FORMULATIONS OF ANTIBODIES THAT BIND HUMAN CD137 AND USES THEREOF

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of U.S. Provisional Patent Application Serial No. 62/793,342 filed on January 16, 2019, and U.S. Provisional Patent Application Serial No. 62/960,501 filed on January 13, 2020, the contents of each of which are herein incorporated by reference in their entireties.

BACKGROUND

In recent years, an increasing body of evidence suggests the immune system operates as a significant barrier to tumor formation and progression. The principle that naturally-occurring T cells with anti-tumor potential or activity exist in a patient with cancer has rationalized the development of immunotherapeutic approaches in oncology. Immune cells, such as T cells, macrophages, and natural killer cells, can exhibit anti-tumor activity and effectively control the occurrence and growth of malignant tumors. Tumor-specific or -associated antigens can induce immune cells to recognize and eliminate malignancies (Chen & Mellman, (2013) *Immunity* 39(1):1-10). In spite of the existence of tumor-specific immune responses, malignant tumors often evade or avoid immune attack through a variety of immunomodulatory mechanisms resulting in the failure to control tumor occurrence and progression (Motz & Coukos, (2013) *Immunity* 39(1):61-730). Indeed, an emerging hallmark of cancer is the exploitation of these immunomodulatory mechanisms and the disablement of anti-tumor immune responses, resulting in tumor evasion and escape from immunological killing (Hanahan and Weinberg (2011) *Cell* 144(5):646-674).

Novel approaches in the immunotherapy of cancer involve counteracting these immune evasion and escape mechanisms and inducing the endogenous immune system to reject tumors. CD137 (alternatively known as "tumor necrosis factor receptor superfamily member 9" (TNFRSF9), 4-1BB, and "induced by lymphocyte activation" (ILA)) is a transmembrane co-stimulatory receptor protein belonging to the tumor necrosis factor superfamily. CD137 is a T cell co-stimulatory receptor induced upon TCR activation (Nam et al., (2005) *Curr Cancer Drug Targets* 5:357-363; Watts et al., (2005) *Annu Rev Immunol* 23:23-68). In addition to its expression

on activated CD4+ and CD8+ T cells, CD137 is also expressed on CD4+CD25+ regulatory T cells, activated natural killer (NK) and NK-T cells, monocytes, neutrophils, and dendritic cells.

Under physiological conditions, CD137 is ligated by CD137 ligand (CD137L), an agonist membrane molecule present on antigen-presenting cells including B cells, monocytes, macrophages, and dendritic cells (Watts et al., (2005) *Annu Rev Immunol* 23:23-68). Upon interaction with its ligand, CD137 leads to increased TCR-induced T-cell proliferation, cytokine production, functional maturation, and prolonged CD8+ T-cell survival. The potential of CD137 co-stimulation using various agonists (*e.g.* agonistic antibodies, recombinant CD137L protein, and CD137-specific aptamers) in enabling the immune system to attack tumors has been documented in numerous models (Dharmadhikari et al., (2016) *Oncoimmunology* 5(4):e1113367 and references therein). A recent report on the clinical evaluation of an agonistic CD137 antibody (Urelumab, BMS-663513; Bristol-Myers Squibb) documented the observation of treatment-related adverse events in human subjects, including indications of severe hepatotoxicity (transaminitis) correlating with antibody dose (Segal et al., (2016) Clin Cancer Res 23(8):1929-1936). In contrast, a different agonistic CD137 antibody (Utomilumab, PF-05082566; Pfizer) tested in combination with an anti-PD-1 antibody (pembrolizumab), though not resulting in any dose-limiting toxicities, showed comparable results to anti-PD-1 antibody therapy alone (Tolcher, A. et al., (2017) Clin Cancer Res 23(18): 5349-5357).

One of the challenges in developing therapeutic antibodies is protein stability. Antibodies have a three-dimensional structure, known as the tertiary structure, that is sensitive to the balance of intra- and intermolecular interactions between amino acid functional groups and the external environment. Non-covalent interactions are critical to maintaining the native folded structure of the antibody. Furthermore, the folded antibody structure is in a state of dynamic equilibrium and any factors shifting the interaction balance can cause the structure to change. This results in unstable large molecules. For example, when the native antibody structure is unfolded to an intermediate state or to a denatured state, the protein variants are prone to aggregation. (Awwad *et al*., Pharmaceutics, 2018, 10, 83; doi:10.3390/pharmaceutics10030083).

Many factors can lead to protein aggregation, these include temperature, mechanical, physical, and freeze/thaw stress. Thus, one of the barriers to antibody development is the development of stable antibody formulations. Excipients have been used to increase the stability of antibody formulations by reducing protein dynamics and motion, increasing confirmation

stability of the antibodies, and inhibiting aggregation. However, the excipient used in one antibody formulation may not be suitable for another antibody due to differences in antibody sequence (Awwad *et al*.). Thus, there continues to be an unmet need for the development of stable antibody formulations, including stable formulations comprising novel agonistic antibodies that bind to human CD137.

SUMMARY

The present disclosure is based, at least in part, on the discovery of novel agonist anti-CD137 antibodies exhibiting protective anti-tumor immunity in animals, and formulations thereof. Notably, the antibodies described herein are efficacious against diverse tumor types, and over a wide dose range. Moreover, as exemplified in the working examples, the antibodies described herein are therapeutically effective against very large tumors. For example, treatment of tumor-bearing mice with agonist anti-CD137 antibodies described herein resulted in complete regression of tumors as large as 1,800 mm^3. As set forth in FIG. 15, treatment of such mice also resulted in protective immunity. And coincident with the observed efficacy were positive immunophenotypic changes in the tumor microenvironment, such as increased immune cell infiltration with concomitant reductions in regulatory T cell and exhausted T cell populations (see, *e.g.*, FIGs. 22A-22D).

As described above, agonism of CD137 has been associated with certain adverse events, including hepatotoxicity-related deaths in humans (see, *e.g.*, Segal et al. (2017) *Clin Cancer Res* 23(8): 1929-1935). Similar toxicities resulting from treatment with agonist anti-CD137 antibodies (such as the 3H3 antibody) have also been observed in animal models (see, *e.g.*, Bartkowiak et al. (2018) *Clin Cancer Res* 24(5):1138-1151). Yet, the agonist anti-CD137 antibodies described herein have minimal effects on the liver, as determined by, *e.g.*, plasma levels of liver enzymes (*e.g.*, alanine aminotransferase (ALT)) and immune cell infiltration. For example, there was no evidence of increased intrahepatic or intrasplenic immune cell infiltration in mice treated with the antibodies. Thus, the antibodies described herein are not only highly efficacious, but also sparing of certain toxicities associated with CD137 agonism.

While the disclosure is not bound by any particular theory or mechanism of action, the superior therapeutic and toxicity-sparing properties of the antibodies described herein are believed to derive in part from one or both of their affinity and the novel epitope to which they

bind. That is, the antibodies described herein share a common, novel epitope that is distinct from that of other agonist anti-CD137 antibodies. And, as exemplified in the working examples, engagement of this epitope by the antibodies described herein gives rise to differentiated *in vitro* activity, such as effects on regulatory T cell proliferation, cytokine production by $CD8^+$ T cells and macrophages, and intracellular signaling, as compared to agonist antibodies that bind to different epitopes of CD137. Furthermore, it has been demonstrated that an affinity range (a "sweet spot") for antibodies is particularly optimal for anti-tumor activity. For example, antibodies of intermediate affinity were shown to be more efficacious against large tumors as compared to antibodies with higher or lower affinity.

The disclosure relates, at least in part, to stable anti-CD137 antibody formulations. Notably, the anti-CD137 antibody formulations of the disclosure maintain the stability of the antibody, or antigen binding fragment thereof, minimize the formation of antibody aggregates (high molecular weight species) and particulates, reduce the percentage of charge variants, and maintain the structural integrity of the antibody.

In one aspect, the disclosure provides a formulation comprising: (a) an anti-CD137 antibody at a concentration of 1 mg/ml to 100 mg/ml, wherein the anti-CD137 antibody comprises heavy and light chain sequences having amino acid sequences set forth in SEQ ID NOs: 4 and 6, respectively , and (b) a buffer comprising histidine.

In another aspect, the disclosure provides a formulation comprising: (a) an anti-CD137 antibody at a concentration of 1 mg/ml to 100 mg/ml, wherein the anti-CD137 antibody comprises heavy and light chain sequences having amino acid sequences set forth in SEQ ID NOs: 4 and 6, respectively, (b) a buffer comprising histidine; and (c) a disaccharide sugar.

In another aspect, the disclosure provides a formulation comprising: (a) an anti-CD137 antibody at a concentration of 1 mg/ml to 100 mg/ml, wherein the anti-CD137 antibody comprises heavy and light chain sequences having amino acid sequences set forth in SEQ ID NOs: 4 and 6, respectively, and (b) a buffer comprising histidine, wherein the formulation has a pH of 5.0-7.0.

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NOs: 4 and 6, respectively, and (b) a buffer comprising histidine; wherein the formulation has a pH of 5.0-7.4.

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In another aspect, the disclosure provides a formulation comprising: (a) an anti-CD137 antibody at a concentration of 1mg/ml to 100 mg/ml, wherein the anti-CD137 antibody comprises heavy and light chain sequences having amino acid sequences set forth in SEQ ID NOs: 4 and 6, respectively, (b) a buffer comprising 10 mM to 100 mM histidine, (c) sucrose at 5%- 15% weight/volume, (d) polysorbate-80 at 0.01%- 0.1% weight/volume (w/v), and (e) NaCl at 50 mM – 200 mM, wherein the pH of the formulation is 5.0 to 7.0.

In another aspect, the disclosure provides a formulation comprising: an anti-CD137 antibody at a concentration of 1 mg/ml to 100 mg/ml, wherein the anti-CD137 antibody comprises heavy and light chain sequences having amino acid sequences set forth in SEQ ID NOs: 4 and 6, respectively, (b) a buffer comprising histidine, (c) a disaccharide sugar, (d) a non-ionic surfactant, and (e) a salt, wherein the pH of the formulation is 5.0 to 7.4.

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In another aspect, the disclosure provides a formulation comprising: (a) an anti-CD137 antibody at a concentration of 1 mg/ml to 100 mg/ml, wherein the anti-CD137 antibody comprises heavy and light chain sequences having amino acid sequences set forth in SEQ ID NOs: 4 and 6, respectively, (b) a buffer comprising 20 mM histidine, (c) sucrose at 10% weight/volume (w/v), (d) polysorbate-80 at 0.03% weight/volume (w/v), and (e) NaCl at 100mM, wherein the pH of the formulation is 6.0.

In any of the foregoing or related aspects of the disclosure, the anti-CD137 antibody comprises a heavy chain CDR3 of DXPFXLDXXYYYYYX (SEQ ID NO: 127), wherein X is any amino acid. In any of the foregoing or related aspects of the disclosure, the anti-CD137 antibody comprises a heavy chain CDR3 of $DX_1X_2X_3X_4LX_5X_6X_7X_8YX_9YYX_{10}$ (SEQ ID NO: 128), wherein X_1 is any amino acid, wherein X_2 is a non-polar amino acid, wherein X_3 is a non-polar amino acid, wherein X_4 is any amino acid, wherein X_5 is a polar amino acid, wherein X_6 is any amino acid, wherein X_7 is any amino acid, wherein X_8 is a polar amino acid, wherein X_9 is a polar amino acid, and wherein X_{10} is any amino acid. In any of the foregoing or related aspects of the disclosure, X_2 is proline, X_3 is phenylalanine or tryptophan, X_5 is aspartic acid or glutamic acid, X_8 is tyrosine, and X_9 is tyrosine.

In any of the foregoing or related aspects of the disclosure, the anti-CD137 antibody of the formulation of the disclosure comprises a heavy chain CDR3 of SEQ ID NO: 68.

In any of the foregoing or related aspects of the disclosure, the anti-CD137 antibody comprises a comprises a heavy chain CDR1 of SEQ ID NO: 48, a heavy chain CDR2 of SEQ ID NO: 56, and a heavy chain CDR3 of SEQ ID NO: 68, and a light chain CDR1 of SEQ ID NO: 69, a light chain CDR2 of SEQ ID NO: 78, and a light chain CDR3 of SEQ ID NO: 89.

In any of the foregoing or related aspects of the disclosure, the anti-CD137 antibody comprises a comprises a heavy chain CDR1 of SEQ ID NO: 51, a heavy chain CDR2 of SEQ ID NO: 108, and a heavy chain CDR3 of SEQ ID NO: 68, and a light chain CDR1 of SEQ ID NO: 69, a light chain CDR2 of SEQ ID NO: 78, and a light chain CDR3 of SEQ ID NO: 89.

In any of the foregoing or related aspects of the disclosure, the anti-CD137 antibody comprises heavy and light chain sequences comprising amino acid sequences having at least 90% identity to SEQ ID NOs: 4 and 6, respectively. In some examples, the anti-CD137 antibody comprises heavy and light chain sequences having amino acid sequences set forth in SEQ ID NOs: 4 and 6, respectively.

In any of the foregoing or related aspects of the disclosure, the anti-CD137 antibody comprises heavy and light chain sequences comprising amino acid sequences having at least 90% identity to SEQ ID NOs: 101 and 6, respectively. In some examples, the anti-CD137 antibody comprises heavy and light chain sequences having amino acid sequences set forth in SEQ ID NOs: 101 and 6, respectively.

In any of the foregoing or related aspects of the disclosure, the antibody comprises an IgG1 heavy chain constant region. In some examples, the IgG1 heavy chain constant region is a wild-type human IgG1 heavy chain constant region. In some examples, the IgG1 heavy chain constant region comprises an amino acid substitution relative to a wild-type human IgG1 heavy chain constant region.

In any of the foregoing or related aspects of the disclosure, the antibody comprises an IgG4 heavy chain constant region. In some examples, the IgG4 heavy chain constant region is a wild-type human IgG4 heavy chain constant region. In some examples, the IgG4 heavy chain constant region comprises an amino acid substitution relative to a wild-type human IgG4 heavy chain constant region.

In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 56 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively, and a buffer comprising histidine.

In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137

antibody comprises heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 135, 139 and 143, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 144, 147 and 150, respectively, and a buffer comprising histidine. [new paragraph]

In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 154 and 159, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 144, 147, 150, respectively, and a buffer comprising histidine.

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histidine, sucrose at about 5%-about 15% weight/volume, polysorbate-80 at about 0.01%-about 0.1% weight/volume (w/v), and NaCl at about 50 mM – 200 mM, wherein the pH of the formulation is about 5.0 to about 7.0.

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In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 135, 139 and 143, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 144, 147 and 150, respectively, a buffer comprising histidine, a disaccharide sugar at about 5%-about 15% weight/volume, a non-ionic surfactant at about 0.01%-about 0.1% weight/volume (w/v), and a salt at about 50 mM – 200 mM, wherein the pH of the formulation is about 5.0 to about 7.4.

In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 154 and 159, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 144, 147 and 150, respectively, a buffer comprising histidine, a disaccharide sugar at about 5%-about 15% weight/volume, a non-ionic surfactant at about 0.01%-about 0.1% weight/volume (w/v), and a salt at about 50 mM – 200 mM, wherein the pH of the formulation is about 5.0 to about 7.4.

In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 56 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively, a buffer comprising about 10 mM to about 100 mM histidine, sucrose at about 5%-about 15% weight/volume, polysorbate-80 at about 0.01%-about 0.1% weight/volume (w/v), and NaCl at about 50 mM – 200 mM, wherein the pH of the formulation is about 5.0 to about 7.4.

In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 135, 139 and 143, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in

SEQ ID NOs: 144, 147 and 150, respectively, a buffer comprising about 10 mM to about 100 mM histidine, sucrose at about 5%-about 15% weight/volume, polysorbate-80 at about 0.01%-about 0.1% weight/volume (w/v), and NaCl at about 50 mM – 200 mM, wherein the pH of the formulation is about 5.0 to about 7.4.

In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 154 and 159, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 144, 147 and 150, respectively, a buffer comprising about 10 mM to about 100 mM histidine, sucrose at about 5%-about 15% weight/volume, polysorbate-80 at about 0.01%-about 0.1% weight/volume (w/v), and NaCl at about 50 mM – 200 mM, wherein the pH of the formulation is about 5.0 to about 7.4.

In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 56 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively, a buffer comprising about 20 mM histidine, sucrose at about 10% weight/volume (w/v), polysorbate-80 at about 0.03% weight/volume (w/v), and NaCl at about 100mM, wherein the pH of the formulation is about 6.0.

In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 135, 139 and 143, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 144, 147 and 150, respectively, a buffer comprising about 20 mM histidine, sucrose at about 10% weight/volume (w/v), polysorbate-80 at about 0.03% weight/volume (w/v), and NaCl at about 100mM, wherein the pH of the formulation is about 6.0.

In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 154 and 159, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 144, 147 and 150, respectively, a buffer comprising about 20 mM histidine,

sucrose at about 10% weight/volume (w/v), polysorbate-80 at about 0.03% weight/volume (w/v), and NaCl at about 100mM, wherein the pH of the formulation is about 6.0.

In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises the heavy and light chain variable sequences set forth in SEQ ID NOs: 4 and 6, respectively, and a buffer comprising histidine.

In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises the heavy and light chain variable sequences set forth in SEQ ID NOs: 4 and 6, respectively, a buffer comprising histidine, and a disaccharide sugar.

In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises the heavy and light chain variable sequences set forth in SEQ ID NOs: 4 and 6, respectively, and a buffer comprising histidine, wherein the formulation has a pH of about 5.0-7.0.

In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises the heavy and light chain variable sequences set forth in SEQ ID NOs: 4 and 6, respectively, a buffer comprising histidine, a disaccharide sugar, a non-ionic surfactant, and a salt, wherein the pH of the formulation is about 5.0 to about 7.0.

In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises the heavy and light chain variable sequences set forth in SEQ ID NOs: 4 and 6, respectively, a buffer comprising histidine, a disaccharide sugar at about 5%-about 15% weight/volume, a non-ionic surfactant at about 0.01%-about 0.1% weight/volume (w/v), and a salt at about 50 mM – 200 mM, wherein the pH of the formulation is about 5.0 to about 7.0.

In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises the heavy and light chain variable sequences set forth in SEQ ID NOs: 4 and 6, respectively, a buffer comprising about 10 mM to about 100 mM histidine, sucrose at about 5%-about 15% weight/volume, polysorbate-80 at about 0.01%-about 0.1% weight/volume (w/v),

and NaCl at about 50 mM – 200 mM, wherein the pH of the formulation is about 5.0 to about 7.0.

In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises the heavy and light chain variable sequences set forth in SEQ ID NOs: 4 and 6, respectively, and a buffer comprising histidine, wherein the formulation has a pH of about 5.0-7.4.

In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises the heavy and light chain variable sequences set forth in SEQ ID NOs: 4 and 6, respectively, a buffer comprising histidine, a disaccharide sugar, a non-ionic surfactant, and a salt, wherein the pH of the formulation is about 5.0 to about 7.4.

In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises the heavy and light chain variable sequences set forth in SEQ ID NOs: 4 and 6, respectively, a buffer comprising histidine, a disaccharide sugar at about 5%-about 15% weight/volume, a non-ionic surfactant at about 0.01%-about 0.1% weight/volume (w/v), and a salt at about 50 mM – 200 mM, wherein the pH of the formulation is about 5.0 to about 7.4.

In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises the heavy and light chain variable sequences set forth in SEQ ID NOs: 4 and 6, respectively, a buffer comprising about 10 mM to about 100 mM histidine, sucrose at about 5%-about 15% weight/volume, polysorbate-80 at about 0.01%-about 0.1% weight/volume (w/v), and NaCl at about 50 mM – 200 mM, wherein the pH of the formulation is about 5.0 to about 7.4.In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises the heavy and light chain variable sequences set forth in SEQ ID NOs: 4 and 6, respectively, a buffer comprising about 20 mM histidine, sucrose at about 10% weight/volume (w/v), polysorbate-80 at about 0.03% weight/volume (w/v), and NaCl at about 100mM, wherein the pH of the formulation is about 6.0.

In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises heavy and light chain amino acid sequences set forth in SEQ ID NOs: 129 and 133, respectively, and a buffer comprising histidine.

In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises heavy and light chain amino acid sequences set forth in SEQ ID NOs: 129 and 133, respectively, a buffer comprising histidine, and a disaccharide sugar.

In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises heavy and light chain amino acid sequences set forth in SEQ ID NOs: 129 and 133, respectively, and a buffer comprising histidine, wherein the formulation has a pH of about 5.0-7.0.

In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises heavy and light chain amino acid sequences set forth in SEQ ID NOs: 129 and 133, respectively, a buffer comprising histidine, a disaccharide sugar, a non-ionic surfactant, and a salt, wherein the pH of the formulation is about 5.0 to about 7.0.

In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises heavy and light chain amino acid sequences set forth in SEQ ID NOs: 129 and 133, respectively, a buffer comprising histidine, a disaccharide sugar at about 5%-about 15% weight/volume, a non-ionic surfactant at about 0.01%-about 0.1% weight/volume (w/v), and a salt at about 50 mM – 200 mM, wherein the pH of the formulation is about 5.0 to about 7.0.

In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises heavy and light chain amino acid sequences set forth in SEQ ID NOs: 129 and 133, respectively, a buffer comprising about 10 mM to about 100 mM histidine, sucrose at about 5%-about 15% weight/volume, polysorbate-80 at about 0.01%-about 0.1% weight/volume (w/v), and NaCl at about 50 mM – 200 mM, wherein the pH of the formulation is about 5.0 to about 7.0.

In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises heavy and light chain amino acid sequences set forth in SEQ ID NOs: 129 and 133, respectively, and a buffer comprising histidine, wherein the formulation has a pH of about 5.0-7.4.

