVSHEDPEVKFNWYVDCGEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP PVLDSDGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLS PGK
296	OX40.21-Vh-hHC-IgG2.5G1-V27	EVQLVQSGGGLVQPCCSLRLSCAGSGFTFSNYAMYWVRQAPGKGLEWVS A ₁ DTDAGTIFYADSVRGRTISRDNAKNSLYLQMNSLRAEDTAVYFCARL GEGYFFDYWGQGITLVTVSSASTKGPSVFPLAPSSRSTSESTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSNFGTQ TYTCNVDHKPSNTKVDKTVKRCCECPAPPELLGGPSVFLFPPKPK DTLMISRTPEVTCVVDVSHEDPEVKFNWYVDCGEVHNAKTKPREEQYN STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP PVLDSDGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLS PGK
297	IgG2.3G1-V27	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSG VHTFPAVLQSSGLYSLSSVTVPSNFGTQTYTCNVDHKPSNTKVDKTV KRCCECPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH EDPEVKFNWYVDCGEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDK SRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK

SEQ ID	Description	Sequence
298	Human IgG1 CH2 with A330S/P331S	PSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEY KCKVSNKALPSSIEKTIKAK
299	Heavy chain - nivolumab	<u>QVQLVESGGGVVQPGRSLRLDCKASGITFSNSGMHWVRQAPCKGL</u> <u>EWVAVFWYDGSKRYADSVKGRFTISRDN SKNTLFLQMNSLRAEDT</u> <u>AVYYCATNDDYWGQCTLVTVSSASTKGPSVFPLAPCSRSTSESTA</u> <u>LGCLVKDYFPEFVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT</u> <u>VPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPCCPAPAEFLG</u> <u>GPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG</u> EVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK LPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEGNV FSCSVMEALHNHYTQKSLSLGLK
300	Light chain - nivolumab	<u>EVLVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPKQAPRLLI</u> <u>YDASNRATGIPARFSGSGSGTDFTLTITSSLEPEDFAVYYCQQSSNWPR</u> <u>TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA</u> <u>KVQWKNVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHK</u> <u>VYACEVTHQGLSPVTKSFNRGEC</u>
301	Heavy chain variable region - nivolumab	QVQLVESGGGVVQPGRSLRLDCKASGITFSNSGMHWVRQAPGKLEWVA VFWYDGSKRYADSVKGRFTISRDN SKNTLFLQMNSLRAEDTAVYYCAT NDDYWGQCTLVTVSS
302	Light chain variable region - nivolumab	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPKQAPRLLIY DASNRATGIPARFSGSGSGTDFTLTITSSLEPEDFAVYYCQQSSNWPRIF FGQGTKVEIK
303	HCDR1 - nivolumab	NSGMH
304	HCDR2 - nivolumab	VIWYDGSKRYADSVKG
305	HCDR3 - nivolumab	NDDY
306	LCDR1 - nivolumab	RASQSVSSYLA
307	LCDR2 - nivolumab	DASNRAT
308	LCDR3 - nivolumab	QQSSNWPR
309	Heavy chain variable region - ipilimumab (from WO01/014424)	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSTMHWRQAPGKLEWVT FISYDGNKKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCAR TCWLCPFDYWGQCTLVTVSS
310	Light chain variable region - ipilimumab (from WO01/014424)	EIVLTQSPCTLSLSPGERATLSCRASQSVSSYLAWYQQKPKQAPRLLI YGAFTSRATGLPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSPPW FGQGTKVEIK
311	HCDR1 - ipilimumab (from WO01/014424)	SYTMH
312	HCDR2 - ipilimumab (from WO01/014424)	FISYDGNKKYYADSVKG
313	HCDR3 - ipilimumab (from	TGWLGPFDY

SEQ ID	Description	Sequence
	WO01/014424)	
314	LCDR1 - ipilimumab (from WO01/014424)	RASQSVGSSYLA
315	LCDR2 - ipilimumab (from WO01/014424)	GAFSRAT
316	LCDR3 - ipilimumab (from WO01/014424)	QQYGSSPWT
317	HCDR2 of OX40.21	AIDTDAGTFYADSVRG
318	VH of OX40.21	EVQLVQSGGGLVQPGGSLRLSCAGSGFTFSSYAMYWVRQAPGKGLE WVSAIDTDAGTFYADSVRGREFTISRDNAKNSLYLQMNSLRAEDTAV YFCARLGEgyFFDYWGQGLVTVSS

[0688] Table 23 provides the sequences of the mature variable regions and heavy and light chains and where indicated, sequences with signal peptides.

Equivalents:

[0689] Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents of the specific embodiments disclosed herein.

REFERENCES CITED IN THE DESCRIPTION

Cited references

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ANTISTOFFER MOD OX40 OG ANVENDELSER DERAFT

PATENTKRAV

1. Isoleret monoklonalt antistof, der binder til humant OX40, hvor antistoffet omfatter et variabelt område af tungkæden omfattende sekvensen ifølge SEQ ID NO: 318 og et variabelt område af letkæden
- 5 omfattende sekvensen ifølge SEQ ID NO: 94.
2. Antistof ifølge krav 1, hvor antistoffet omfatter en tungkæde omfattende sekvensen ifølge SEQ ID NO: 124 og en letkæde omfattende sekvensen ifølge SEQ ID NO: 116.
3. Antistof ifølge krav 1, hvor antistoffet omfatter konstante tung- og letkædeområder.
4. Antistof ifølge et hvilket som helst af kravene 1-3, hvor det konstante tungkædeområde mangler et
- 10 C-terminalt lysin.
5. Antistof ifølge et hvilket som helst af kravene 1-4, hvor antistoffet stimulerer et antigenspecifikt T-cellerespons.
6. Antistof ifølge et hvilket som helst af kravene 1-5, hvor antistoffet binder til opløseligt, humant OX40 med en KD på 10 nM eller mindre, målt ved Biacore.
- 15 7. Antistof ifølge et hvilket som helst af kravene 1-6, hvor antistoffet binder til hele eller en del af sekvensen DVVSSKPKCTWCNLR (SEQ ID NO: 178) af humant OX40 (SEQ ID NO: 2).
8. Antistof ifølge et hvilket som helst af kravene 1-7, der er en IgG1-isotype.
9. Antistof ifølge et hvilket som helst af kravene 1-8, der er et humant antistof.
10. Nukleinsyre, der koder for det variable tung- og letkædeområde af antistoffet ifølge et hvilket som
- 20 helst af kravene 1-9.
11. Ekspressionsvektor, der omfatter nukleinsyren ifølge krav 10.
12. Celle transformeret med (i) ekspressionsvektoren ifølge krav 11 eller (ii) en ekspressionsvektor omfattende nukleinsyren, der koder for det variable område af tungkæden af antistoffet ifølge et hvilket som
- 25 helst af kravene 1-9, og en separat ekspressionsvektor, der omfatter nukleinsyren, der koder for det variable område af letkæden af antistoffet ifølge et hvilket som helst af kravene 1-9.
13. Farmaceutisk sammensætning, der omfatter antistoffet ifølge et hvilket som helst af kravene 1-9 og en bærer.
14. Farmaceutisk sammensætning ifølge krav 13, der endvidere omfatter mindst et andet anticancermiddel.
- 30 15. Farmaceutisk sammensætning ifølge krav 14, hvor det mindst ene andet anticancermiddel vælges fra gruppen bestående af: et anti-PD-1-antistof og et CTLA-4-antistof.
16. Antistof ifølge et hvilket som helst af kravene 1-9 til anvendelse i en fremgangsmåde til behandling af cancer hvor fremgangsmåden omfatter indgivelse af antistoffet til et individ.
17. Farmaceutisk sammensætning ifølge et hvilket som helst af kravene 13-15 til anvendelse i en
- 35 fremgangsmåde til behandling af cancer, hvor fremgangsmåden omfatter indgivelse af sammensætningen til et individ.

- 2 -

18. Antistof til anvendelse ifølge krav 16 eller sammensætning til anvendelse ifølge krav 17, hvor canceren vælges fra gruppen bestående af: cervixcancer, colorektal cancer, blærecancer og ovariecancer.
19. Farmaceutisk sammensætning, der omfatter antistoffet ifølge et hvilket som helst af kravene 1-9, og anti-PD-1-antistoffet nivolumab til anvendelse i en fremgangsmåde til behandling af cancer, hvor
5 fremgangsmåden omfatter indgivelse af sammensætningen til et individ.
20. Farmaceutisk sammensætning, der omfatter antistoffet ifølge et hvilket som helst af kravene 1-9, og anti-CTLA-4-antistoffet ipilimumab til anvendelse i en fremgangsmåde til behandling af cancer, hvor fremgangsmåden omfatter indgivelse af sammensætningen til et individ.
21. Antistof til anvendelse ifølge krav 16, hvor fremgangsmåden endvidere omfatter indgivelse af anti-
10 PD-1-antistoffet nivolumab til individet.
22. Antistof til anvendelse ifølge krav 16, hvor fremgangsmåden endvidere omfatter indgivelse af anti-CTLA-4- antistoffet ipilimumab til individet.

DRAWINGS

Anti-OX40 3F4 VH (hIgG1)

V segment: 1-08

D segment: 6-6

J segment: JH5b

1	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S
	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GCT	GAG	GTG	AAG	AAG	CCT	GGG	GCC	TCA
	CDR1																
52	V	K	V	S	C	K	A	S	G	N	T	F	T	S	Y	D	V
	GIG	AAG	GTC	TCC	TGC	AAG	GCT	TCT	GGA	AAC	ACC	TTC	ACC	AGT	TAT	GAT	GTC
	CDR2																
103	N	W	V	R	Q	A	T	G	Q	G	L	E	W	M	G	W	M
	AAC	TGG	GIG	CGA	CAG	GCC	ACT	GGA	CAA	GGG	CTT	GAG	TGG	ATG	GGA	TGG	ATG
154	N	P	N	S	G	N	T	G	Y	A	P	K	F	Q	G	R	V
	AAC	CCT	AAC	AGT	GGT	AAC	ACA	GGC	TAT	GCA	CCG	AAG	TTC	CAG	GGC	AGA	GTC
205	T	M	T	R	N	T	S	T	S	T	A	Y	M	E	L	S	S
	ACC	ATG	ACC	AGG	AAC	ACC	TCC	ATA	AGC	ACA	GCC	TAC	ATG	GAG	CTG	AGC	AGC
	CDR3																
256	L	R	S	E	D	T	A	V	Y	Y	C	A	R	I	Y	S	S
	CTG	AGA	TCT	GAG	GAC	ACG	GCC	GTT	TAT	TAC	TGT	GCG	AGA	ATA	TAT	AGC	AGC
307	S	Y	N	W	F	D	P	W	G	Q	G	T	L	V	T	V	S
	TCG	TAC	AAC	TGG	TTC	GAC	CCC	TGG	GGC	CAG	GGA	ACC	CTG	GTC	ACC	GTC	TCC
358	S																
	TCA																

Figure 1A

Anti-OX40 3F4 VK (hKappa)

V segment: L6

J segment: JK4

```

      E   I   V   L   T   Q   S   P   A   T   L   S   L   S   P   G   E
1    GAA ATT GTG TTG ACA CAG TCT CCA GCC ACC CTG TCT TTG TCT CCA GGG GAA

      _CDR1_
      R   A   L   L   S   C   R   A   S   Q   S   V   S   S   Y   L   A
52   ACA GCC ACC CTC TCC TGC AGC GCC ACT CAG ACT GTT AGC ACC TAC TTA GCC

      _CDR2_
      W   Y   Q   Q   K   P   G   Q   A   P   R   L   L   I   Y   D   A
103  TGG TAC CAA CAG AAA CCT GGC CAG GCT CCC AGG CTC CTC ATC TAT GAT GCA

      S   N   R   A   T   G   I   P   A   R   F   S   G   S   G   S   G
154  TCC AAC AGG GCC ACT GGC ATC CCA GCC AGG TTC AGT GGC AGT GGG TCT GGG

      L   D   F   T   L   T   I   S   S   L   E   P   E   D   F   A   V
205  ACA GAC TTC ACT CTC ACC ATC AGC AGC CTA GAG CCT GAA GAT TTT GCA GTT

      _CDR3_
      Y   Y   C   Q   Q   R   S   N   W   P   L   T   F   G   G   G   T
256  TAT TAC TGT CAG CAG CGT AGC AAC TGG CCT CTC ACT TTC GGC GGA GGG ACC

      K   V   E   L   K
307  AAG GTG GAG ATC AAA

```

Figure 1B

Anti-OX40 14B6 VH (hIgG1)

V segment: 5-51

D segment: 3-9

J segment: JH2

```

      E   V   Q   L   E   Q   S   G   A   E   V   K   K   P   G   E   S
1    GAG GTG CAG CTG GAG CAG TCT GGA GCA GAG GTG AAA AAG CCC GGG GAG TCT

      L   K   I   S   C   K   G   S   G   Y   S   F   T   S   N   W   I
52   CTG AAG ATC TCC TGT AAG GGT TCT GGA TAC AGC TTT ACC AGC AAC TGG ATC

      G   W   V   R   Q   M   P   G   K   G   L   E   W   M   G   F   I
103  GGC TGG GTG CGC CAG ATG CCC GGG AAA GGC CTG GAG TGG ATG GGG TTC ATC

      Y   P   G   D   S   D   T   R   Y   S   P   S   F   Q   G   Q   V
154  TAT CCT GGT GAC TCT GAT ACC AGG TAC AGC CCG TCC TTC CAA GGC CAG GTC

      T   I   S   A   D   K   S   I   S   T   A   Y   L   Q   W   S   S
205  ACC ATC TCA GCC GAC AAG TCC ATC AGC ACC GCC TAC CTG CAG TGG AGC AGC

      L   K   A   S   D   I   A   M   Y   Y   C   A   R   Y   G   D   D
256  CTC AAG GCC TCG GAC ATC GCC ATG TAT TAC TGT GCG AGA TAT GGG GAT GAC

      W   Y   F   D   L   W   G   R   G   T   L   V   T   V   S   S
      TGG TAC TTC GAT CTC TGG GGC CGT GGC ACC CTG GTC ACT GTC TCC TCA

```

Figure 2A

Anti-OX40 14B6 VK1 (hKappa)

V segment: L6

J segment: JK5

```

      E   I   V   L   T   Q   S   P   A   T   L   S   L   S   P   G   E
1    GAA ATT CTG TTG ACA CAG TCT CCA GCC ACC CTG TCT TTG TCT CCA GCG GAA

      _CDR1_
      R   A   T   L   S   C   R   A   S   Q   S   V   S   S   Y   L   A
52   AGA GCC ACC CTC TCC TGC AGG GCC AGT CAG AGT GTT AGC AGC TAC TTA GCC

      _CDR2_
      W   F   Q   Q   R   P   G   Q   A   P   R   L   L   I   Y   D   A
103  TGG TTC CAA CAG AGA CCT GGC CAG GCT CCC AGG CTC CTC ATC TAT GAT GCA

      S   N   R   A   T   G   I   P   A   R   F   S   G   S   G   S   G
154  TCC AAC AGG GCC ACT GGC ATC CCA GCC AGG TTC AGT GGC AGT GGG TCT GGG

      T   D   F   S   L   T   I   S   S   L   E   P   E   D   F   A   V
205  ACA GAC TTC TCT CTC ACC ATC AGC AGC CTA GAG CCT GAA GAT TTT GCA GTT

      _CDR3_
      Y   Y   C   Q   Q   R   G   D   W   P   I   T   F   G   Q   G   T
256  TAT TAC TGT CAG CAC CGT GGC GAC TGG CCC ATC ACC TTC GCG CAA GCG ACA

      R   L   E   T   K
307  CGA CTG GAG ATT AAA

```

Figure 2B

Anti-OX40 14B6 VK2 (hKappa)

V segment: L15

J segment: JK5

```

      D   L   Q   M   T   Q   S   P   S   S   L   S   A   S   V   G   D
1    GAC ATC CAG ATG ACC CAG TCT CCA TCC TCA CTG TCT GCA TCT GTA GGA GAC

      _CDR1_
      R   V   T   T   T   C   R   A   S   Q   G   I   S   S   W   L   A
52   AGA GTC ACC ATC ACT TGT CGG GCG AGT CAG GGT ATT AGC AGC TGG TTA GCC

      _CDR2_
      W   Y   Q   Q   K   P   E   K   A   P   K   S   L   I   Y   A   A
103  TGG TAT CAG CAG AAA CCA GAG AAA GCC CCT AAG TCC CTG ATC TAT GCT GCA

      S   S   L   Q   S   G   V   P   S   R   F   S   G   S   G   S   G
154  TCC AGT TGG CAA AGT GGG GTC CCA TCA AGG TTC AGC GGC AGT GGA TCT GGG

      T   D   E   T   L   T   I   S   S   L   Q   P   E   D   F   A   T
205  ACA GAT TCC ACT CTC ACC ATC AGC AGC CTG CAG CCT GAA GAT TTT GCA ACT

      _CDR3_
      Y   Y   C   Q   Q   Y   N   S   Y   P   R   I   T   F   G   Q   G
256  TAT TAC TGC CAA CAC TAT AAT ACT TAC CCT CCG ATC ACC TTC CGC CAA GCG

      T   R   L   E   I   K
307  ACA CGA CTG GAG ATT AAA

```

Figure 2C

Anti-OX40 23H3 VH (hIgG1)

V segment: DP-44

J segment: JH4b

1	E	V	Q	L	V	Q	S	G	G	G	L	V	H	P	G	G	S
	GAG	GTT	CAG	CTG	GTG	CAG	TCT	GGG	GGA	GGC	TTG	GTA	CAT	OCT	GGG	GGG	TCC
	CDR1																
52	L	R	L	S	C	A	G	S	G	F	T	F	S	N	Y	A	M
	CTG	AGA	CTC	TCC	TGT	GCA	GGC	TCT	GGA	TTC	ACC	TTC	AGT	AAC	TAT	GCT	ATG
	CDR2																
103	V	W	V	R	Q	A	P	G	K	G	L	E	W	V	S	A	I
	TAC	TGG	GTT	CGC	CAG	GCT	CCA	GGA	AAA	GGT	CTG	GAG	TGG	GTA	TCA	GCC	ATT
	CDR3																
154	G	I	G	G	D	T	F	Y	T	D	S	V	K	G	R	F	T
	GGT	ATT	GGT	GGT	GAC	ACA	TTC	TAT	ACA	GAC	TCC	GTG	AAG	GGC	CGA	TTC	ACC
205	E	S	R	D	N	A	K	N	S	L	S	L	Q	M	N	S	L
	ATC	TCC	AGA	GAC	AAT	GCC	AAG	AAC	TCC	TTG	TCT	CTT	CAA	ATG	AAC	AGC	CTG
	CDR3																
256	R	A	E	D	M	A	V	Y	Y	C	A	R	M	G	T	G	Y
	AGA	GCC	GAG	GAC	ATG	GCT	GTG	TAT	TAC	TGT	GCA	AGA	ATG	GGA	ACT	GGG	TAC
307	F	F	D	Y	W	G	Q	G	T	L	V	T	V	S	S		
	TTC	TTT	GAC	TAC	TGG	GGC	CAG	GGA	ACC	CTG	GTC	ACC	GTC	TCC	TCA		

Figure 3A

Anti-OX40 23H3 VK (hKappa)

V segment: L6

J segment: JK3

```

      E   I   V   L   T   Q   S   P   A   T   L   S   L   S   P   G   E
1    GAA ATT GTG TTG ACA CAG TCT CCA GCC ACC CTG TCT TTG TCT CCA GGG GAA

      _CDR1_
      R   A   T   L   S   C   R   A   S   Q   S   V   S   S   Y   L   A
52   AGA GCC ACC CTC TCC TGC AGG GCC AGT CAG AGT GTT AGC AGC TAC TTA GCC

      _CDR2_
      W   Y   Q   Q   K   P   G   Q   A   P   R   L   L   I   Y   L   A
103  TGG TAC CAA CAG AAA CCT GGC CAG GCT CCC AGG CTC CTC ATC TAT GAT GCA

      S   N   R   A   T   G   I   P   A   R   F   S   G   S   G   S   G
154  TCC AAC AGG GCC ACT GGC ATC CCA GCC AGG TTC AGT GGC AGT GGG TCT GGG

      T   D   F   T   L   T   I   S   S   L   E   P   E   D   F   A   V
205  ACA GAC TTC ACT CTC ACC ATC AGC AGC CTA GAG CCT GAA GAT TTT GCA GTT

      _CDR3_
      Y   Y   C   Q   Q   R   S   N   W   P   L   T   F   C   P   G   T
256  TAT TAC TGT CAG CAG CGT AGC AAC TGG CCT CTC ACT TTC GGC CCT GGG ACC

      K   V   D   T   K
307  AAA GTG GAT ATC AAA

```

Figure 3B

Anti-OX40 6E1 VH (hIgG1)

V segment: 3-30.3

D segment: 3-10

J segment: JH1

```

1      Q   V   Q   L   V   E   S   G   G   G   V   V   Q   P   G   R   S
      CAG GTG CAG CTG GTG GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG TCC

                                         _CDR1_
52      L   R   L   S   C   A   A   S   G   F   T   F   S   S   F   A   M
      CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGC TTT GCT ATG

                                         _CDR2_
103     H   W   V   R   Q   A   P   G   K   G   L   E   W   V   T   V   L
      CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG ACA GTT ATT

154     S   Y   D   G   S   L   K   Y   Y   T   E   S   V   K   G   R   F
      TCA TAT CAT CGA ACC ATT AAA TAC TAC ACA GAC TCC GTG AAG GCC CGA TTC

205     T   F   S   R   D   N   S   K   N   T   L   Y   L   Q   M   N   S
      ACC TTC TCC AGA CAC AAT TCC AAG AAC ACT CTG TAT CTG CAA ATC AAC AGC

                                         _CDR3_
256     L   R   A   E   D   T   A   V   Y   Y   C   T   R   D   G   N   Y
      CTG AGA GCT GAG GAC ACG GCT GTG TAT TAC TGT ACG AGA GAT GGA AAC TAT

307     G   S   A   R   Y   F   Q   H   W   G   Q   G   T   L   V   T   V
      GGT TCG GCG AGA TAC TTC CAG CAC TGG GGC CAG GGC ACC CTG GTC ACC GTC

358     S   S
      TCC TCA

```

Figure 4A

Anti-OX40 6E1 VK1 (hKappa)

V segment: L15

J segment: JK1

```

      D   L   Q   M   T   Q   S   P   S   S   L   S   A   S   V   C   D
1    GAC ATC CAG ATG ACC CAG TCT CCA TCC TCA CTG TCT GCA TCT GTA GCA GAC

      _CDR1_
      R   V   T   T   T   C   R   A   S   Q   G   I   S   S   W   L   A
52   AGA GTC ACC ATC ACT TGT CGG GCG AGT CAG GGT ATT AGC AGC TGG TTA GCC

      _CDR2_
      W   Y   Q   Q   K   P   E   K   A   P   K   S   L   I   Y   A   A
103  TGG TAT CAG CAG AAA CCA GAG AAA GCC CCT AAG TCC CTG ATC TAT GCT GCA

      S   S   L   Q   S   G   V   P   S   R   F   S   G   S   G   S   G
154  TCC AGT TCG CAA AGT GGG GTC CCA TCA AGG TTC AGC GGC AGT GGA TCT GGG

      T   D   F   T   L   T   I   S   S   L   Q   P   E   D   F   A   T
205  ACA GAT TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT GAA GAT TTT GCA ACT

      _CDR3_
      Y   Y   C   Q   Q   Y   N   S   Y   P   R   T   F   G   Q   G   T
256  TAT TAC TGC CAA CAG TAT AAT AGT TAC CCT CGG ACG TTC GGC CAA GGG ACC

      K   V   E   T   K
307  AAG GTG GAA ATC AAA

```

Figure 4B

Anti-OX40 6E1 VK2 (hKappa)

V segment: L6

J segment: JK2

```

      E   I   V   L   T   Q   S   P   A   T   L   S   L   S   P   G   E
1    GAA ATT GTG TTG ACA CAG TCT CCA GCC ACC CTG TCT TTG TCT CCA GGG GAA

      _CDR1_
      R   A   T   L   S   C   R   A   S   Q   S   V   S   S   Y   L   A
52   AGA GCC ACC CTC TCC TGC AGG GCC AGT CAG AGT GTT AGC AGC TAC TTA GCC

      _CDR2_
      W   Y   Q   Q   K   P   G   Q   A   P   R   L   L   I   Y   D   A
103  TGG TAC CAA CAG AAA CCT GGC CAG GCT CCC AGG CTC CTC ATC TAT GAT GCA

      S   N   R   A   T   G   I   P   A   R   F   S   G   S   G   S   G
154  TCC AAC AGG GCC ACT GGC ATC CCA GCC AGG TTC AGT GGC AGT GGG TCT GGG

      T   D   F   T   L   T   I   S   S   L   E   P   E   D   F   A   V
205  ACA GAC TTC ACT CTC ACC ATC AGC AGC CTA GAG CCT GAA GAT TTT GCA GTT

      _CDR3_
      Y   Y   C   Q   Q   R   S   N   W   P   Y   T   F   G   Q   G   T
256  TAT TAC TGT CAG CAG CGT AGC AAC TGG CCG TAC ACT TTT GGC CAG GGG ACC

      K   L   E   -   K
307  AAG CTC CAG ATC AAA

```

Figure 4C

Anti-OX40 18E9 VH (hIgG1)