In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises heavy and light chain amino acid sequences set forth in SEQ ID NOs: 129 and 133, respectively, a buffer comprising histidine, a disaccharide sugar, a non-ionic surfactant, and a salt, wherein the pH of the formulation is about 5.0 to about 7.4.

In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises heavy and light chain amino acid sequences set forth in SEQ ID NOs: 129 and 133, respectively, a buffer comprising histidine, a disaccharide sugar at about 5%-about 15% weight/volume, a non-ionic surfactant at about 0.01%-about 0.1% weight/volume (w/v), and a salt at about 50 mM – 200 mM, wherein the pH of the formulation is about 5.0 to about 7.4.

In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises heavy and light chain amino acid sequences set forth in SEQ ID NOs: 129 and 133, respectively, a buffer comprising about 10 mM to about 100 mM histidine, sucrose at about 5%-about 15% weight/volume, polysorbate-80 at about 0.01%-about 0.1% weight/volume (w/v), and NaCl at about 50 mM – 200 mM, wherein the pH of the formulation is about 5.0 to about 7.4.

In some examples, the disclosure provides a formulation comprising an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises heavy and light chain amino acid sequences set forth in SEQ ID NOs: 129 and 133, respectively, a buffer comprising about 20 mM histidine, sucrose at about 10% weight/volume (w/v), polysorbate-80 at about 0.03% weight/volume (w/v), and NaCl at about 100mM, wherein the pH of the formulation is about 6.0.

In any of the foregoing or related examples of the disclosure, the formulation of the disclosure comprises histidine. In some examples, the formulation of the disclosure comprises

about 10 mM histidine to about 100 mM histidine. In some examples, the formulation comprises about 20 mM histidine.

In any of the foregoing or related examples of the disclosure, the formulation of the disclosure comprises a disaccharide sugar. In some examples, the disaccharide sugar is selected from sucrose, lactose, maltose, and trehalose. In some examples, the disaccharide sugar is sucrose. In some examples, the formulation of the disclosure comprises the disaccharide sugar at about 5%-about 15% weight/volume. In some examples, the formulation of the disclosure comprises the disaccharide sugar at about 10% weight/volume.

In any of the foregoing or related examples of the disclosure, the formulation of the disclosure comprises a salt. In some examples, the salt is NaCl. In some examples, the formulation of the disclosure comprises salt at a concentration of about 50 mM - 200 mM. In some examples, the formulation of the disclosure comprises salt at a concentration of about 100 mM.

In any of the foregoing or related examples of the disclosure, the formulation of the disclosure has a pH of about 5.0-7.0. In some examples, the formulation of the disclosure has a pH of about 6.0.

In any of the foregoing or related examples of the disclosure, the formulation of the disclosure has a pH of about 5.0-8.0. In some examples, the formulation of the disclosure has a pH of about 5.0-7.4.

In any of the foregoing or related examples of the disclosure, the formulation of the disclosure comprises a non-ionic surfactant. In some examples, the non-ionic surfactant is a polysorbate. In some examples, the polysorbate is polysorbate-80. In some examples, the formulation of the disclosure comprises the non-ionic surfactant is at about 0.01%-about 0.1% weight/volume (w/v). In some examples, the formulation of the disclosure comprises the non-ionic surfactant is at about 0.03% weight/volume (w/v).

In any of the foregoing or related examples of the disclosure, the formulation of the disclosure comprises an anti-CD137 antibody at a concentration of about 1mg/ml to about 100 mg/ml. In some examples, the formulation of the disclosure comprises the anti-CD137 antibody at a concentration of about 5 mg/ml to about 15 mg/ml. In some examples, the formulation of the disclosure comprises the anti-CD137 antibody at a concentration of about 15 mg/ml to about 30 mg/ml. In some examples, the formulation of the disclosure comprises the anti-CD137

antibody at a concentration of about 30 mg/ml to about 45 mg/ml. In some examples, the formulation of the disclosure comprises the anti-CD137 antibody at a concentration of about 45 mg/ml to about 60 mg/ml. In some examples, the formulation of the disclosure comprises the anti-CD137 antibody at a concentration of about 60 mg/ml to about 75 mg/ml. In some examples, the formulation of the disclosure comprises the anti-CD137 antibody at a concentration of about 75 mg/ml to about 90 mg/ml. In some examples, the formulation of the disclosure comprises the anti-CD137 antibody at a concentration of about 85 mg/ml to about 100 mg/ml. In some examples, the formulation of the disclosure comprises the anti-CD137 antibody at a concentration of about 5 mg/ml. In some examples, the formulation of the disclosure comprises the anti-CD137 antibody at a concentration of about 10 mg/ml. In some examples, the formulation of the disclosure comprises the anti-CD137 antibody at a concentration of about 15 mg/ml. In some examples, the formulation of the disclosure comprises the anti-CD137 antibody at a concentration of about 20 mg/ml.

In a further aspect, the disclosure provides use of the formulation as described herein in the manufacture of a medicament for inducing or enhancing dimerization of human CD137 trimers in a subject that has cancer or a tumor. In a further aspect, the disclosure provides use of the formulation as described herein in the manufacture of a medicament for inducing or enhancing multimerization of human CD137 trimers in a subject that has cancer or a tumor. In a further aspect, the disclosure provides use of the formulation as described herein in the manufacture of a medicament for inducing or enhancing T cell activation in a subject that has cancer or a tumor.

In a further aspect, the disclosure provides use of the formulation as described herein in the manufacture of a medicament for inducing or enhancing a cytotoxic T cell response in a subject that has cancer or a tumor. In another aspect, the disclosure provides use of the formulation as described herein in the manufacture of a medicament for inducing or enhancing cytokine production of an immune cell in a subject that has cancer or a tumor. In another aspect, the disclosure provides use of the formulation as described herein in the manufacture of a medicament for inducing or enhancing T cell proliferation in a subject that has cancer or a tumor.

In another aspect, the disclosure provides use of the formulation as described herein in the manufacture of a medicament for reducing or inhibiting tumor growth. In another aspect, the disclosure provides use of the formulation as described herein in the manufacture of a medicament for treating a disorder mediated by human CD137 in a subject that has cancer or a tumor. In another

aspect, the disclosure provides use of the formulation as described herein in the manufacture of a medicament for treating cancer in a subject.

In yet another aspect, the disclosure provides use of the formulation as described herein in the manufacture of a medicament for inducing an anti-tumor memory immune response.

In some examples, the disclosure provides a method for inducing or enhancing dimerization of human CD137 trimers in a subject, comprising administering to a subject in need thereof, an effective amount of the formulation of the disclosure.

In some examples, the disclosure provides a method for inducing or enhancing multimerization of human CD137 trimers in a subject, comprising administering to a subject in need thereof, an effective amount of the formulation of the disclosure.

In some examples, the disclosure provides a method for inducing or enhancing T cell activation in a subject, comprising administering to a subject in need thereof, an effective amount of the formulation of the disclosure. In some examples, the T cell activation occurs in a tumor microenvironment.

In some examples, the disclosure provides a method for inducing or enhancing a cytotoxic T cell response in a subject, comprising administering to a subject in need thereof, an effective amount of the formulation of the disclosure. In some examples, the cytotoxic T cell response occurs in a tumor microenvironment.

In some examples, the disclosure provides a method for inducing or enhancing cytokine production of an immune cell in a subject, comprising administering to a subject in need thereof, an effective amount of the formulation of the disclosure. In some examples, the cytokine produced is IL-2, TNFα, IL-13, IFN-γ, or combinations thereof. In some examples, the cytokine production occurs in a tumor microenvironment.

In some examples, the disclosure provides a method for inducing or enhancing T cell proliferation in a subject, comprising administering to a subject in need thereof, an effective amount of the formulation of the disclosure. In some examples, the T cell proliferation occurs in a tumor microenvironment.

In some examples, the disclosure provides a method for reducing or inhibiting tumor growth, comprising administering to a subject in need thereof, an effective amount of the formulation of the disclosure.

In some examples, the disclosure provides a method for treating a disorder mediated by human CD137 in a subject, comprising administering to a subject in need thereof, an effective amount of the formulation of the disclosure.

In some examples, the disclosure provides a method for treating cancer in a subject, comprising administering to a subject in need thereof, an effective amount of the formulation of the disclosure.

In any of the foregoing examples, infiltration of immune cells into a tumor microenvironment is increased after administration of the formulation. In some examples, the immune cells express CD45.

In any of the forgoing examples, the quantity of T regulatory (Treg) cells is reduced in a tumor microenvironment after administration of the formulation. In some examples, the Treg cells express CD4, FOXP-3 and CD25.

In any of the forgoing examples, the quantity of macrophages is reduced in a tumor microenvironment after administration of the isolated monoclonal antibody or antigen binding portion. In some examples, the macrophages express CD45 and CD11b.

In any of the forgoing examples, T cell exhaustion is reduced in a tumor microenvironment after administration of the isolated monoclonal antibody or antigen binding portion. In some examples, reduction of T cell exhaustion comprises a decrease in expression of TIGIT, PD-1, LAG-3, or combinations thereof.

In any of the foregoing examples, the cancer is selected from the group consisting of melanoma, glioma, renal, breast, hematological, and head and neck cancer. In some examples, the hematological cancer is a B cell lymphoma.

In some examples, the disclosure provides a method of inducing an anti-tumor memory immune response, comprising administering to a subject in need thereof, an effective amount of the formulation of the disclosure.

In any of the foregoing examples, the anti-CD137 antibody binds Fc gamma receptor.

In any of the foregoing examples, depletion of CD4+ T cells, CD8+ T cells, Natural Killer cells, or combinations thereof, reduces the efficacy of the formulation.

In another aspect, the disclosure provides a kit comprising a container comprising the formulation of the disclosure, and a package insert comprising instructions for administration of the formulation, for treating or delaying progression of cancer or reducing or inhibiting tumor growth in a subject in need thereof.

In another aspect, the disclosure provides a kit comprising a container comprising the formulation of the disclosure, and a package insert comprising instructions for administration of

the formulation alone or in combination with another agent, for treating or delaying progression of cancer or reducing or inhibiting tumor growth in a subject in need thereof.

In another aspect, the disclosure provides for the use of the formulation of the disclosure, for the manufacture of a medicament for treating or delaying progression of cancer or reducing or inhibiting tumor growth in a subject in need thereof.

In some examples, the disclosure provides a formulation of the disclosure for use in the manufacture of a medicament for treating or delaying progression of cancer or reducing or inhibiting tumor growth in a subject in need thereof.

In another aspect, the disclosure provides a formulation of the disclosure for use as a medicament.

In view of the foregoing, in some examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds human CD137, wherein the antibody or antigen binding portion binds human CD137 with an affinity (K_D) of between about 40 nM to about 100 nM. In some examples, the disclosure provides an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds to human CD137, wherein the antibody or antigen binding portion binds human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 110 nM). In some examples, the affinity of the anti-CD137 antibody to human CD137 is at least two (*e.g.*, at least three, four, five, six, seven, eight, nine, or 10) fold higher than the affinity of mAb10 for mouse CD137. In some examples, the affinity of the anti-CD137 antibody is no greater than 500, 450, 400, 350, 300, 250, 200, 250, 200, 175, 150, 125, 110, or 100 nM. In some examples, the affinity of the anti-CD137 antibody to human CD137 is at least two (*e.g.*, at least three, four, five, six, seven, eight, nine, or 10) fold higher than the affinity of mAb10 for mouse CD137, but no greater than 500, 450, 400, 350, 300, 250, 200, 250, 200, 175, 150, 125, 110, or 100 nM.

In some examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds to human CD137, wherein the antibody or antigen binding portion binds to an epitope on human CD137 comprising one or more (*e.g.*, one, two, three, four, five, six, seven, eight, nine, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or all 25) of amino acids 111-132 of SEQ ID NO:3. In some examples, the disclosure provides an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds to human CD137, wherein the antibody or antigen binding portion binds to an

epitope within amino acids 111-132 of SEQ ID NO:3. In some examples, the disclosure provides an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds to human CD137, wherein the antibody or antigen binding portion binds to all or a portion of amino acids 111-132 of SEQ ID NO:3. In some examples, the epitope comprises K114 of SEQ ID NO: 3. In some examples, the epitope comprises residues E111, T113, and K114 of SEQ ID NO: 3. In some examples, the epitope comprises residues E111, T113, K114, N126 and I132 of SEQ ID NO: 3. In some examples, the epitope comprises residues E111, T113, K114 and P135 of SEQ ID NO: 3. In some examples, the epitope comprises residues E111, T113, K114, N126, I132 and P135 of SEQ ID NO: 3. In some examples, the antibody or antigen binding portion thereof binds to human CD137 with an affinity of between about 30 nM and about 100 nM (*e.g.*, between about 30 nM and about 110 nM).

In some examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds to human CD137, wherein the antibody or antigen binding portion binds human CD137 with an affinity (K_D) of about 40-100 nM (*e.g.*, between about 40 nM and about 100 nM) and binds to an epitope on human CD137 comprising K114 of SEQ ID NO: 3. In some examples, the disclosure provides an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds to human CD137, wherein the antibody or antigen binding portion binds human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM) and binds to an epitope on human CD137 comprising K114 of SEQ ID NO: 3. In some examples, the epitope comprises residues E111, T113, and K114 of SEQ ID NO: 3. In some examples, the epitope comprises residues E111, T113, K114, N126 and I132 of SEQ ID NO: 3. In some examples, the epitope comprises residues E111, T113, K114 and P135 of SEQ ID NO: 3. In some examples, the epitope comprises residues E111, T113, K114, N126, I132 and P135 of SEQ ID NO: 3.

In some examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds to human CD137, wherein the antibody or antigen binding portion binds human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, about 30 nM to about 100 nM) and binds to an epitope on human CD137 comprising a sequence of one or more amino acid residues corresponding to amino acid positions 111 to 135 of SEQ ID NO: 3. In some examples, the epitope comprises 2, 3, 4, 5, 6, 7, 8, 9, 10,

11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 amino acid residues corresponding to amino acid positions 111 to 135 of SEQ ID NO: 3.

In some examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds to human CD137, wherein the antibody or antigen binding portion binds human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM) and binds to an epitope on human CD137 located within amino acid residues 111-135 of SEQ ID NO: 3. In some examples, the epitope is at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15 amino acids. In some examples, the epitope is fewer than 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6 or 5 amino acids.

In some examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds to human CD137, wherein the antibody or antigen binding portion binds human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM) and binds to an epitope on human CD137 comprising ELTK (corresponding to amino acid residues 111-114 of SEQ ID NO: 3). In some examples, the epitope further comprises one or more residues N126, I132 and P135 of SEQ ID NO: 3.

In any of the foregoing examples, the epitope is a non-linear epitope. In any of the foregoing examples, mutation of residue K114 of SEQ ID NO: 3 abrogates binding of the antibody or antigen binding portion thereof to human CD137.

In any of the foregoing examples, the antibody or antigen binding portion described herein binds human CD137 with an affinity (K_D) of about 30-100 nM, 30-95 nM, 45-95 nM, 50-90 nM, 55-85 nM, 60-80 nM, 65-75 nM, 55-75 nM, 40-70 nM, 50-80 nM, or 60-90 nM. In some examples, the antibody or antigen binding portion binds to a non-ligand binding region of the extracellular domain of human CD137. In some examples, the antibody or antigen binding portion does not inhibit the interaction between CD137 and CD137L. In some examples, the non-ligand binding region spans cysteine rich domain (CRD) III and CRD IV. In any of the foregoing examples, the antibody or antigen binding portion does not inhibit the formation of a trimer of CD137:CD137L monomers.

In some examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds human CD137, wherein the antibody or antigen binding portion:

(i) binds human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM);

(ii) binds to a non-ligand binding region of the extracellular domain of human CD137; and

(iii) binds to an epitope on human CD137 comprising K114 of SEQ ID NO: 3.

In some examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds human CD137, wherein the antibody or antigen binding portion:

(i) binds human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM);

(ii) does not inhibit the interaction between human CD137 and human CD137 ligand; and

(iii) binds to an epitope on human CD137 comprising K114 of SEQ ID NO: 3.

In some examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds human CD137, wherein the antibody or antigen binding portion: (i) binds human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM) and (ii) does not inhibit the formation of a trimer of CD137:CD137L monomers (that is, a CD137:CD137L trimer:trimer complex). In some examples, the disclosure features an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds human CD137, wherein the antibody or antigen binding portion: (i) binds human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM) and (ii) binds to a non-ligand binding region of the extracellular domain of human CD137. In some examples, the disclosure features an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds human CD137, wherein the antibody or antigen binding portion: (i) binds human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM) and (ii) does not inhibit the interaction between human CD137 and CD137 ligand.

In any of the foregoing examples, the antibody or antigen binding portion comprises a heavy chain CDR3 comprising the amino acid sequence DXXXXLXXXXYXYYX (SEQ ID

NO: 126), wherein X is any amino acid. In some examples, the antibody or antigen binding portion comprises a heavy chain CDR3 comprising the amino acid sequence DXPFXLDXXYYYYYX (SEQ ID NO: 127), wherein X is any amino acid. In any of the foregoing examples, mutation of residues D95, L100, Y100E, Y100G, Y100H, or combinations thereof, of the heavy chain CDR3, to alanine results in loss of binding to human CD137. In any of the foregoing examples, mutation of residues P97, F98, D100A, Y100D, Y100F, or combinations thereof, to alanine results in reduction of binding to human CD137. In any of the foregoing examples, the antibody or antigen binding portion comprises heavy and light chain CDRs, wherein heavy chain CDR3 comprises the amino acid sequence set forth in SEQ ID NO: 68.

In other examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds to human CD137, wherein

(i) the antibody or antigen binding portion binds human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM); and

(ii) the antibody or antigen binding portion comprises a heavy chain CDR3 comprising the amino acid sequence DXXXXLXXXXYXYYX (SEQ ID NO: 126), wherein X is any amino acid. In some examples, X is any amino acid except alanine.

In another example, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds to human CD137, wherein

(i) the antibody or antigen binding portion binds human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM); and

(ii) the antibody or antigen binding portion comprises a heavy chain CDR3 comprising the amino acid sequence $DX_1X_2X_3X_4LX_5X_6X_7X_8YX_9YYX_{10}$ (SEQ ID NO: 128), wherein X_1 is any amino acid, wherein X_2 is a non-polar amino acid, wherein X_3 is a non-polar amino acid, wherein X_4 is any amino acid, wherein X_5 is a polar amino acid, wherein X_6 is any amino acid, wherein X_7 is any amino acid, wherein X_8 is a polar amino acid, wherein X_9 is a polar amino acid, and wherein X_{10} is any amino acid. In some examples, X_2 is proline, X_3 is phenylalanine or tryptophan, X_5 is aspartic acid or glutamic acid, X_8 is tyrosine, and X_9 is tyrosine.

In other examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds to human CD137, wherein

(i) the antibody or antigen binding portion binds human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM); and

(ii) the antibody or antigen binding portion thereof specifically binds to an epitope on human CD137 comprising one or more residues E111, T113, K114, N126, I132 and P135 of SEQ ID NO: 3.

In other examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds to human CD137, wherein

(i) the antibody or antigen binding portion binds human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM);

(ii) the antibody or antigen binding portion thereof specifically binds to an epitope on human CD137 comprising one or more residues E111, T113, K114, N126, I132 and P135 of SEQ ID NO: 3;

(iii) the antibody or antigen binding portion comprises a heavy chain CDR3 comprising the amino acid sequence DXXXXLXXXXYXYYX (SEQ ID NO: 126), wherein X is any amino acid; or

(iv) combinations thereof. In some examples, X is any amino acid except alanine.

In other examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds to human CD137, wherein

(i) the antibody or antigen binding portion binds human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM);

(ii) the antibody or antigen binding portion thereof specifically binds to an epitope on human CD137 comprising one or more residues E111, T113, K114, N126, I132 and P135 of SEQ ID NO: 3;

(iii) the antibody or antigen binding portion comprises a heavy chain CDR3 comprising the amino acid sequence $DX_1X_2X_3X_4LX_5X_6X_7X_8YX_9YYX_{10}$ (SEQ ID NO: 128), wherein X_1 is any amino acid, wherein X_2 is a non-polar amino acid, wherein X_3 is a non-polar amino acid, wherein X_4 is any amino acid, wherein X_5 is a polar amino acid, wherein X_6 is any amino acid, wherein X_7 is any amino acid, wherein X_8 is a polar amino acid, wherein X_9 is a polar amino acid, and wherein X_{10} is any amino acid; or

(iv) combinations thereof. In some examples, X_2 is proline, X_3 is phenylalanine or tryptophan, X_5 is aspartic acid or glutamic acid, X_8 is tyrosine, and X_9 is tyrosine.

In other examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds to human CD137, wherein

(i) the antibody or antigen binding portion binds human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM);

(ii) the antibody or antigen binding portion thereof specifically binds to an epitope on human CD137 comprising one or more residues E111, T113, K114, N126, I132 and P135 of SEQ ID NO: 3; and

(iii) the antibody or antigen binding portion comprises a heavy chain CDR3 comprising the amino acid sequence DXXXXLXXXXYXYYX (SEQ ID NO: 126), wherein X is any amino acid. In some examples, X is any amino acid except alanine.

In other examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds to human CD137, wherein

(i) the antibody or antigen binding portion binds human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM);

(ii) the antibody or antigen binding portion thereof specifically binds to an epitope on human CD137 comprising one or more residues E111, T113, K114, N126, I132 and P135 of SEQ ID NO: 3; and

(iii) the antibody or antigen binding portion comprises a heavy chain CDR3 comprising the amino acid sequence $DX_1X_2X_3X_4LX_5X_6X_7X_8YX_9YYX_{10}$ (SEQ ID NO: 128), wherein X_1 is any amino acid, wherein X_2 is a non-polar amino acid, wherein X_3 is a non-polar amino acid, wherein X_4 is any amino acid, wherein X_5 is a polar amino acid, wherein X_6 is any amino acid, wherein X_7 is any amino acid, wherein X_8 is a polar amino acid, wherein X_9 is a polar amino acid, and wherein X_{10} is any amino acid. In some examples, X_2 is proline, X_3 is phenylalanine or tryptophan, X_5 is aspartic acid or glutamic acid, X_8 is tyrosine, and X_9 is tyrosine.