V segment: DP-44

D segment: 3-9

J segment: JH4b

```

      E   V   Q   L   V   Q   S   G   G   G   L   V   H   P   G   G   S
1    GAG GTT CAG CTG GTG CAG TCT GGG GGA GGC TTG GTT CAT CCT GGG GGG TCC

                                     _CDR1_
      L   R   L   S   C   A   H   S   G   F   T   F   T   S   S   A   M
52   CTG AGA CTC TCC TGT GCA CAC TCT GGA TTC ACC TTC ACT AGC TCT GCT ATG

                                     _CDR2_
      H   W   V   R   Q   A   P   G   K   G   L   E   W   I   S   A   I
103  CAC TGG GTT CGC CAG GCT CCA GGA AAA GGT CTG GAA TGG ATA TCA GCT ATT

      G   T   G   G   D   T   Y   Y   A   D   S   V   K   G   R   F   T
154  GGT ACT GGT GGT GAC ACA TAC TAT GCA GAC TCC GTG AAG GGC CGA TTC ACC

      T   S   R   D   N   A   K   N   S   L   Y   L   Q   I   N   S   L
205  ATC TCC AGA GAC AAT GCC AAG AAC TCC TTG TAT CTT CAA ATA AAC AGC CTG

                                     _CDR3_
      R   A   E   D   M   A   V   Y   Y   C   A   R   D   F   Y   D   I
256  AGA GCC GAG GAC ATG GCT GTA TAT TAC TGT GCA AGA GAC TTG TAC GAT ATT

      L   T   G   T   F   D   Y   W   G   Q   G   T   L   V   T   V   S
307  TTG ACT GGT ATC TTT GAC TAC TGG GGC CAG GGA ACC CTG GTC ACC GTC TCC

      S
358  TCA

```

Figure 5A

Anti-OX40 18E9 VK (hKappa)

V segment: L5

J segment: JK1

```

      L   L   Q   M   T   Q   S   P   S   S   V   S   A   S   V   G   D
1    GAC ATC CAG ATG ACC CAG TCT CCA TCT TCC GTG TCT GCA TCT GTA GGA GAC

      _CDR1_
      R   V   T   T   T   C   R   A   S   Q   G   I   S   S   W   L   A
52   AGA GTC ACC ATC ACT TGT CGG GCG AGT CAG GGT ATT AGC AGC TGG TTA GCC

      _CDR2_
      W   Y   Q   H   K   P   G   K   A   P   K   L   L   I   Y   A   A
103  TGG TAT CAG CAT AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC TAT GCT GCA

      S   S   L   Q   S   G   V   P   S   R   F   S   G   S   G   S   G
154  TCC AGT TTG CAA AGT GGG GTC CCA TCA AGG TTC AGC GGC AGT GGA TCT GGG

      T   D   F   T   L   T   I   S   S   L   Q   P   E   D   F   A   T
205  ACA GAT TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT GAA GAT TTT GCA ACT

      _CDR3_
      Y   Y   C   Q   Q   A   N   S   F   P   S   T   F   G   Q   G   T
256  TAC TAT TGT CAA CAG GCT AAT AGT TTC CCT TCG ACG TTC GGC CAA GGG ACC

      K   V   E   T   K
307  AAG GTG GAA ATC AAA

```

Figure 5B

Anti-OX40 8B11 VH (hIgG1)

V segment: DP-44

J segment: JH4b

```

1      E I Q L V Q S G G G L V H P G G S
    GAA ATT CAG CTG GTG CAG TCT GGG GGA GGC TTG GTA CAT CCT GGG GGG TCC

52      L R L S C A G S G F T F S S D A M
    CTG AGA CTC TCC TGT GCA GGC TCT GGA TTC ACC TTC AGT AGC GAT GCT ATG

103      Y W V R Q A P C K C L E W V S A I
    TAC TGG GTT CGC CAG GCT CCA GGA AAA GGT CTG GAG TGG GTA TCA GCT ATT

154      C I G G D T Y Y T D S V M G R F T
    GGT ATT GGT GGT GAC ACA TAC TAT ACA GAC TCC GTG ATG GGC CGA TTC ACC

205      T S R D N A K N S L Y L Q M N S L
    ATC TCC AGA GAC AAT GCC AAG AAC TCC TTG TAT CTT CAA ATG AAC AGC CTG

256      R A E D M A V Y Y C A R L G M G Y
    AGA GCC GAG GAC ATG GCT GTG TAT TAC TGT GCA AGG CTG GGG ATG GGG TAC

307      Y F D Y W G Q G T L V T V S S
    TAC TTT CAC TAC TCC GCC CAG GCA ACC CTC GTC ACC GTC TCC TCA

```

Figure 6A

Anti-OX40 8B11 VK (hKappa)

V segment: L6

J segment: JK1

```

      E   I   V   L   T   Q   S   P   A   T   L   S   L   S   P   G   E
1    GAA ATT GTG TTG ACA CAG TCT CCA GCC ACC CTG TCT TTG TCT CCA GGG GAA

      CDR1
      R   A   T   L   S   C   R   A   S   Q   S   V   S   S   Y   L   A
52   AGA GCC ACC CTC TCC TGC AGG GCC AGT CAG AGT GTT AGC AGC TAC TTA GCC

      CDR2
      W   Y   Q   Q   K   P   G   Q   A   P   R   L   L   L   Y   L   A
103  TGG TAC CAA CAG AAA CCT GGC CAG GCT CCC AGG CTC CTC ATC TAT GAT GCA

      S   N   R   A   T   G   I   P   A   R   F   S   G   S   G   S   G
154  TCC AAC AGG GCC ACT GGC ATC CCA GCC AGG TTC AGT GGC AGT GGG TCT GGG

      T   D   F   T   L   T   I   S   S   L   E   P   E   D   F   A   V
205  ACA GAC TTC ACT CTC ACC ATC AGC AGC CTA GAG CCT GAA GAT TTT GCA GTT

      CDR3
      Y   Y   C   Q   Q   R   S   N   W   P   P   T   F   G   Q   G   T
256  TAT TAC TGT CAG CAG CGT AGC AAC TGG CCT CCG ACG TTC GGC CAA GGG ACC

      K   V   E   T   K
307  AAG GTG GAA ATC AAA

```

Figure 6B

Anti-OX40 20B3 VH (hIgG2)

V segment: 3-13

J segment: JH4b

```

      E   V   Q   L   V   E   S   G   G   G   L   V   Q   P   G   G   S
1    GAG GTG CAG CTG GTG GAG TCT GGG GGA GGC TTG GTA CAG CCT GGG GGG TCC

                                     _CDR1_
      L   R   L   S   C   A   A   S   G   F   T   F   S   S   Y   D   M
52   CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGC TAC GAC ATG

                                     _CDR2_
      H   W   V   R   Q   T   T   G   K   G   L   E   W   V   S   V   I
103  CAC TGG GTC CGC CAA ACT ACA GGA AAA GGT CTG GAG TGG GTC TCA GTT ATT

      G   T   A   G   D   T   Y   Y   P   G   S   V   K   G   R   F   T
154  GGT ACT GCT GGT GAC ACA TAC TAT CCA GGC TCC GTG AAG GGC CGA TTC ACC

      I   S   R   E   N   A   K   N   S   L   Y   L   Q   M   N   S   L
205  ATC TCC AGA GAA AAT GCC AAG AAC TCC TTG TAT CTT CAA ATG AAC AGC CTG

                                     _CDR3_
      R   A   G   D   T   A   V   Y   Y   C   A   R   G   G   M   G   N
256  AGA GCC GGG GAC ACG GCT GTG TAT TAC TGT GCA AGA GGG GGG ATG GGG AAC

      Y   F   D   Y   W   G   Q   G   T   L   V   T   V   S   S
307  TAC TTT GAC TAC TGG GGC CAG GGA ACC CTG GTC ACC GTC TCC TCA

```

Figure 7A

Anti-OX40 20B3 VK (hKappa)

V segment: L6

J segment: JK4

```

      E   I   V   L   T   Q   S   P   A   T   L   S   L   S   P   G   E
1    GAA ATT GTG TTG ACA CAG TCT CCA GCC ACC CTG TCT TTG TCT CCA GGG GAA

      _CDR1_
      R   A   T   L   S   C   R   A   S   Q   S   V   S   S   Y   L   A
52   AGA GCC ACC CTC TCC TGC AGG GCC AGT CAG AGT GTT AGC AGC TAC TTA GCC

      _CDR2_
      W   Y   Q   Q   K   P   G   Q   A   P   R   L   L   I   Y   D   A
103  TGG TAC CAA CAG AAA CCT GGC CAG GCT CCC AGG CTC CTC ATC TAT GAT GCA

      S   N   R   A   T   G   I   P   A   R   F   S   G   S   G   S   G
154  TCC AAC AGG GCC ACT GGC ATC CCA GCC AGG TTC AGT GGC AGT GGG TCT GGG

      L   D   F   L   L   L   I   S   S   L   E   P   E   D   F   A   V
205  ACA GAC TTC ACT CTC ACC ATC ACC ACC CTA GAG CCT GAA GAT TTT GCA GTT

      _CDR3_
      Y   Y   C   Q   Q   R   S   N   W   P   L   T   F   G   G   G   T
256  TAT TAC TGT CAG CAG CGT AGC AAC TGG CCG CTC ACT TTC GGC GGA GGG ACC

      K   V   E   L   K
307  AAG GTG GAG ATC AAA

```

Figure 7B

Anti-OX40 14A2 VH (hIgG1)

V segment: 3-30.3

J segment: JH5b

```

      Q   V   Q   L   V   E   S   G   G   G   V   V   Q   P   G   R   S
1    CAG GTG CAG CTG GTG GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG TCC

                                     _CDR1_
      L   R   L   S   C   A   A   S   G   F   T   F   S   N   Y   A   L
52   CLG AGA CAC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AAC TAT GCT CTG

      _CDR2_
      H   W   V   R   Q   A   P   C   K   C   L   E   W   V   A   L   L
103  CAC TCG CAC CCC CAG GCT CCA GCC AAG GGC CTG GAC TCG CTG CCA CTT ATA

      S   Y   D   G   S   R   K   H   Y   A   D   S   V   K   G   R   F
154  TCA TAT GAT GGA AGC AGG AAA CAC TAC GCA GAC TCC GTG AAG GGC CGA TTC

      S   I   S   R   D   N   S   K   N   T   L   Y   L   Q   M   N   S
205  AGT ATC TCC AGA GAC AAT TCC AAG AAC ACA CTG TAT CTG CAA ATG AAC AGC

                                     _CDR3_
      L   R   A   E   D   T   A   V   Y   Y   C   A   S   L   T   M   V
256  CTG AGA GCT GAG GAC ACG GCT GTG TAT TAC TGT GCG AGT CTT ACT ATG GTT

      R   E   G   G   Q   G   T   L   V   T   V   S   S
307  CCG GAG GGG GGC CAG GGA ACC CTG GTC ACC GTC TCC TCA

```

Figure 8A

Anti-OX40 14A2 VK1 (hKappa)

V segment: A27

J segment: JK3

```

      E   I   V   L   T   Q   S   P   G   T   L   S   L   S   P   G   E
1    GAA ATT GTG TTG ACG CAG TCT CCA GGC ACC CTG TCT TTG TCT CCA GGG GAA

      _CDR1_
      R   A   T   L   S   C   R   A   S   Q   S   V   S   S   S   Y   L
52   AGA GCC ACC CTC TCC TGC AGG GCC AGT CAG AGT GTT AGC AGC AGC TAC TTA

      _CDR2_
      A   W   Y   Q   Q   K   P   G   Q   A   P   R   L   L   I   Y   C
103  GCC TGG TAC CAG CAG AAA CCT GGC CAG GCT CCC AGG CTC CTC ATC TAT GGT

      A   S   S   R   A   T   G   I   P   D   R   F   S   G   S   G   S
154  GCA TCC AGC AGG GCC ACT GGC ATC CCA GAC AGG TTC AGT GGC AGT GGG TCT

      G   T   D   F   T   L   T   I   S   R   L   E   P   E   D   F   A
205  GGG ACA GAC TTC ACT CTC ACC ATC AGC AGA CTG GAG CCT GAA GAT TTT GCA

      _CDR3_
      V   Y   Y   C   Q   Q   Y   G   S   S   P   F   T   F   G   P   G
256  GTG TAT TAC TGT CAG CAG TAT GGT AGC TCA CCA TTC ACT TTC GGC CCT GGG

      T   K   V   D   I   K
307  ACC AAA GTG GAT ATC AAA

```

Figure 8B

Anti-OX40 14A2 VK2 (hKappa)

V segment: O14/O4

J segment: JK4

```

      L   L   Q   L   T   Q   S   P   S   S   L   S   A   S   V   G   D
1    GAC ATC CAG TTG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC

      _CDR1_
      R   V   T   T   T   C   R   V   S   Q   G   I   S   S   Y   L   N
52   AGA GTC ACC ATC ACT TGC CGG GTG AGT CAG GGC ATT AGC AGT TAT TTA AAT

      _CDR2_
      W   Y   R   Q   K   P   G   K   V   P   K   L   L   I   Y   S   A
103  TGG TAT CGG CAG AAA CCA GGG AAA GTT CCT AAG CTC CTG ATC TAT AGT GCA

      S   N   L   Q   S   G   V   P   S   R   F   S   G   S   G   S   G
154  TCC AAT TTG CAA TCT GGA GTC CCA TCT CGG TTC AGT GGC AGT GGA TCT GGG

      T   D   F   T   L   T   I   S   S   L   Q   P   E   D   V   A   T
205  ACA GAT TTC ACT CTC ACT ATC AGC AGC CTG CAG CCT GAA GAT GTT GCA ACT

      _CDR3_
      Y   Y   G   Q   R   T   Y   N   A   P   Y   T   F   G   G   G   T
256  TAT TAC GGT CAA CGG ACT TAC AAT GCC CCT TAC ACT TTC GGC GGA GGG ACC

      K   V   E   T   K
307  AAG GTG GAG ATC AAA

```

Figure 8C

Anti-OX40 20C1 VH (hIgG1)

V segment: DP-44

J segment: JH4b

```

      E  A  Q  L  V  Q  S  G  G  G  L  V  H  P  G  G  S
1    GAG GCT CAG CTG GTG CAG TCT GGG GGA GGC TTG GTT CAT CCT GGG GGG TCC

                                     _CDR1_
      L  R  L  S  C  A  D  S  G  F  T  F  S  S  Y  A  M
52   CTG AGA CTC TCC TGT GCA GAC TCT GGA TTC ACC TTC AGT AGC TAT GCT ATG

      _CDR2_
      Y  W  V  R  Q  A  P  G  K  G  L  E  W  V  S  A  I
103  TAC TGG GTT CGC CAG GCT CCA GGA AAA GGT CTG GAG TGG GTA TCA GCT ATT

      D  T  D  G  G  T  F  Y  A  D  S  V  R  G  R  F  T
154  GAT ACT GAT GGT GGC ACA TTC TAT GCA GAC TCC GTG CGG GGC CGA TTC ACC

      C  S  R  D  N  A  K  N  S  L  Y  L  Q  M  N  G  L
205  ATC TCC AGA GAC AAT GCC AAG AAC TCC TTG TAT CTT CAA ATG AAC GGC CTG

                                     _CDR3_
      R  A  E  D  M  A  V  Y  F  C  A  R  L  G  E  G  Y
256  AGA GCC GAG GAC ATG GCT GTG TAT TTC TGT GCA AGA CTT GGG GAA GGG TAC

      F  F  D  Y  W  G  Q  G  T  L  V  T  V  S  S
307  TTC TTT GAC TAC TGG GGC CAG GGA ACC CTG GTC ACC GTC TCC TCA

```

Figure 9A

Anti-OX40 20C1 VK (hKappa)

V segment: L6

J segment: JK4

```

      E   I   V   L   T   Q   S   P   A   T   L   S   L   S   P   G   E
1    GAA ATT GTG TTG ACA CAG TCT CCA GCC ACC CTG TCT TTG TCT CCA GGG GAA

      _CDR1_
      R   A   L   L   S   C   R   A   S   Q   S   V   S   S   Y   L   A
52   AGA GCC ACC CTC TCC TGC AGG GCC AGT CAG AGT GTT AGC AGC TAC TTA GCC

      _CDR2_
      W   Y   Q   Q   K   P   G   Q   A   P   R   L   L   I   Y   D   A
103  TGG TAC CAA CAG AAA CCT GGC CAG GCT CCC AGG CTC CTC ATC TAT GAT GCA

      S   N   R   A   T   G   I   P   A   R   F   S   G   S   G   S   G
154  TCC AAC AGG GCC ACT GGC ATC CCA GCC AGG TTC AGT GGC AGT GGG TCT GGG

      L   D   F   L   L   L   I   S   S   L   E   P   E   D   F   A   V
205  ACA GAC TTC ACT CTC ACC ATC AGC AGC CTA GAG CCT GAA GAT TTT GCA GTT

      _CDR3_
      Y   Y   C   Q   Q   R   S   N   W   P   P   T   F   G   G   G   T
256  TAT TAC TGT CAG CAC CGT ACC AAC TGG CCT CCC ACT TTC CCC CCA GCG ACC

      K   V   E   L   K
307  AAG GTG GAG ATC AAA

```

Figure 9B

Anti-OX-40.21 VH

```

      A2V                      H13Q
      ~~~~                    ~~~~

      20C1 VH
      ~~~~~
      E V Q L V Q S G G G L V Q P G
1   GAG GTT CAG CTG GTG CAG TCT GGG GGA GGC TTG GTT CAG CCT GGS
      D24G
      ~~~~

      20C1 VH
      ~~~~~
      G S L R L S C A G S G F T F S
46  GGG TCC CTG AGA CTC TCC TGT GCA GGC TCT GGA TTC ACC TTC AGT
      20C1 VH
      ~~~~~
      S Y A M Y W V R Q A P C K C L
91  AGC TAT GCT ATG TAC TGG GTT CGC CAG GGT CCA GGA AAA GGT CTG
      G55A
      ~~~~

      20C1 VH
      ~~~~~
      E W V S A I D T D A G T F Y A
136 GAG TGG GTA TCA GCT ATT GAT ACT GAT GCT GGC ACA TTC TAT GCA
      20C1 VH
      ~~~~~
      D S V R G R F T I S R D N A K
181 GAC TCC GTG CCG GGC CGA TTC ACC ATC TCC AGA CAC AAT GCC AAG
      G82bs M87T
      ~~~~

      20C1 VH
      ~~~~~
      N S L Y L Q M N S L R A E D T
226 AAC TCC TTG TAT CTT CAA ATG AAC AGC CTG AGA GCC GAG GAC ACG
      20C1 VH
      ~~~~~
      A V Y F C A R L G E G Y F F D
271 GCT GTG TAT TTC TGT GCA AGA CTT GGG GAA GGG TAC TTC TTT GAC
      20C1 VH
      ~~~~~

      C gamma1
      ~~~~~
      Y W G Q G T L V I V S S A S T
316 TAC TGG GGC CAG GGA ACC CTG GTC ACC GTC TCC TCA GCT AGC ACC
      C gamma1
      ~~~~~
      K G P S V F P L A P S S K S T
361 AAG GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC
      C gamma1
      ~~~~~
      S G G T A A L G C L V K D Y F
406 TCT GGG GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG GAC TAC TTC
      C gamma1
      ~~~~~
      P E P V T V S W N S G A L T S
451 CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG ACC AGC
      C gamma1
      ~~~~~
      G V H T F P A V L Q S S G L Y
496 GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC TAC
      C gamma1
      ~~~~~

```

S L S S V V T V P S S S L G T
 541 TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC
 C gamma1
 ~~~~~  
 Q T Y I C N V N H K P S N T K  
 586 CAG ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG  
 C gamma1  
 ~~~~~  
 V D K R V E P K S C D K T H I
 631 CTC CAC AAG AGA GTT CAG CCC AAA TCT TCT GAC AAA ACT CAC ACA
 C gamma1
 ~~~~~  
 C P P C P A P E L L G G P S V  
 676 TGC CCA CCG TGC CCA GCA CCT GAA CTC CTG GGG GGA CCG TCA GTC  
 C gamma1  
 ~~~~~  
 F L F P P K P K D T L M I S R
 721 TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC CTC ATG ATC TCC CGG
 C gamma1
 ~~~~~  
 T P E V T C V V V D V S H E D  
 766 ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC GAA GAC  
 C gamma1  
 ~~~~~  
 P E V K F N W Y V D G V E V H
 811 CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT
 C gamma1
 ~~~~~  
 N A K T K P R E E Q Y N S T Y  
 856 AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC  
 C gamma1  
 ~~~~~  
 R V V S V L T V L H Q D W L N
 901 CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT
 C gamma1
 ~~~~~  
 G K E Y K C K V S N K A L P A  
 946 GGC AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GCC CTC CCA GCC  
 C gamma1  
 ~~~~~  
 P I E K T I S K A K G Q P R E
 991 CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAA
 C gamma1
 ~~~~~  
 P Q V Y T L P P S R E E M T K  
 1036 CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAG GAG ATG ACC AAG  
 C gamma1  
 ~~~~~  
 N Q V S L T C L V K G F Y P S
 1081 AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC
 C gamma1
 ~~~~~  
 D I A V E W E S N G Q P E N N  
 1126 GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC  
 C gamma1  
 ~~~~~  
 Y K T T P P V L D S D G S F F
 1171 TAC AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC
 C gamma1
 ~~~~~  
 L Y S K L T V D K S R W Q Q G  
 1216 CTC TAT AGC AAG CTC ACC GTG CAC AAG ACC ACC TGG CAG CAG GCG  
 C gamma1

```

~~~~~
 N V F S C S V M H E A L H N H
1261 AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG GCT CTG CAC AAC CAC
 C gamma1
~~~~~
  Y   T   Q   K   S   L   S   L   S   P   G   *
1306 TAC ACG CAG AAG AGC CTC TCC CTG TCC CCG GGT TGA

```

Figure 10A

## Anti-OX-40.21 VK

## 20C1 VK

~~~~~  
 E I V L T Q S P A T L S L S P
 1 GAA ATT GTG TTG ACA CAG TCT CCA GCC ACC CTG TCT TTG TCT CCA
 20C1 VK
 ~~~~~

G E R A T L S C R A S Q S V S  
 46 GGG GAA AGA GCC ACC CTC TCC TGC AGG GCC AGT CAG AGT GTT AGC  
 20C1 VK  
 ~~~~~

S Y L A W Y Q Q K P G Q A P R
 91 ACC TAC TTA GCC TGG TAC CAA CAG AAA CCT CGC CAG GCT CCC AGG
 20C1 VK
 ~~~~~

L L I Y D A S N R A T G I P A  
 136 CTC CTC ATC TAT GAT GCA TCC AAC AGG GCC ACT GGC ATC CCA GCC  
 20C1 VK  
 ~~~~~

R F S G S G S G T D F T L T I
 181 AGG TTC AGT GGC AGT GGG TCT GGG ACA GAC TTC ACT CTC ACC ATC
 20C1 VK
 ~~~~~

S S L E P E D F A V Y Y C Q Q  
 226 AGC AGC CTA GAG CCT GAA GAT TTT GCA GTT TAT TAC TGT CAG CAG  
 20C1 VK  
 ~~~~~

R S N W P P T F G G G T K V E
 271 CGT AGC AAC TGG CCT CCC ACT TTC GGC GGA GGG ACC AAG GTG GAG
 20C1 VK
 ~~~~~

## C kappa

~~~~~  
 I K R T V A A P S V F I F P P
 316 ATC AAA CGT ACG GTG CCT GCA CCA TCT GTC TTC ATC TTC CCG CCA
 C kappa
 ~~~~~

S D E Q L K S G T A S V V C L  
 361 TCT GAT GAG CAG TTG AAA TCT GGA ACT GCC TCT GTT GTG TGC CTG  
 C kappa  
 ~~~~~

L N N F Y P R E A K V Q W K V
 406 CTG AAT AAC TTC TAT CCC AGA GAG GCC AAA GTA CAG TGG AAG GTG
 C kappa
 ~~~~~

D N A L Q S G N S Q E S V T E  
 451 GAT AAC GCC CTC CAA TCG GGT AAC TCC CAG GAG AGT GTC ACA GAG  
 C kappa  
 ~~~~~

Q D S K D S T Y S L S S T L T
 496 CAG GAC AGC AAG GAC AGC ACC TAC AGC CTC AGC AGC ACC CTG ACG
 C kappa
 ~~~~~

L S K A D Y E K H K V Y A C E  
 541 CTG AGC AAA GCA GAC TAC GAG AAA CAC AAA GTC TAC GCC TGC GAA  
 C kappa  
 ~~~~~

V T H Q C L S S P V T K S F N
 586 CTC ACC CAT CAG GGC CTG ACC TCC CCC CTC ACA AAG ACC TTC AAC
 C kappa
 ~~~~~

~~~~~  
R G E C *
631 AGG GGA GAG TGT TAG

Figure 10B

Anti-OX40 Antibody binding to primary human CD4+/CD25+ T cells

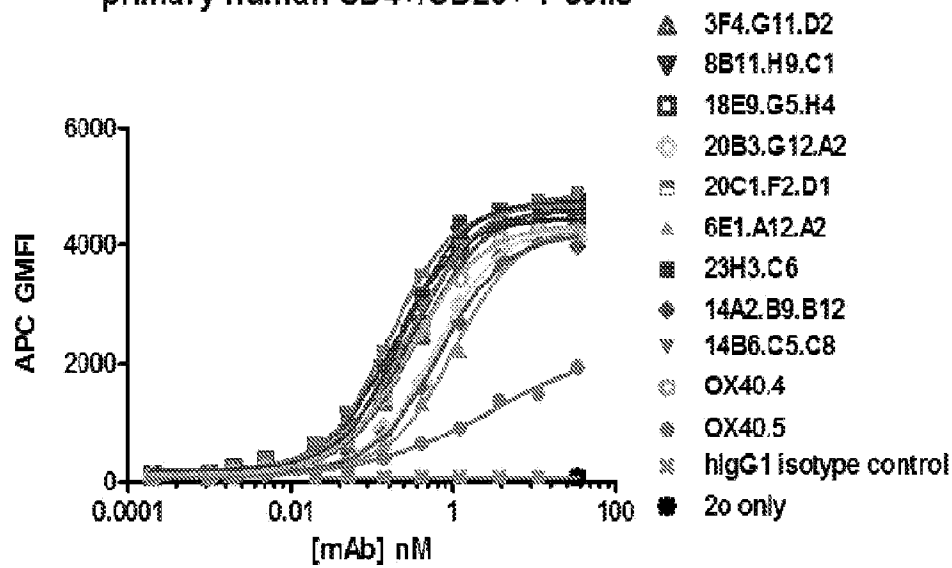


Figure 11A

Binding of recombinant anti-OX40 antibody transfected cell culture supernatants to primary human CD4+/CD25+ T cells

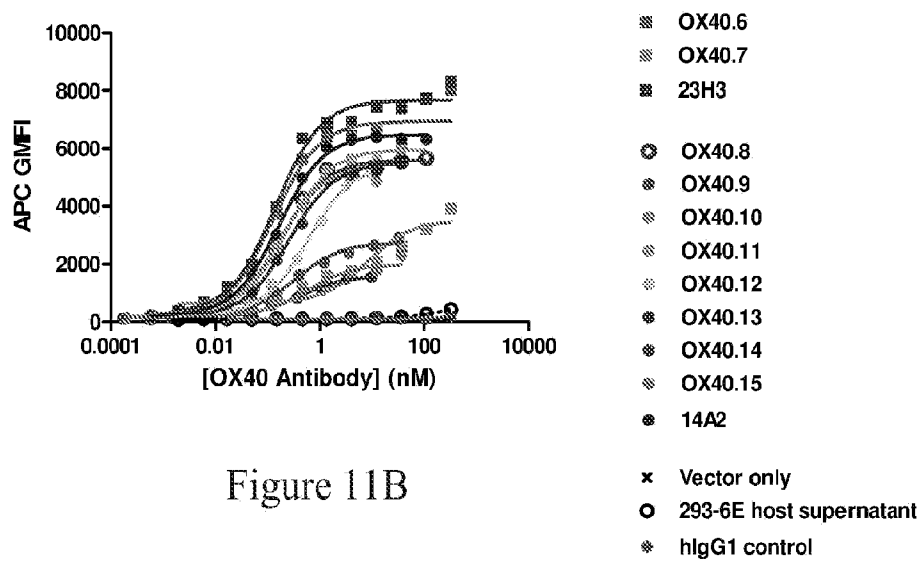


Figure 11B

**Recombinant anti-OX40 antibody binding to
primary human CD4+/CD25+ T cells**

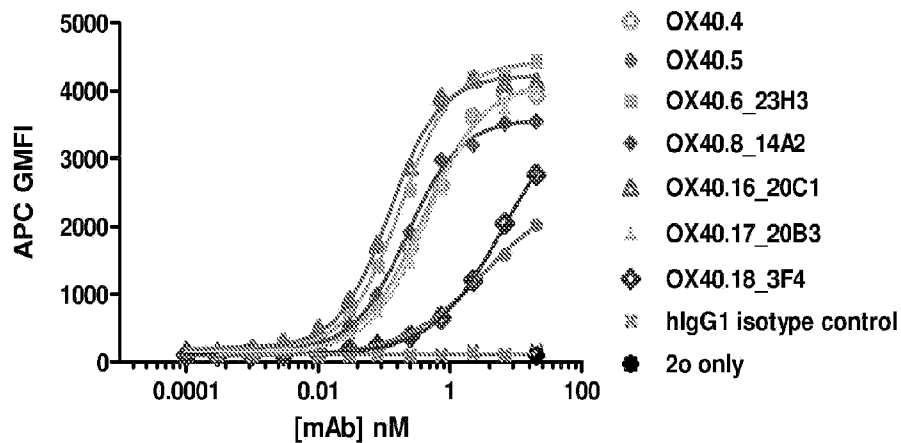


Figure 11C

**Recombinant anti-OX40 antibody binding to
primary human CD4+/CD25+ T cells**

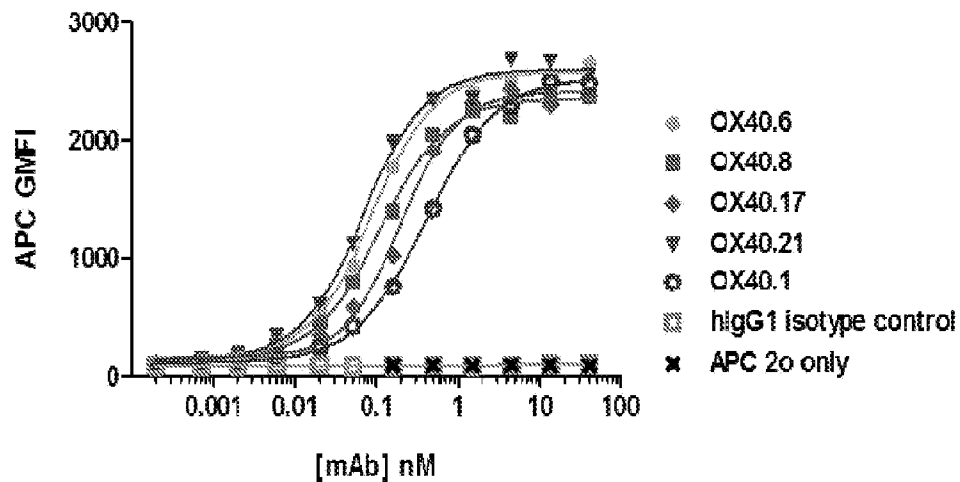


Figure 11D

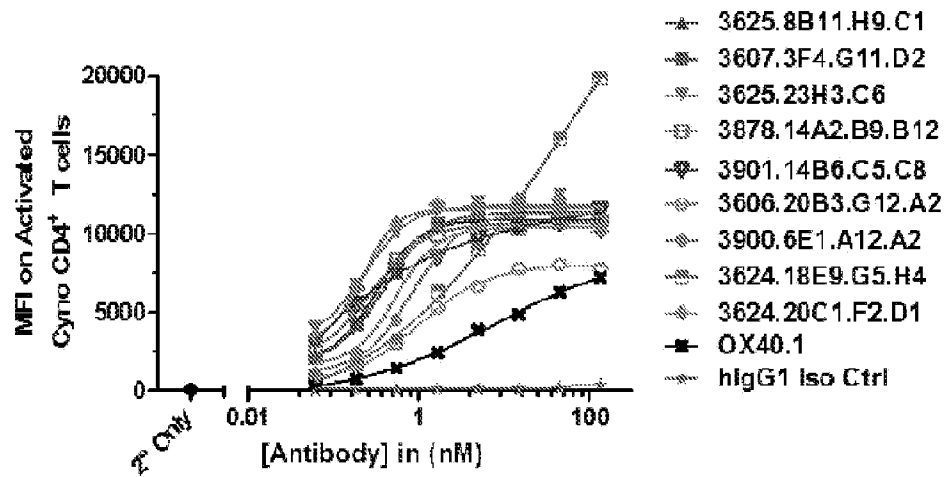


Figure 12A

Anti-OX40 Antibody binding to primary cynomolgous
macaque CD4⁺/CD25⁺ T cells

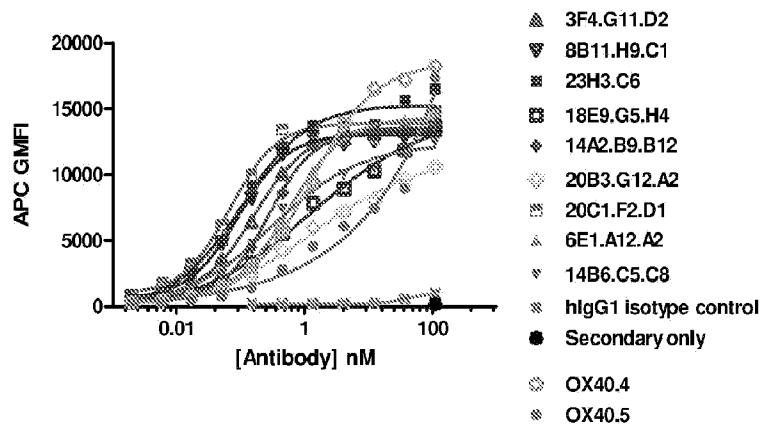


Figure 12B

Recombinant anti-OX40 antibody binding to
primary cynomolgous macaque CD4⁺/CD25⁺ T cells

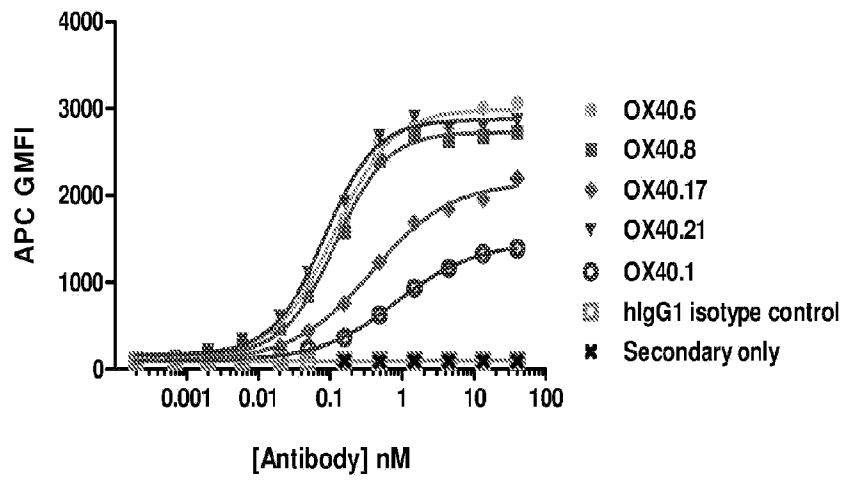
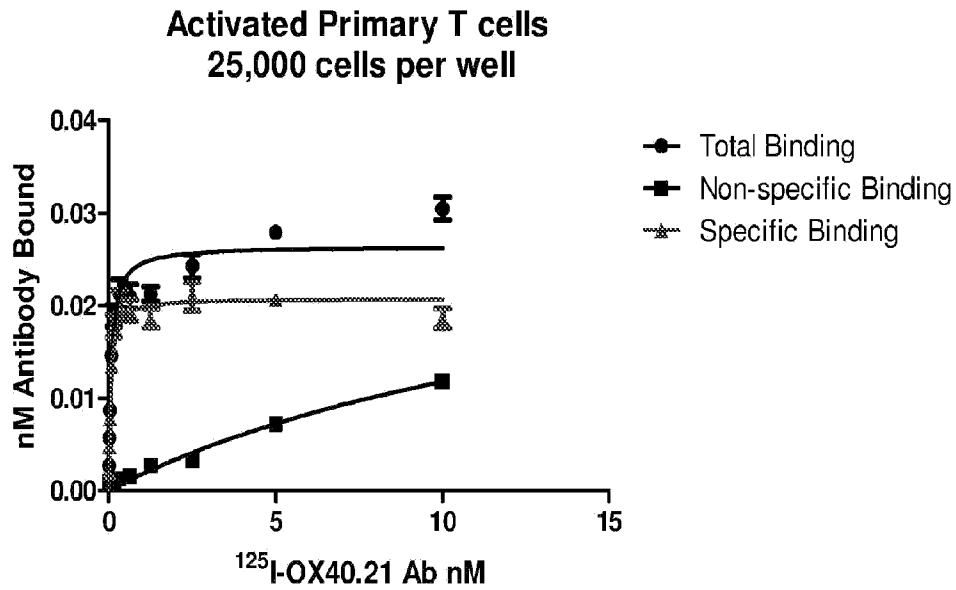


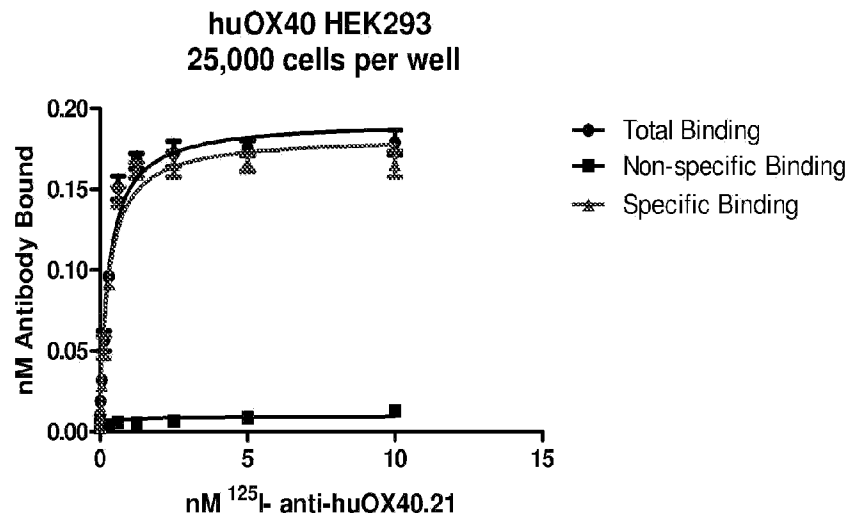
Figure 12C



	Specific Binding Donor 6 25e3
Bmax	0.02081
Kd	0.04966

Receptors per cell = Bmax (6e10)/# cells per well
 = 0.021*6e10/25,000
 = 50,400 OX-40 receptors per cell

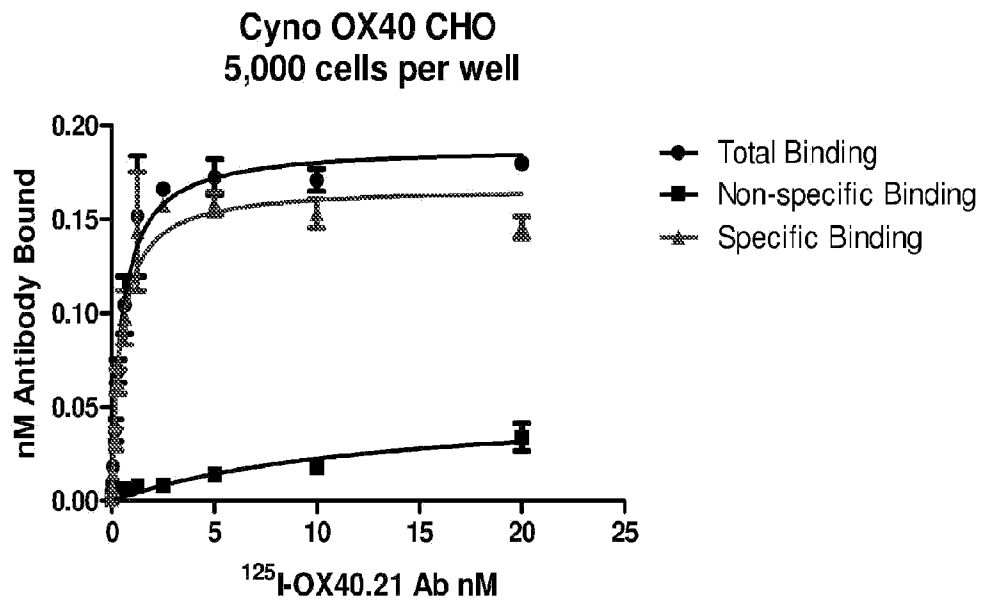
Figure 13A



	Specific Binding huOX 25e3
Bmax	0.1829
Kd	0.2911

Receptors per cell = Bmax (6e10)/# cells per well
 = 0.183*6e10/25,000
 = 439,200 OX40 receptors per cell

Figure 13B



	Specific Binding Cyno OX40 5e3
Bmax	0.1674
Kd	0.4422

Receptors per cell = Bmax (6e10)/# cells per well
 = 0.167*6e10/5,000
 = 2,004,000 OX-40 receptors per cell