In any of the foregoing examples, the epitope comprises K114. In any of the foregoing examples, the epitope comprises E111, T113 and K114. In any of the foregoing examples, the epitope comprises E11, T113, K114, N126 and I132. In any of the foregoing examples, the epitope comprises residues E111, T113, K114, N126, I132 and P135 of SEQ ID NO: 3.

In other examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds to human CD137, wherein

(i) the antibody or antigen binding portion binds human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM); and

(ii) the antibody or antigen binding portion thereof specifically binds to an epitope comprising a sequence of one or more amino acid residues corresponding to amino acid positions 111 to 135 of SEQ ID NO: 3.

In other examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds to human CD137, wherein

(i) the antibody or antigen binding portion binds human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM);

(ii) the antibody or antigen binding portion thereof specifically binds to an epitope comprising a sequence of one or more amino acid residues corresponding to amino acid positions 111 to 135 of SEQ ID NO: 3;

(iii) the antibody or antigen binding portion comprises a heavy chain CDR3 comprising the amino acid sequence DXXXXLXXXXYXYYX (SEQ ID NO: 126), wherein X is any amino acid; or

(iv) combinations thereof. In some examples, X is any amino acid except alanine.

In other examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds to human CD137, wherein

(i) the antibody or antigen binding portion binds human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM);

(ii) the antibody or antigen binding portion thereof specifically binds to an epitope comprising a sequence of one or more amino acid residues corresponding to amino acid positions 111 to 135 of SEQ ID NO: 3;

(iii) the antibody or antigen binding portion comprises a heavy chain CDR3 comprising the amino acid sequence $DX_1X_2X_3X_4LX_5X_6X_7X_8YX_9YYX_{10}$ (SEQ ID NO: 128), wherein X_1 is any amino acid, wherein X_2 is a non-polar amino acid, wherein X_3 is a non-polar amino acid, wherein X_4 is any amino acid, wherein X_5 is a polar amino acid, wherein X_6 is any amino acid, wherein X_7 is any amino acid, wherein X_8 is a polar amino acid, wherein X_9 is a polar amino acid, and wherein X_{10} is any amino acid; or

(iv) combinations thereof. In some examples, X_2 is proline, X_3 is phenylalanine or tryptophan, X_5 is aspartic acid or glutamic acid, X_8 is tyrosine, and X_9 is tyrosine.

In another examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds to human CD137, wherein

(i) the antibody or antigen binding portion binds human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM);

(ii) the antibody or antigen binding portion thereof specifically binds to an epitope comprising a sequence of one or more amino acid residues corresponding to amino acid positions 111 to 135 of SEQ ID NO: 3; and

(iii) the antibody or antigen binding portion comprises a heavy chain CDR3 comprising the amino acid sequence DXXXXLXXXXYXYYX (SEQ ID NO: 126), wherein X is any amino acid. In some examples, X is any amino acid except alanine.

In another examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds to human CD137, wherein

(i) the antibody or antigen binding portion binds human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM);

(ii) the antibody or antigen binding portion thereof specifically binds to an epitope comprising a sequence of one or more amino acid residues corresponding to amino acid positions 111 to 135 of SEQ ID NO: 3; and

(iii) the antibody or antigen binding portion comprises a heavy chain CDR3 comprising the amino acid sequence $DX_1X_2X_3X_4LX_5X_6X_7X_8YX_9YYX_{10}$ (SEQ ID NO: 128), wherein X_1 is any amino acid, wherein X_2 is a non-polar amino acid, wherein X_3 is a non-polar amino acid, wherein X_4 is any amino acid, wherein X_5 is a polar amino acid, wherein X_6 is any amino acid, wherein X_7 is any amino acid, wherein X_8 is a polar amino acid, wherein X_9 is a polar amino acid, and wherein X_{10} is any amino acid. In some examples, X_2 is proline, X_3 is phenylalanine or tryptophan, X_5 is aspartic acid or glutamic acid, X_8 is tyrosine, and X_9 is tyrosine.

In any of the foregoing examples, the epitope comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 amino acid residues corresponding to amino acid positions 111 to 135 of SEQ ID NO: 3.

In some examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds to human CD137, wherein

(i) the antibody or antigen binding portion binds human CD137 with an affinity of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM); and

(ii) the antibody or antigen binding portion thereof specifically binds to an epitope comprising ELTK (corresponding to amino acid residues 111-114 of SEQ ID NO: 3).

In some examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds to human CD137, wherein

(i) the antibody or antigen binding portion binds human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM);

(ii) the antibody or antigen binding portion thereof specifically binds to an epitope comprising ELTK (corresponding to amino acid residues 111-114 of SEQ ID NO: 3);

(iii) the antibody or antigen binding portion comprises a heavy chain CDR3 comprising the amino acid sequence DXXXXLXXXXYXYYX (SEQ ID NO: 126), wherein X is any amino acid; or

(iv) combinations thereof. In some examples, X is any amino acid except alanine.

In some examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds to human CD137, wherein

(i) the antibody or antigen binding portion binds human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM);

(ii) the antibody or antigen binding portion thereof specifically binds to an epitope comprising ELTK (corresponding to amino acid residues 111-114 of SEQ ID NO: 3);

(iii) the antibody or antigen binding portion comprises a heavy chain CDR3 comprising the amino acid sequence $DX_1X_2X_3X_4LX_5X_6X_7X_8YX_9YYX_{10}$ (SEQ ID NO: 128), wherein X_1 is any amino acid, wherein X_2 is a non-polar amino acid, wherein X_3 is a non-polar amino acid, wherein X_4 is any amino acid, wherein X_5 is a polar amino acid, wherein X_6 is any amino acid, wherein X_7 is any amino acid, wherein X_8 is a polar amino acid, wherein X_9 is a polar amino acid, and wherein X_{10} is any amino acid; or

(iv) combinations thereof. In some examples, X_2 is proline, X_3 is phenylalanine or tryptophan, X_5 is aspartic acid or glutamic acid, X_8 is tyrosine, and X_9 is tyrosine.

In some examples, the disclosure provides an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds to human CD137, wherein

(i) the antibody or antigen binding portion binds human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM);

(ii) the antibody or antigen binding portion thereof specifically binds to an epitope comprising ELTK (corresponding to amino acid residues 111-114 of SEQ ID NO: 3); and

(iii) the antibody or antigen binding portion comprises a heavy chain CDR3 comprising the amino acid sequence DXXXXLXXXXYXYYX (SEQ ID NO: 126), wherein X is any amino acid. In some examples, X is any amino acid except alanine.

In some examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds to human CD137, wherein

(i) the antibody or antigen binding portion binds human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM);

(ii) the antibody or antigen binding portion thereof specifically binds to an epitope comprising ELTK (corresponding to amino acid residues 111-114 of SEQ ID NO: 3); and

(iii) the antibody or antigen binding portion comprises a heavy chain CDR3 comprising the amino acid sequence $DX_1X_2X_3X_4LX_5X_6X_7X_8YX_9YYX_{10}$ (SEQ ID NO: 128), wherein X_1 is any amino acid, wherein X_2 is a non-polar amino acid, wherein X_3 is a non-polar amino acid, wherein X_4 is any amino acid, wherein X_5 is a polar amino acid, wherein X_6 is any amino acid, wherein X_7 is any amino acid, wherein X_8 is a polar amino acid, wherein X_9 is a polar amino acid, and wherein X_{10} is any amino acid. In some examples, X_2 is proline, X_3 is phenylalanine or tryptophan, X_5 is aspartic acid or glutamic acid, X_8 is tyrosine, and X_9 is tyrosine

In any of the foregoing examples, the epitope comprises the residues ELTK of SEQ ID NO: 3 (corresponding to amino acid residues 111-114 of SEQ ID NO: 3). In some examples, the epitope comprises ELTK of SEQ ID NO: 3 (corresponding to amino acid residues 111-114 of SEQ ID NO: 3) and residues N126, I132 and P135 of SEQ ID NO: 3.

In any of the foregoing examples, the epitope is a non-linear epitope. In some examples, mutation of residue K114 of human CD137 (SEQ ID NO: 3) abrogates binding of the antibody or antigen binding portion thereof to human CD137.

In any of the foregoing examples, the antibody or antigen binding portion thereof comprises a heavy chain CDR3 comprising the amino acid sequence DXPFXLDXXYYYYYX (SEQ ID NO: 128), wherein X is any amino acid. In some examples, mutation of residues D95, L100, Y100E, Y100G, Y100H, or combinations thereof, of the heavy chain CDR3 of the antibody or antigen binding portion described herein, results in loss of binding to human CD137. In some examples, mutation of residues P97, F98, D100A, Y100D, Y100F, or combinations

thereof, of the heavy chain CDR3 of the antibody or antigen binding portion described herein, to alanine results in reduction of binding to human CD137. In other examples, mutation of residues P97, F98, D100A, Y100D, Y100F, or combinations thereof, of the heavy chain CDR3 of the antibody or antigen binding portion described herein, to any residue except alanine, results in an increase in binding to human CD137.

In any of the foregoing examples, the antibody or antigen binding portion thereof, binds human CD137 with an (K_D) of about 45-95 nM, 50-90 nM, 55-85 nM, 60-80 nM, 65-75 nM, 55-75 nM, 40-70 nM, 50-80 nM, or 60-90 nM. In any of the foregoing examples, the antibody or antigen binding portion thereof, binds human CD137 with an (K_D) of about 45 nM to about 95 nM, about 50 to about 90 nM, about 55 to about 85 nM, about 60 to about 80 nM, about 65 to about 75 nM, about 55 to about 75 nM, about 40 to about 70 nM, about 50 to about 80 nM, or about 60 to about 90 nM.

In any of the foregoing examples, the antibody or antigen binding portion thereof comprises heavy and light chain CDRs, wherein heavy chain CDR3 comprises the amino acid sequence set forth in SEQ ID NO: 68.

In any of the foregoing examples, the antibody or antigen binding portion thereof comprises heavy and light chain CDRs selected from the group consisting of:

(a) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 56 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively; and

(b) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 51, 108 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively.

In some examples, the agonistic isolated monoclonal antibody or antigen-binding portion thereof comprises heavy and light chain CDRs selected from the group consisting of:

(a) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 135, 139 and 143, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 144, 147 and 150, respectively; and

(b) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 137, 141 and 143, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 144, 147 and 150, respectively.

In some examples, the agonistic isolated monoclonal antibody or antigen-binding portion thereof comprises heavy and light chain CDRs selected from the group consisting of:

(a) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 154 and 159, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 144, 147 and 150, respectively; and

(b) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 51, 156 159 respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 144, 147 and 150, respectively.

In any of the foregoing examples, the antibody or antigen binding portion thereof comprises 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: 4 and 101; and wherein the light chain variable region comprises an amino acid sequence of SEQ ID NO: 6.

In any of the foregoing examples, the antibody or antigen binding portion thereof comprises heavy and light chain variable regions, comprising amino acid sequences selected from the group consisting of:

(a) SEQ ID NO: 4 and 6, respectively; and

(b) SEQ ID NO: 101 and 6, respectively.

In any of the foregoing examples, the antibody or antigen binding portion thereof comprises heavy and light chain variable regions, wherein the heavy chain variable region comprises an amino acid sequence which is at least 90% identical to the amino acid sequence selected from the group consisting of SEQ ID NOs: 4 and 101; and wherein the light chain variable region comprises an amino acid sequence which is at least 90% identical to the amino acid sequence of SEQ ID NO: 6.

In any of the foregoing examples, the antibody or antigen binding portion thereof comprises heavy and light chain variable regions comprising amino acid sequences at least 90% identical to the amino acid sequences selected from the group consisting of:

(a) SEQ ID NO: 4 and 6, respectively; and

(b) SEQ ID NO: 101 and 6, respectively.

In any of the foregoing examples, the antibody or antigen binding portion comprises heavy and light chains comprising amino acid sequences selected from the group consisting of:

(a) SEQ ID NOs: 129 and 133, respectively; and

(b) SEQ ID NOs: 131 and 133, respectively.

In any of the foregoing examples, the isolated monoclonal antibody, or antigen binding portion thereof described herein, is an agonist of human CD137 activity.

In any of the foregoing examples, the isolated monoclonal antibody, or antigen binding portion thereof described herein, competes with mAb1 or an antigen binding fragment of mAb1, for binding to the epitope of human CD137.

In some examples, the formulations described herein comprise an isolated monoclonal antibody that specifically binds CD137, or an antigen binding portion thereof, wherein the antibody or antigen binding portion thereof comprises heavy and light chain CDRs selected from the group consisting of:

(a) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 56 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively;

(b) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 56 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 70, 79 and 90, respectively;

(c) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 56 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 71, 80 and 91, respectively;

(d) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 56 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 72, 81 and 92, respectively;

(e) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 56 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 73, 82 and 91, respectively;

(f) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 56 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 74, 83 and 93, respectively;

(g) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 56 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 75, 84 and 91, respectively;

(h) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 56 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 74, 85 and 94, respectively;

(i) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 56 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 76, 86 and 95, respectively;

(j) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 56 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 77, 87 and 93, respectively;

(k) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 56 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 88 and 90, respectively;

(l) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 49, 57 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively;

(m) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 49, 58 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively;

(n) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 49, 59 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively;

(o) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 49, 60 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively;

(p) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 50, 61 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively;

(q) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 50, 58 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively;

(r) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 51, 62 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively;

(s) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 52, 63 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively;

(t) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 50, 64 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively;

(u) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 50, 65 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively;

(v) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 51, 108 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively;

(w) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 107, 56 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively; and

(x) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 56 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 109, 110 and 92, respectively.

In other examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds human CD137, wherein the antibody or antigen binding portion thereof comprises 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: 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 101 and 103; and wherein the light chain variable region comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 6, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46 and 105.

In other examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds human CD137, wherein the

antibody or antigen binding portion comprises heavy and light chain variable regions encoded by nucleotide sequences selected from the group consisting of:

(a) SEQ ID NOs: 5 and 7, respectively; and

(b) SEQ ID NOs: 102 and 7, respectively.

In other examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds human CD137, wherein the antibody or antigen binding portion thereof comprises heavy and light chain variable regions encoded by nucleotide sequences selected from the group consisting of:

(a) SEQ ID NO: 5 and 7, respectively;

(b) SEQ ID NO: 5 and 29, respectively;

(c) SEQ ID NO: 5 and 31, respectively;

(d) SEQ ID NO: 5 and 33, respectively;

(e) SEQ ID NO: 5 and 35, respectively;

(f) SEQ ID NO: 5 and 37, respectively;

(g) SEQ ID NO: 5 and 39, respectively;

(h) SEQ ID NO: 5 and 41, respectively;

(i) SEQ ID NO: 5 and 43, respectively;

(j) SEQ ID NO: 5 and 45, respectively;

(k) SEQ ID NO: 5 and 47, respectively;

(l) SEQ ID NO: 9 and 7, respectively;

(m) SEQ ID NO: 11 and 7, respectively;

(n) SEQ ID NO: 13 and 7, respectively;

(o) SEQ ID NO: 15 and 7, respectively;

(p) SEQ ID NO: 17 and 7, respectively;

(q) SEQ ID NO: 19 and 7, respectively;

(r) SEQ ID NO: 21 and 7, respectively;

(s) SEQ ID NO: 23 and 7, respectively;

(t) SEQ ID NO: 25 and 7, respectively;

(u) SEQ ID NO: 27 and 7, respectively;

(v) SEQ ID NO: 102 and 7, respectively;

(w) SEQ ID NO: 104 and 7, respectively; and

(x) SEQ ID NO: 5 and 106, respectively.

In yet other examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds human CD137, wherein the antibody or antigen binding portion thereof comprises heavy and light chain CDRs, wherein heavy chain CDR3 comprises the amino acid sequence set forth in SEQ ID NO: 68.

In another example, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds human CD137, wherein the antibody or antigen binding portion thereof comprises heavy and light chain CDRs, wherein heavy chain CDR3 comprises the amino acid sequence DXXXXLXXXXYXYYX (SEQ ID NO: 126), wherein X is any amino acid. In some examples, X is any amino acid except for alanine.

In some examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds human CD137, wherein the antibody or antigen binding portion thereof comprises heavy and light chain CDRs, wherein heavy chain CDR3 comprises the amino acid sequence DXPFXLDXXYYYYYX (SEQ ID NO: 127), wherein X is any amino acid. In some examples, X is any amino acid except for alanine.

In yet other examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds human CD137, wherein the antibody or antigen binding portion thereof comprises heavy and light chain CDRs, wherein heavy chain CDR3 comprises the amino acid sequence DXXXXLXXXXYXYYX (SEQ ID NO: 126), wherein X is any amino acid, and wherein mutation of residues D95, L100, Y100E, Y100G, Y100H, or combinations thereof, results in loss of binding to human CD137.

In other examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds human CD137, wherein the antibody or antigen binding portion thereof comprises heavy and light chain CDRs, wherein heavy chain CDR3 comprises the amino acid sequence DXPFXLDXXYYYYYX (SEQ ID NO: 127), wherein X is any amino acid, and wherein mutation of residues P97, F98, D100A, Y100D, Y100F, or combinations thereof to alanine results in reduction of binding to human CD137.

In some examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds human CD137, wherein the antibody or antigen binding portion thereof comprises heavy and light chain CDRs, wherein heavy chain CDR3 comprises the amino acid sequence DXPFXLDXXYYYYYX (SEQ ID NO: 127),

wherein X is any amino acid, and wherein mutation of residues P97, F98, D100A, Y100D, Y100F, or combinations thereof to any residue except alanine, results in an increase in binding to human CD137.

In yet other examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds human CD137, wherein the antibody or antigen binding portion thereof comprises heavy and light chain CDRs, wherein heavy chain CDR3 comprises the amino acid sequence DX1X2X3X4LX5X6X7X8YX9YYX10 (SEQ ID NO: 128) wherein X1 is any amino acid, wherein X2 is a non-polar amino acid, wherein X3 is a non-polar amino acid, wherein X4 is any amino acid, wherein X5 is a polar amino acid, wherein X6 is any amino acid, wherein X7 is any amino acid, wherein X8 is a polar amino acid, wherein X9 is a polar amino acid, and wherein X10 is any amino acid. In some examples, wherein X2 is proline, wherein X3 is phenylalanine or tryptophan, wherein X5 is aspartic acid or glutamic acid wherein X8 is tyrosine, and wherein X9 is tyrosine.

In some examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds human CD137, wherein the antibody or antigen binding portion thereof comprises heavy and light chain variable regions comprising amino acid sequences selected from the group consisting of:

(a) SEQ ID NO: 4 and 6, respectively;
(b) SEQ ID NO: 4 and 28, respectively;
(c) SEQ ID NO: 4 and 30, respectively;
(d) SEQ ID NO: 4 and 32, respectively;
(e) SEQ ID NO: 4 and 34, respectively;
(f) SEQ ID NO: 4 and 36, respectively;
(g) SEQ ID NO: 4 and 38, respectively;
(h) SEQ ID NO: 4 and 40, respectively;
(i) SEQ ID NO: 4 and 42, respectively;
(j) SEQ ID NO: 4 and 44, respectively;
(k) SEQ ID NO: 4 and 46, respectively;
(l) SEQ ID NO: 8 and 6, respectively;
(m) SEQ ID NO: 10 and 6, respectively;
(n) SEQ ID NO: 12 and 6, respectively;

(o) SEQ ID NO: 14 and 6, respectively;

(p) SEQ ID NO: 16 and 6, respectively;

(q) SEQ ID NO: 18 and 6, respectively;

(r) SEQ ID NO: 20 and 6, respectively;

(s) SEQ ID NO: 22 and 6, respectively;

(t) SEQ ID NO: 24 and 6, respectively;

(u) SEQ ID NO: 26 and 6, respectively;

(v) SEQ ID NO: 101 and 6, respectively;

(w) SEQ ID NO: 103 and 6, respectively; and

(x) SEQ ID NO: 4 and 105, respectively.

In other examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds human CD137wherein the antibody or antigen binding portion thereof comprises heavy and light chain variable regions, wherein the heavy chain variable region comprises an amino acid sequence which is at least 90% identical to the amino acid sequence selected from the group consisting of SEQ ID NOs: 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 101 and 103; and wherein the light chain variable region comprises an amino acid sequence which is at least 90% identical to the amino acid sequence selected from the group consisting of SEQ ID NOs: 6, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46 and 105.

In some examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds human CD137, wherein the antibody or antigen binding portion thereof comprises heavy and light chain variable regions comprising amino acid sequences at least 90% identical to the amino acid sequences selected from the group consisting of:

(a) SEQ ID NO: 4 and 6, respectively;

(b) SEQ ID NO: 4 and 28, respectively;

(c) SEQ ID NO: 4 and 30, respectively;

(d) SEQ ID NO: 4 and 32, respectively;

(e) SEQ ID NO: 4 and 34, respectively;

(f) SEQ ID NO: 4 and 36, respectively;

(g) SEQ ID NO: 4 and 38, respectively;

(h) SEQ ID NO: 4 and 40, respectively;

(i) SEQ ID NO: 4 and 42, respectively;

(j) SEQ ID NO: 4 and 44, respectively;

(k) SEQ ID NO: 4 and 46, respectively;

(l) SEQ ID NO: 8 and 6, respectively;

(m) SEQ ID NO: 10 and 6, respectively;

(n) SEQ ID NO: 12 and 6, respectively;

(o) SEQ ID NO: 14 and 6, respectively;

(p) SEQ ID NO: 16 and 6, respectively;

(q) SEQ ID NO: 18 and 6, respectively;

(r) SEQ ID NO: 20 and 6, respectively;

(s) SEQ ID NO: 22 and 6, respectively;

(t) SEQ ID NO: 24 and 6, respectively;

(u) SEQ ID NO: 26 and 6, respectively;

(v) SEQ ID NO: 101 and 6, respectively;

(w) SEQ ID NO: 103 and 6, respectively; and

(x) SEQ ID NO: 4 and 105, respectively.

In some examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds human CD137, wherein the antibody or antigen binding portion thereof comprises heavy and light chain sequences comprising amino acid sequences selected from the group consisting of:

(a) SEQ ID NOs: 129 and 133, respectively; and

(b) SEQ ID NOs: 131 and 133, respectively.

In some examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds human CD137, wherein the antibody or antigen binding portion thereof comprises heavy and light chain sequences having amino acid sequences set forth in SEQ ID NOs: 129 and 133, respectively.

In some examples, the formulations described herein comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds human CD137, wherein the antibody or antigen binding portion thereof comprises heavy and light chain sequences having amino acid sequences set forth in SEQ ID NOs: 131 and 133, respectively

In any of the foregoing examples, the antibody or antigen binding portion specifically binds to and agonizes human CD137.

In any of the foregoing examples, the isolated monoclonal antibody or antigen binding portion thereof, exhibits at least one or more of the following properties selected from the group consisting of:

(a) induces or enhances dimerization of CD137 trimers;

(b) induces or enhances multimerization of CD137 trimers;

(c) induces or enhances T cell activation;

(d) induces or enhances a cytotoxic T cell response;

(e) induces or enhances T cell proliferation;

(f) induces or enhances cytokine production; and

(g) any combination of properties (a)-(f).

In any of the foregoing examples, the isolated monoclonal antibody or antigen binding portion thereof, exhibits at least one or more of the following properties relative to a reference antibody that binds human CD137, selected from the group consisting of:

(a) does not induce or enhance intrahepatic T cell activation;

(b) does not induce or enhance intrahepatic T cell proliferation;

(c) does not induce or enhance intrasplenic T cell activation;

(d) does not induce or enhance intrasplenic T cell proliferation;

(e) does not induce or enhance macrophage activation;

(f) does not induce or enhance macrophage differentiation;

(g) does not induce or enhance alanine aminotransferase (ALT) activity; and

(h) any combination of properties (a) – (g). In some examples, the reference antibody is urelumab.

In any of the foregoing examples, the isolated monoclonal antibody or antigen binding portion thereof, induces or enhances human CD137-mediated T cell activation in the tumor microenvironment, but does not significantly induce or enhance human CD137-mediated T cell activation in the spleen and/or liver.

In any of the foregoing examples, the isolated monoclonal antibody or antigen binding portion thereof, induces or enhances T cell activation in the tumor microenvironment, but does not significantly induce or enhance T cell activation in the spleen and/or liver.

In any of the foregoing examples, the isolated monoclonal antibody or antigen binding portion thereof, induces or enhances human CD137-mediated cytotoxic T cell response in the tumor microenvironment, but does not significantly induce or enhance human CD137-mediated cytotoxic T cell response in the spleen and/or liver.

In any of the foregoing examples, the isolated monoclonal antibody or antigen binding portion thereof, induces or enhances a cytotoxic T cell response in the tumor microenvironment, but does not significantly induce or enhance a T cell response in the spleen and/or liver.

In any of the foregoing examples, the isolated monoclonal antibody or antigen binding portion thereof, induces human CD137-mediated T cell proliferation in the tumor microenvironment, but does not significantly induce human CD137-mediated T cell proliferation in the spleen and/or liver.

In any of the foregoing examples, the isolated monoclonal antibody or antigen binding portion thereof, induces T cell proliferation in the tumor microenvironment, but does not significantly induce T cell proliferation in the spleen and/or liver.

In any of the foregoing examples, the isolated monoclonal antibody or antigen binding portion thereof, induces human CD137-mediated T cell infiltration in the tumor microenvironment, but does not significantly induce human CD137-mediated T cell infiltration in the spleen and/or liver.

In any of the foregoing examples, the isolated monoclonal antibody or antigen binding portion thereof, induces T cell infiltration in the tumor microenvironment, but does not significantly induce T cell infiltration in the spleen and/or liver.

In any of the foregoing examples, the isolated monoclonal antibody or antigen binding fragment thereof, induces or enhances human CD137-mediated cytokine production in the tumor microenvironment, but does not significantly induce or enhance human CD137-mediated cytokine production in the spleen and/or liver.

In any of the foregoing examples, the properties of the antibody or antigen binding portion described herein, are not Fc gamma receptor binding dependent. In some examples, the properties of the antibody or antigen binding portion described herein, are enhanced by Fc gamma receptor binding.

In any of the foregoing examples, the isolated monoclonal antibody or antigen binding portion thereof cross competes with mAb1 (*i.e.*, an antibody comprising the heavy and light chain

variable sequences of SEQ ID NOs: 4 and 6, respectively). In some examples, the isolated monoclonal antibody or antigen binding portion thereof cross competes with mAb1 (*i.e.*, an antibody comprising the heavy and light chain variable sequences of SEQ ID NOs: 4 and 6, respectively), mab8 (*i.e.*, an antibody comprising the heavy and light chain variable sequences of SEQ ID NOs: 101 and 6, respectively) or mAb10 (*i.e.*, an antibody comprising the heavy and light chain variable sequences of SEQ ID NOs: 26 and 6, respectively). In some examples, the isolated monoclonal antibody or antigen binding portion thereof cross competes with mab8 (*i.e.*, an antibody comprising the heavy and light chain variable sequences of SEQ ID NOs: 101 and 6, respectively). In some examples, the isolated monoclonal antibody or antigen binding portion thereof cross competes with mAb10 (*i.e.*, an antibody comprising the heavy and light chain variable sequences of SEQ ID NOs: 26 and 6, respectively).

In any of the foregoing examples, the isolated monoclonal antibody or antigen binding portion thereof comprises at least the functional properties of mAb1 (*i.e.*, an antibody comprising the heavy and light chain variable sequences of SEQ ID NOs: 4 and 6, respectively). In some examples, the isolated monoclonal antibody or antigen binding portion thereof comprises at least the functional properties of mAb1 (*i.e.*, an antibody comprising the heavy and light chain variable sequences of SEQ ID NOs: 4 and 6, respectively), mab8 (*i.e.*, an antibody comprising the heavy and light chain variable sequences of SEQ ID NOs: 101 and 6, respectively) or mAb10 (*i.e.*, an antibody comprising the heavy and light chain variable sequences of SEQ ID NOs: 26 and 6, respectively). In some examples, the isolated monoclonal antibody or antigen binding portion thereof comprises at least the functional properties of mab8 (*i.e.*, an antibody comprising the heavy and light chain variable sequences of SEQ ID NOs: 101 and 6, respectively). In some examples, the isolated monoclonal antibody or antigen binding portion thereof comprises at least the functional properties of mAb10 (*i.e.*, an antibody comprising the heavy and light chain variable sequences of SEQ ID NOs: 26 and 6, respectively).

In any of the foregoing examples, the isolated monoclonal antibody or antigen binding portion thereof has a K_D value at least equivalent to mAb1 (*i.e.*, an antibody comprising the heavy and light chain variable sequences of SEQ ID NOs: 4 and 6, respectively). In some examples, the isolated monoclonal antibody or antigen binding portion thereof has a K_D value at least equivalent to mAb1 (*i.e.*, an antibody comprising the heavy and light chain variable sequences of SEQ ID NOs: 4 and 6, respectively), mab8 (*i.e.*, an antibody comprising the heavy and light chain variable

sequences of SEQ ID NOs: 101 and 6, respectively) or mAb10 (*i.e.*, an antibody comprising the heavy and light chain variable sequences of SEQ ID NOs: 26 and 6, respectively). In some examples, the isolated monoclonal antibody or antigen binding portion thereof has a K_D value at least equivalent to mab8 (*i.e.*, an antibody comprising the heavy and light chain variable sequences of SEQ ID NOs: 101 and 6, respectively). In some examples, the isolated monoclonal antibody or antigen binding portion thereof has a K_D value at least equivalent to mAb10 (*i.e.*, an antibody comprising the heavy and light chain variable sequences of SEQ ID NOs: 26 and 6, respectively).

In any of the foregoing examples, the isolated monoclonal antibody or antigen binding portion thereof, cross-reacts with cynomolgus CD137 and/or mouse CD137.

In any of the foregoing examples, the isolated monoclonal antibody, or antigen binding portion thereof, is selected from the group consisting of an IgG1, an IgG2, and IgG3, an IgG4, and IgM, and IgA1, and IgA2, and IgD, and an IgE antibody. In some examples, the isolated monoclonal antibody, or antigen binding portion thereof, is an IgG1 antibody or IgG4 antibody.

In any of the foregoing examples, the isolated monoclonal antibody comprises a wild-type IgG1 or wild-type IgG4 heavy chain constant region. In some examples, the isolated monoclonal antibody comprises a mutant IgG1 heavy chain constant region. In some examples, the isolated monoclonal antibody comprises a mutant IgG4 heavy chain constant region. In some examples, the mutant IgG4 heavy chain constant region comprises a substitution at Ser228. In some examples, the mutant IgG4 heavy chain constant region comprises substitution S228P.

In any of the foregoing examples, the isolated monoclonal antibody, or antigen binding portion thereof, binds to an epitope of CD137, wherein the amino acid residues comprising the epitope bound by the antibody are located within 4 angstroms of the amino acid residues comprising the paratope of the mAb1 antibody, described herein.

In any of the foregoing examples, the isolated monoclonal antibody, or antigen binding portion thereof, binds to an epitope of CD137, wherein a mutation of the epitope bound by the antibody inhibits, reduces, or blocks binding to both the antibody and to antibody mAb1.

In any of the foregoing examples, the isolated antibody, or antigen binding portion thereof, is fully human or humanized *(i.e.*, a fully human or humanized antibody or antigen binding portion thereof).

In some examples, the disclosure provides a pharmaceutical composition comprising an isolated monoclonal antibody or antigen binding portion thereof, as described herein, and a pharmaceutically acceptable carrier.

In other examples, the disclosure provides a nucleic acid comprising a nucleotide sequence encoding the light chain, heavy chain, or both light and heavy chains of an isolated monoclonal antibody, or antigen binding portion thereof, described herein. In some examples, the nucleic acid comprises SEQ ID NOs: 5 and 7. In some examples, the nucleic acid comprises SEQ ID NOs: 102 and 7. In some examples, the disclosure provides an expression vector comprising the nucleic acid described herein. In other examples, the disclosure provides a cell transformed with an expression vector described herein.

In another example, the disclosure provides a method for producing an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds human CD137, the method comprising maintaining a cell described herein under conditions permitting expression of the monoclonal antibody or antigen binding portion thereof. In some examples, the method for producing the monoclonal antibody that specifically binds human CD137, or antigen binding portion thereof, further comprises obtaining the monoclonal antibody or antigen binding portion thereof.

In yet another example, the disclosure provides a method for inducing or enhancing dimerization of human CD137 trimers in a subject, comprising administering to a subject in need thereof, an effective amount of an isolated monoclonal antibody, or antigen binding portion thereof, as described herein, or a pharmaceutical composition described herein.

In another example, the disclosure provides a method for inducing or enhancing multimerization of human CD137 trimers in a subject, comprising administering to a subject in need thereof, an effective amount of an isolated monoclonal antibody, or antigen binding portion thereof, as described herein, or a pharmaceutical composition described herein.

In other examples, the disclosure provides a method for inducing or enhancing T cell activation mediated by human CD137 in a subject, comprising administering to a subject in need thereof, an effective amount of an isolated monoclonal antibody, or antigen binding portion thereof, as described herein, or a pharmaceutical composition described herein. In some examples, T cell activation occurs in a tumor microenvironment. In other examples, T cell activation does not significantly occur in the spleen and/or liver of the subject.

In another example, the disclosure provides a method for inducing or enhancing a cytotoxic T cell response mediated by human CD137 in a subject, comprising administering to a subject in need thereof, an effective amount of an isolated monoclonal antibody, or antigen binding portion thereof, as described herein, or a pharmaceutical composition described herein. In some examples, the cytotoxic T cell response occurs in a tumor microenvironment. In other examples, the cytotoxic T cell response does not significantly occur in the spleen and/or liver of the subject.

In some examples, the disclosure provides a method for inducing or enhancing cytokine production mediated by human CD137 in a subject, comprising administering to a subject in need thereof, an effective amount of an isolated monoclonal antibody, or antigen binding portion thereof, as described herein, or a pharmaceutical composition described herein. In some examples, the cytokine produced is IL-2, TNFα, IL-13, IFN-γ, or combinations thereof. In some examples, the cytokine produced is IL-2. In some examples, the cytokine produced is TNFα. In some examples, the cytokine produced is IL-13. In some examples, the cytokine produced is IFN-γ. In some examples, the cytokine produced is IL-2 and TNFα. In some examples, the cytokine produced is IL-2 and IL-13. In some examples, the cytokine produced is IL-2 and IFN-γ. In some examples, the cytokine produced is TNFα and IL-13. In some examples, the cytokine produced is TNFα and IFN-γ. In some examples, the cytokine produced is IL-13 and IFN-γ. In some examples, the cytokine produced is IL-2, TNFα and IL-13. In some examples, the cytokine produced is IL-2, TNFα and IFN-γ. In some examples, the cytokine produced is IFN-γ TNFα and IL-13. In other examples, cytokine production occurs in a tumor microenvironment. In yet other examples, cytokine production does not significantly occur in the spleen and/or liver of the subject.

In another example, the disclosure provides a method for inducing or enhancing T cell proliferation mediated by human CD137 in a subject, comprising administering to a subject in need thereof, an effective amount of an isolated monoclonal antibody, or antigen binding portion thereof, as described herein, or a pharmaceutical composition described herein. In some examples, T cell proliferation occurs in a tumor microenvironment. In other examples, T cell proliferation does not significantly occur in the spleen and/or liver of the subject.

In another example, the disclosure provides a method for reducing or inhibiting tumor growth, comprising administering to a subject in need thereof, an effective amount of an isolated monoclonal antibody, or antigen binding portion thereof, as described herein, or a pharmaceutical composition described herein.

In yet another example, the disclosure provides a method for treating a disorder mediated by human CD137 in a subject, comprising administering to a subject in need thereof, an effective amount of an isolated monoclonal antibody, or antigen binding portion thereof, as described herein, or a pharmaceutical composition described herein.

In some examples, the disclosure provides a method for treating cancer in a subject, comprising administering to a subject in need thereof, an effective amount of an isolated monoclonal antibody, or antigen binding portion thereof, as described herein, or a pharmaceutical composition described herein. In some examples, the cancer is selected from the group consisting of melanoma, glioma, renal, breast, hematological and head and neck cancer. In some examples, the hematological cancer is a B cell lymphoma.

In some examples, the disclosure provides a method of inducing an anti-tumor memory immune response, comprising administering to a subject in need thereof, an effective amount of an isolated monoclonal antibody, or antigen binding portion thereof, as described herein, or a pharmaceutical composition described herein.

In any of the foregoing examples, infiltration of immune cells into a tumor microenvironment is increased after administration of an antibody or antigen binding portion. In some examples, immune cells express CD45.

In any of the foregoing examples, quantity of T regulatory (Treg) cells is reduced in a tumor microenvironment after administration of an antibody or antigen binding portion. In some examples, Treg cells express CD4, FOXP-3 and CD24.

In any of the foregoing examples, quantity of macrophages cells is reduced in a tumor microenvironment after administration of a monoclonal antibody or antigen binding portion. In some examples, macrophages express CD45 and CD11b.

In any of the foregoing examples, T cell exhaustion is reduced after administration of an antibody or antigen binding portion. In some examples, reduction of T cell exhaustion comprises a decrease in expression of TIGIT, PD-1, LAG-3 or a combination thereof. In some examples, reduction of T cell exhaustion comprises a decrease in expression of TIGIT and PD-1.

In any of the foregoing examples, depletion of CD4+ T cells, CD8+ T cells, Natural Killer cells, or combinations thereof, reduces the efficacy of the antibody or antigen binding portion thereof.

In another example, the disclosure provides a method for detecting the presence or absence of human CD137 in a biological sample, comprising:

(a) contacting a biological sample with an antibody or antigen-binding portion described herein, wherein the antibody or antigen-binding portion is labeled with a detectable substance; and

(b) detecting the antibody or antigen-binding portion bound to human CD137 to thereby detect the presence or absence of human CD137 in the biological sample.

In another example, the disclosure provides a kit comprising a container comprising an antibody or antigen-binding portion described herein, and an optional pharmaceutically acceptable carrier, or a pharmaceutical composition described herein, and a package insert comprising instructions for administration of the antibody or pharmaceutical composition, for treating or delaying progression of cancer or reducing or inhibiting tumor growth in a subject in need thereof.

In another example, the disclosure provides a kit comprising a container comprising an antibody or antigen-binding portion described herein, and an optional pharmaceutically acceptable carrier, or a pharmaceutical composition described herein, and a package insert comprising instructions for administration of the antibody or pharmaceutical composition alone or in combination with another agent, for treating or delaying progression of cancer or reducing or inhibiting tumor growth in a subject in need thereof.

In another example, the disclosure provides use of an isolated monoclonal antibody, or antigen binding portion thereof, as described herein, to induce or enhance T cell activation mediated by human CD137 in a subject. In other examples, the disclosure provides use of an isolated monoclonal antibody, or antigen binding portion thereof, as described herein, to induce or enhance multimerization of human CD137 trimers in a subject. In another example, the disclosure provides use of an isolated monoclonal antibody, or antigen binding portion thereof, as described herein, to induce or enhance a cytotoxic T cell response mediated by human CD137 in a subject. In other examples, the disclosure provides use of an isolated monoclonal antibody, or antigen binding portion thereof, as described herein, to induce or enhance cytokine production mediated by human CD137 in a subject. In another example, the disclosure provides use of an isolated monoclonal antibody, or antigen binding portion thereof, as described herein, to induce or enhance T cell proliferation mediated by human CD137 in a subject.

In another example, the disclosure provides use of an isolated monoclonal antibody, or antigen binding portion thereof, as described herein, to reduce or inhibit tumor growth in a subject in need thereof. In other examples, the disclosure provides use of an isolated monoclonal antibody, or antigen binding portion thereof, as described herein, to treat a disorder mediated by human CD137 in a subject in need thereof. In another example, the disclosure provides use of an isolated monoclonal antibody, or antigen binding portion thereof, as described herein, to treat cancer in a subject in need thereof.

In another example, the disclosure provides use of an isolated monoclonal antibody, or antigen binding portion thereof, as described herein, for the manufacture of a medicament for treating or delaying progression of cancer or reducing or inhibiting tumor growth in a subject in need thereof. In other examples, the disclosure provides an isolated monoclonal antibody, or antigen binding portion thereof, as described herein, in the manufacture of a medicament for treating or delaying progression of cancer or reducing or inhibiting tumor growth in a subject in need thereof. In another example, the disclosure provides an isolated monoclonal antibody or antigen binding portion thereof, as described herein, for use as a medicament.

BRIEF DESCRIPTION OF THE DRAWINGS

The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

FIG. 1 provides graphs depicting the distribution of binding affinities of affinity matured clones of the parental anti-CD137 antibody mAb1.

FIG. 2 provides a schematic showing the results of mAb1 CDRH3 alanine scanning, as measured by binding affinity (K_D) to human or mouse CD137.

FIG. 3A shows the amino acid sequence of human CD137 wherein residues comprising an epitope bound by mAb1, mAb4 or mAb5 are indicated in bold.

FIG. 3B is a graph depicting kinetic binding data of mAb1 to the extracellular domain of mouse and rat CD137 as determined by surface plasmon resonance.

FIG. 3C provides x-ray crystallography images of human CD137 bound to CD137L(shown in grey) and residues E111, T113, K114 and P135 shown as spheres.

FIG. 3D provides x-ray crystallography images of human CD137 bound to CD137L (shown in grey) in trimeric formation, and residues E111, T113, K114 and P135 shown as spheres.

FIG. 4A provides a scatterplot of flow cytometric data depicting an increase in TIGIT (top) or PD-1 (bottom) expression on CD44+ T cells in response to anti-CD137 antibodies.

FIG. 4B provides graphs depicting the quantification of CD8+ CD44+ T cells expressing TIGIT (top) or PD-1 (bottom) in the spleen of mice after treatment with anti-CD137 antibodies.

FIG. 4C provides graphs depicting the quantification of CD8+ T cells in the spleen of mice after treatment with anti-CD137 antibodies, as percentage of CD45+ cells (left) or cell number per spleen (right).

FIG. 5A provides graphs showing individual CT26 tumor volumes in mice after treatment with anti-CD137 antibodies at indicated dosages.

FIG. 5B is a graph showing the mean tumor volumes provided in FIG. 5A.

FIG. 5C is a Kaplan-Meier graph showing overall survival of mice with tumors after treatment with anti-CD137 antibodies.

FIG. 5D is a graph showing tumor volume in mice re-challenged with tumorigenic CT26 cells.

FIG. 6A provides graphs showing individual CT26 tumor volumes in mice after treatment with parental and affinity-matured anti-CD137 antibodies.

FIG. 6B is a graph providing the mean tumor volumes provided in FIG. 6A.

FIG. 7 provides graphs depicting the percentage of CD8+ or CD4+ T cells, from splenic T cells (top) and tumor infiltrating leukocytes (bottom) after treatment with anti-CD137 antibodies at indicated dosages.

FIG. 8 provides graphs showing individual tumor volumes when mice were treated with mAb1, with or without lymphocyte depleting antibodies. CD4+ T cells were depleted with GK1.5 (middle graph), CD8+ T cells were depleted with YTS169.4 (second graph from the right), and NK cells were depleted with an anti-asialo-GM1 antibody (last graph on the right).