Figure 13C

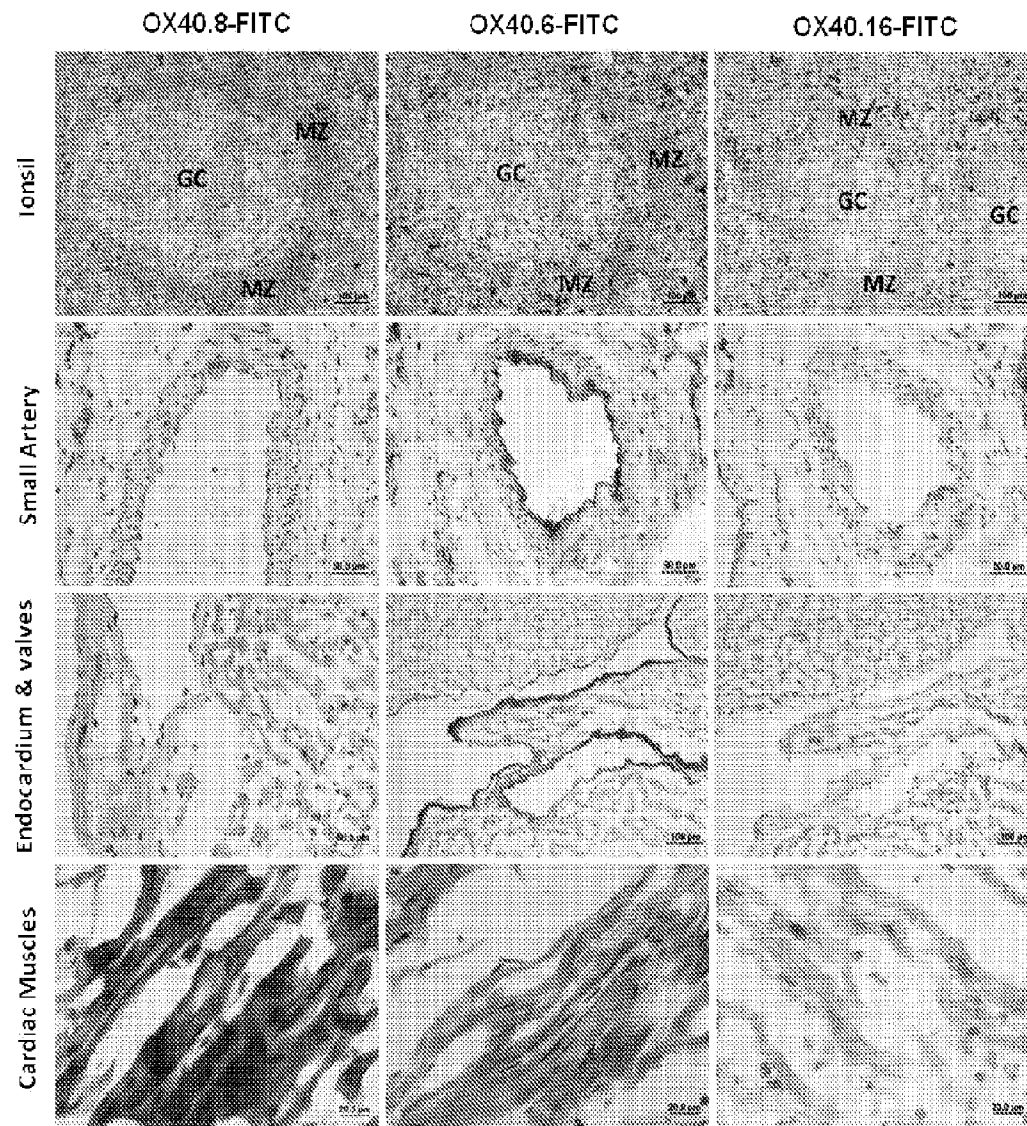


Figure 14A

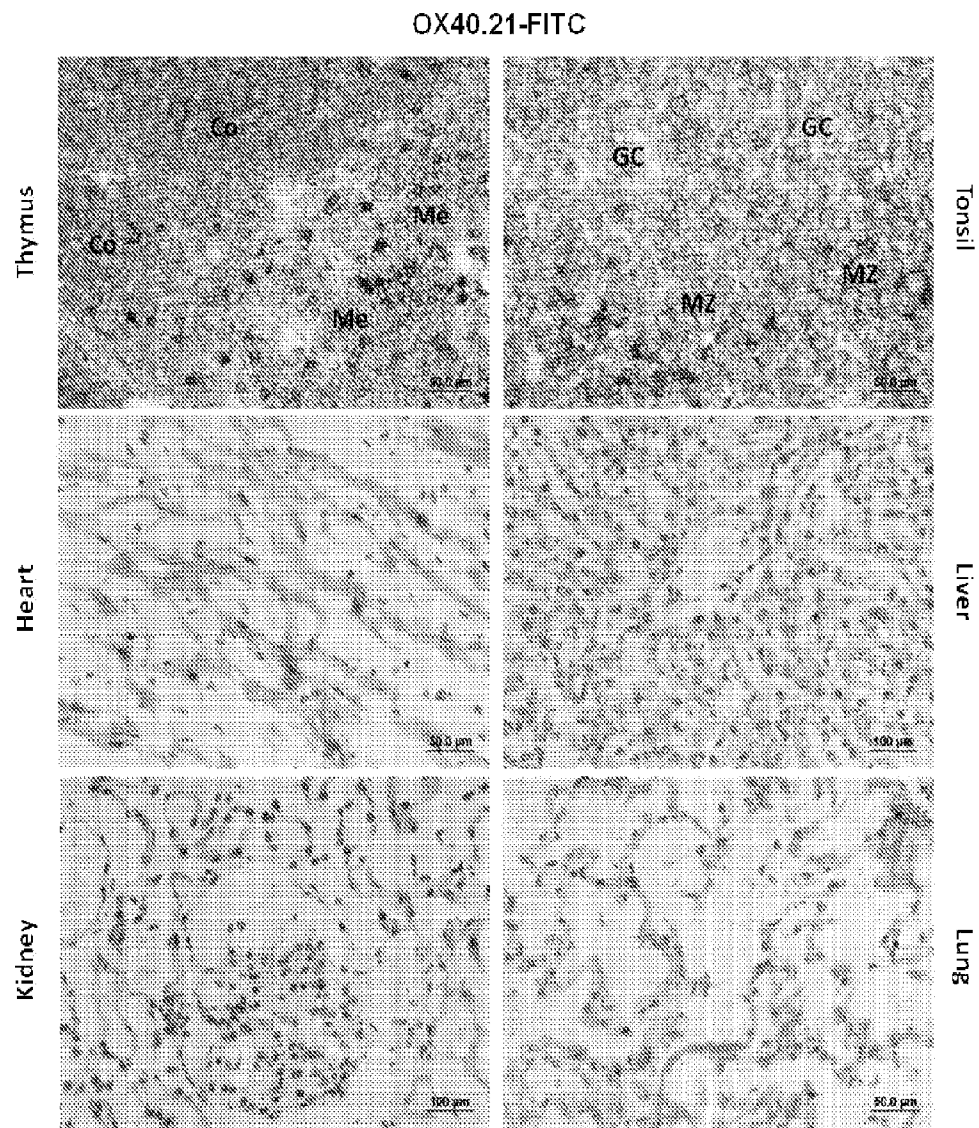


Figure 14B

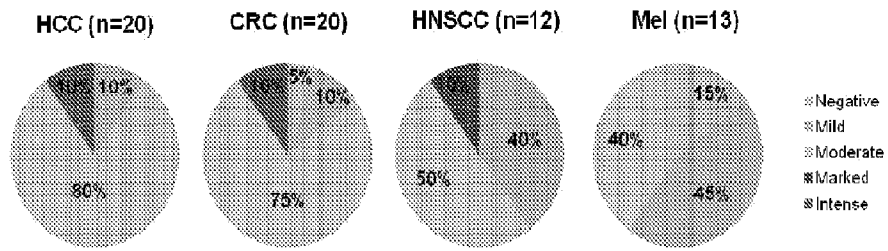


Figure 15A

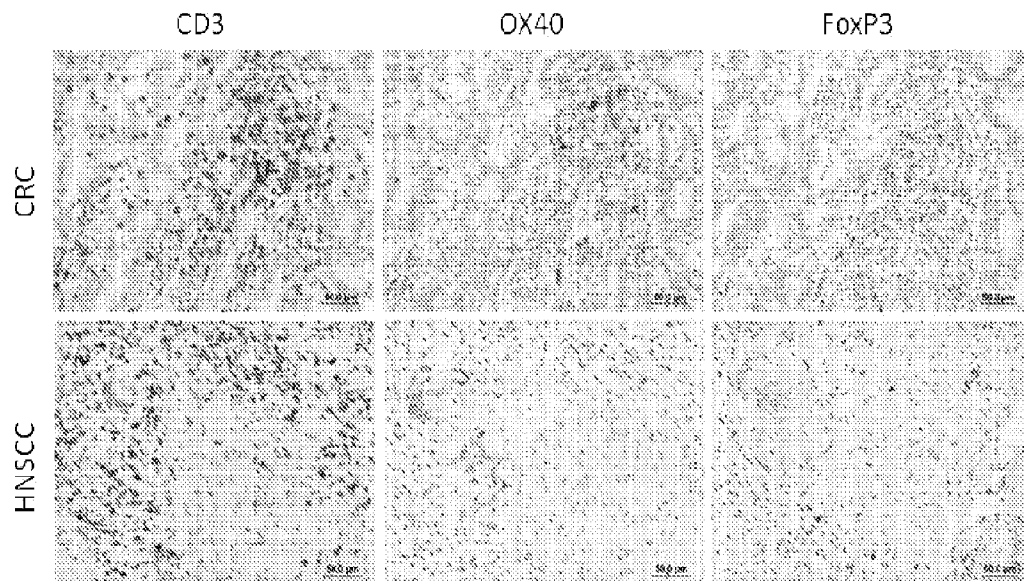


Figure 15B

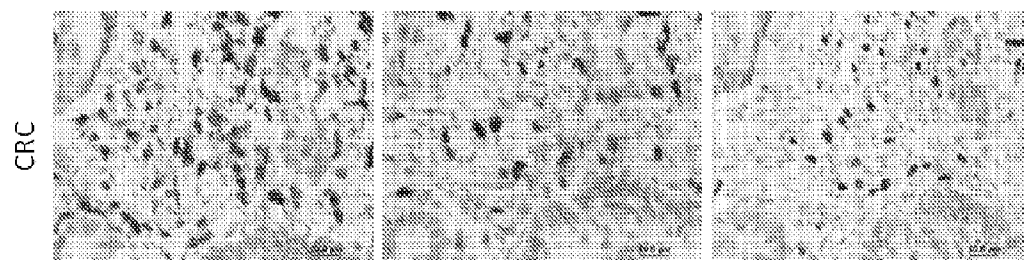


Figure 15C

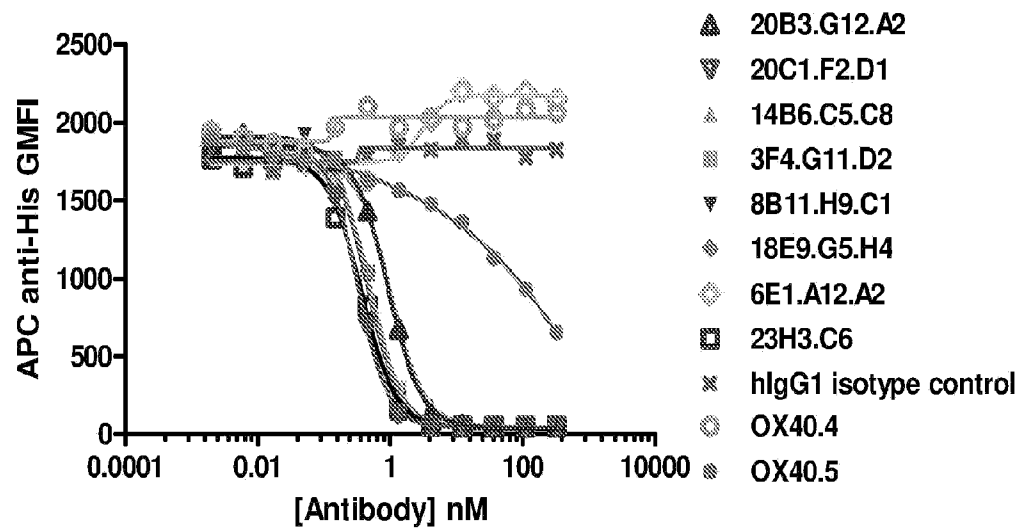


Figure 16

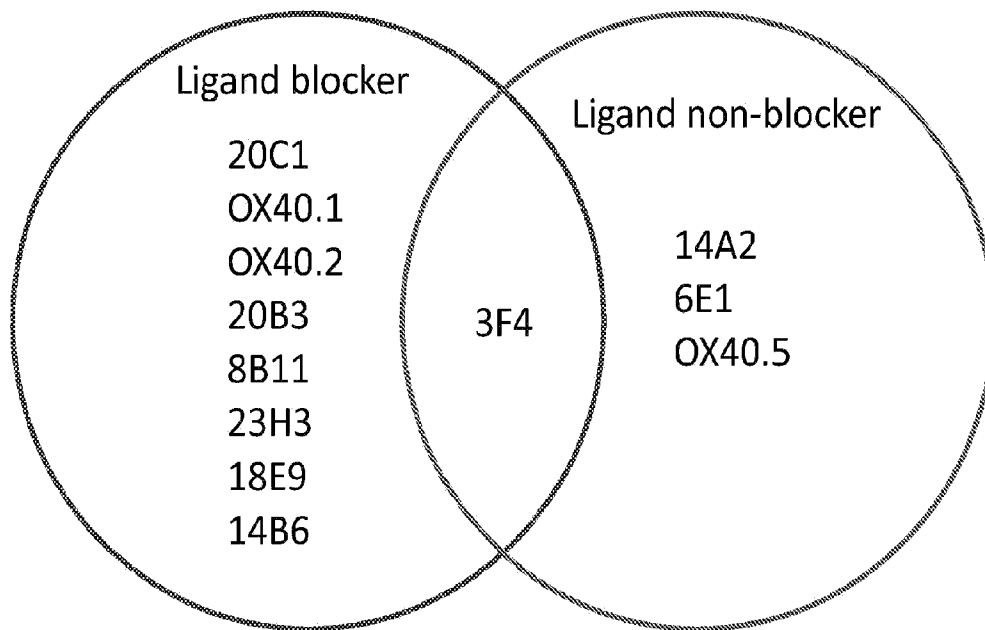


Figure 17

- 3F4.G11.D2
- ▲ 8B11.H9.C1
- ◆ 20C1.F2.D1
- ▼ 23H3.C6
- 6E1.A12.A2
- 14A2.B9.B12
- ▽ 14B6.C5.C8
- ▨ 18E9.G5
- 20B3.G12.A2
- ✕ OX40.1
- ✦ hlgG1 iso ctrl
- * PE-L106 only
- ▤ PE-mG1 iso ctrl
- Unstained cells

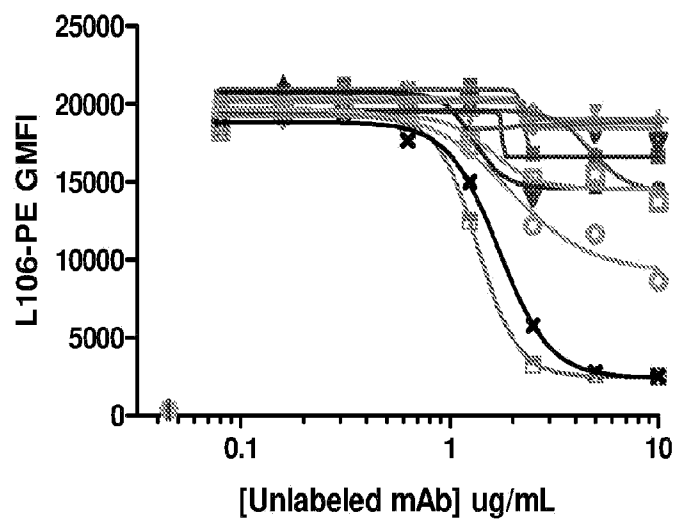


Figure 18

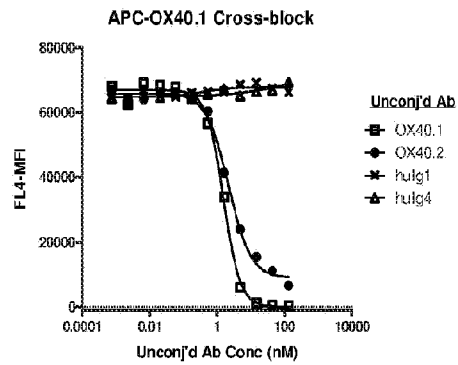


Figure 19A

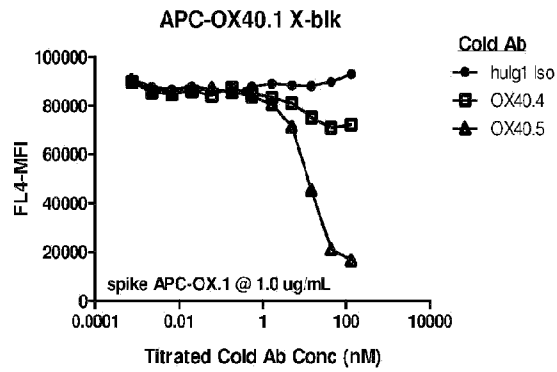
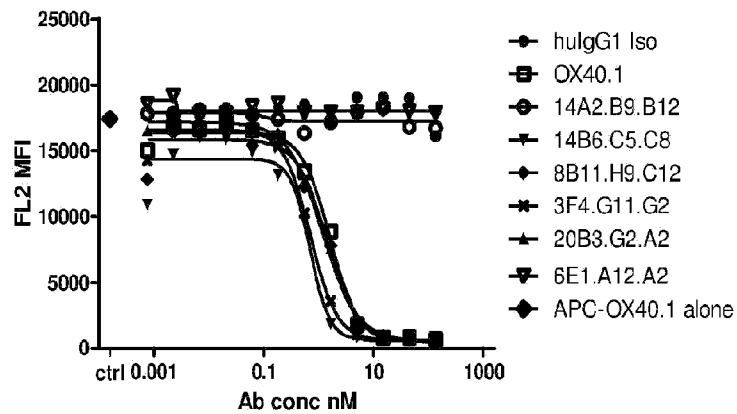


Figure 19B

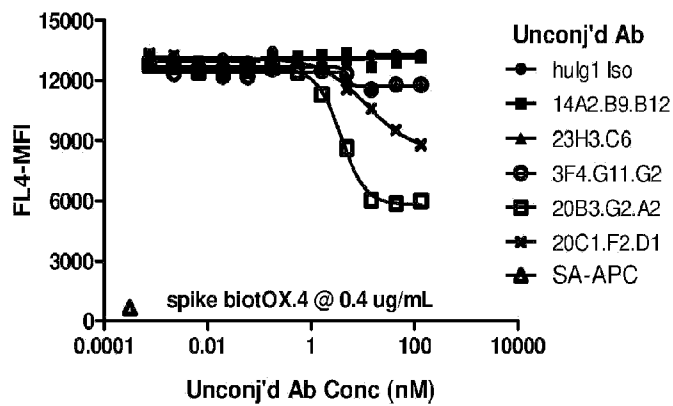
**OX40 HuMab cross-block of OX40.1 binding
to HT1080-hOX40 cells**



	IC50
OX40.1	1.589
14A2.B9.B12	0.1037
14B6.C5.C8	0.6997
8B11.H9.C12	1.410
3F4.G11.G2	0.7062
20B3.G2.A2	1.165
6E1.A12.A2	~ 0.002489

Figure 19C

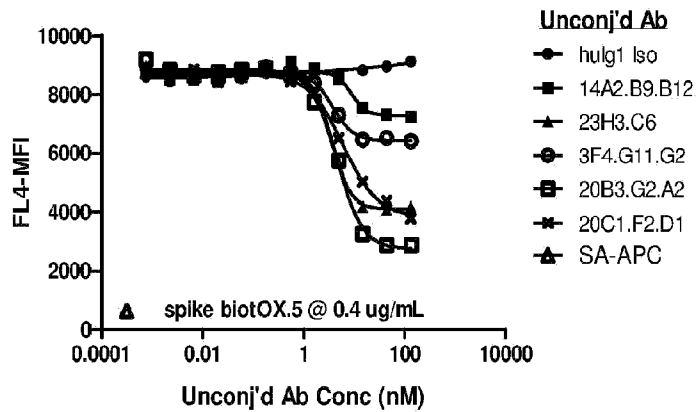
Cross-block of the Binding of biotOX40.4



	14A2.B9.B12	23H3.C6	3F4.G11.G2	20B3.G2.A2	20C1.F2.D1
EC50				3.862	12.06

Figure 19D

Cross-block of the Binding of biotOX40.5



	14A2.B9.B12	23H3.C6	3F4.G11.G2	20B3.G2.A2	20C1.F2.D1
EC50	8.888	3.684	3.714	4.539	6.134

Figure 19E

Cross-block of the Binding of biotOX40.4

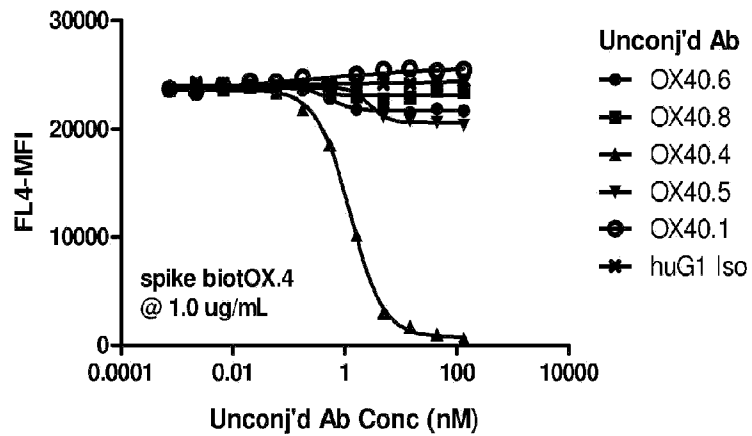
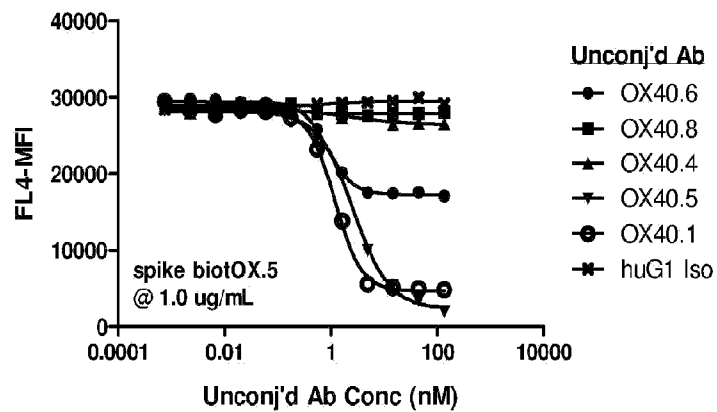


Figure 19F

Cross-block of the Binding of biotOX40.5



	OX40.6	OX40.8	OX40.4	OX40.5	OX40.1
EC50	0.857			2.669	1.190

Figure 19G

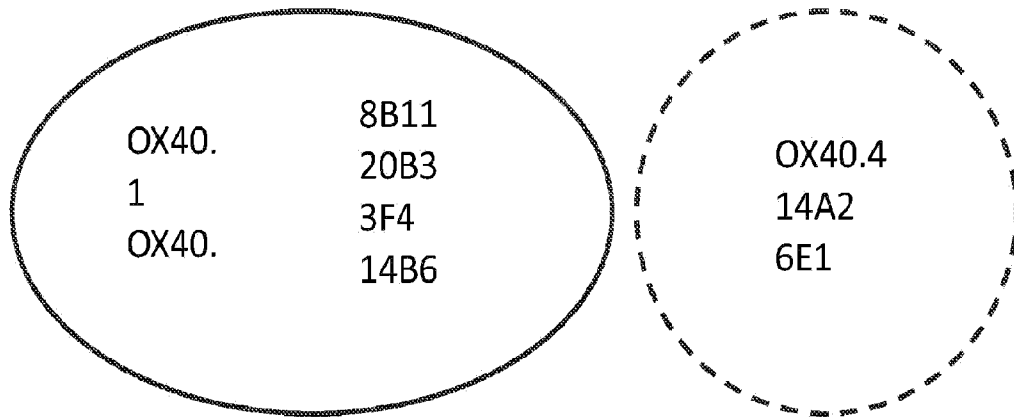


Figure 19H

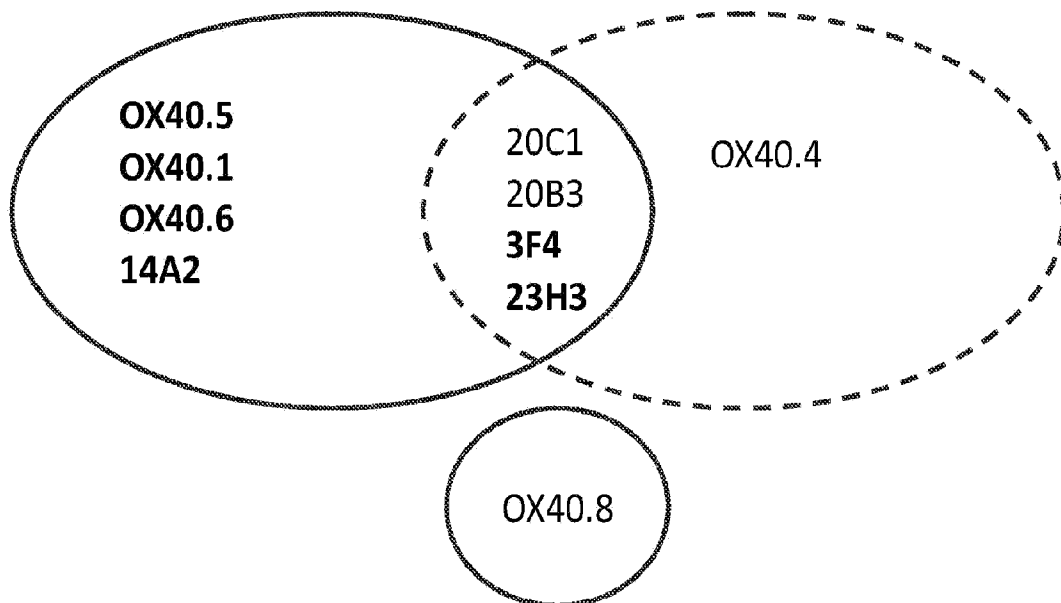


Figure 19I

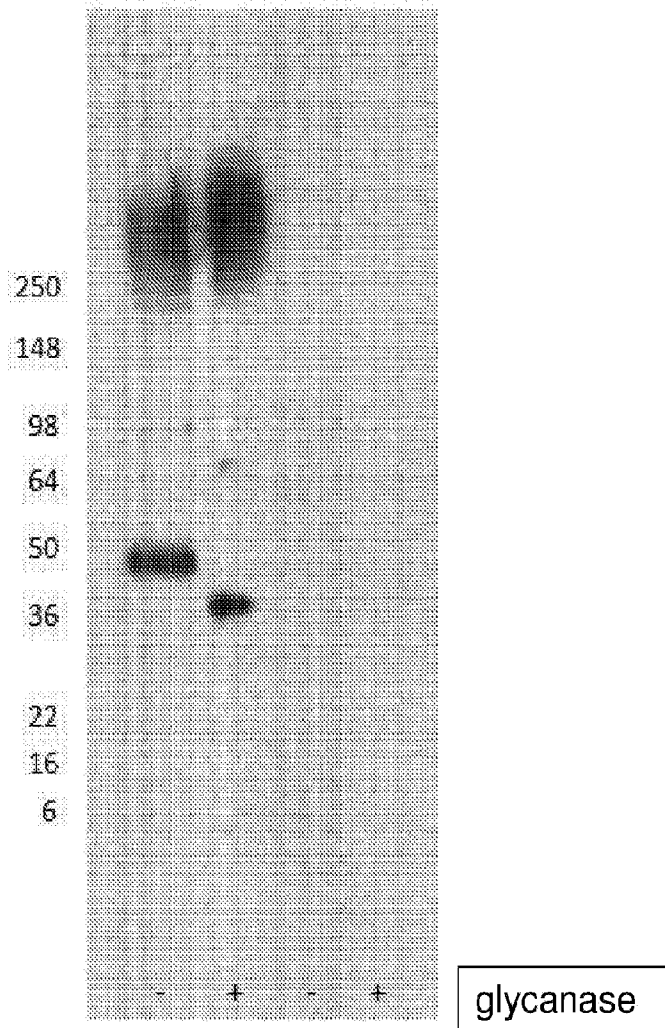


Figure 20A

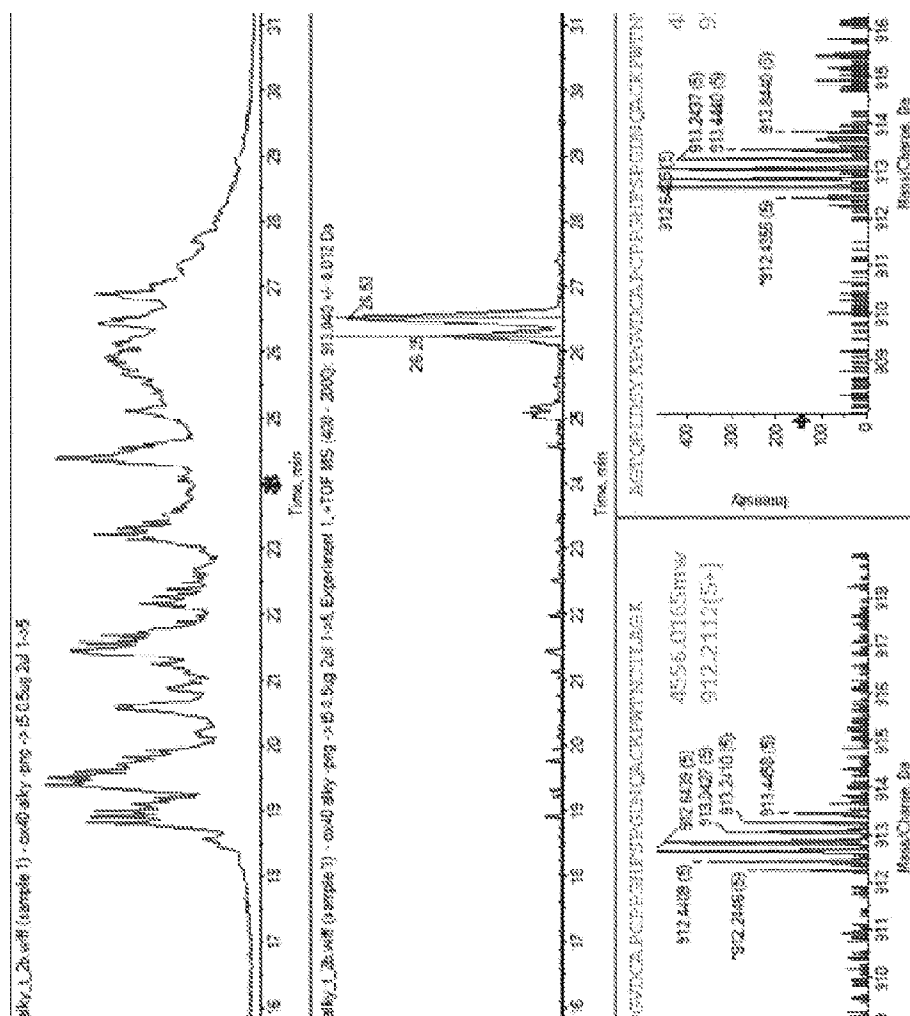


Figure 20B

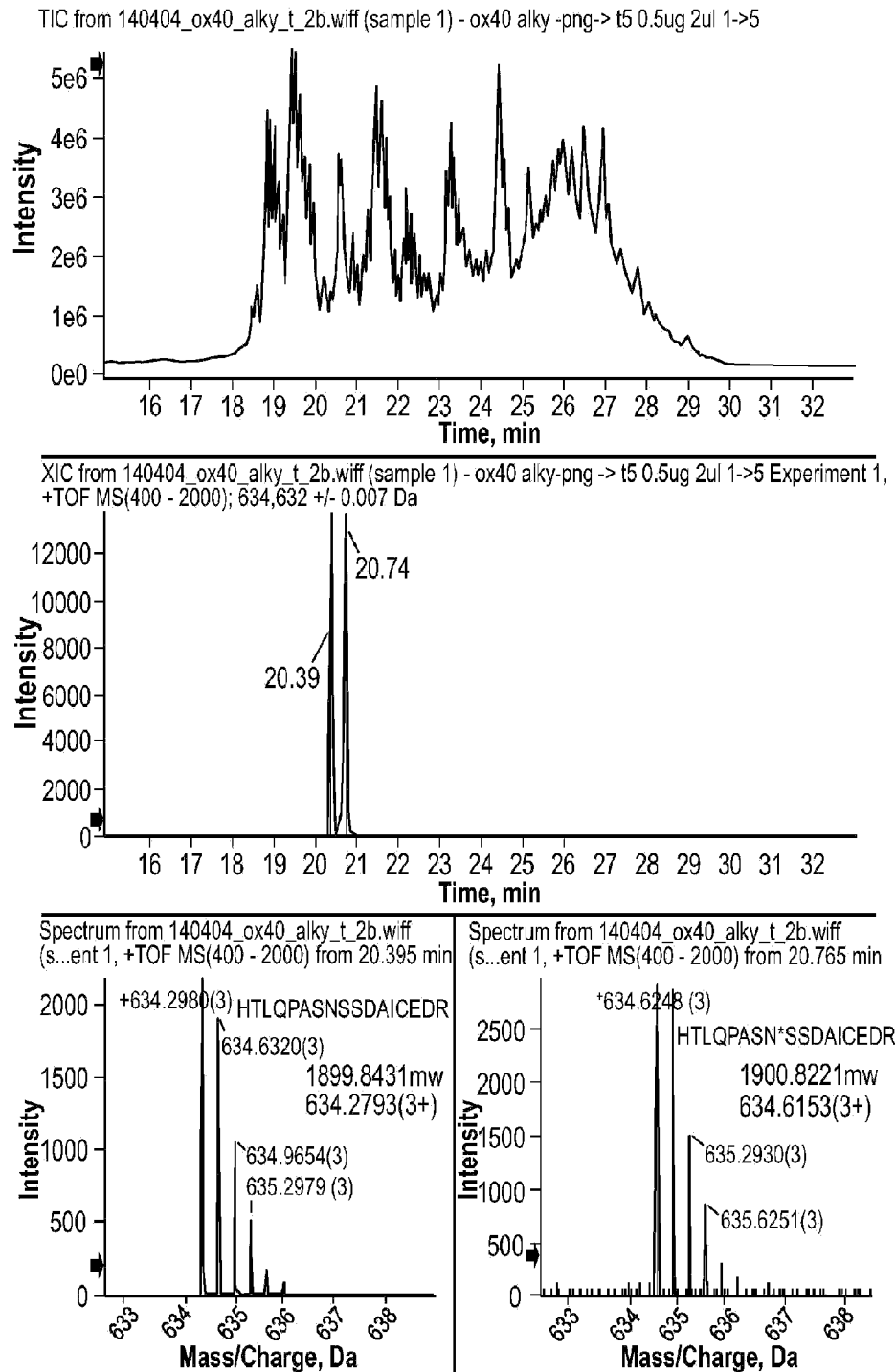


Figure 20C

* 42 * * *
 LHCVGDTYPS NDRCCHECRP GNGMVSRCSR SQNTVCRPCG PGFYNDVVSS
 | | | | |
 * * * * *
 KPCKPCTWCN LRSGSERKQL CTATQDTVCR CRAGTQPLDS VKPGVDCAPC
 | | | | |
 PPGHFSPGDN QACKPWTNCT LAGKHTLOPA SNSSDAICED RDPPATQPQE
 TQGPPARPIT VQTEAWPRT SQGPSTRPVE VPGGRAVHHH HHHH