FIG. 9 provides graphs showing individual tumor volumes in mice having either CT26 tumors (colon carcinoma), EMT-6 tumors (breast carcinoma), A20 tumors (B cell lymphoma), or MC38 tumors (colon carcinoma) and treated with mAb8 or isotype control antibody.

FIGs. 10A-10C show the *in vivo* anti-tumor efficacy of anti-CD137 antibodies administered at 150 μg/mouse. Individual tumor volumes are shown in **10A**, mean tumor volumes are shown in **10B** and percent survival is shown in **10C**.

FIGs. 11A-11C show the *in vivo* anti-tumor efficacy of anti-CD137 antibodies administered at 20 μg/mouse. Individual tumor volumes are shown in **11A**, mean tumor volumes are shown in **11B** and percent survival is shown in **11C**.

FIG. 12 provides graphs showing individual tumor volumes in mice having CT26 tumors and treated with varying doses of mAb1 (*i.e.,* 12.5, 25, 50, 100 or 200μg) or isotype control.

FIGs. 13A and 13B show the contribution of Fc binding in the anti-tumor efficacy of mAb1. **FIG. 13A** shows mAb1 as an IgG4 isotype or an IgG4 aglycosylated isotype. Mean tumor volumes are shown on the top and individual tumor volumes are shown on the bottom. **FIG. 13B** shows mAb1 as an IgG4 isotype or an IgG1 aglycosylated isotype. Mean tumor volumes are shown on the top and individual tumor volumes are shown on the bottom.

FIGs. 14A-14D show the *in vivo* anti-tumor efficacy of anti-CD137 antibodies in mice with large established tumors (i.e., 500mm^3) prior to receiving treatment. Individual tumor volumes are shown in **14A and 14D**, mean tumor volumes are shown in **14B** and percent survival is shown in **14C**.

FIG. 15 provides a Kaplan-Meier survival graph showing protective anti-tumor immunity in mice previously treated with mAb1, mAb8 or isotype control from FIGs. 14A-14C and considered cured, re-challenged with CT26 cells in an opposing flank.

FIG. 16A provides scatterplots of flow cytometric data showing the expansion of CD45+ intrahepatic T cells following treatment with anti-CD137 antibodies at indicated dosages.

FIG. 16B provides graphs depicting the quantification of intrahepatic CD8+ T cells (left) and CD4+ T cells (right) following treatment with anti-CD137 antibodies at indicated dosages.

FIG. 17A provides graphs depicting the percentage of CD3+, CD4+, or CD8+ T cells, from splenic T cells after treatment of mice with affinity-matured anti-CD137 antibodies.

FIG. 17B provides graphs depicting the percentage of CD3+, CD4+, or CD8+ T cells from liver T cells after treatment of mice with affinity-matured anti-CD137 antibodies.

FIG. 18A provides graphs depicting the percentage of splenic CD8+CD44+ T cells expressing TIGIT, PD-1, or LAG3 after treatment of mice with affinity-matured anti-CD137 antibodies.

FIG. 18B provides graphs depicting the percentage of liver CD8+CD44+ T cells expressing TIGIT, PD-1, or LAG3 after treatment of mice with affinity-matured anti-CD137 antibodies.

FIG. 19A provides graphs depicting the percentage of splenic CD4+CD44+ T cells expressing TIGIT, PD-1, or LAG3 after treatment of mice with affinity-matured anti-CD137 antibodies.

FIG. 19B provides graphs depicting the percentage of liver CD4+CD44+ T cells expressing TIGIT, PD-1, or LAG3 after treatment of mice with affinity-matured anti-CD137 antibodies.

FIGs. 20A-20C provide graphs of *in vivo* indicators of toxicity resulting from multiple administrations of anti-CD137 antibodies mAb1, mAb8 or 3H3 at varying doses. **FIG. 20A** is a graph showing percentage of CD8+ T cells in the liver after administration of the anti-CD137 antibodies. **FIG. 20B** is a graph showing alanine aminotransferase (ALT) activity in the plasma of mice administered anti-CD137 antibodies. **FIG. 20C** is a graph showing the levels of TNFα in the plasma of mice administered anti-CD137 antibodies.

FIG. 21 provides representative images of sectioned livers stained with hematoxylin and eosin (H&E) from mice treated with mAb1, mAb8, 3H3 or isotype control as described in FIGs. 20A-20C. Arrows indicate infiltration of immune cells.

FIGs. 22A-22D provide representative FACS plots showing immune cell reprogramming in the tumor microenvironment. Mice having CT26 tumors were administered multiple doses of mAb8 or isotype control (days 0, 3, 6 and 9). **FIG. 22A** shows overall immune cell infiltration based on CD45 expression. **FIG. 22B** shows reduction in Treg cells as measured by FOXP-3 and CD25 expression. **FIG. 22C** shows reduction of T-cell exhaustion as measured by PD-1 and TIGIT expression. **FIG. 22D** shows reduction of tumor-associated macrophages as measured by F4/80 and CD11b expression.

FIG. 23 shows immunophenotyping analysis of spleens from mice having CT26 tumors and treated with either anti-CD137 antibodies mAb1 and 3H3, or isotype control.

FIG. 24 is a graph showing the concentration of IL-2 (pg/ml) produced by murine T cells in an OVA stimulation assay, when stimulated with the anti-CD137 antibodies indicated. Along with Atezolizumab (anti-PD-L1 antibody), a murine anti-PD-1 (RMP1-14) was used as a comparator.

FIGs. 25A and 25B are graphs showing the percentage of murine CD8+ T cells expressing either CD25 (**25A**) or TIGIT (**25B**) when stimulated with the anti-CD137 antibodies indicated, in an OVA stimulation assay. Along with Atezolizumab (anti-PD-L1 antibody), a murine anti-PD-1 (RMP1-14) and murine anti-CD137 (3H3) were used as comparators.

FIG. 26 provides bar graphs depicting the quantification of cytokines (IL-2, TNFα, IL-13, and IFN-γ) produced by CD3+ T cells following incubation with plate-bound anti-CD137 antibodies. Cytokine levels are shown as fold increase over baseline activation by an anti-CD3 antibody.

FIGs. 27A-27C provide graphs depicting the dose-response of IFN-γ production in a mixed lymphocyte reaction following treatment with anti-CD137 antibodies. An anti-PD1 antibody (Keytruda; Merck) was used as a control.

FIG. 28 is a graph showing IFN-γ production from human T cells co-cultured with CHO cells engineered to express CD32 (CHO-CD32 cells) in the presence of anti-CD137 antibodies mAb1, mAb8, mAb4 or mAb5, or isotype control.

FIG. 29 is a graph showing proliferation of Treg cells when co-cultured with CHO cells engineered to express CD32 (CHO-CD32 cells) in the presence or absence of anti-CD137 antibodies mAb1, mAb8, mAb4 or mAb5, isotype control.

FIG. 30 provides graphs showing NFκβ and SRF signaling in CCL-119 cells transduced with luciferase reporters for NFκβ or SRF in the presence of mAb1, mAB8, mAb4 or mAb5 at varying concentrations.

FIG. 31 provides graphs showing induction of IL-6, TNFα, or IL-27 by bone marrow-derived mouse macrophages stimulated with TLR9 agonist CpG in the presence of anti-CD137 antibodies mAb1, 3H3 or LOB12.3, or isotype control.

FIG. 32 provides a graph showing induction of TNFα by human monocyte derived macrophages stimulated with LPS in the presence of anti-CD137 antibodies mAb1, mAb4 or mAb5, or isotype control.

FIG. 33 provides a graph showing effect of anti-CD137 antibodies on macrophage differentiation as determined by CD64 expression of THP1 monocytes cultured with PMA in the presence of anti-CD137 antibodies mAb1, mAb4 or mAb5, or isotype control.

FIGs. 34A-34C provides graphs showing percentage of hCD45+, hCD8+ or hCD4+ from immunocompetent mice that received human PBMCs and anti-CD137 antibodies mAb1, mAb4 or mAb5, or isotype control.

FIG. 35 graphically depicts cIEF charge variants analysis of mAb1 at high concentration (100 mg/mL) in three buffers with different pH and stored at either 4°C or 25°C temperatures up to 4 weeks.

FIG. 36 graphically depicts the cIEF charge variants analysis of mAb1 at 5 mg/mL in three buffers with different pH at 40°C for up to 4 weeks.

FIG. 37 depicts the size-exclusion chromatography profile of mAb1 after diluting 10-fold into 5%, 0.5% or 0.1% dextrose solutions, 0.9% saline, or pure water and incubating at room temperature for three days. The term dextrose is used interchangeably with the term glucose.

FIG. 38 graphically depicts the Dynamic Light Scattering (DLS) results of mAb1 after diluting 10-fold into 5%, 0.5% or 0.1% dextrose solutions, 0.9% saline, or pure water and incubating at room temperature for 3 days

FIG. 39 graphically depicts the micro-flow imaging analysis of subvisible particles between 2-80 mm. The analysis was performed using mAb1 at 10 mg/mL in a formulation of the disclosure after going through three cycles of freeze-thaw between -30°C/room temperature and three passes through a needle with a built in 5µm filter or a vented needle with a built in 5µm filter.

DETAILED DESCRIPTION

The present disclosure provides various formulations of an anti-CD137 antibody, or antigen binding fragments thereof, that specifically bind to human CD137 and agonize human CD137. In some embodiments, the formulations of the disclosure include (i) an anti-CD137 antibody or antigen binding fragment thereof, (ii) a buffer (*e.g.*, histidine), (iii) a disaccharide sugar (*e.g.*, sucrose); (iv) a non-ionic surfactant (*e.g.*, polysorbate 80); and (v) a salt (*e.g.*, NaCl). In some embodiments, the formulations of the disclosure have a pH of about 5.0 to about 7.0. In some embodiments, the formulations of the disclosure have a pH of about 5.0 to about 7.4. The disclosure also provides methods for treating cancer, or reducing or inhibiting tumor growth in a patient comprising administering a formulation of the disclosure to the patient. The disclosure

also provides methods for inducing or enhancing T cell activation in a patient comprising administering a formulation of the disclosure to the patient.

The present disclosure is based, at least in part, on the discovery that the formulations of the disclosure are stable and minimize the formation of antibody aggregates and particulates. In particular, the formulations of the disclosure were shown to provide an anti-CD137 agonist antibody, mAb1, with excellent stability, no significant loss of monomeric antibody, and no significant amount of degradation. In particular, it was surprisingly discovered that an anti-CD137 antibody was stable at high concentrations and under forced degradation conditions (*e.g.*, elevated temperature) when formulated in histidine buffer at pH 5.8. Likewise, it was discovered that there was a reduction in acidic/basic species when the anti-CD137 antibody was formulated in a buffer at pH 6.0 and at pH 6.5. It was also discovered that the anti-CD137 formulations of the disclosure had excellent stability with no significant loss of monomeric antibody. Furthermore, it was discovered that the addition of sucrose to the anti-CD137 formulations of the disclosure resulted in improved antibody stability at elevated temperatures.

Accordingly, in some embodiments, the present disclosure provides stable anti-CD137 antibody formulations. In some embodiments, the present disclosure provides stable anti-CD137 antibody formulations comprising (i) a buffer comprising about 10 mM to about 100 mM histidine, (ii) sucrose at about 5%-about 15% weight/volume, (iii) polysorbate-80 at about 0.01%-about 0.1% weight/volume (w/v), and (iv) NaCl at about 50 mM – 200 mM, wherein the pH of the formulation is about 5.0 to about 7.0. In some embodiments, the pH of the formulation is about 5.0 to about 7.4. In some embodiments, the pH of the formulation is about 5.0 to about 8.0.

Cancer therapy with agonist anti-CD137 antibodies has been shown to induce immune-mediated tumor rejections in mice, and analogous agents of this kind are currently being tested in cancer patients. Previous reports have indicated that administration of anti-CD137 antibodies can induce significant accumulations of polyclonal infiltrates of T lymphocytes in the liver (Dubrot et al., (2010) Cancer Immunology, Immunotherapy 59(8):1223-1233), suggestive of hepatic inflammation and the potential for drug-induced liver toxicity. A recent report on the clinical evaluation of an agonistic anti-CD137 antibody (Urelumab, BMS-663513; Bristol-Myers Squibb) documented the observation of treatment-related adverse events in human subjects, including

indications of severe hepatotoxicity (transaminitis) correlating with antibody dose (Segal et al., (2016) Clin Cancer Res 23(8):1929-1936).

The present disclosure provides isolated monoclonal antibodies, or antigen binding portions thereof, that specifically bind to an epitope of human CD137 and agonize human CD137, and formulations thereof. In some embodiments, the antibody or antigen binding portion thereof competes with mAb1 for binding to the epitope of human CD137. In some aspects, the anti-CD137 agonist antibodies of the disclosure induce cytokine production and expansion of CD8+ T cells in the tumor microenvironment, and protective anti-tumor immunity *in vivo* with a concomitant reduction in the potential for toxicity-related events, as compared to the anti-mouse CD137 3H3 antibody (Melero et al. (1997) Nature Medicine 3(6):682-685; Uno et al. (2006) Nature Medicine 12(6):693-696) and to at least two anti-human CD137 antibodies in clinical development (BMS-663513/Urelumab, Bristol-Meyers Squibb, and PF-05082566/Utomilumab, Pfizer).

Definitions

Terms used in the claims and specification are defined as set forth below unless otherwise specified.

It must be noted that, as used in the specification and the appended claims, the singular forms "a," "an" and "the" include plural referents unless the context clearly dictates otherwise. Further, unless otherwise required by context, singular terms shall include pluralities and plural terms shall include the singular.

As used herein, "about" will be understood by persons of ordinary skill and will vary to some extent depending on the context in which it is used. If there are uses of the term which are not clear to persons of ordinary skill given the context in which it is used, "about" will mean up to plus or minus 10% of the particular value.

As used herein, the term "agonist" refers to any molecule that partially or fully promotes, induces, increases, and/or activates a biological activity of a native polypeptide disclosed herein (*e.g.*, CD137). Suitable agonist molecules specifically include agonist antibodies or antibody fragments, fragments or amino acid sequence variants of native polypeptides, peptides, antisense oligonucleotides, small organic molecules, etc. In some embodiments, activation in the presence of the agonist is observed in a dose-dependent manner. In some embodiments, the measured signal (*e.g.*, biological activity) is at least about 5%, at least about 10%, at least about 15%, at least about

20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, or at least about 100% higher than the signal measured with a negative control under comparable conditions. Also disclosed herein, are methods of identifying agonists suitable for use in the methods of the disclosure. For example, these methods include, but are not limited to, binding assays such as enzyme-linked immuno-absorbent assay (ELISA), FORTE BIO© systems, and radioimmunoassay (RIA). These assays determine the ability of an agonist to bind the polypeptide of interest (*e.g.*, a receptor or ligand, *e.g.*, CD137) and therefore indicate the ability of the agonist to promote, increase or activate the activity of the polypeptide. Efficacy of an agonist can also be determined using functional assays, such as the ability of an agonist to activate or promote the function of the polypeptide. For example, a functional assay may comprise contacting a polypeptide with a candidate agonist molecule and measuring a detectable change in one or more biological activities normally associated with the polypeptide. The potency of an agonist is usually defined by its EC_{50} value (concentration required to activate 50% of the agonist response). The lower the EC_{50} value the greater the potency of the agonist and the lower the concentration that is required to activate the maximum biological response.

As used herein, the term ”alanine scanning” refers to a technique used to determine the contribution of a specific wild-type residue to the stability or function(s) (*e.g.*, binding affinity) of a given protein or polypeptide. The technique involves the substitution of an alanine residue for a wild-type residue in a polypeptide, followed by an assessment of the stability or function(s) (*e.g.*, binding affinity) of the alanine-substituted derivative or mutant polypeptide and comparison to the wild-type polypeptide. Techniques to substitute alanine for a wild-type residue in a polypeptide are known in the art.

The term "ameliorating" refers to any therapeutically beneficial result in the treatment of a disease state, *e.g.*, cancer, including prophylaxis, lessening in the severity or progression, remission, or cure thereof.

As used herein, the term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function in a manner similar to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, *e.g.*, hydroxyproline, γ-

carboxyglutamate, and O-phosphoserine. Amino acid analogs refer to compounds that have the same basic chemical structure as a naturally occurring amino acid, *i.e.*, a carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, *e.g.*, homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs have modified R groups (*e.g.*, norleucine) or modified peptide backbones, but retain the same basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refers to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that function in a manner similar to a naturally occurring amino acid.

Amino acids can be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, can be referred to by their commonly accepted single-letter codes. As used here, a “polar amino acid” refers to an amino acid comprising a side chain that prefers to reside in an aqueous environment. In some embodiments, a polar amino acid is selected from the group consisting of: arginine, asparagine, aspartic acid, glutamic acid, glutamine, histidine, lysine, serine, theronine and tyrosine. Polar amino acids can be positive, negatively or neutrally charged. As used herein, a “non-polar amino acid” refers to an amino acid selected from the group consisting of: alanine, cysteine, glycine, isoleucine, leucine, methionine, phenylalanine, proline, tryptophan and valine.

As used herein, an "amino acid substitution" refers to the replacement of at least one existing amino acid residue in a predetermined amino acid sequence (an amino acid sequence of a starting polypeptide) with a second, different "replacement" amino acid residue. An "amino acid insertion" refers to the incorporation of at least one additional amino acid into a predetermined amino acid sequence. While the insertion will usually consist of the insertion of one or two amino acid residues, larger "peptide insertions," can also be made, *e.g.* insertion of about three to about five or even up to about ten, fifteen, or twenty amino acid residues. The inserted residue(s) may be naturally occurring or non- naturally occurring as disclosed above. An "amino acid deletion" refers to the removal of at least one amino acid residue from a predetermined amino acid sequence.

As used herein, the term “amount” or “level” refers to a detectable quantity, level or abundance of a substance (*e.g.*, a protein). When referring to a polypeptide, such as those described herein, the terms “level of expression” or “expression level” in general are used interchangeably

and generally refer to a detectable amount of a polypeptide in a biological sample (*e.g.*, on the surface of a cell).

As used herein, the term "anti-CD137 agonist antibody" (used interchangeably with the term "anti-CD137 antibody") refers to an antibody that specifically binds to CD137 and partially or fully promotes, induces, increases, and/or activates CD137 biological activity, response, and/or downstream pathway(s) mediated by CD137 signaling or other CD137-mediated function. In some embodiments, an anti-CD137 agonist antibody binds to CD137 and allows binding of CD137L. In some embodiments, an anti-CD137 agonist antibody binds to CD137 and induces multimerization of CD137. In some embodiments, an anti-CD137 agonist antibody binds to CD137 and induces the dimerization of CD137 trimers. In some embodiments, an anti-CD137 agonist antibody binds to CD137 and induces the multimerization of CD137 trimers. Examples of anti-CD137 agonist antibodies are provided herein. Methods for detecting formation of a trimer:trimer complex are known to those of skill in the art. For example, electron microscopy has been shown to detect such complexes, *see*, *e.g.*, Won, E. The Journal of Biological Chemistry, Vol. 285 (12): 9202-9210 (2010)

As used herein, the term “anti-CD137 mAb1” (used interchangeably with “mAb1”) refers to an exemplary anti-CD137 agonist antibody that comprises the variable heavy chain (V_H) amino acid sequence:

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTY YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDSPFLLDDYYYYYYMDVW GKGTTVTVSS (SEQ ID NO: 4),

and the variable light chain (V_L) amino acid sequence:

DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPS RFSGSGSGTDFTLTISSLQPEDFATYYCQQGHLFPITFGGGTKVEIK (SEQ ID NO: 6).

As used herein, the term “anti-CD137 mAb8” (used interchangeably with “mAb8”) refers to an exemplary anti-CD137 agonist antibody that comprises the variable heavy chain ((V_H) amino acid sequence:

EVQLLESGGGLVQPGGSLRLSCAASGFTFRNYAMSWVRQAPGKGLEWVSAISGSGDTT YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDSPFLLDDYYYYYYMDV WGKGTTVTVSS (SEQ ID NO: 101);

and the variable light chain (V_L) amino acid sequence:

DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPS
RFSGSGSGTDFTLTISSLQPEDFATYYCQQGHLFPITFGGGTKVEIK (SEQ ID NO: 6).

As used herein, the term "anti-CD137 mAb10" (used interchangeably with "mAb10") refers to an exemplary anti-CD137 agonist antibody that comprises the variable heavy chain ((V_H) amino acid sequence:

EVQLLESGGGLVQPGGSLRLSCAASGFTFYGYAMSWVRQAPGKGLEWVAAISGSGDST
YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDSPFLLDDYYYYYYMDV
WGKGTTVTVSS (SEQ ID NO: 26);

and the variable light chain (V_L) amino acid sequence:

DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASSLQSGVPS
RFSGSGSGTDFTLTISSLQPEDFATYYCQQGHLFPITFGGGTKVEIK (SEQ ID NO: 6).

As used herein, the term "antibody" refers to a whole antibody comprising two light chain polypeptides and two heavy chain polypeptides. Whole antibodies include different antibody isotypes including IgM, IgG, IgA, IgD, and IgE antibodies. The term "antibody" includes a polyclonal antibody, a monoclonal antibody, a chimerized or chimeric antibody, a humanized antibody, a primatized antibody, a deimmunized antibody, and a fully human antibody. The antibody can be made in or derived from any of a variety of species, *e.g.*, mammals such as humans, non-human primates (*e.g.*, orangutan, baboons, or chimpanzees), horses, cattle, pigs, sheep, goats, dogs, cats, rabbits, guinea pigs, gerbils, hamsters, rats, and mice. The antibody can be a purified or a recombinant antibody.

As used herein, the terms "antibody fragment," "antigen-binding fragment," "antigen binding portion" or similar terms refer to a fragment of an antibody that retains the ability to bind to a target antigen (*e.g.*, CD137) and inhibit the activity of the target antigen. Such fragments include, *e.g.*, a single chain antibody, a single chain Fv fragment (scFv), an Fd fragment, a Fab fragment, a Fab' fragment, or an $F(ab')_2$ fragment. An scFv fragment is a single polypeptide chain that includes both the heavy and light chain variable regions of the antibody from which the scFv is derived. In addition, intrabodies, minibodies, triabodies, and diabodies are also included in the definition of antibody and are compatible for use in the methods described herein. See, *e.g.*, Todorovska et al., (2001) *J. Immunol. Methods* 248(1):47-66; Hudson and Kortt, (1999) *J. Immunol. Methods* 231(1):177-189; Poljak, (1994) *Structure* 2(12):1121-1123; Rondon and

Marasco, (1997) *Annu. Rev. Microbiol.* 51:257-283, the disclosures of each of which are incorporated herein by reference in their entirety.

As used herein, the term "antibody fragment" also includes, *e.g.*, single domain antibodies such as camelized single domain antibodies. See, *e.g.*, Muyldermans et al., (2001) *Trends Biochem. Sci.* 26:230-235; Nuttall et al., (2000) *Curr. Pharm. Biotech.* 1:253-263; Reichmann et al., (1999) *J. Immunol. Meth.* 231:25-38; PCT application publication nos. WO 94/04678 and WO 94/25591; and U.S. Patent No:. 6,005,079, all of which are incorporated herein by reference in their entireties. In some embodiments, the disclosure provides single domain antibodies comprising two VH domains with modifications such that single domain antibodies are formed.

In some embodiment, an antigen-binding fragment includes the variable region of a heavy chain polypeptide and the variable region of a light chain polypeptide. In some embodiments, an antigen-binding fragment described herein comprises the CDRs of the light chain and heavy chain polypeptide of an antibody.

The term "antigen presenting cell" or "APC" is a cell that displays foreign antigen complexed with MHC on its surface. T cells recognize this complex using T cell receptor (TCR). Examples of APCs include, but are not limited to, dendritic cells (DCs), peripheral blood mononuclear cells (PBMC), monocytes (such as THP-1), B lymphoblastoid cells (such as C1R.A2, 1518 B-LCL) and monocyte-derived dendritic cells (DCs). Some APCs internalize antigens either by phagocytosis or by receptor-mediated endocytosis.

The term "antigen presentation" refers to the process by which APCs capture antigens and enables their recognition by T cells, *e.g.*, as a component of an MHC-I and/or MHC-II conjugate.

As used herein, the term "apoptosis" refers to the process of programmed cell death that occurs in multicellular organisms (*e.g.* humans). The highly-regulated biochemical and molecular events that result in apoptosis can lead to observable and characteristic morphological changes to a cell, including membrane blebbing, cell volume shrinkage, chromosomal DNA condensation and fragmentation, and mRNA decay. A common method to identify cells, including T cells, undergoing apoptosis is to expose cells to a fluorophore-conjugated protein (Annexin V). Annexin V is commonly used to detect apoptotic cells by its ability to bind to phosphatidylserine on the outer leaflet of the plasma membrane, which is an early indicator that the cell is undergoing the process of apoptosis.

As used herein, the term "binds to immobilized CD137," refers to the ability of a human antibody of the disclosure to bind to CD137, for example, expressed on the surface of a cell or which is attached to a solid support.

As used herein, the term "bispecific" or "bifunctional antibody" refers to 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, (1990) *Clin. Exp. Immunol.* 79:315-321; Kostelny et al., (1992) *J. Immunol.* 148:1547-1553.

Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chain/light-chain pairs have different specificities (Milstein and Cuello, (1983) *Nature* 305:537-539). Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion of the heavy chain variable region is preferably with an immunoglobulin heavy-chain constant domain, including at least part of the hinge, CH2, and CH3 regions. For further details of illustrative currently known methods for generating bispecific antibodies see, *e.g.*, Suresh et al., (1986) *Methods Enzymol.* 121:210; PCT Publication No. WO 96/27011; Brennan et al., (1985) *Science* 229:81; Shalaby et al., *J. Exp. Med.* (1992) 175:217-225; Kostelny et al., (1992) *J. Immunol.* 148(5):1547-1553; Hollinger et al., (1993) *Proc. Natl. Acad. Sci. USA* 90:6444-6448; Gruber et al., (1994) *J. Immunol.* 152:5368; and Tutt et al., (1991) *J. Immunol.* 147:60. Bispecific antibodies also include cross-linked or heteroconjugate antibodies. Heteroconjugate antibodies may be made using any convenient cross-linking methods. Suitable cross-linking agents are well known in the art, and are disclosed in U.S. Pat. No. 4,676,980, along with a number of cross-linking techniques.

Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. See, *e.g.*, Kostelny et al. (1992) J Immunol 148(5):1547-1553. The leucine zipper peptides from the Fos and Jun proteins may be linked to the Fab′ portions of two different antibodies by gene fusion. The antibody homodimers may be reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al. (1993) Proc Natl Acad Sci USA 90:6444-6448 has provided an

alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (VH) connected to a light-chain variable domain (VL) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the VH and VL domains of one fragment are forced to pair with the complementary VL and VH domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (scFv) dimers has also been reported. See, *e.g.*, Gruber et al. (1994) J Immunol 152:5368. Alternatively, the antibodies can be "linear antibodies" as described in, *e.g.*, Zapata et al. (1995) Protein Eng. 8(10):1057-1062. Briefly, these antibodies comprise a pair of tandem Fd segments (VH-CH1-VH-CH1) which form a pair of antigen binding regions. Linear antibodies can be bispecific or monospecific.

Antibodies with more than two valencies (*e.g.*, trispecific antibodies) are contemplated and described in, *e.g.*, Tutt et al. (1991) J Immunol 147:60.

The disclosure also embraces variant forms of multi-specific antibodies such as the dual variable domain immunoglobulin (DVD-Ig) molecules described in Wu et al. (2007) Nat Biotechnol 25(11): 1290-1297. The DVD-Ig molecules are designed such that two different light chain variable domains (VL) from two different parent antibodies are linked in tandem directly or via a short linker by recombinant DNA techniques, followed by the light chain constant domain. Similarly, the heavy chain comprises two different heavy chain variable domains (VH) linked in tandem, followed by the constant domain CH1 and Fc region. Methods for making DVD-Ig molecules from two parent antibodies are further described in, *e.g.*, PCT Publication Nos. WO 08/024188 and WO 07/024715. In some embodiments, the bispecific antibody is a Fabs-in-Tandem immunoglobulin, in which the light chain variable region with a second specificity is fused to the heavy chain variable region of a whole antibody. Such antibodies are described in, *e.g.*, International Patent Application Publication No. WO 2015/103072.

As used herein, "cancer antigen" or "tumor antigen" refers to (i) tumor- specific antigens, (ii) tumor- associated antigens, (iii) cells that express tumor- specific antigens, (iv) cells that express tumor- associated antigens, (v) embryonic antigens on tumors, (vi) autologous tumor cells, (vii) tumor- specific membrane antigens, (viii) tumor- associated membrane antigens, (ix) growth factor receptors, (x) growth factor ligands, and (xi) any other type of antigen or antigen-presenting cell or material that is associated with a cancer.

The term "carcinoma" is art recognized and refers to malignancies of epithelial or endocrine tissues including respiratory system carcinomas, gastrointestinal system carcinomas, genitourinary system carcinomas, testicular carcinomas, breast carcinomas, prostatic carcinomas, endocrine system carcinomas, and melanomas. The anti-CD137 antibodies described herein can be used to treat patients who have, who are suspected of having, or who may be at high risk for developing any type of cancer, including renal carcinoma or melanoma. Exemplary carcinomas include those forming from tissue of the cervix, lung, prostate, breast, head and neck, colon and ovary. The term also includes carcinosarcomas, which include malignant tumors composed of carcinomatous and sarcomatous tissues. An "adenocarcinoma" refers to a carcinoma derived from glandular tissue or in which the tumor cells form recognizable glandular structures.

As used herein the term "compete", when used in the context of antigen-binding proteins (*e.g.*, immunoglobulins, antibodies, or antigen-binding fragments thereof) that compete for binding to the same epitope, refers to a interaction between antigen-binding proteins as determined by an assay (*e.g.*, a competitive binding assay; a cross-blocking assay), wherein a test antigen-binding protein (*e.g.*, a test antibody) inhibits (*e.g.*, reduces or blocks) specific binding of a reference antigen-binding protein (*e.g.*, a reference antibody, such as mAb1) to a common antigen (*e.g.*, CD137 or a fragment thereof). In some embodiments, the antibodies described herein cross compete with mAb1 (i.e., an antibody comprising the heavy and light chain variable sequences of SEQ ID NOs: 4 and 6, respectively), mab8 (*i.e.*, an antibody comprising the heavy and light chain variable sequences of SEQ ID NOs: 101 and 6, respectively) or mAb10 (*i.e.*, an antibody comprising the heavy and light chain variable sequences of SEQ ID NOs: 26 and 6, respectively).

A polypeptide or amino acid sequence "derived from" a designated polypeptide or protein refers to the origin of the polypeptide. Preferably, the polypeptide or amino acid sequence which is derived from a particular sequence has an amino acid sequence that is essentially identical to that sequence or a portion thereof, wherein the portion consists of at least 10-20 amino acids, preferably at least 20-30 amino acids, more preferably at least 30-50 amino acids, or which is otherwise identifiable to one of ordinary skill in the art as having its origin in the sequence. Polypeptides derived from another peptide may have one or more mutations relative to the starting polypeptide, *e.g.*, one or more amino acid residues which have been substituted with another amino acid residue or which has one or more amino acid residue insertions or deletions.

A polypeptide can comprise an amino acid sequence which is not naturally occurring. Such variants necessarily have less than 100% sequence identity or similarity with the starting molecule. In certain embodiments, the variant will have an amino acid sequence from about 75% to less than 100% amino acid sequence identity or similarity with the amino acid sequence of the starting polypeptide, more preferably from about 80% to less than 100%, more preferably from about 85% to less than 100%, more preferably from about 90% to less than 100% (*e.g.*, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%) and most preferably from about 95% to less than 100%, *e.g.*, over the length of the variant molecule.

In certain embodiments, there is one amino acid difference between a starting polypeptide sequence and the sequence derived there from. Identity or similarity with respect to this sequence is defined herein as the percentage of amino acid residues in the candidate sequence that are identical (i.e., same residue) with the starting amino acid residues, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. In certain embodiments, a polypeptide consists of, consists essentially of, or comprises an amino acid sequence selected from a sequence set forth in any one of Tables 22-27. In certain embodiments, a polypeptide includes an amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to an amino acid sequence selected from a sequence set forth in any one of Tables 22-27. In certain embodiments, a polypeptide includes a contiguous amino acid sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a contiguous amino acid sequence selected from a sequence set forth in any one of Tables 22-27. In certain embodiments, a polypeptide includes an amino acid sequence having at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 200, 300, 400, or 500 (or any integer within these numbers) contiguous amino acids of an amino acid sequence selected from a sequence set forth in any one of Tables 22-27.

In certain embodiments, the antibodies of the disclosure are encoded by a nucleotide sequence. Nucleotide sequences of the invention can be useful for a number of applications, including: cloning, gene therapy, protein expression and purification, mutation introduction, DNA vaccination of a host in need thereof, antibody generation for, *e.g.*, passive immunization, PCR, primer and probe generation, and the like. In certain embodiments, the nucleotide sequence of the invention comprises, consists of, or consists essentially of, a nucleotide sequence selected from a

sequence set forth in any one of Tables 22-27. In certain embodiments, a nucleotide sequence includes a nucleotide sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a nucleotide sequence selected from a sequence set forth in any one of Tables 22-27. In certain embodiments, a nucleotide sequence includes a contiguous nucleotide sequence at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a contiguous nucleotide sequence selected from a sequence set forth in any one of Tables 22-27. In certain embodiments, a nucleotide sequence includes a nucleotide sequence having at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 200, 300, 400, or 500 (or any integer within these numbers) contiguous nucleotides of a nucleotide sequence selected from a sequence set forth in any one of Tables 22-27.

It will also be understood by one of ordinary skill in the art that the antibodies suitable for use in the methods disclosed herein may be altered such that they vary in sequence from the naturally occurring or native sequences from which they were derived, while retaining the desirable activity of the native sequences. For example, nucleotide or amino acid substitutions leading to conservative substitutions or changes at "non-essential" amino acid residues may be made. Mutations may be introduced by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis.

The antibodies suitable for use in the methods disclosed herein may comprise conservative amino acid substitutions at one or more amino acid residues, *e.g.*, at essential or non-essential amino acid residues. A "conservative amino acid substitution" is one 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, including 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), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a nonessential amino acid residue in a binding polypeptide is preferably replaced with another amino acid residue from the same side chain family. In certain embodiments, a string of amino acids can be replaced with a structurally similar string that differs in order and/or composition of side chain family members.

Alternatively, in certain embodiments, mutations may be introduced randomly along all or part of a coding sequence, such as by saturation mutagenesis, and the resultant mutants can be incorporated into binding polypeptides of the invention and screened for their ability to bind to the desired target.

As used herein, the term antigen "cross-presentation" refers to presentation of exogenous protein antigens to T cells via MHC class I and class II molecules on APCs.

As used herein, the term "cross-reacts" refers to the ability of an antibody of the disclosure to bind to CD137 from a different species. For example, an antibody of the present disclosure which binds human CD137 may also bind another species of CD137. As used herein, cross-reactivity is 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 CD137. 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.

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.

As used herein, the term "dimerization" refers to the formation of a macromolecular complex by two, usually non-covalently bound, macromolecules, such as proteins or multimers of proteins. Homodimerization refers to the process of dimerization when the macromolecules (*e.g.*, proteins) are identical in nature. Heterodimerization refers to the process of dimerization when the macromolecules (*e.g.*, proteins) are non-identical in nature. Methods for determining dimerization are known to those of skill in the art. For example, such methods include, but are not limited to, yeast two-hybrid assay, fluorescence resonance energy transfer (FRET), bioluminescence resonance energy transfer (BRET), protein mass spectrometry, evanescent wave methods, size exclusion chromatography, analytical ultracentrifugation, scattering techniques, NMR spectroscopy, isothermal titration calorimetry, fluorescence anisotropy, fluorescence correlation spectroscopy (FCS), fluorescence recovery after photobleaching (FRAP), proximity imaging (PRIM) and bimolecular fluorescence complementation (BiFC) (see *e.g.,* Gell D.A., Grant R.P., Mackay J.P. (2012) The Detection and Quantitation of Protein Oligomerization. In: Matthews J.M. (eds) Protein Dimerization and Oligomerization in Biology. Advances in Experimental Medicine

and Biology, vol 747. Springer, New York, NY; and Xie, Q. *et al.* Methods Mol Biol, 2011; 680: 3-28).

As used herein, the terms "dimerization of CD137" refers to the dimerization of two CD137 trimers. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance dimerization of CD137. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance dimerization of CD137 relative to the amount of dimerization in the absence of an anti-CD137 agonist antibody. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance dimerization of CD137 relative to the amount of dimerization in the presence of a reference anti-CD137 agonist antibody. In some embodiments, dimerization is increased by at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100%.

As used herein, the term "EC_{50}" refers to the concentration of an antibody or an antigen-binding portion thereof, which induces a response, either in an *in vitro* or an *in vivo* assay, which is 50% of the maximal response, *i.e.*, halfway between the maximal response and the baseline.

As used herein, the term "effective dose" or "effective dosage" is defined as an amount sufficient to achieve or at least partially achieve the desired effect. The term "therapeutically effective dose" is defined as an amount sufficient to cure or at least partially arrest the disease and its complications in a patient already suffering from the disease. Amounts effective for this use will depend upon the severity of the disorder being treated and the general state of the patient's own immune system.

As used herein, the term "epitope" or "antigenic determinant" refers to a determinant or site on an antigen (*e.g.*, CD137) to which an antigen-binding protein (*e.g.*, an immunoglobulin, antibody, or antigen-binding fragment) specifically binds. The epitopes of protein antigens can be demarcated into "linear epitopes" and "conformational epitopes". As used herein, the term "linear epitope" refers to an epitope formed from a contiguous, linear sequence of linked amino acids. Linear epitopes of protein antigens are typically retained upon exposure to chemical denaturants (*e.g.*, acids, bases, solvents, cross-linking reagents, chaotropic agents, disulfide bond reducing agents) or physical denaturants (*e.g.* thermal heat, radioactivity, or mechanical shear or stress). In some embodiments, an epitope is non-linear, also referred to as an interrupted epitope. As used herein, the term "conformational epitope" or "non-linear epitope" refers to an epitope formed from noncontiguous amino acids juxtaposed by tertiary folding of a polypeptide. Conformational

epitopes are typically lost upon treatment with denaturants. 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. In some embodiments, an epitope includes fewer than 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6 or 5 amino acids in a unique spatial conformation. Generally, an antibody, or antigen-binding fragment thereof, specific for a particular target molecule will preferentially recognize and bind to a specific epitope on the target molecule within a complex mixture of proteins and/or macromolecules. In some embodiments, an epitope does not include all amino acids of the extracellular domain of human CD137.

Also encompassed by the present disclosure are antibodies that bind to an epitope on CD137 which comprises all or a portion of an epitope recognized by the particular antibodies described herein (*e.g.*, the same or an overlapping region or a region between or spanning the region).

As used herein, the term "epitope mapping" refers to a process or method of identifying the binding site, or epitope, of an antibody, or antigen binding fragment thereof, on its target protein antigen. Epitope mapping methods and techniques are provided herein.

As used herein, the term "CD137" refers to a specific member of the tumor necrosis factor receptor (TNFR) family of transmembrane proteins. Alternative names and acronyms for CD137 in the art include "tumor necrosis factor receptor superfamily member 9" (TNFRSF9), 4-1BB and "induced by lymphocyte activation" (ILA) (Alderson et al., (1994) Eur J Immunol 24(9):2219-2227; Schwarz et al., (1993) Gene 134(2):295-298). An exemplary amino acid sequence of full-length human CD137, including leader, transmembrane, and cytoplasmic domains is set forth in Table 23 (SEQ ID NO: 3) and here:

MGNSCYNIVATLLLVLNFERTRSLQDPCSNCPAGTFCDNNRNQICSPCPPNSFSSAGGQR
TCDICRQCKGVFRTRKECSSTSNAECDCTPGFHCLGAGCSMCEQDCKQGQELTKKGCK
DCCFGTFNDQKRGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGASSVTPPAP
AREPGHSPQIISFFLALTSTALLFLLFFLTLRFSVVKRGRKKLLYIFKQPFMR
PVQTTQEEDGCSCRFPEEEEGGCEL.

As used herein, the term "CD137L" or "CD137 ligand" refers to a member of the tumor necrosis factor (TNF) family of transmembrane proteins. Alternative names and acronyms for CD137L in the art include "tumor necrosis factor superfamily member 9" (TNFSF9) and 4-1BB

ligand (4-1BBL) (Alderson et al., (1994) Eur J Immunol 24(9):2219-2227). An exemplary amino acid sequence of full-length CD137L is set forth in Table 23 (SEQ ID NO: 97).

As used herein, the terms "Fc-mediated effector functions" or "Fc effector functions" refer to the biological activities of an antibody other than the antibody's primary function and purpose. For example, the effector functions of a therapeutic agnostic antibody are the biological activities other than the activation of the target protein or pathway. Examples of antibody effect functions include C1q binding and complement dependent cytotoxicity; Fc receptor binding; antibody-dependent cell-mediated cytotoxicity (ADCC); phagocytosis; down regulation of cell surface receptors (*e.g.*, B cell receptor); lack of activation of platelets that express Fc receptor; and B cell activation. Many effector functions begin with Fc binding to an Fcγ receptor.

As used herein, the term "Fc receptor" refers to a polypeptide found on the surface of immune effector cells, which is bound by the Fc region of an antibody. In some embodiments, the Fc receptor is an Fcγ receptor. There are three subclasses of Fcγ receptors, FcγRI (CD64), FcγRII (CD32) and FγcRIII (CD16). All four IgG isotypes (IgG1, IgG2, IgG3 and IgG4) bind and activate Fc receptors FcγRI, FcγRIIA and FcγRIIIA. FcγRIIB is an inhibitory receptor, and therefore antibody binding to this receptor does not activate complement and cellular responses. FcγRI is a high affinity receptor that binds to IgG in monomeric form, whereas FcγRIIA and FcγRIIA are low affinity receptors that bind IgG only in multimeric form and have slightly lower affinity. The binding of an antibody to an Fc receptor and/or C1q is governed by specific residues or domains within the Fc regions. Binding also depends on residues located within the hinge region and within the CH2 portion of the antibody. In some embodiments, the agonistic and/or therapeutic activity of the antibodies described herein is dependent on binding of the Fc region to the Fc receptor (*e.g.*, FcγR). In some embodiments, the agonistic and/or therapeutic activity of the antibodies described herein is enhanced by binding of the Fc region to the Fc receptor (*e.g.*, FcγR).

As used herein, the term "glycosylation pattern" is defined as the pattern of carbohydrate units that are covalently attached to a protein, more specifically to an immunoglobulin protein. A glycosylation pattern of a heterologous antibody can be characterized as being substantially similar to glycosylation patterns which occur naturally on antibodies produced by the species of the nonhuman transgenic animal, when one of ordinary skill in the art would recognize the glycosylation pattern of the heterologous antibody as being more similar to said pattern of

glycosylation in the species of the nonhuman transgenic animal than to the species from which the CH genes of the transgene were derived.

As used herein, the term "hematological cancer" includes a lymphoma, leukemia, myeloma or a lymphoid malignancy, as well as a cancer of the spleen and 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, Waldenstrom 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.