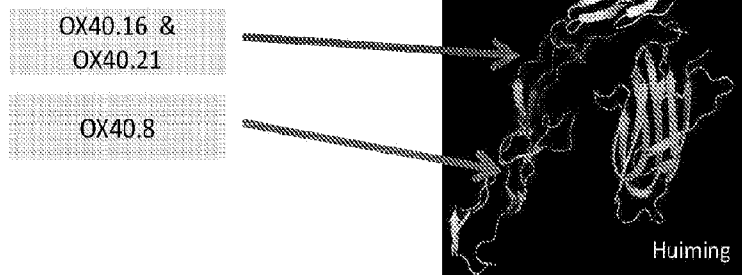


Figure 20D

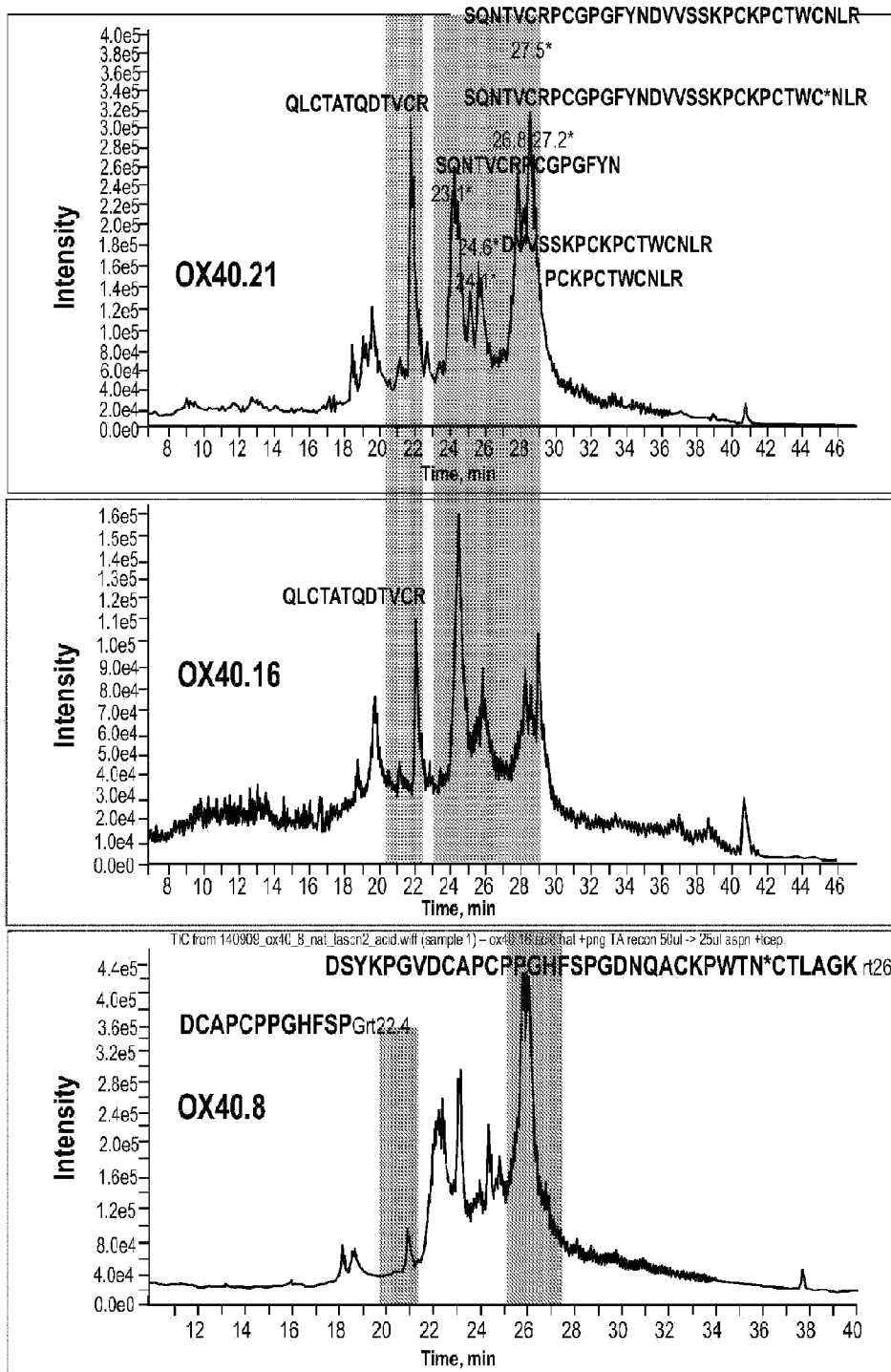


Figure 20E

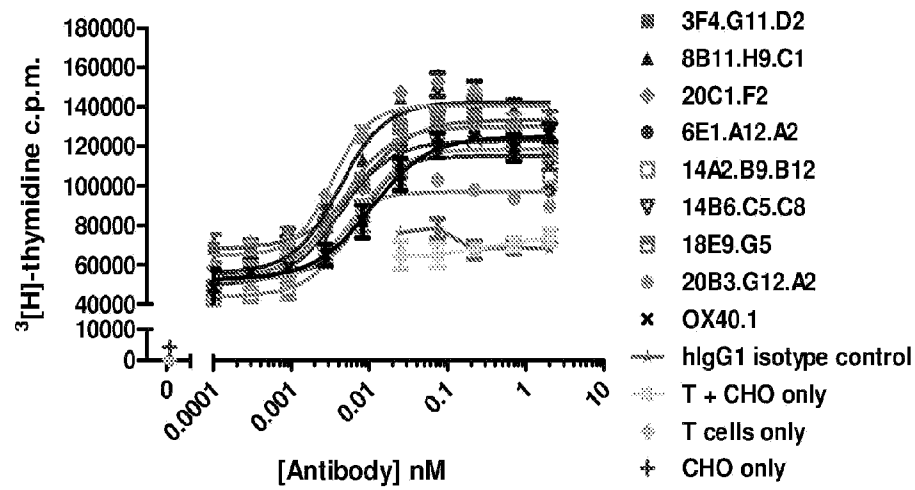


Figure 21A

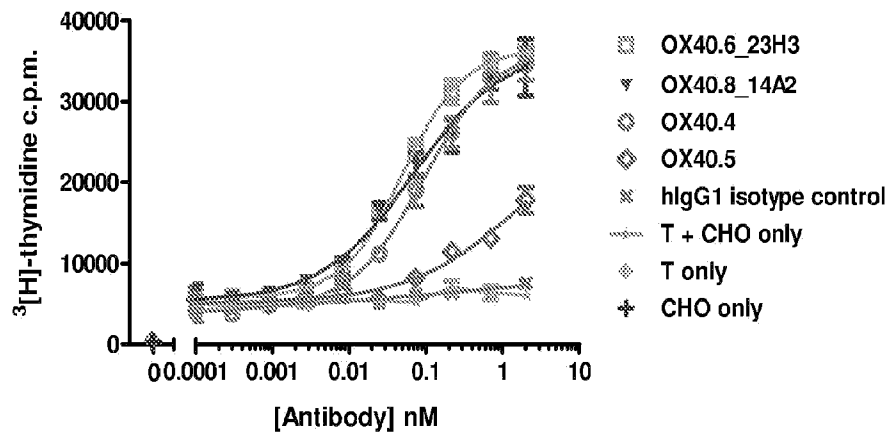


Figure 21B

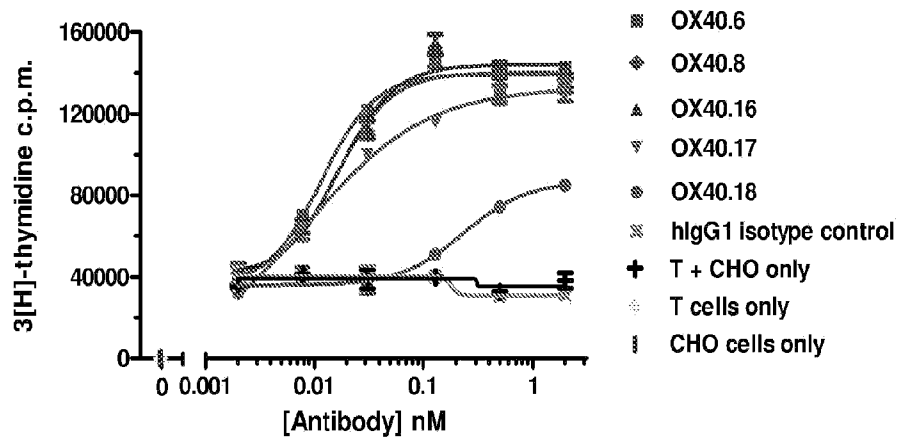


Figure 21C

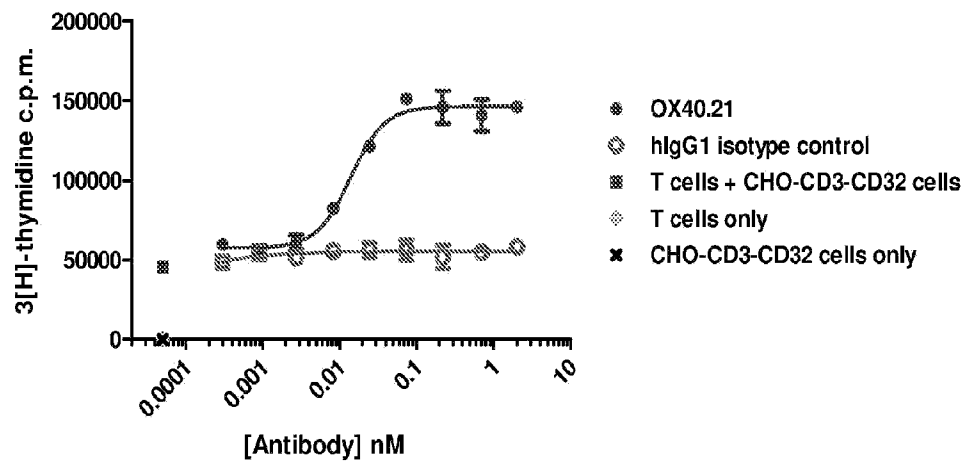


Figure 21D

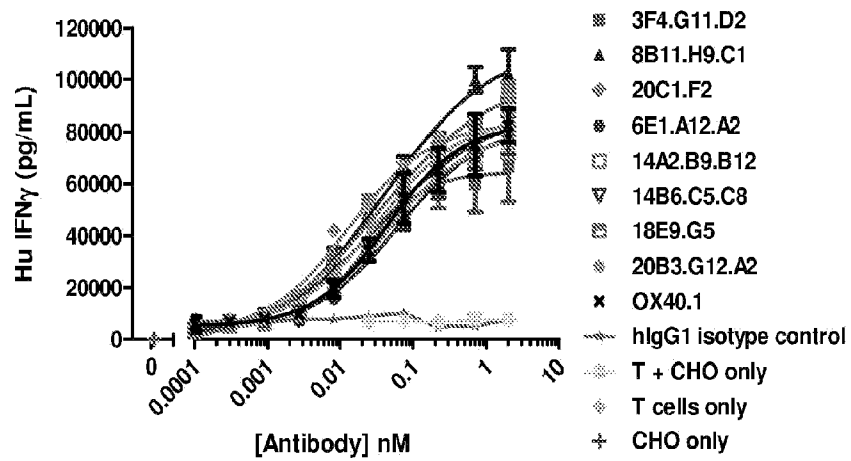


Figure 22A

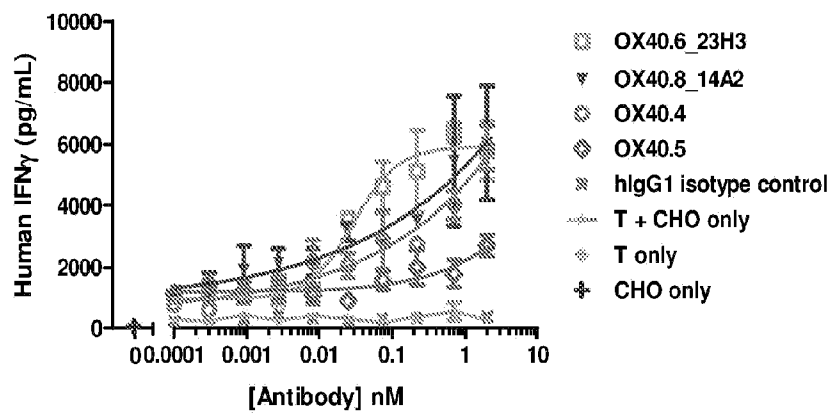


Figure 22B

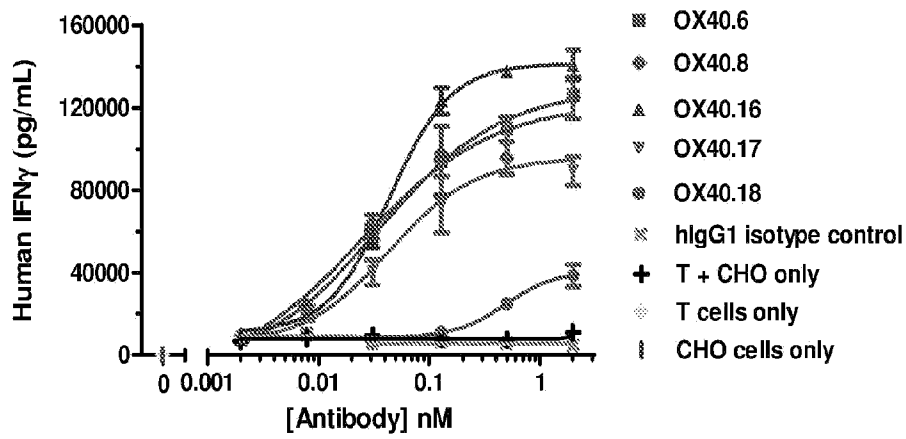


Figure 22C

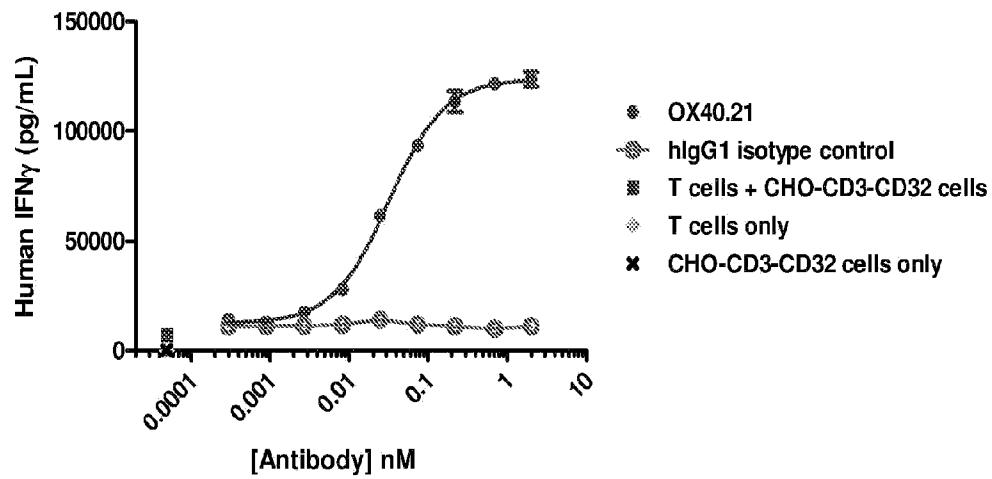
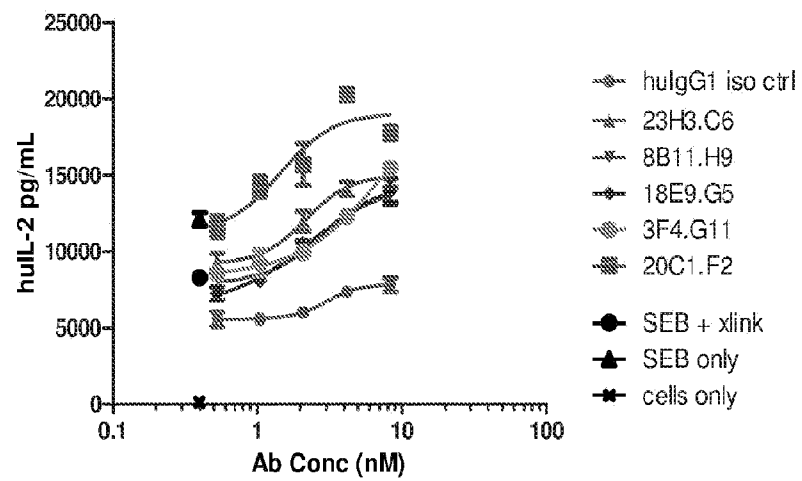


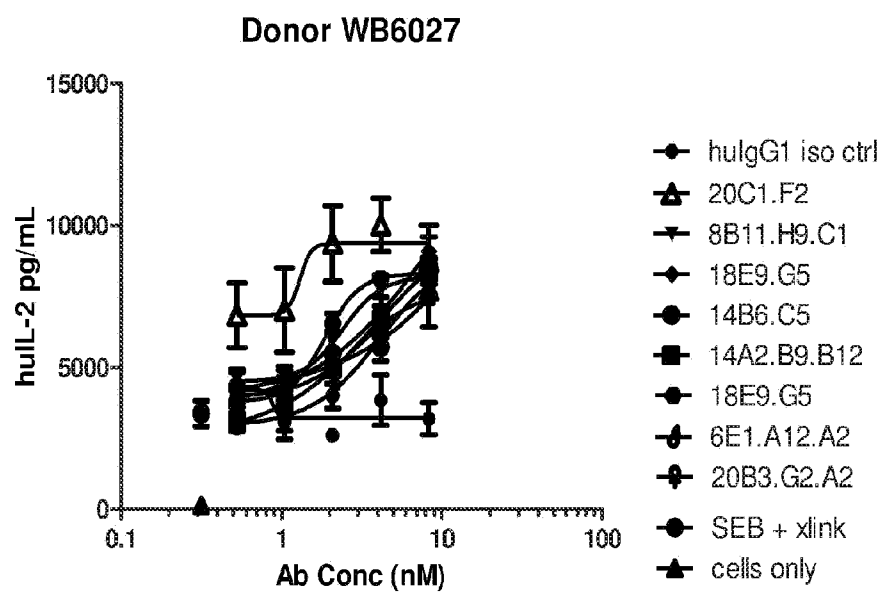
Figure 22D

Donor WB5522



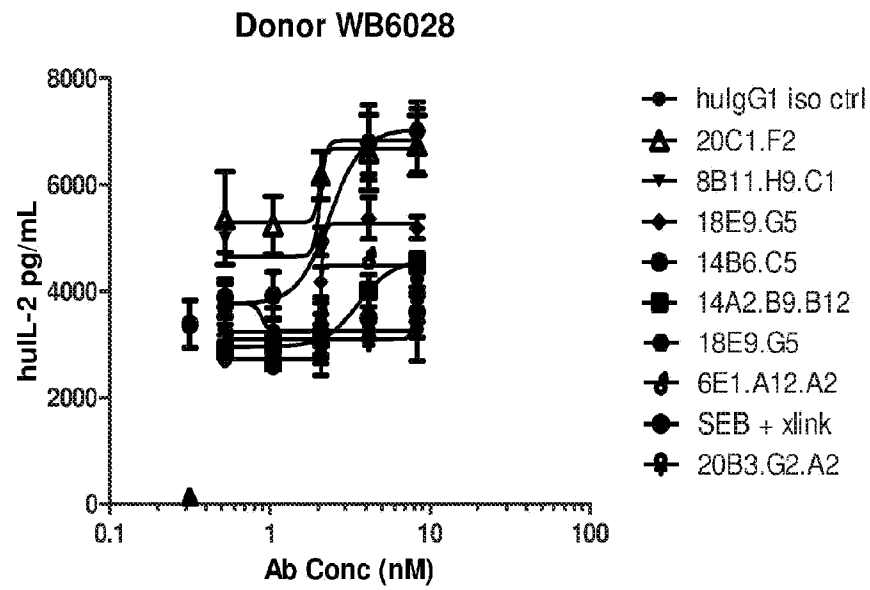
	EC50 (nM)
23H3.C6	2.177
8B11.H9	2.801
18E9.G5	2.395
3F4.G11	6.916
20C1.F2	1.459

Figure 23A



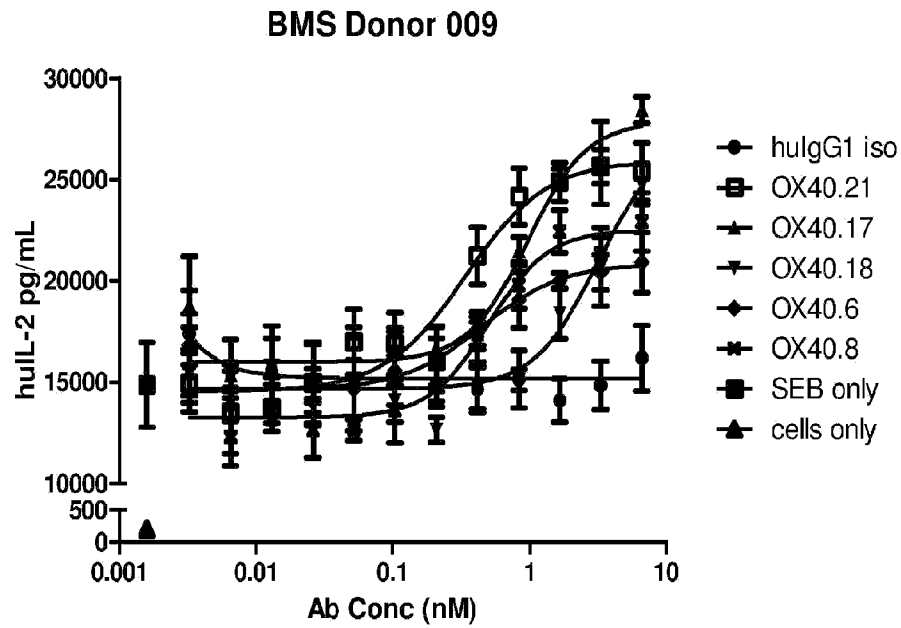
	EC50 (nM)
20C1.F2	1.30
8B11.H9.C1	2.409
3F4.G11.D2	11.94
14B6.C5	~ 1274
14A2.B9.B12	3.816
18E9.G5	1.865
6E1.A12.A2	4.113
20B3.G2.A2	3.112

Figure 23B



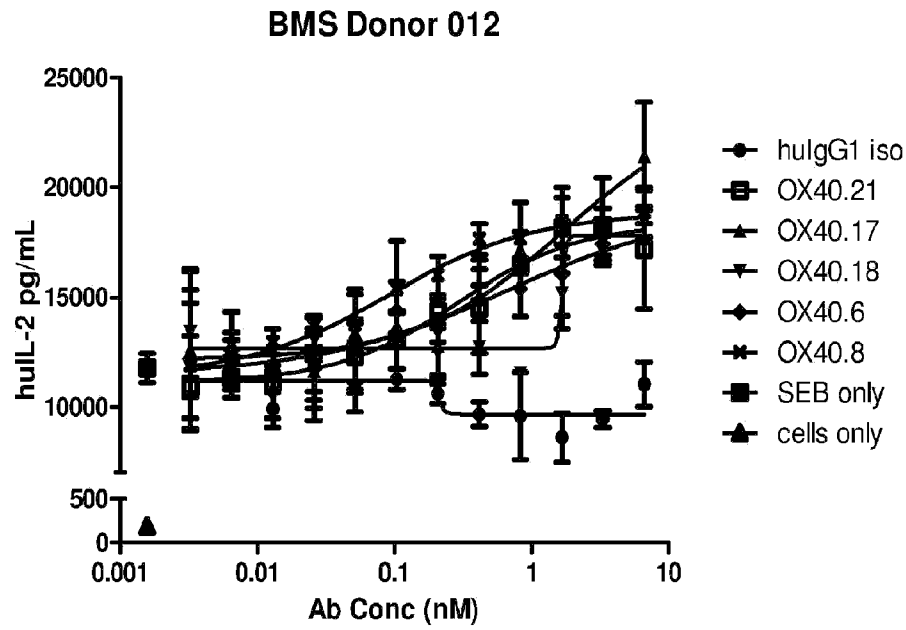
	EC50
20C1.F2	~ 2.045
8B11.H9.C1	~ 2.061
3F4.G11.D2	~ 2.099
14B6.C5	
14A2.B9.B12	3.608
18E9.G5	2.379
6E1.A12.A2	~ 2.092
20B3.G2.A2	~ 8.295