As used herein, the term "human antibody" includes antibodies having variable and constant regions (if present) of human germline immunoglobulin sequences. Human antibodies of the disclosure can 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*) (See, *e.g.*, Lonberg et al., (1994) *Nature* 368(6474): 856-859); Lonberg, (1994) *Handbook of Experimental Pharmacology* 113:49-101; Lonberg & Huszar, (1995) *Intern. Rev. Immunol*. 13:65-93, and Harding & Lonberg, (1995) *Ann. N.Y. Acad. Sci.* 764:536-546). However, the term "human antibody" does not 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 (*i.e*. humanized antibodies).

As used herein, the term "heterologous antibody" is defined in relation to the transgenic non-human organism producing such an antibody. This term refers to an antibody having an amino

acid sequence or an encoding nucleic acid sequence corresponding to that found in an organism not consisting of the transgenic non-human animal, and generally from a species other than that of the transgenic non-human animal.

The terms “inducing an immune response” and “enhancing an immune response” are used interchangeably and refer to the stimulation of an immune response (*i.e.*, either passive or adaptive) to a particular antigen. The term “induce” as used with respect to inducing CDC or ADCC refer to the stimulation of particular direct cell killing mechanisms.

As used herein, a subject “in need of prevention,” “in need of treatment,” or “in need thereof,” refers to one, who by the judgment of an appropriate medical practitioner (*e.g.*, a doctor, a nurse, or a nurse practitioner in the case of humans; a veterinarian in the case of non-human mammals), would reasonably benefit from a given treatment (such as treatment with a composition comprising an anti-CD137 antibody).

The term "*in vivo*" refers to processes that occur in a living organism.

As used herein, the term “isolated antibody” is intended to refer to an antibody which is substantially free of other antibodies having different antigenic specificities (*e.g.*, an isolated antibody that specifically binds to human CD137 is substantially free of antibodies that specifically bind antigens other than CD137). An isolated antibody that specifically binds to an epitope may, however, have cross-reactivity to other CD137 proteins from different species. However, the antibody continues to display specific binding to human CD137 in a specific binding assay as described herein. In addition, an isolated antibody is typically substantially free of other cellular material and/or chemicals. In some embodiments, a combination of “isolated” antibodies having different CD137 specificities is combined in a well-defined composition.

As used herein, the term “isolated nucleic acid molecule” refers to nucleic acids encoding antibodies or antibody portions (*e.g.*, V_H, V_L, CDR3) that bind to CD137, is intended to refer to a nucleic acid molecule in which the nucleotide sequences encoding the antibody or antibody portion are free of other nucleotide sequences encoding antibodies or antibody portions that bind antigens other than CD137, which other sequences may naturally flank the nucleic acid in human genomic DNA. For example, a sequence selected from a sequence set forth in any one of Tables 22-27corresponds to the nucleotide sequences comprising the heavy chain (V_H) and light chain (V_L) variable regions of anti-CD137 antibody monoclonal antibodies described herein.

As used herein, "isotype" refers to the antibody class (*e.g.*, IgM or IgGl) that is encoded by heavy chain constant region genes. In some embodiments, a human monoclonal antibody of the disclosure is of the IgG1 isotype. In some embodiments, a human monoclonal antibody of the disclosure is of the IgG1 isotype and comprises a mutation. In some embodiments, a human monoclonal antibody of the disclosure is of the IgG2 isotype. In some embodiments, a human monoclonal antibody of the disclosure is of the IgG3 isotype. In some embodiments, a human monoclonal antibody of the disclosure is of the IgG4 isotype. In some embodiments, a human monoclonal antibody of the disclosure is of the IgG4 isotype and comprises a mutation. In some embodiments, the mutation is a substitution at Ser228. In some embodiments, the substitution at Ser228 is S228P.

As used herein, the term "isotype switching" refers to the phenomenon by which the class, or isotype, of an antibody changes from one Ig class to one of the other Ig classes.

As used herein the term "KD" or "K_D" refers to the equilibrium dissociation constant of a binding reaction between an antibody and an antigen. The value of K_D is a numeric representation of the ratio of the antibody off-rate constant (kd) to the antibody on-rate constant (ka). The value of K_D is inversely related to the binding affinity of an antibody to an antigen. The smaller the K_D value the greater the affinity of the antibody for its antigen. Affinity is the strength of binding of a single molecule to its ligand and is typically measured and reported by the equilibrium dissociation constant (K_D), which is used to evaluate and rank order strengths of bimolecular interactions.

As used herein, the term "kd" or "k_d" (alternatively "koff" or "k_{off}") is intended to refer to the off-rate constant for the dissociation of an antibody from an antibody/antigen complex. The value of kd is a numeric representation of the fraction of complexes that decay or dissociate per second, and is expressed in units sec^{-1}.

As used herein, the term "ka" or "k_a" (alternatively "kon" or "k_{on}") is intended to refer to the on-rate constant for the association of an antibody with an antigen. The value of ka is a numeric representation of the number of antibody/antigen complexes formed per second in a 1 molar (1M) solution of antibody and antigen, and is expressed in units $M^{-1}sec^{-1}$.

As used herein, the terms "linked," "fused", or "fusion", are used interchangeably. These terms refer to the joining together of two more elements or components or domains, by whatever means including chemical conjugation or recombinant means. Methods of chemical conjugation (*e.g.*, using heterobifunctional crosslinking agents) are known in the art.

As used herein, "local administration" or "local delivery," refers to delivery that does not rely upon transport of the composition or agent to its intended target tissue or site via the vascular system. For example, the composition may be delivered by injection or implantation of the composition or agent or by injection or implantation of a device containing the composition or agent. Following local administration in the vicinity of a target tissue or site, the composition or agent, or one or more components thereof, may diffuse to the intended target tissue or site.

As used herein, "MHC molecules" refers to two types of molecules, MHC class I and MHC class II. MHC class I molecules present antigen to specific CD8+ T cells and MHC class II molecules present antigen to specific CD4+ T cells. Antigens delivered exogenously to APCs are processed primarily for association with MHC class II. In contrast, antigens delivered endogenously to APCs are processed primarily for association with MHC class I.

As used herein, the term "monoclonal antibody" refers to an antibody which displays a single binding specificity and affinity for a particular epitope. Accordingly, the term "human monoclonal antibody" refers to an antibody which displays a single binding specificity and which has variable and optional constant regions derived from human germline immunoglobulin sequences. In some embodiments, human monoclonal antibodies are produced by a hybridoma which includes a B cell obtained from a transgenic non-human animal, *e.g.*, a transgenic mouse, having a genome comprising a human heavy chain transgene and a light chain transgene fused to an immortalized cell.

As used herein, the term "multimerization" refers to the formation of a macromolecular complex comprising more than two macromolecules such as proteins, typically bound by non-covalent interactions. Methods for determining multimerization are known to those of skill in the art and are described *supra* for dimerization. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance multimerization of CD137. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance multimerization of CD137 relative to the amount of multimerization in the absence of an anti-CD137 agonist antibody. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance multimerization of CD137 relative to the amount of multimerization in the presence of a reference anti-CD137 agonist antibody. In some embodiments, multimerization is increased by at least 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100%.

As used herein, the term “naturally-occurring” 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.

As used herein, the term “nonswitched isotype” refers to the isotypic class of heavy chain that is produced when no isotype switching has taken place; the CH gene encoding the nonswitched isotype is typically the first CH gene immediately downstream from the functionally rearranged VDJ gene. Isotype switching has been classified as classical or non-classical isotype switching. Classical isotype switching occurs by recombination events which involve at least one switch sequence region in the transgene. Non-classical isotype switching may occur by, for example, homologous recombination between human σ_μ and human $\sum_\mu$ (δ-associated deletion). Alternative non-classical switching mechanisms, such as intertransgene and/or interchromosomal recombination, among others, may occur and effectuate isotype switching.

As used herein, the term "nucleic acid" refers to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double- stranded form. Unless specifically limited, the term encompasses nucleic acids containing known analogues of natural nucleotides that have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally occurring nucleotides. Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (*e.g.*, degenerate codon substitutions) and complementary sequences and as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions can be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzer et al., Nucleic Acid Res. 19:5081, 1991; Ohtsuka et al., Biol. Chem. 260:2605-2608, 1985; and Cassol et al, 1992; Rossolini et al, Mol. Cell. Probes 8:91-98, 1994). For arginine and leucine, modifications at the second base can also be conservative. The term nucleic acid is used interchangeably with gene, cDNA, and mRNA encoded by a gene.

Polynucleotides used herein can be composed of any polyribonucleotide or polydeoxribonucleotide, which can be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double- stranded regions, single- and double- stranded RNA, and RNA that is mixture of single- and double- stranded regions, hybrid molecules comprising DNA and RNA

that can be single- stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide can also contain one or more modified bases or DNA or RNA backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

A nucleic acid is “operably linked” when it is placed into a functional relationship with another nucleic acid sequence. For instance, a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence. With respect to transcription regulatory sequences, operably linked means that the DNA sequences being linked are contiguous and, where necessary to join two protein coding regions, contiguous and in reading frame. For switch sequences, operably linked indicates that the sequences are capable of effecting switch recombination.

As used herein, the term “paratope”, also “antigen-binding site” refers to a portion of an antibody, or antigen-binding fragment thereof, which recognizes and binds to an epitope on an antigen, comprising the set of complementarity determining regions (CDRs) located within variable heavy and light chains.

As used herein, “parenteral administration,” “administered parenterally,” and other grammatically equivalent phrases, refer to modes of administration other than enteral and topical administration, usually by injection, and include, without limitation, intravenous, intranasal, intraocular, intramuscular, intraarterial, intrathecal, intracapsular, intraorbital, intracardiac, intradermal, intraperitoneal, transtracheal, subcutaneous, subcuticular, intraarticular, subcapsular, subarachnoid, intraspinal, epidural, intracerebral, intracranial, intracarotid and intrasternal injection and infusion.

As used herein, the term “patient” includes human and other mammalian subjects that receive either prophylactic or therapeutic treatment.

The term "percent identity," in the context of two or more nucleic acid or polypeptide sequences, refer to two or more sequences or subsequences that have a specified percentage of nucleotides or amino acid residues that are the same, when compared and aligned for maximum correspondence, as measured using one of the sequence comparison algorithms described below

(*e.g.*, BLASTP and BLASTN or other algorithms available to persons of skill) or by visual inspection. Depending on the application, the "percent identity" can exist over a region of the sequence being compared, *e.g.*, over a functional domain, or, alternatively, exist over the full length of the two sequences to be compared. For sequence comparison, typically one sequence acts as a reference sequence to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

Optimal alignment of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith & Waterman, Adv. Appl. Math. 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, J. Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson & Lipman, Proc. Nat'l. Acad. Sci. USA 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, Wis.), or by visual inspection (see generally Ausubel et al., infra).

One example of an algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul et al., J. Mol. Biol. 215:403-410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information website.

As generally used herein, “pharmaceutically acceptable” refers to those compounds, materials, compositions, and/or dosage forms which are, within the scope of sound medical judgment, suitable for use in contact with the tissues, organs, and/or bodily fluids of human beings and animals without excessive toxicity, irritation, allergic response, or other problems or complications commensurate with a reasonable benefit/risk ratio.

As used herein, a “pharmaceutically acceptable carrier” refers to, and includes, any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like that are physiologically compatible. The compositions can include a pharmaceutically acceptable salt, *e.g.*, an acid addition salt or a base addition salt (see, *e.g.*, Berge et al. (1977) *J Pharm Sci* 66:1-19).

As used herein, the terms "polypeptide," "peptide", and "protein" are used interchangeably to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers and non-naturally occurring amino acid polymer.

As used herein, the term "preventing" when used in relation to a condition, refers to administration of a composition which reduces the frequency of, or delays the onset of, symptoms of a medical condition in a subject relative to a subject which does not receive the composition.

As used herein, the term "purified" or "isolated" as applied to any of the proteins (antibodies or fragments) described herein refers to a polypeptide that has been separated or purified from components (*e.g.*, proteins or other naturally-occurring biological or organic molecules) which naturally accompany it, *e.g.*, other proteins, lipids, and nucleic acid in a prokaryote expressing the proteins. Typically, a polypeptide is purified when it constitutes at least 60 (*e.g.*, at least 65, 70, 75, 80, 85, 90, 92, 95, 97, or 99) %, by weight, of the total protein in a sample.

As used herein, the term "rearranged" refers to a configuration of a heavy chain or light chain immunoglobulin locus wherein a V segment is positioned immediately adjacent to a D-J or J segment in a conformation encoding essentially a complete V_H or V_L domain, respectively. A rearranged immunoglobulin gene locus can be identified by comparison to germline DNA; a rearranged locus will have at least one recombined heptamer/nonamer homology element.

As used herein, the term "receptor clustering" refers to a cellular process that results in grouping or local accumulation of a set of receptors at a particular cellular location, often to induce or amplify a signaling response. Many protein receptors bind cognate ligands and cluster, i.e., form dimers, trimers, oligomers or multimers, upon binding their cognate ligands. For example, the PDGF receptor and TNF receptor superfamily members form dimers and trimers upon ligand binding, respectively. Cognate ligand-induced clustering (*e.g.*, dimerization, multimerization) induces signal transduction through the receptor. Accordingly, the antibodies, or antigen-binding fragments thereof, of the present disclosure can activate a receptor by binding to more than one receptor and induce or stabilize dimerization, trimerization, and/or multimerization with or without cognate ligand binding.

Receptor clustering and multimerization is needed for TNFR signaling (Wajant (2015) Cell Death Differ 22(11):1727-1741), and in particular for TNFRSF activation. 4-1BB (CD137), CD40, GITR, CD27, DR3, DR5, and Fas are some of the TNFSF receptors known to require clustering in order to trigger downstream signaling. Experimental evidence that the 4-1BB receptor must be cross-linked to signal comes from Rabu et al. These authors reported that a 1-trimer form of human 4-1BBL had no activating effects on human T cells whereas cross-linking the protein into 2- or more trimers led to a strongly activating protein (Rabu et al., (2005) J Biol Chem 280:41472-41481). Accordingly, in some embodiments, an anti-CD137 agonist antibody induces the multimerization of 2 or more trimers of CD137.

As used herein, the term "recombinant host cell" (or simply "host cell") is intended to refer to 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.

As used herein, the term "recombinant human antibody" 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 which 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 molecules that encode the light chain and heavy chain immunoglobulin polypeptides in response to an antigen may not have sequence identity with the original nucleic acid molecules, but instead will be substantially identical or similar (*i.e.*, have at least 80% identity).

As used herein, the term "reference antibody" (used interchangeably with "reference mAb") or "reference antigen-binding protein" refers to an antibody, or an antigen-binding fragment thereof, that binds to a specific epitope on human CD137 and is used to establish a relationship between itself and one or more distinct antibodies. In some embodiments, the relationship is the binding of the reference antibody and the one or more distinct antibodies to the same epitope on CD137. As used herein, the term connotes an anti-CD137 antibody that is useful in a test or assay, such as those described herein, (*e.g.*, a competitive binding assay), as a competitor, wherein the assay is useful for the discovery, identification or development, of one or more distinct antibodies that bind to the same epitope. The variable heavy (V_H) and light chain (V_L) amino acid sequences of an exemplary reference antibody (mAb1) are provided in Table 23 (V_H1, SEQ ID NO. 4; V_H2, SEQ ID NO. 6). In some embodiments, the term connotes an anti-CD137 antibody that is useful in a test or assay, as a comparator, wherein the assay is useful for distinguishing characteristics of the antibodies (*e.g.*, hepatotoxicity, anti-tumor efficacy). In some embodiments, the reference antibody is urelumab. In some embodiments, the reference antibody is utomilumab.

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. Typically, the antibody binds with an equilibrium dissociation constant (K_D) of approximately less than 10^{-6} M, such as approximately less than 10^{-7}, 10^{-8} M, 10^{-9} M or 10^{-10} M or even lower when determined by surface plasmon resonance (SPR) technology in a BIACORE 2000 instrument using recombinant human CD137 as the analyte and the antibody as the ligand and 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. 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."

As used herein, the term "switch sequence" refers to those DNA sequences responsible for switch recombination. A "switch donor" sequence, typically a μ switch region, will be 5' (*i.e.*, upstream) of the construct region to be deleted during the switch recombination. The "switch acceptor" region will be between the construct region to be deleted and the replacement constant region (*e.g.*, γ, ε, etc.). As there is no specific site where recombination always occurs, the final gene sequence will typically not be predictable from the construct.

As used herein, the term "subject" includes any human or non-human animal. For example, the methods and compositions of the present invention can be used to treat a subject with an immune disorder. 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.*

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.

The percent identity between two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % homology = # of identical positions/total # of positions x 100), 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.

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.

The nucleic acid and protein sequences of the present disclosure 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 of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to the protein molecules of the invention. 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 http://www.ncbi.nlm.nih.gov.

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 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).

The nucleic acid compositions of the present disclosure, while often in a native sequence (except for modified restriction sites and the like), from either cDNA, genomic or mixtures thereof 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 (where "derived" indicates that a sequence is identical or modified from another sequence).

As used herein, the term "tumor microenvironment" (alternatively "cancer microenvironment"; abbreviated TME) refers to the cellular environment or milieu in which the tumor or neoplasm exists, including surrounding blood vessels as well as non-cancerous cells

including, but not limited to, immune cells, fibroblasts, bone marrow-derived inflammatory cells, and lymphocytes. Signaling molecules and the extracellular matrix also comprise the TME. The tumor and the surrounding microenvironment are closely related and interact constantly. Tumors can influence the microenvironment by releasing extracellular signals, promoting tumor angiogenesis and inducing peripheral immune tolerance, while the immune cells in the microenvironment can affect the growth and evolution of tumor cells.

The term "T cell" refers to a type of white blood cell that can be distinguished from other white blood cells by the presence of a T cell receptor on the cell surface. There are several subsets of T cells, including, but not limited to, T helper cells (a.k.a. T_H cells or $CD4^+$ T cells) and subtypes, including T_H1, T_H2, T_H3, T_H17, T_H9, and T_{FH} cells, cytotoxic T cells (*i.e.,* T_C cells, $CD8^+$ T cells, cytotoxic T lymphocytes, T-killer cells, killer T cells), memory T cells and subtypes, including central memory T cells (T_{CM} cells), effector memory T cells (T_{EM} and T_{EMRA} cells), and resident memory T cells (T_{RM} cells), regulatory T cells (a.k.a. T_{reg} cells or suppressor T cells) and subtypes, including $CD4^+$ $FOXP3^+$ T_{reg} cells, $CD4^+FOXP3^-$ T_{reg} cells, Tr1 cells, Th3 cells, and $T_{reg}17$ cells, natural killer T cells (a.k.a. NKT cells), mucosal associated invariant T cells (MAITs), and gamma delta T cells (γδ T cells), including Vγ9/Vδ2 T cells. Any one or more of the aforementioned or unmentioned T cells may be the target cell type for a method of use of the invention.

As used herein, the term "T cell activation" or "activation of T cells" refers to a cellular process in which mature T cells, which express antigen-specific T cell receptors on their surfaces, recognize their cognate antigens and respond by entering the cell cycle, secreting cytokines or lytic enzymes, and initiating or becoming competent to perform cell-based effector functions. T cell activation requires at least two signals to become fully activated. The first occurs after engagement of the T cell antigen-specific receptor (TCR) by the antigen-major histocompatibility complex (MHC), and the second by subsequent engagement of co-stimulatory molecules (*e.g.*, CD28). These signals are transmitted to the nucleus and result in clonal expansion of T cells, upregulation of activation markers on the cell surface, differentiation into effector cells, induction of cytotoxicity or cytokine secretion, induction of apoptosis, or a combination thereof.

As used herein, the term "T cell-mediated response" refers to any response mediated by T cells, including, but not limited to, 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.

As used herein, the terms "therapeutically effective amount" or "therapeutically effective dose," or similar terms used herein are intended to mean an amount of an agent (*e.g.*, an anti-CD137 antibody or an antigen-binding fragment thereof) that will elicit the desired biological or medical response (*e.g.*, an improvement in one or more symptoms of a cancer).

The terms "treat," "treating," and "treatment," as used herein, refer to therapeutic or preventative measures described herein. The methods of "treatment" employ administration to a subject, in need of such treatment, a human antibody of the present disclosure, for example, a subject in need of an enhanced immune response against a particular antigen or a subject who ultimately may acquire such a disorder, in order to prevent, cure, delay, reduce the severity of, or ameliorate one or more symptoms of the disorder or recurring disorder, or in order to prolong the survival of a subject beyond that expected in the absence of such treatment.

As used herein, the term "unrearranged" or "germline configuration" refers to the configuration wherein the V segment is not recombined so as to be immediately adjacent to a D or J segment.

As used herein, the term "vector" 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, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this disclosure pertains. Preferred methods and materials are described below, although methods and materials similar or equivalent to those described herein can also be used in the practice or testing of the presently disclosed methods and compositions. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety.

Anti-CD137 Formulations

The disclosure provides formulations comprising an antibody or antigen binding fragments thereof that bind to human CD137 [hereinafter an "anti-CD137 antibody" or an "anti-human CD137 antibody"]. The anti-CD137 antibody formulations of the disclosure maintain the antibody, or antigen binding fragment thereof, under stable conditions, minimize the formation of antibody aggregates (high molecular weight species) and particulates, reduce the percentage of charge variants, and maintain the structural integrity of the antibody.

In one aspect, the disclosure provides, at least in part, various formulations of an anti-CD137 antibody, or antigen binding fragment thereof. In some embodiments, the formulations of the disclosure comprising anti-CD137, or an antigen binding fragment thereof, also include: (i) a buffer (*e.g.*, histidine), (ii) a disaccharide sugar (*e.g.*, sucrose), (iii) a non-ionic surfactant (*e.g.*, polysorbate 80), and/or (iv) a salt (*e.g.*, NaCl). In some embodiments, the formulations of the disclosure have a pH of about 5.0 to about 7.0. In some embodiments, the formulations of the disclosure have a pH of about 5.0 to about 7.4. In some embodiments, the pH of the formulation is about 5.0 to about 8.0. In some embodiments, the formulations of the disclosure further contain one or more solubilizers, diluents, binders, stabilizers, salts, lipophilic solvents, amino acids, chelators, or preservatives.