Figure 23C



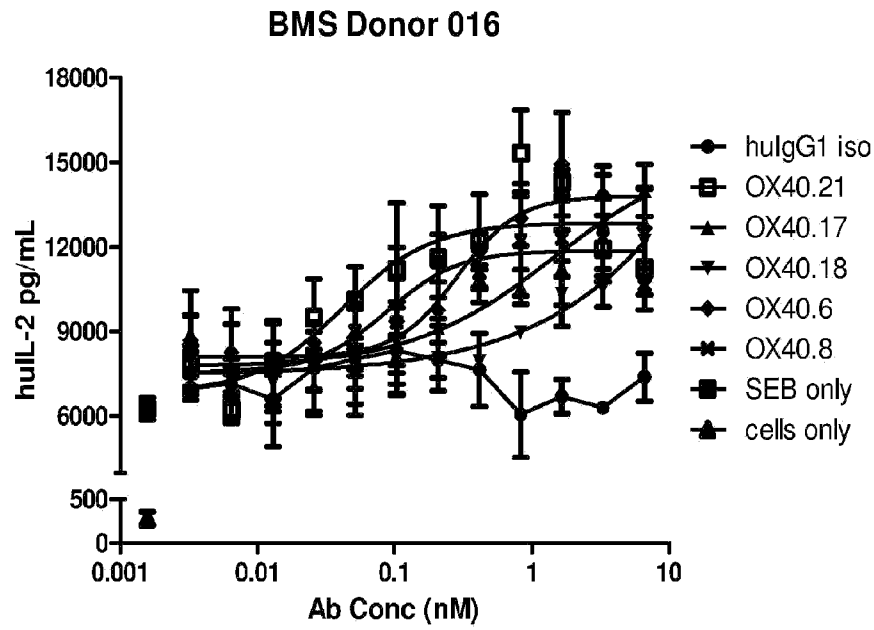
	EC50
OX40.21	0.343
OX40.17	0.965
OX40.18	3.210
OX40.6	0.451
OX40.8	0.503

Figure 23D



	EC50
OX40.21	0.288
OX40.17	1.741
OX40.18	~ 1.669
OX40.6	0.656
OX40.8	0.093

Figure 23E



	EC50
OX40.21	0.042
OX40.17	1.396
OX40.18	~ 100.8
OX40.6	0.287
OX40.8	0.089

Figure 23F

**NK92 Lysis of activated CD4+ Tcells
OX40 mAbs**

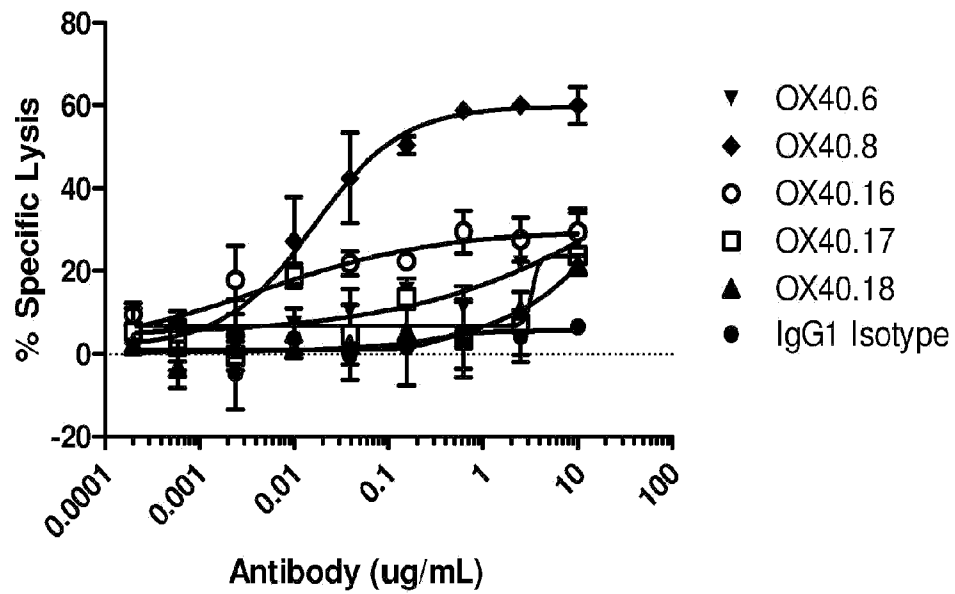


Figure 24

Target cell donor 1

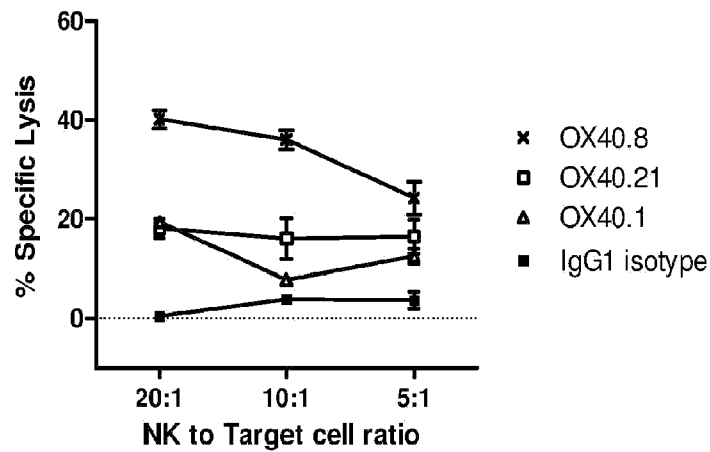


Figure 25A

Target cell donor 2

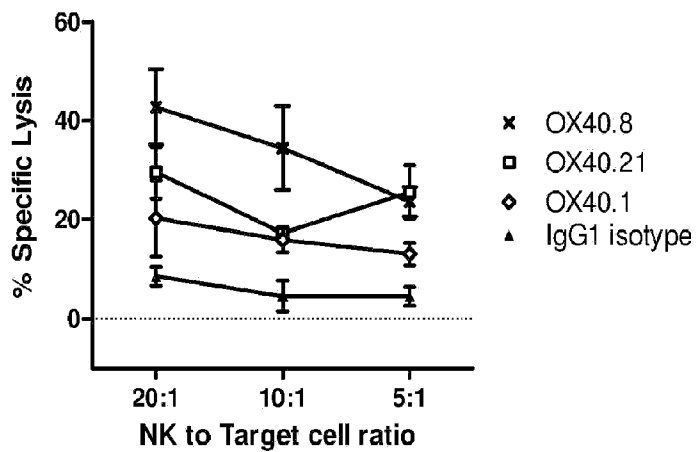


Figure 25B

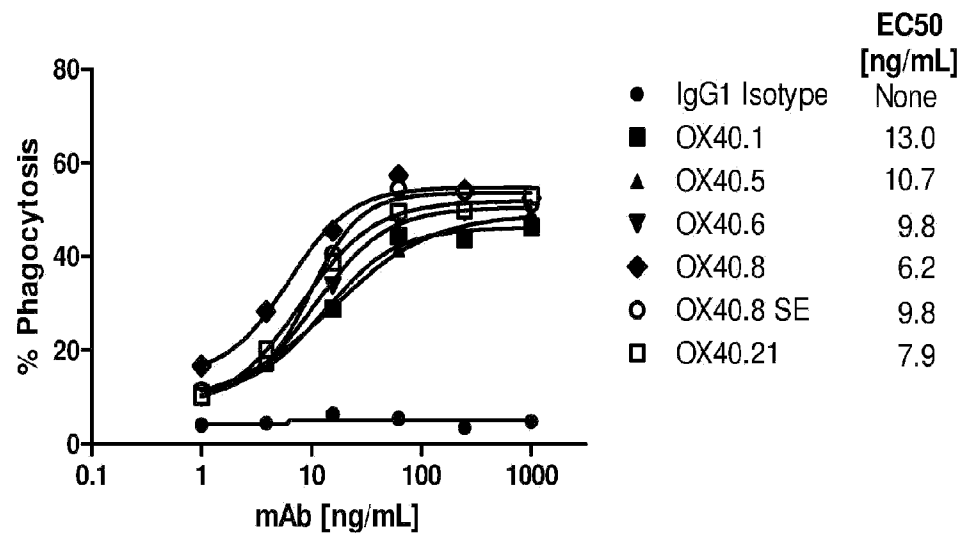


Figure 26

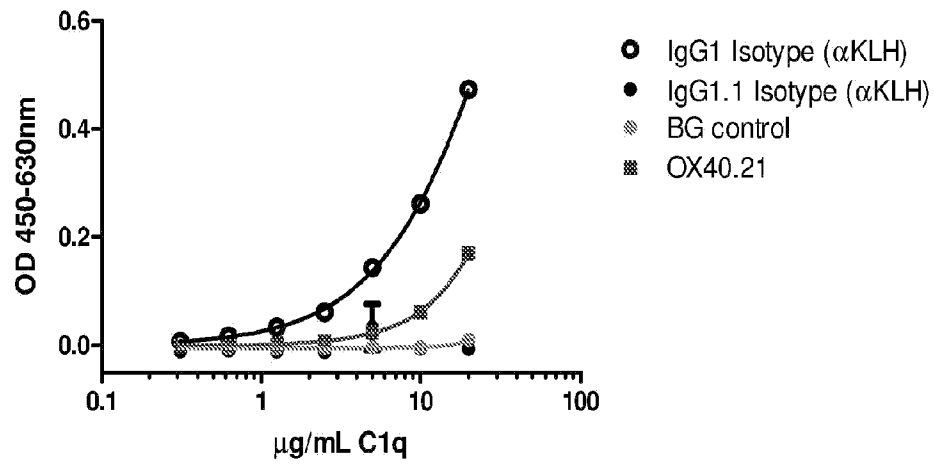


Figure 27

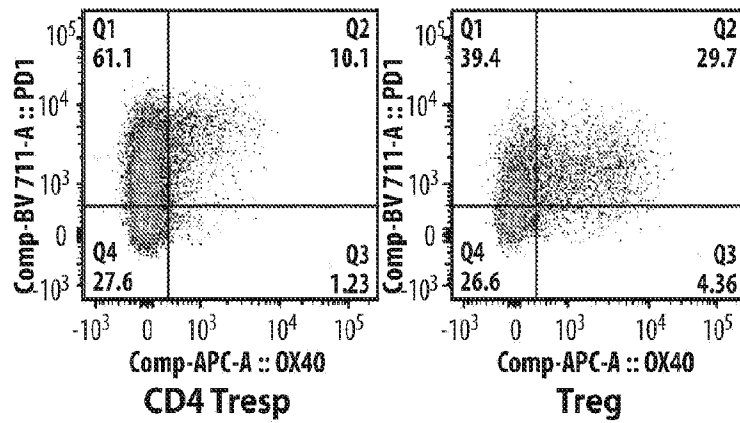


Figure 28A

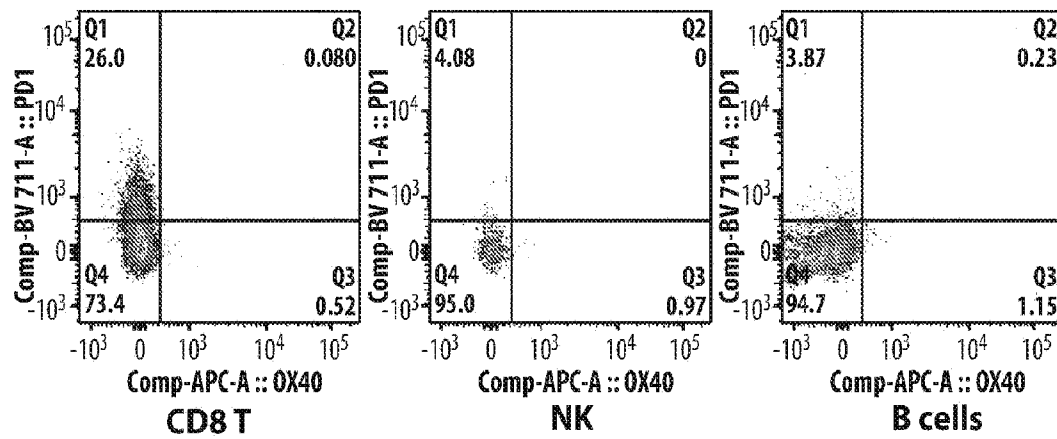
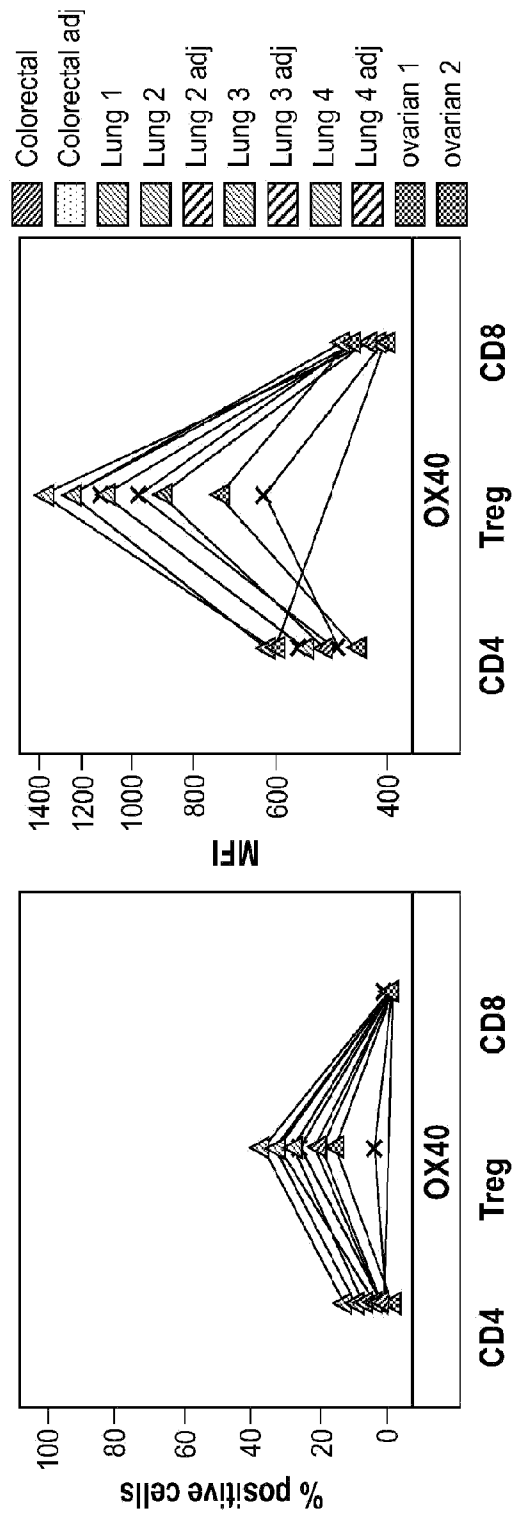


Figure 28B



x adj norm
▲ TIL

Figure 28C

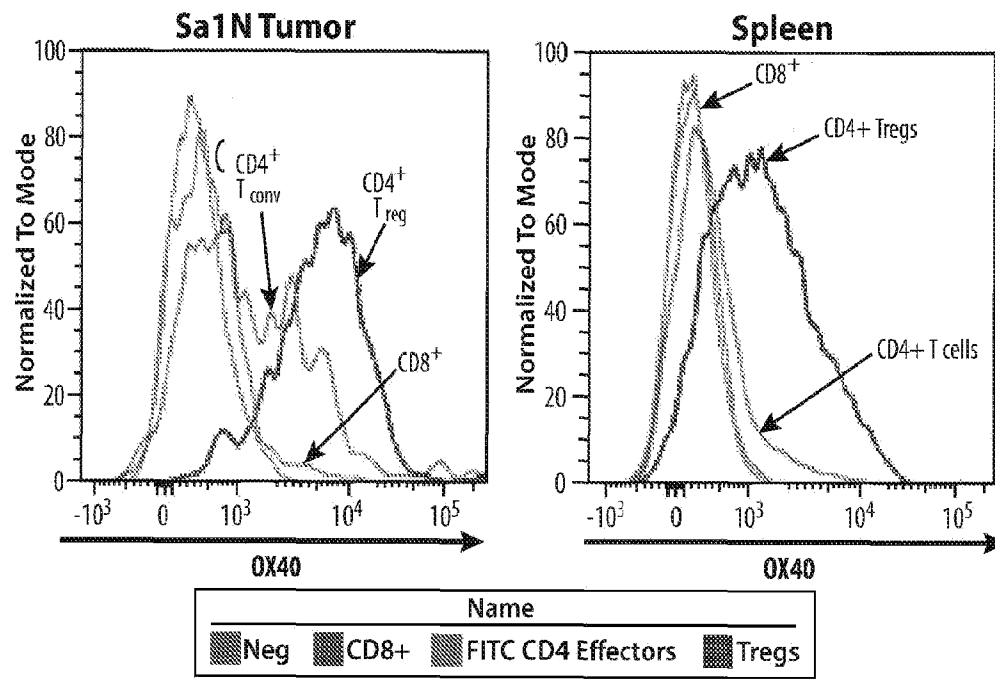


Figure 28D

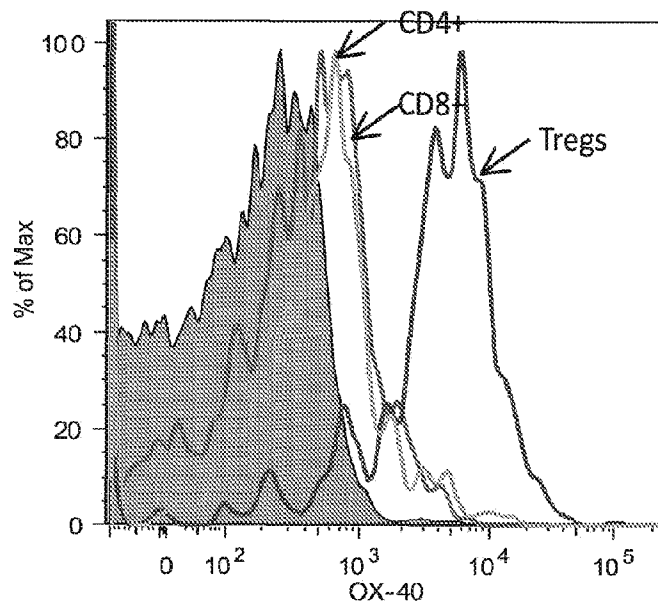


Figure 28E

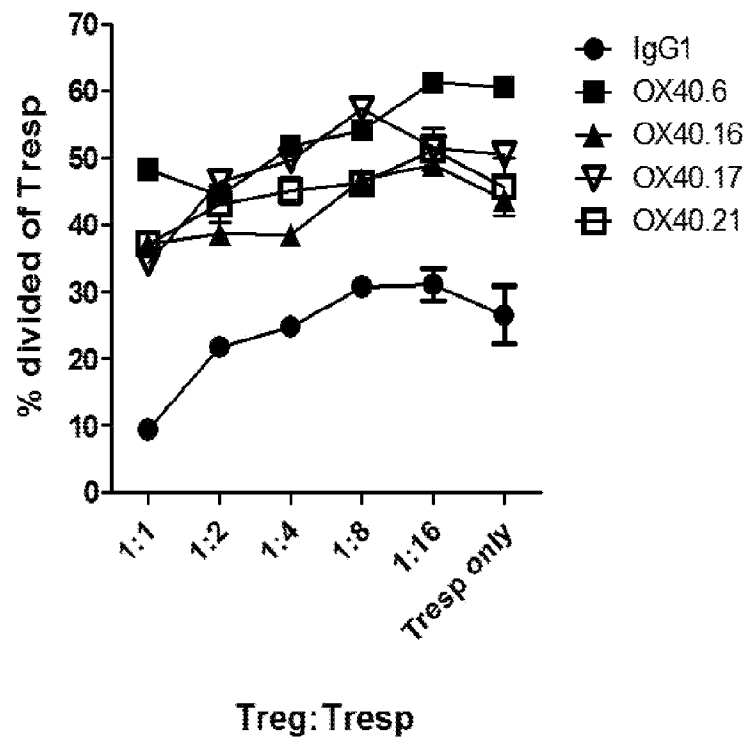


Figure 29

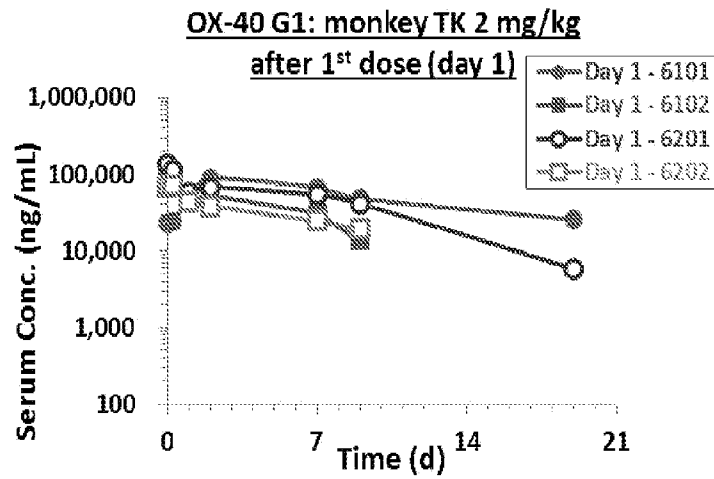


Figure 30A

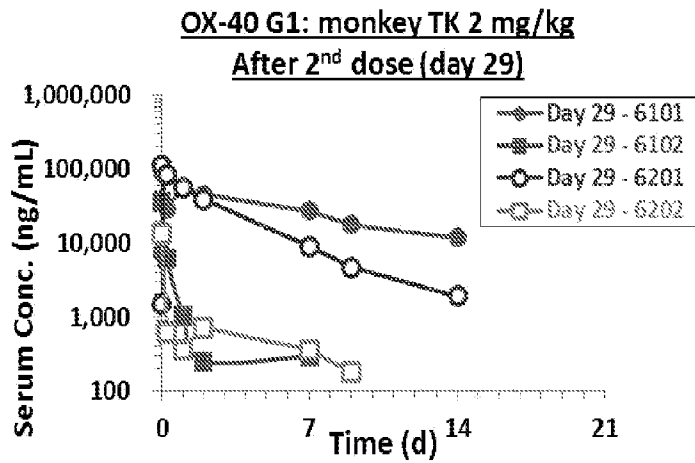


Figure 30B

Percentage Antigenicity Split by Donor

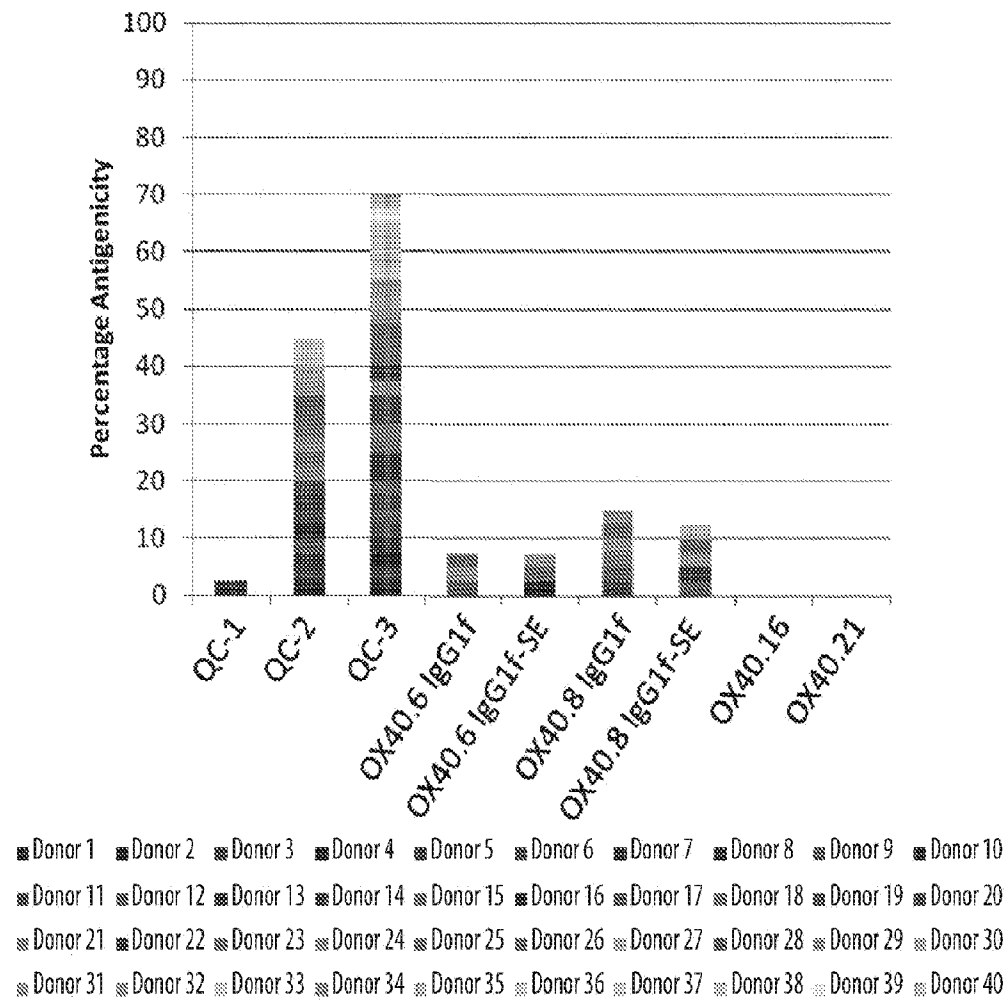


Figure 31

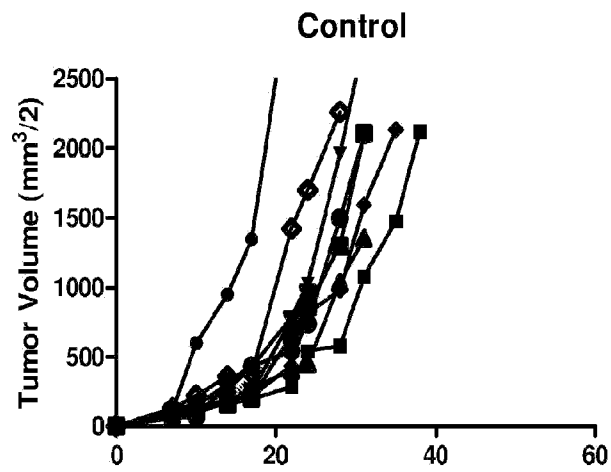


Figure 32A

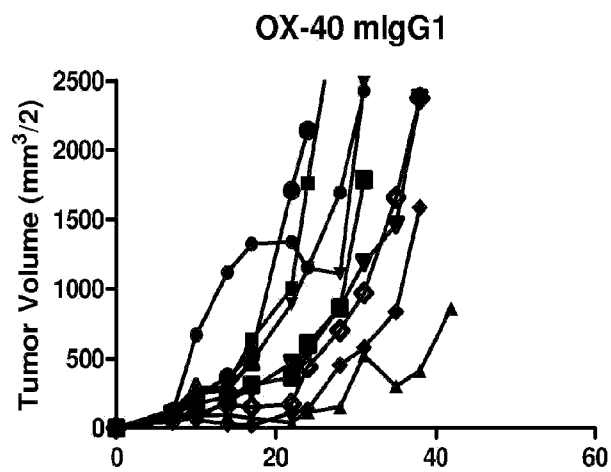


Figure 32B

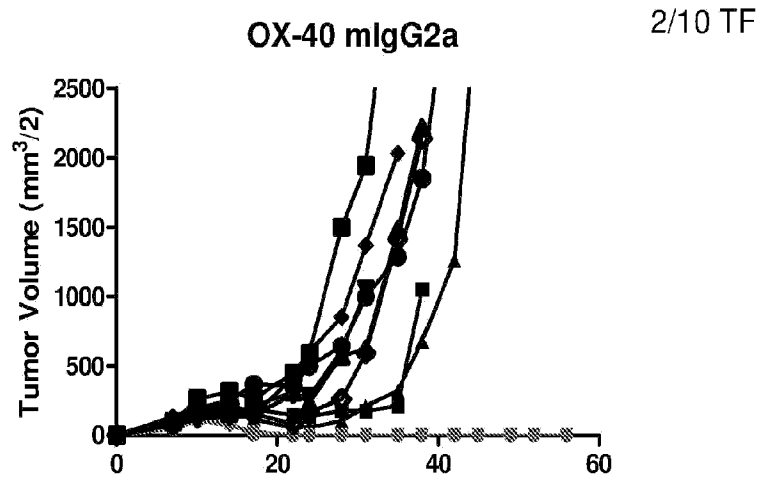
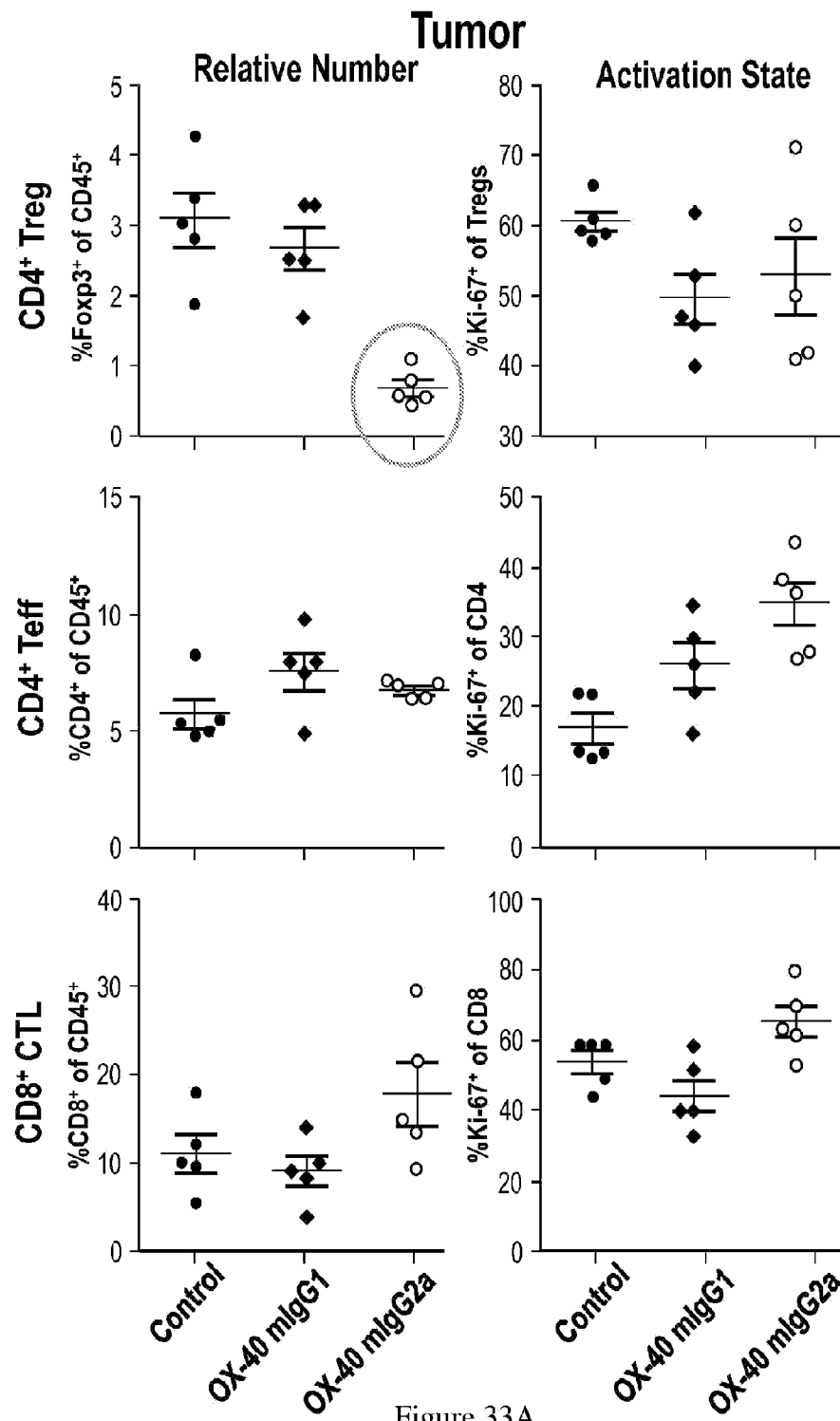


Figure 32C



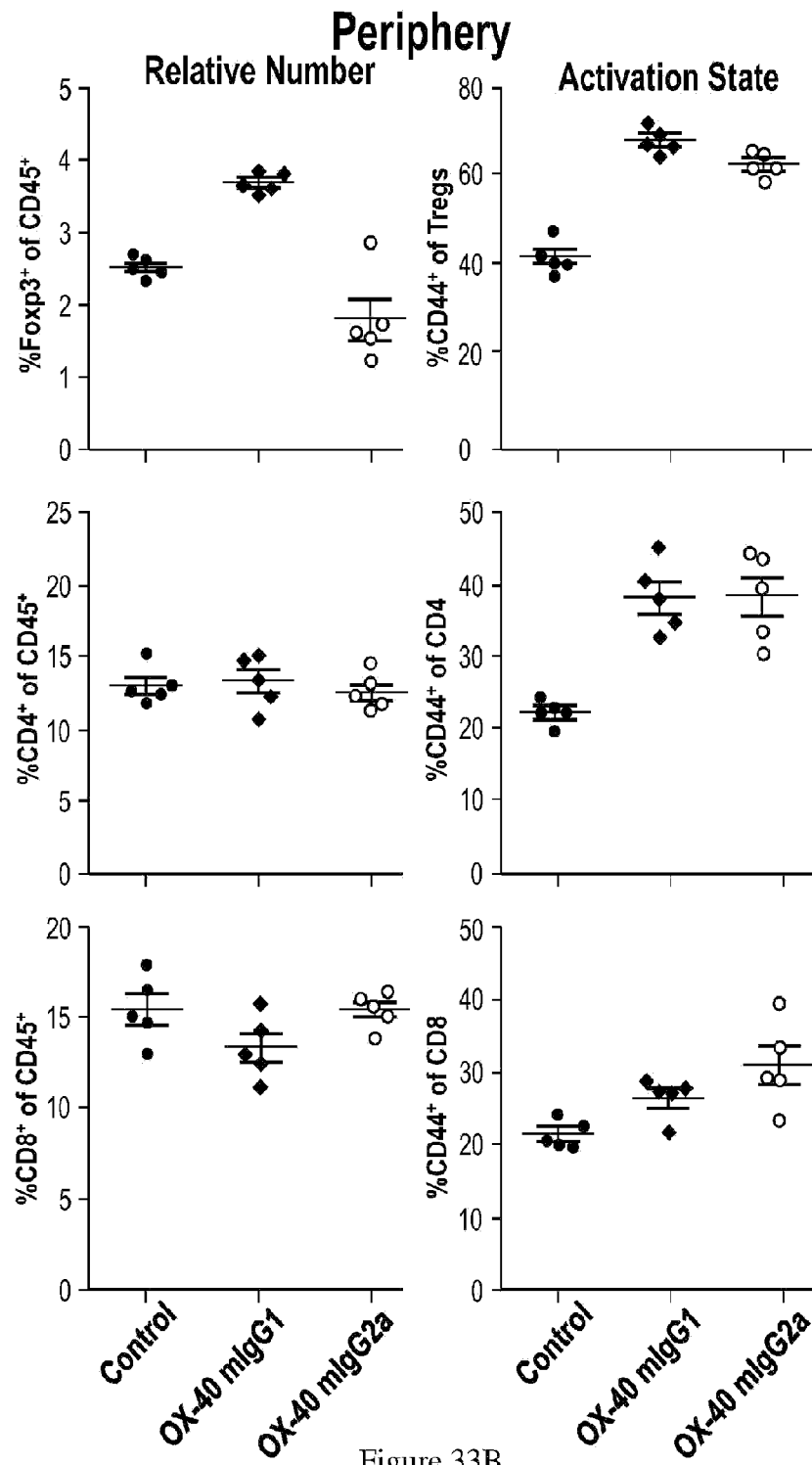


Figure 33B

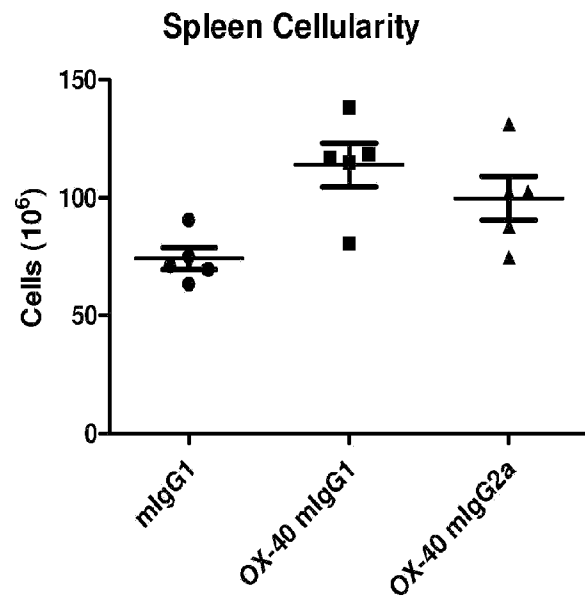


Figure 33C

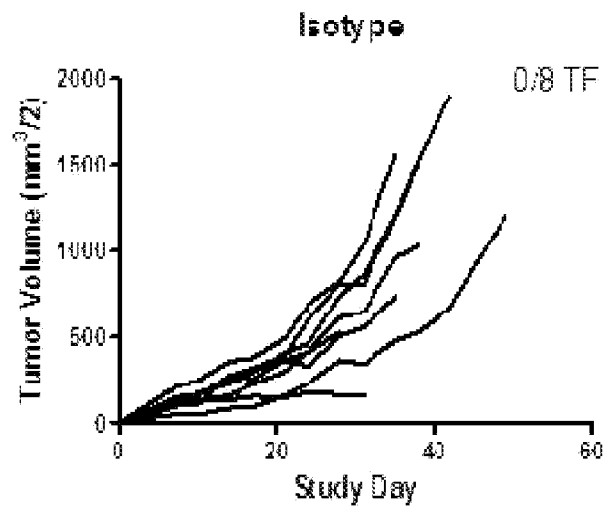


Figure 34A

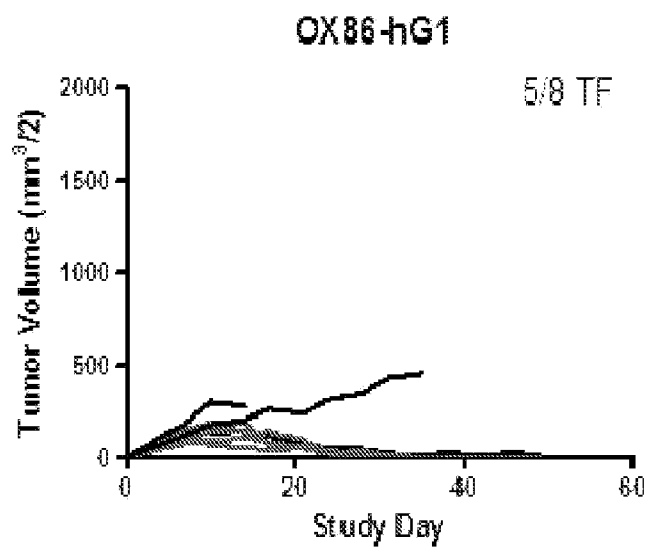


Figure 34B

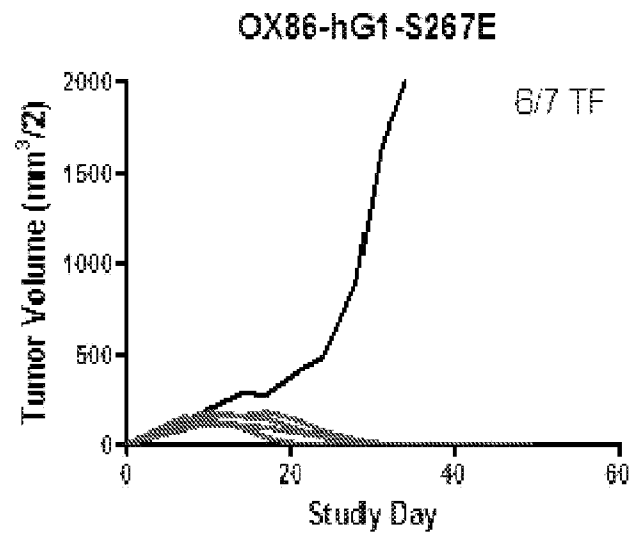


Figure 34C

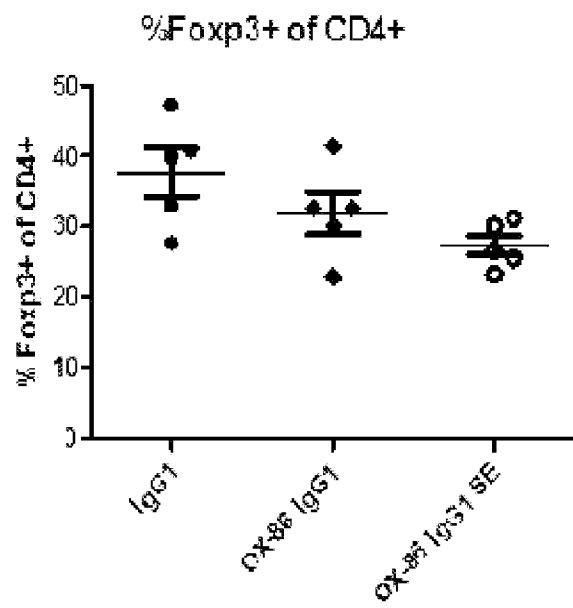


Figure 35A

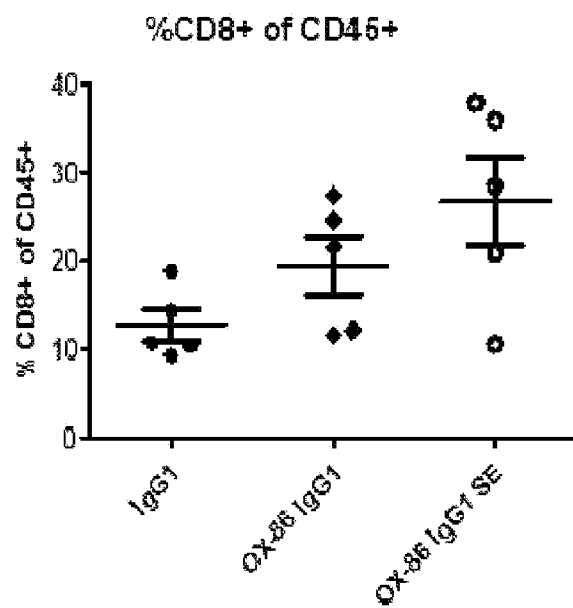


Figure 35B

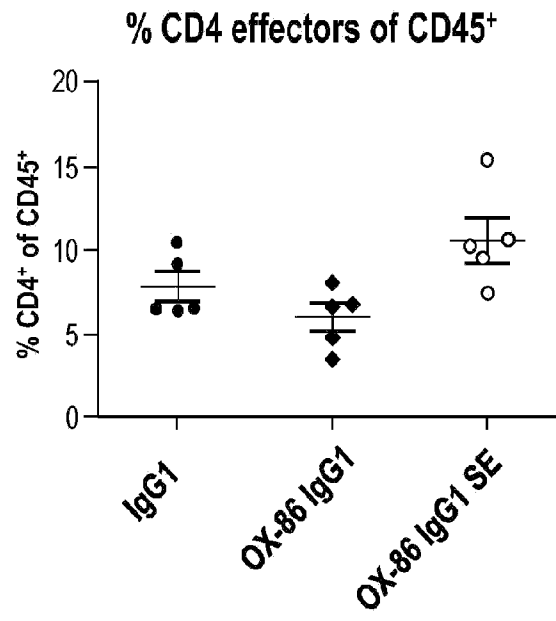


Figure 35C

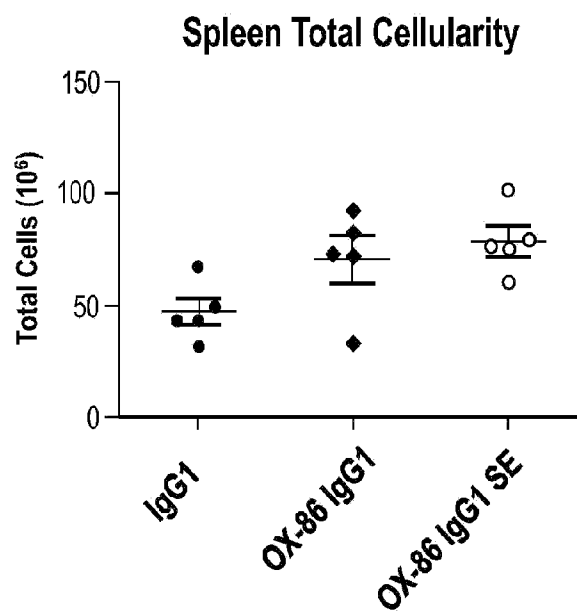


Figure 35D

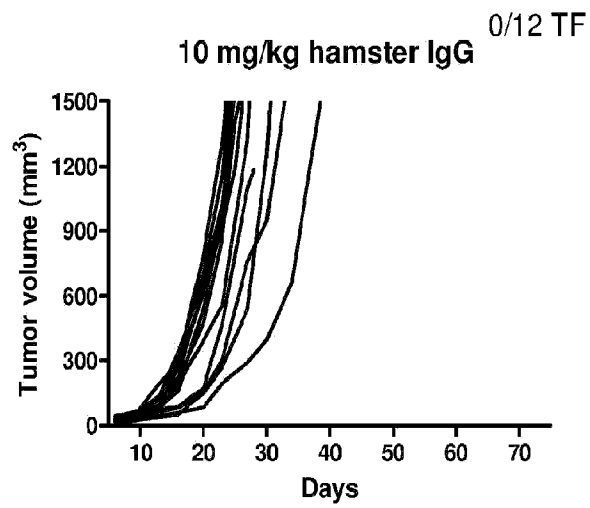


Figure 36A

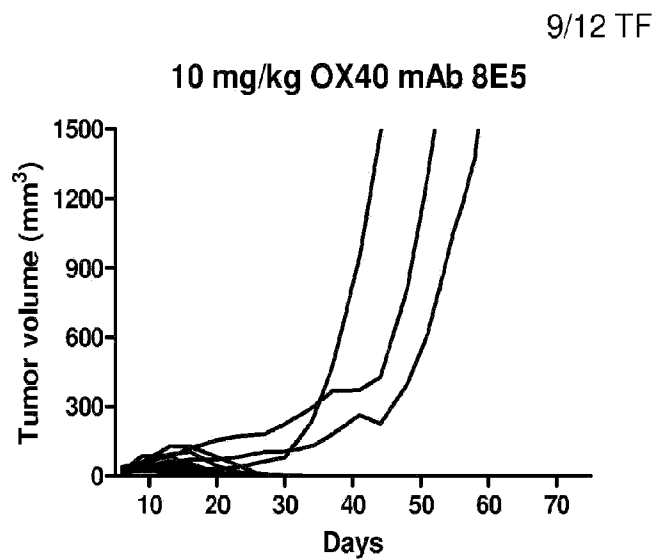


Figure 36B

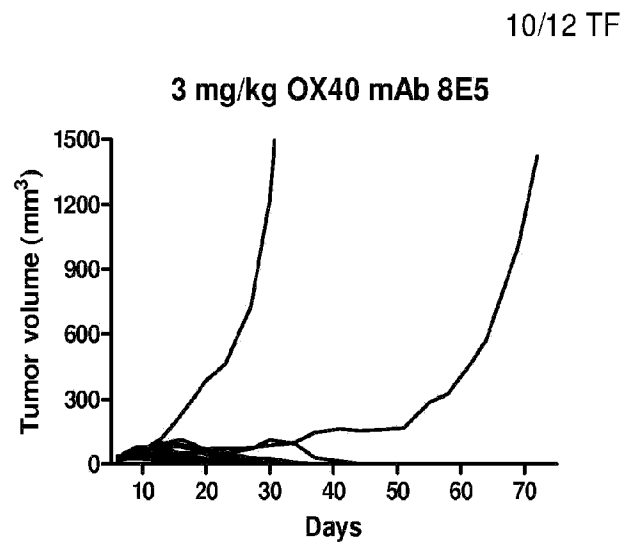


Figure 36C

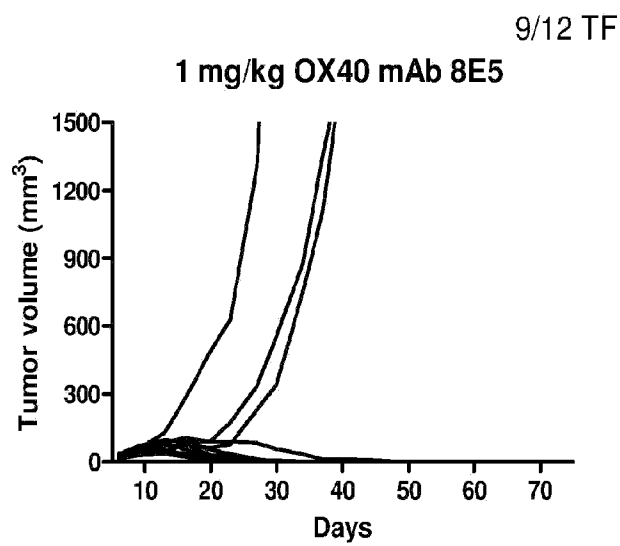


Figure 36D

10/12 TF

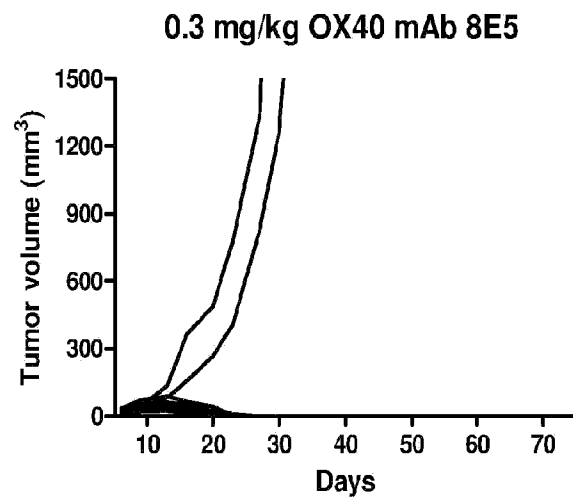


Figure 36E

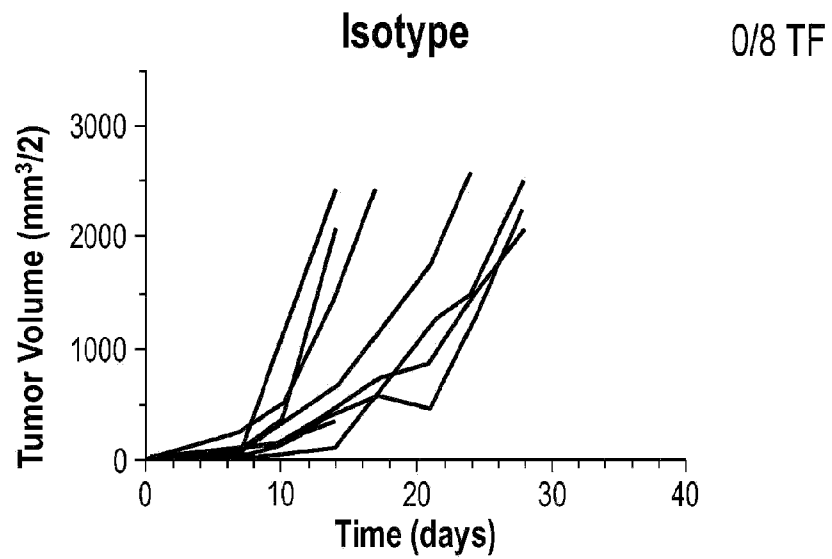


Figure 37A

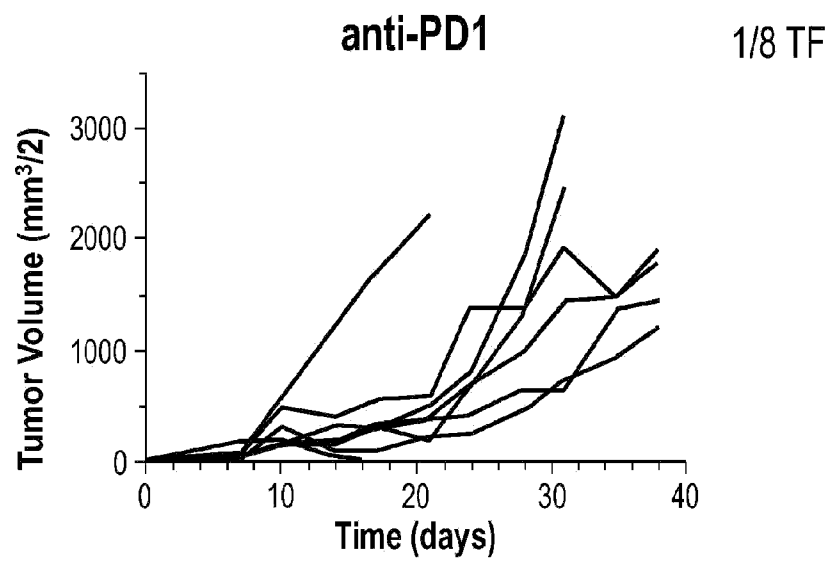


Figure 37B

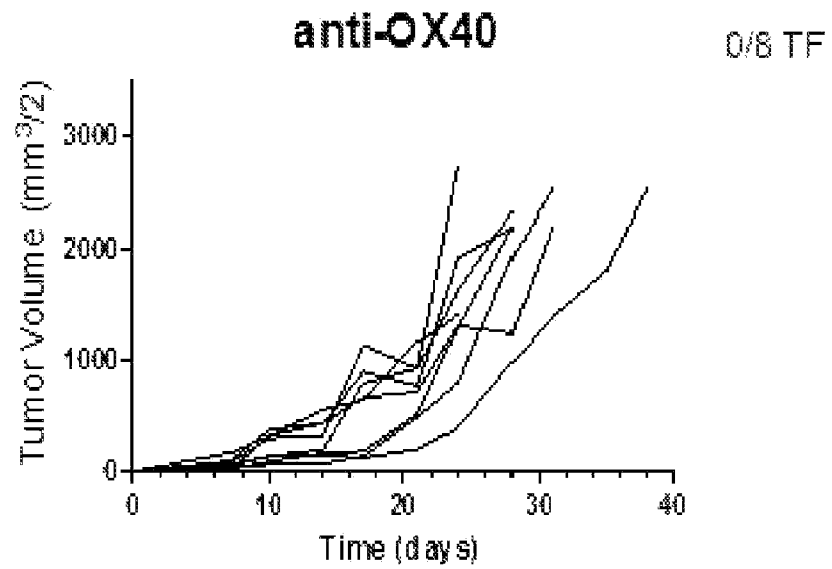


Figure 37C

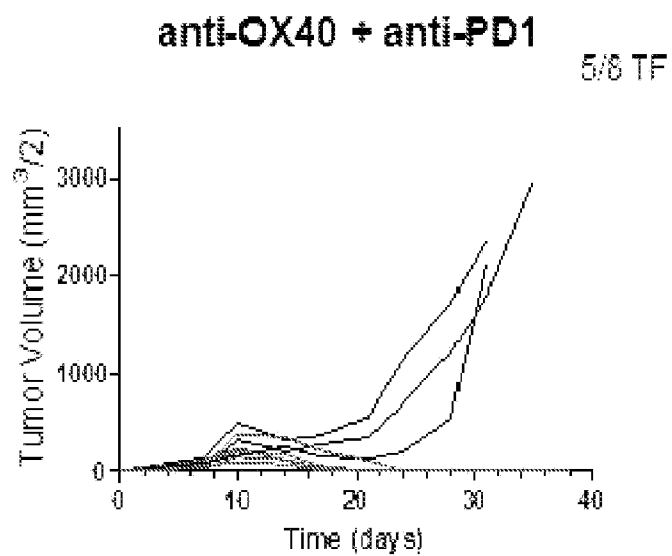


Figure 37D

KLH Ex vivo T cell response, Day 22

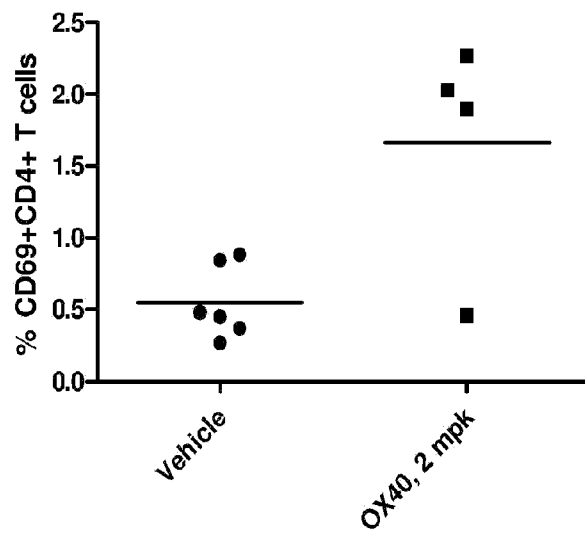


Figure 38A

KLH Ex vivo T cell response, Day 41

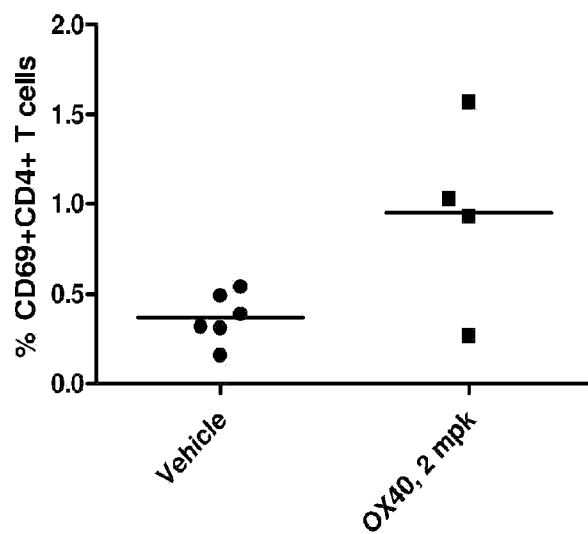


Figure 38B

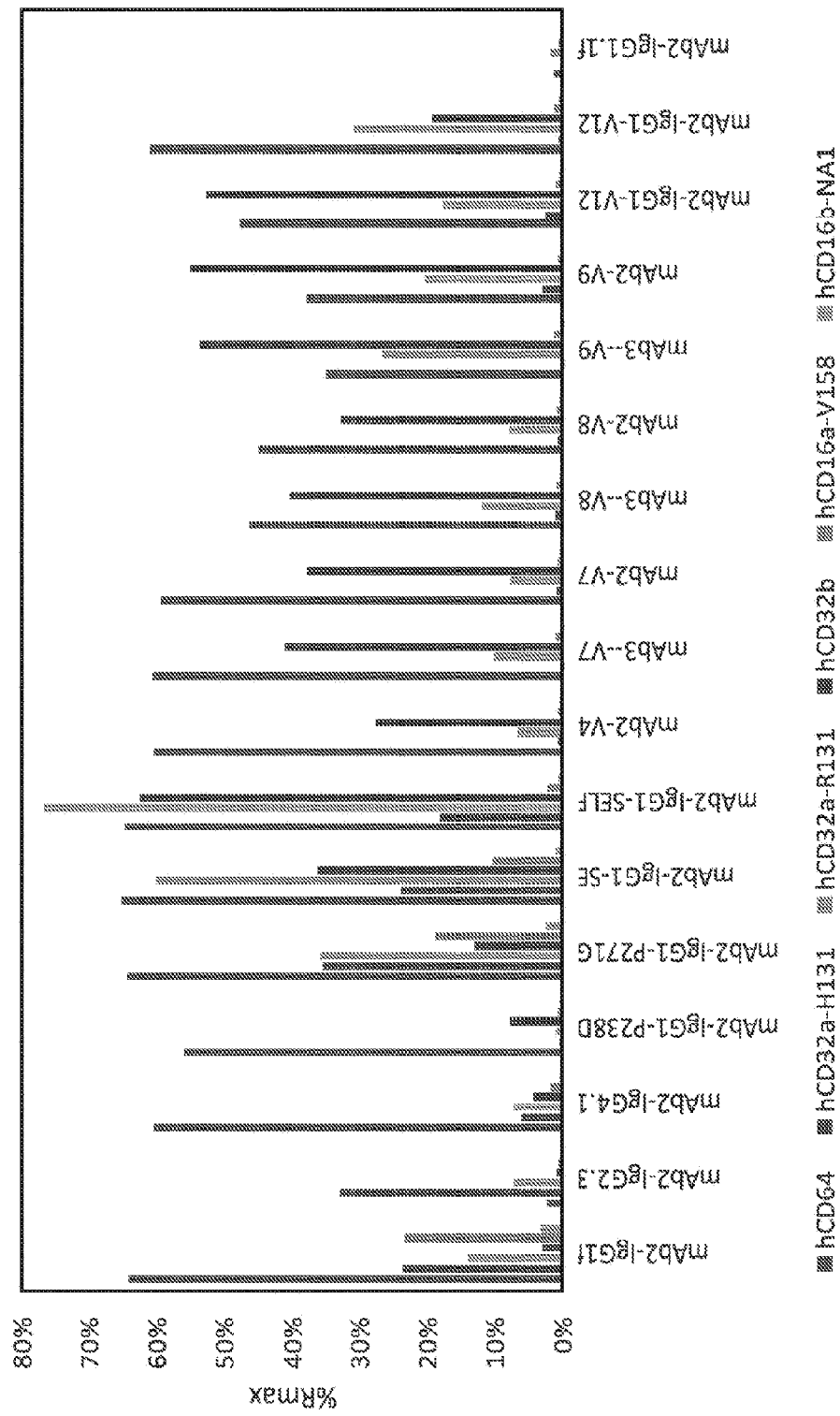


Figure 39

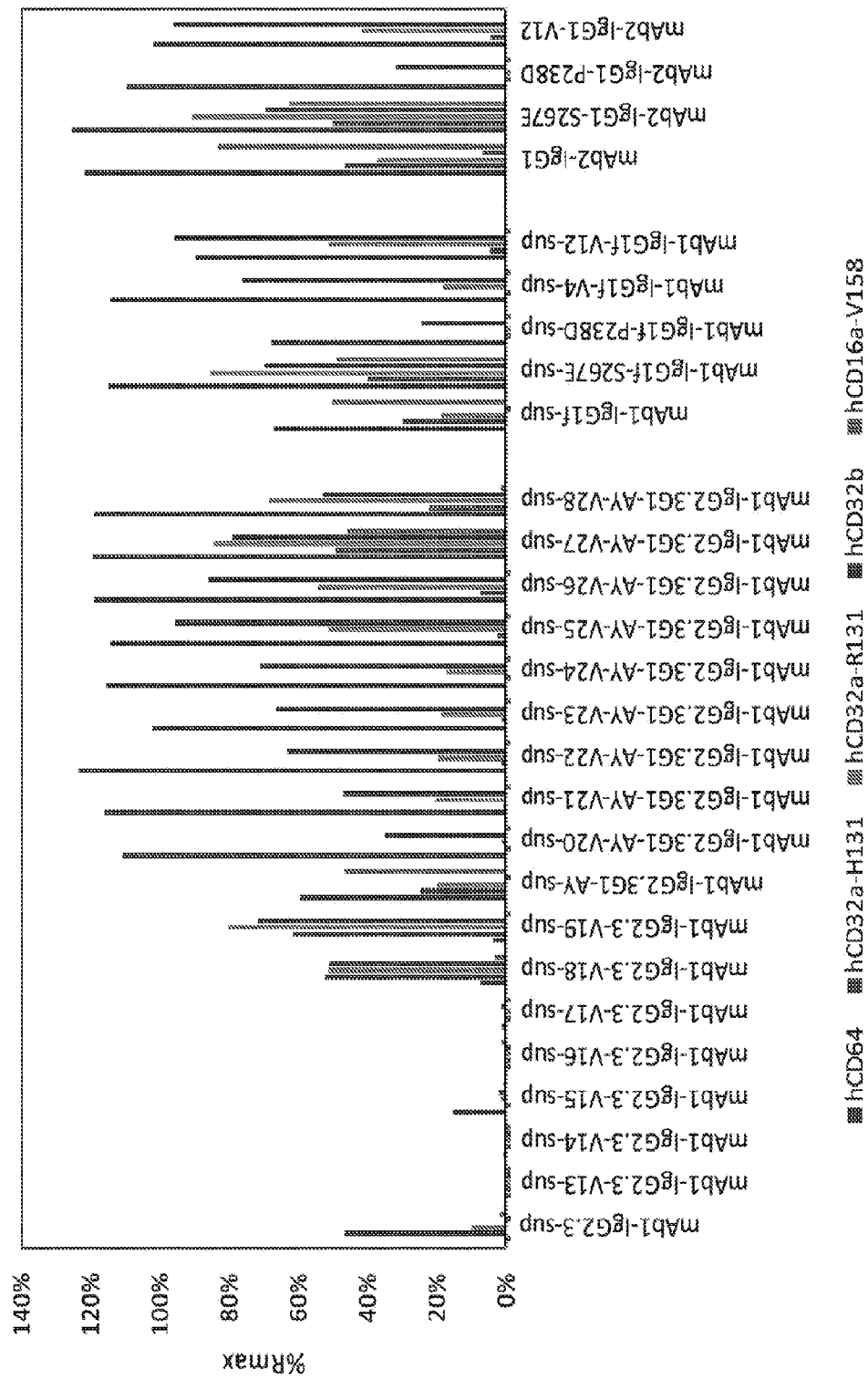


Figure 40

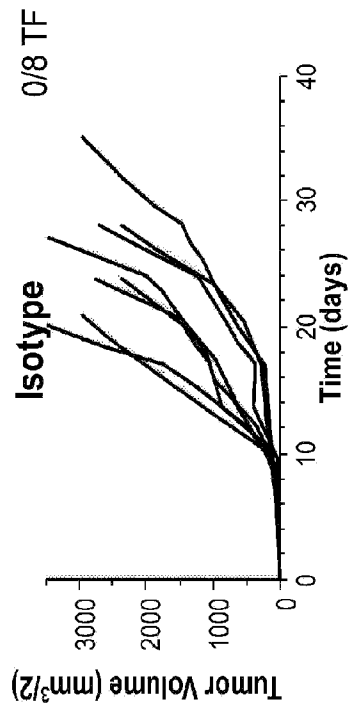


Figure 41A

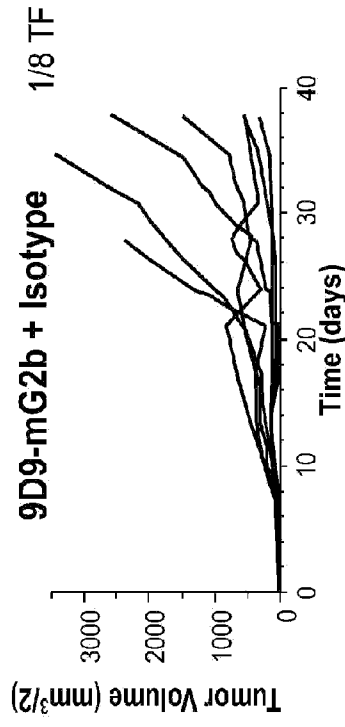


Figure 41B

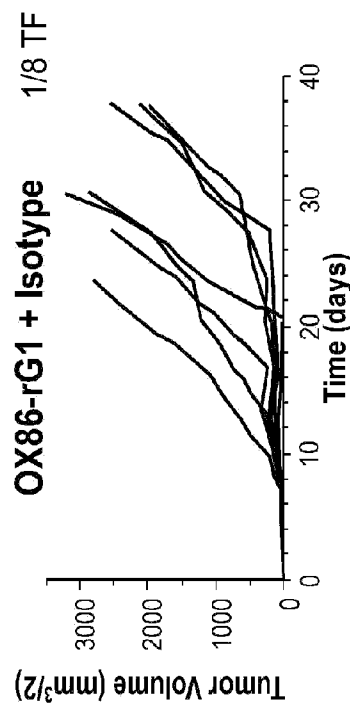


Figure 41C

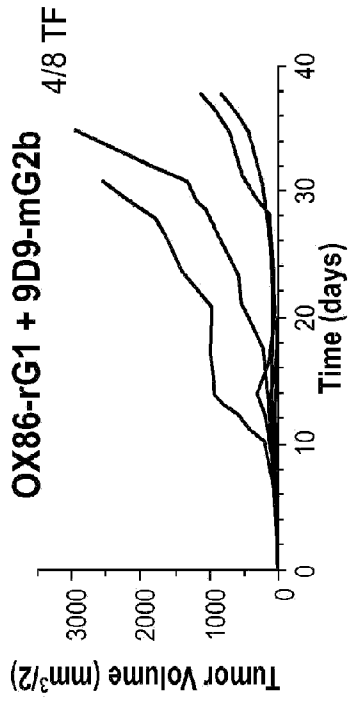


Figure 41D

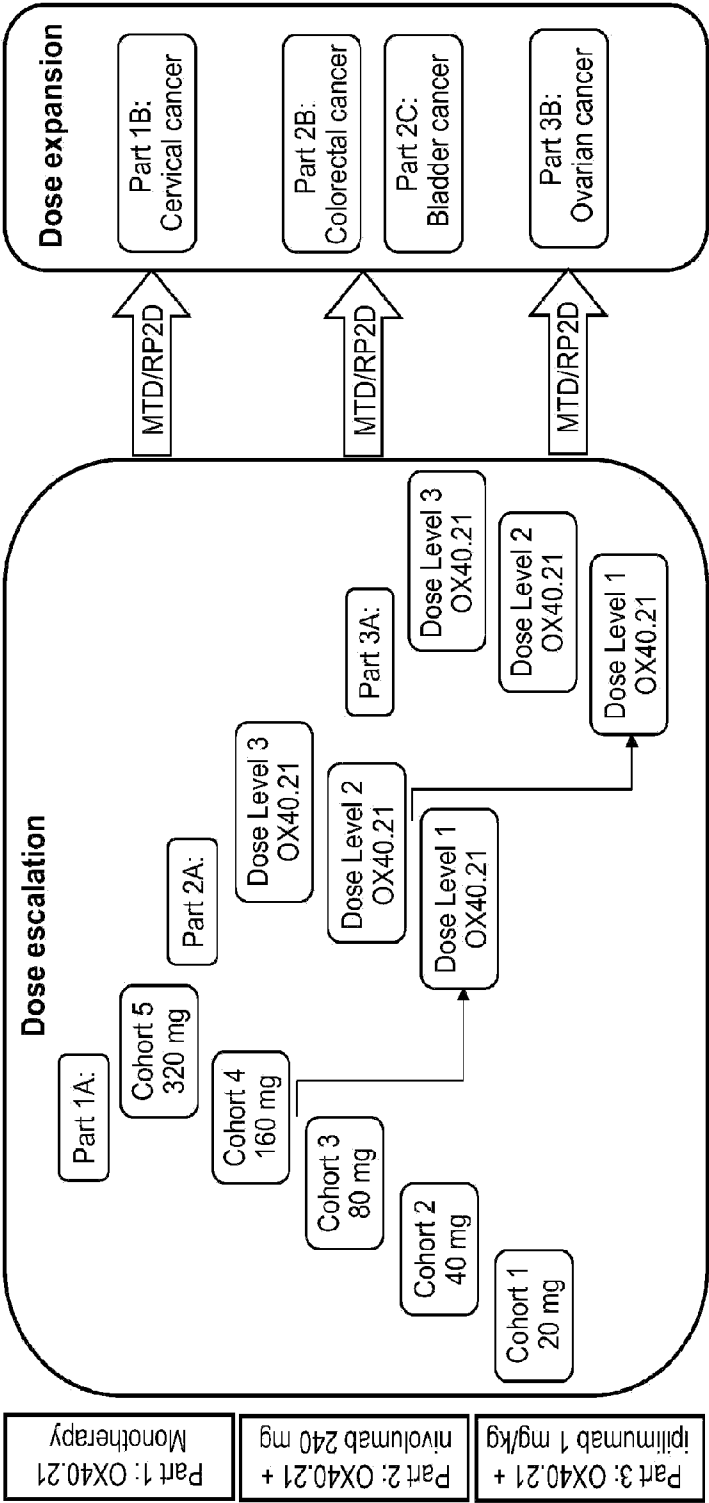


Figure 42

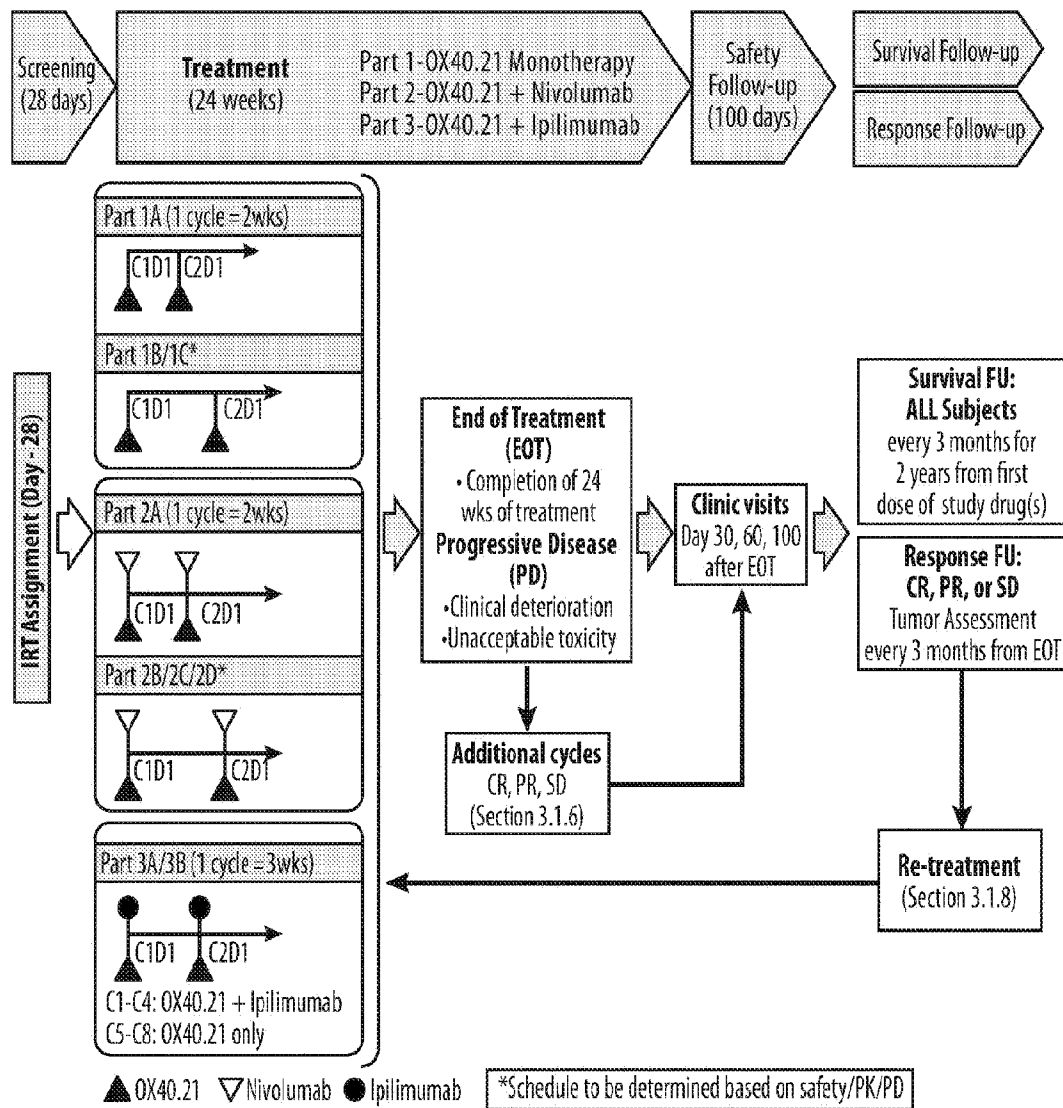


Figure 43

SEKVENSLISTE

Sekvenslisten er udeladt af skriftet og kan hentes fra det Europæiske Patent Register.

The Sequence Listing was omitted from the document and can be downloaded from the European Patent Register.