(i) Buffering Agents

In some embodiments, buffering agents are included in antibody formulations to improve stability and/or control the pH of the formulation. As exemplified in the working examples described herein, the anti-CD137 antibody was stable at high concentrations and under forced degradation conditions when formulated in histidine buffer.

In some embodiments, buffering agents useful in the formulations described herein include, *e.g.*, salts of citric acid, ascorbic acid, gluconic acid, carbonic acid, tartaric acid, succinic acid, acetic acid, or phthalic acid. In some embodiments, the buffer is a Tris-based or phosphate buffer.

In some embodiments, the formulations described herein include one or more amino acids, which can, among other things, provide buffering capacity. Suitable amino acids for use in the formulations of the disclosure include, *e.g.*, histidine, glycine, and serine. In some embodiments, the formulations of the disclosure do not include a free amino acid as a buffering agent. In some embodiments, the formulations of the disclosure include one free amino acid (*e.g.*, histidine) as a buffering agent. In some embodiments, the formulations of the disclosure include two or more (*e.g.*, two, three, four, five, six, or seven or more) different amino acids as buffering agents, *e.g.*, serine and histidine.

The buffering agents are generally used at concentrations between approximately 10 mM and 100 mM, depending, in part, on the buffering capacity required. In some embodiments, a formulation described herein includes a buffering agent at a concentration of less than, or approximately, 100 (*e.g.*, less than, or approximately, 90, 80, 70, 60, 50, 40, 30, 25, 20, 15, or 10) mM. In some embodiments, a formulation described herein contains a buffering agent at a concentration of at least 10 (*e.g.*, at least 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100 or more) mM. In some embodiments, a formulation described herein includes a buffering agent at a concentration of between about 10 mM to 20 mM, 15 mM to 20 mM, 10 mM to 25 mM, 15 mM to 25 mM, 20 mM to 25 mM, 10 mM to 30 mM, 15 mM to 30 mM, 20 mM to 30 mM, 25 mM to 30 mM, 10 mM to 40 mM, 15 mM to 40 mM, 20 mM to 40 mM, 25 mM to 40 mM, 30 mM to 40 mM, 10 mM to 50 mM, 15 mM to 50 mM, 20 mM to 50 mM, 25 mM to 50 mM, 30 mM to 50 mM, 40 mM to 50 mM, 10 mM to 100 mM, 15 mM to 100 mM, 20 mM to 100 mM, 25 mM to 100 mM, 30 mM to 100 mM, 40 mM to 100 mM, or 50 to 100 mM. It is understood that in embodiments where a formulation of the disclosure contains two or more (*e.g.*, at least two, three, four, five, six, seven, eight, nine, or 10 or more) different buffering agents, each of the two or more buffering agents can independently be present at, *e.g.*, one of the above described concentrations.

In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 10-100 mM. In some embodiments, the formulation of the

disclosure includes a buffer comprising histidine at a concentration of about 15-100 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 20-100 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 25-100 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine concentration of about 30-100 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 40-100 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 50-100 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 10-50 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 15-50 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 20-50 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 25-50 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 30-50 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 40-50 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 10-40 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 15-40 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 20-40 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 25-40 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 30-40 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 10-30 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 15-30 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 20-30 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 25-30 mM. In some

embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 10-25 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 15-25 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 20-25 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 10-20 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 15-20 mM.

In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 10 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 11 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 12 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 13 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 14 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 15 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 16 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 17 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 18 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 19 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 20 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 21 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 22 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 23 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 24 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 25 mM. In some embodiments, the formulation of the

disclosure includes a buffer comprising histidine at a concentration of about 26 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 27 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 28 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 29 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 30 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 35 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 40 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 45 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 50 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 55 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 60 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 65 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 70 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 75 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 80 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 85 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 90 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 95 mM. In some embodiments, the formulation of the disclosure includes a buffer comprising histidine at a concentration of about 100 mM.

(ii) Carbohydrate Excipients

In some embodiments, carbohydrate excipients are added to antibody formulations of the disclosure to improve stability. As provided in the working examples, it was discovered that the

addition of sucrose to the anti-CD137 formulations of the disclosure resulted in improved stability at elevated temperatures.

In some embodiments, any of the formulations described herein contain a carbohydrate excipient. Suitable carbohydrate excipients are described in, *e.g.*, Katakam and Banga (1995) *J Pharm Pharmacol* 47(2):103-107; Andya et al. (2003) *AAPS PharmSci* 5(2): Article 10; and Shire (2009) "Current Trends in Monoclonal Antibody Development and Manufacturing," Volume 11, Springer, 354 pages. Carbohydrate excipients suitable for use in the formulations described herein include, without limitation, monosaccharides such as fructose, maltose, galactose, glucose, D-mannose, and sorbose; disaccharides such as lactose, sucrose, trehalose, and cellobiose; polysaccharides such as maltodextrins, dextrans, and starches; and sugar alcohols such as mannitol, xylitol, maltitol, lactitol, and sorbitol. In some embodiments, the carbohydrate excipient is a disaccharide or disaccharide sugar. In some embodiments, the disaccharide sugar is sucrose. In some embodiments, a carbohydrate excipient is present in a formulation of the disclosure at a concentration of at least, or approximately, 5 (*e.g.*, at least, or approximately, 5.0, 5.5, 6.0, 6.5, 7.0, 7.5, 8.0, 8.5, 9.0, 9.5, 10.0, 10.5, 11.0, 11.5, 12.0, 12.5, 13.0, 13.5, 14.0, 14.5, 15.0 or more) % weight/volume (w/v). In embodiments where a formulation of the disclosure contains two or more (*e.g.*, at least two, three, four, five, six, seven, eight, nine, or 10 or more) different carbohydrate excipients (*e.g.*, sorbitol and mannitol), each excipient can, independently, be present at any of the above-described concentrations.

In some embodiments of the disclosure, the carbohydrate excipient is present in an amount of from about 5-15% (w/v) (5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15%). In some embodiments, the carbohydrate excipient is present in an amount from about 6% to about 15% (w/v). In some embodiments, the carbohydrate excipient is present in an amount from about 8% to about 15% (w/v). In some embodiments, the carbohydrate excipient is present in an amount from about 10% to about 15% (w/v). In some embodiments, the carbohydrate excipient is present in an amount from about 12% to about 15% (w/v). In some embodiments, the carbohydrate excipient is present in an amount from about 14% to about 15% (w/v). In some embodiments, the carbohydrate excipient is present in an amount from about 5% to about 12% (w/v). In some embodiments, the carbohydrate excipient is present in an amount from about 6% to about 12% (w/v). In some embodiments, the carbohydrate excipient is present in an amount from about 8% to about 12% (w/v). In some embodiments, the carbohydrate excipient is present in an amount

from about 10% to about 12% (w/v). In some embodiments, the carbohydrate excipient is present in an amount from about 5% to about 10% (w/v). In some embodiments, the carbohydrate excipient is present in an amount from about 6% to about 10% (w/v). In some embodiments, the carbohydrate excipient is present in an amount from about 8% to about 10% (w/v). In some embodiments, the carbohydrate excipient is a disaccharide sugar. In some embodiments, the carbohydrate excipient is sucrose.

In some embodiments, the carbohydrate excipient is present in an amount of about 5% (w/v). In some embodiments, the carbohydrate excipient is present in an amount of about 6% (w/v). In some embodiments, the carbohydrate excipient is present in an amount of about 7% (w/v). In some embodiments, the carbohydrate excipient is present in an amount of about 8% (w/v). In some embodiments, the carbohydrate excipient is present in an amount of about 9% (w/v). In some embodiments, the carbohydrate excipient is present in an amount of about 10% (w/v). In some embodiments, the carbohydrate excipient is present in an amount of about 11% (w/v). In some embodiments, the carbohydrate excipient is present in an amount of about 12% (w/v). In some embodiments, the carbohydrate excipient is present in an amount of about 13% (w/v). In some embodiments, the carbohydrate excipient is present in an amount of about 14% (w/v). In some embodiments, the carbohydrate excipient is present in an amount of about 15% (w/v). In some embodiments, the carbohydrate excipient is a disaccharide sugar. In some embodiments, the carbohydrate excipient is sucrose. In some embodiments, the carbohydrate excipient is trehalose.

In some embodiments, the formulation of the disclosure includes a disaccharide sugar. In some embodiments, the formulation of the disclosure includes sucrose. In some embodiments, the carbohydrate excipient is trehalose.

In some embodiments, the formulations of the disclosure include sucrose in an amount from about 5% to about 15% (w/v). In some embodiments, the formulations of the disclosure include sucrose in an amount from about 6% to about 15% (w/v). In some embodiments, the formulations of the disclosure include sucrose in an amount from about 8% to about 15% (w/v). In some embodiments, the formulations of the disclosure include sucrose in an amount from about 10% to about 15% (w/v). In some embodiments, the formulations of the disclosure include sucrose in an amount from about 12% to about 15% (w/v). In some embodiments, the formulations of the disclosure include sucrose in an amount from about 14% to about 15% (w/v).

In some embodiments, the formulations of the disclosure include sucrose in an amount from about 5% to about 12% (w/v). In some embodiments, the formulations of the disclosure include sucrose in an amount from about 6% to about 12% (w/v). In some embodiments, the formulations of the disclosure include sucrose in an amount from about 8% to about 12% (w/v). In some embodiments, the formulations of the disclosure include sucrose in an amount from about 10% to about 12% (w/v). In some embodiments, the formulations of the disclosure include sucrose in an amount from about 5% to about 10% (w/v). In some embodiments, the formulations of the disclosure include sucrose in an amount from about 6% to about 10% (w/v). In some embodiments, the formulations of the disclosure include sucrose in an amount from about 8% to about 10% (w/v).

In some embodiments, the formulations of the disclosure include sucrose at about 5% (w/v). In some embodiments, the formulations of the disclosure include sucrose at about 6% (w/v). In some embodiments, the formulations of the disclosure include sucrose at about 7% (w/v). In some embodiments, the formulations of the disclosure include sucrose at about 8% (w/v). In some embodiments, the formulations of the disclosure include sucrose at about 9% (w/v). In some embodiments, the formulations of the disclosure include sucrose at about 10% (w/v). In some embodiments, the formulations of the disclosure include sucrose at about 11% (w/v). In some embodiments, the formulations of the disclosure include sucrose at about 12% (w/v). In some embodiments, the formulations of the disclosure include sucrose at about 13% (w/v). In some embodiments, the formulations of the disclosure include sucrose at about 14% (w/v). In some embodiments, the formulations of the disclosure include sucrose at about 15% (w/v).

(iii) Surfactants

In some embodiments, the antibody formulations of the disclosure comprise a surfactant. As used herein, a surfactant is a surface active agent that is amphipathic in nature. In some embodiments, surfactants are added to the formulations herein to provide stability, reduce and/or prevent aggregation or to prevent and/or inhibit protein damage during processing conditions such as purification, filtration, freeze-drying, transportation, storage, and delivery. In some embodiments of the present disclosure, a surfactant is useful for providing stability to the active ingredient(s).

In some embodiments, the formulations of the disclosure contain a surfactant such as an anionic, cationic, or non-ionic surfactant. In some embodiments, the surfactant is polyoxyethylene sorbitan fatty acid esters (Polysorbates, sold under the trade name TWEEN®) including Polysorbate-20 (polyoxyethylene sorbitan monolaurate), Polysorbate-40 (polyoxyethylene sorbitan monopalmitate), Polysorbate-60 (polyoxyethylene sorbitan monostearate), and Polysorbate-80 (polyoxyethylene sorbitan monooleate); polyoxyethylene alkyl ethers such as BRIJ® 58 and BRIJ® 35; poloxamers (*e.g.*, poloxamer 188); TRITON® X-100 and TRITON® X-114; NP40; Span 20, Span 40, Span 60, Span 65, Span 80 and Span 85; copolymers of ethylene and propylene glycol (*e.g.*, the PLURONIC® series of nonionic surfactants such as PLURONIC® F68, PLURONIC® 10R5, PLURONIC® F108, PLURONIC® F127, PLURONIC® F38, PLURONIC® L44, PLURONIC® L62; and sodium dodecyl sulfate (SDS). In some embodiments, the surfactant is a non-ionic surfactant. In some embodiments, the surfactant is a polysorbate. In some embodiments, the surfactant is polysorbate 80.

The amount of surfactant to be included in the formulations of the invention is an amount sufficient to perform the desired function, i.e. a minimal amount necessary to stabilize the active pharmaceutical ingredient (*i.e.*, the anti-CD137 antibody or antigen binding fragment thereof) in the formulation. All percentages for the surfactant are listed as w/v %.

In some embodiments, the formulations described herein contain a surfactant (*e.g.*, any of the pharmaceutically-acceptable surfactants described herein or known in the art) at a concentration of at least, or approximately, 0.01 (*e.g.*, at least, or approximately, 0.02, 0.03, 0.04, 0.05, 0.06, 0.07, 0.08, 0.09, 0.1, or more) w/v %. In some embodiments, formulation of the disclosure contains no more than 0.1 (*e.g.*, no more than 0.09, 0.08, 0.07, 0.06, 0.05, 0.04, 0.03, 0.02, or 0.01) w/v % of a pharmaceutically-acceptable surfactant.

In some embodiments, the formulation of the disclosure includes a surfactant at a concentration of from about 0.01% to about 0.1% w/v. In some embodiments, the formulation of the disclosure includes a surfactant in an amount from about 0.01% to about 0.09% w/v; from about 0.01% to about 0.08% w/v; from about 0.01% to about 0.07% w/v; from about 0.01% to about 0.06% w/v; from about 0.01% to about 0.05% w/v; from about 0.01% to about 0.04% w/v; from about 0.01% to about 0.03% w/v, or from about 0.01% to about 0.02% w/v.

In some embodiments, the formulation of the disclosure includes a surfactant in an amount of about 0.01% w/v. In some embodiments, the formulation of the disclosure includes a

surfactant in an amount of about 0.02% w/v. In some embodiments, the formulation of the disclosure includes a surfactant in an amount of about 0.025% w/v. In some embodiments, the formulation of the disclosure includes a surfactant in an amount of about 0.03% w/v. In some embodiments, the formulation of the disclosure includes a surfactant in an amount of about 0.035% w/v. In some embodiments, the formulation of the disclosure includes a surfactant in an amount of about 0.04% w/v. In some embodiments, the formulation of the disclosure includes a surfactant in an amount of about 0.05% w/v. In some embodiments, the formulation of the disclosure includes a surfactant in an amount of about 0.06% w/v. In some embodiments, the formulation of the disclosure includes a surfactant in an amount of about 0.07% w/v. In some embodiments, the formulation of the disclosure includes a surfactant in an amount of about 0.08% w/v. In some embodiments, the formulation of the disclosure includes a surfactant in an amount of about 0.09% w/v. In some embodiments, the formulation of the disclosure includes a surfactant in an amount of about 0.1% w/v.

In some embodiments, the surfactant in the formulation of the disclosure is polysorbate 80. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount from about 0.01% to about 0.1% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount from about 0.01% to about 0.09% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount from about 0.01% to about 0.08% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount from about 0.01% to about 0.07% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount from about 0.01% to about 0.06% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount from about 0.01% to about 0.05% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount from about 0.01% to about 0.04% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount from about 0.01% to about 0.03% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount from about 0.01% to about 0.02% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount from about 0.02% to about 0.1% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount from about 0.02% to about 0.09% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount from about 0.02% to about 0.08% w/v. In some

embodiments, the formulation of the disclosure includes polysorbate 80 in an amount from about 0.02% to about 0.07% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount from about 0.02% to about 0.06% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount from about 0.02% to about 0.05% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount from about 0.02% to about 0.04% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount from about 0.02% to about 0.035% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount from about 0.02% to about 0.03% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount from about 0.025% to about 0.05% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount from about 0.025% to about 0.04% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount from about 0.025% to about 0.035% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount from about 0.025% to about 0.03% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount from about 0.03% to about 0.1% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount from about 0.03% to about 0.09% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount from about 0.03% to about 0.08% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount from about 0.03% to about 0.07% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount from about 0.03% to about 0.06% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount from about 0.03% to about 0.05% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount from about 0.03% to about 0.04% w/v.

In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount of about 0.01% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount of about 0.015% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount of about 0.02% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount of about 0.025% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount of

about 0.03% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount of about 0.035% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount of about 0.04% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount of about 0.045% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount of about 0.05% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount of about 0.055% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount of about 0.06% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount of about 0.065% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount of about 0.07% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount of about 0.075% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount of about 0.08% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount of about 0.085% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount of about 0.09% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount of about 0.095% w/v. In some embodiments, the formulation of the disclosure includes polysorbate 80 in an amount of about 0.1% w/v.

(iv) Salts

In some embodiments, a salt can be included in the antibody formulations described herein to provide stability to the formulation. In some embodiments, the formulations described herein contain a salt, *e.g.*, sodium chloride, potassium chloride, or magnesium chloride. In some embodiments, a formulation described herein contains a salt at a concentration of at least 50 (*e.g.*, at least 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, or 200, or more) mM. In some embodiments, a formulation of the disclosure includes a salt at a concentration of less than, or approximately, 200 (*e.g.*, less than, or approximately, 195, 190, 185, 180, 175, 170, 165, 160, 155, 150, 145, 140, 135, 130, 125, 120, 115, 110, 105, 100, 95, 90, 85, 80, 75, 70, 65, 60, 55, or 50) mM. In some embodiments, a formulation of the disclosure includes a salt at a concentration of between about 50 mM to 100 mM, 60 mM to 100 mM, 70 mM to 100 mM, 80 mM to 100

mM, 90 mM to 100 mM, 50 mM to 120 mM, 60 mM to 120 mM, 70 mM to 120 mM, 80 mM to 120 mM, 90 mM to 120 mM, 100 mM to 120 mM, 110 mM to 120 mM, 50 mM to 150 mM, 60 mM to 150 mM, 70 mM to 150 mM, 80 mM to 150 mM, 90 mM to 150 mM, 100 mM to 150 mM, 110 mM to 150 mM, 120 mM to 150 mM, 130 mM to 150 mM, 140 mM to 150 mM, 50 mM to 200 mM, 60 mM to 200 mM, 70 mM to 200 mM, 80 mM to 200 mM, 90 mM to 200 mM, 100 mM to 200 mM, 110 mM to 200 mM, 120 mM to 200 mM, 130 mM to 200 mM, 140 mM to 200 mM, 150 mM to 200 mM, 160 mM to 200 mM, 170 mM to 200 mM, 180 mM to 200 mM, or 190 mM to 200 mM.

It is understood that in embodiments where a formulation of the disclosure contains two or more (*e.g.*, at least two, three, four, five, six, seven, eight, nine, or 10 or more) different salts, each of the two or more salts can independently be present at, *e.g.*, one of the above described concentrations.

In some embodiments, the formulations of the disclosure comprise NaCl. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 50-100 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 60-100 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 70-100 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 80-100 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 90-100 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 90-110 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 95-105 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 50-120 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 80-120 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 100-120 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 50-150 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 80-150 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 100-150 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 120-150 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 50-200 mM. In some embodiments, the formulations of

the disclosure include NaCl at a concentration of about 80-200 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 100-200 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 120-200 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 150-200 mM.

In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 50 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 60 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 70 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 75 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 80 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 85 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 90 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 95 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 100 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 105 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 110 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 115 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 120 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 125 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 130 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 140 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 150 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 160 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 170 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 180 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 190 mM. In some embodiments, the formulations of the disclosure include NaCl at a concentration of about 200 mM.

(v) pH

It was discovered that the pH of the anti-CD137 antibody formulations of the disclosure affect the stability of the formulations. As provided in the working examples, improved stability was observed when the anti-CD137 antibody was formulated in histidine buffer at pH 5.8 as compared to formulations comprising glutamic acid at pH 4.5 or Tris at pH 7.5.

In some embodiments, the formulations described herein include a buffering or pH-adjusting agent. In some embodiments, any of the formulations described herein have, or can be adjusted to have, a physiologically acceptable pH. As used herein, "physiologically acceptable pH" is a pH that is between, and inclusive of, pH 5 and pH 7, and in some embodiments of the formualtions described herein, a pH that is between, and inclusive of, pH 5 and pH 8. Accordingly, as used herein, a physiologically acceptable pH is inclusive of particular pH values such as 5.0, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6.0, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7.0, 7.1, 7.2, 7.3, 7.4, 7.5, 7.6, 7.7, 7.8, 7.9, and 8.0. In some embodiments, physiologically acceptable pH is at least pH 5 (*e.g.*, at least pH 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8 or 5.9), but less than pH 7 (*e.g.*, less than pH 6.9, 6.8, 6.7, 6.6, 6.5, 6.4, 6.3, 6.2, or 6.1). That is, in some embodiments physiologically acceptable pH is, *e.g.*, at least pH 5.0, but less than pH 7.0. In some embodiments, a physiologically acceptable pH is between pH 5.0 and pH 7.0. In some embodiments, a physiologically acceptable pH is between pH 5.5 and pH 6.5. In some embodiments, a physiologically acceptable pH is, *e.g.*, pH 6. In some embodiments, the pH of an antibody formulation described herein is between approximately 5.0 and 7.0, inclusive (*e.g.*, approximately 5.0, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6.0, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, and 7.0). In some embodiments, physiologically acceptable pH is at least pH 5 (*e.g.*, at least pH 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8 or 5.9), but less than pH 8 (*e.g.*, less than pH 7.9, 7.8, 7.7, 7.6, 7.5, 7.4, 7.3, 7.2, or 7.1). That is, in some embodiments physiologically acceptable pH is, *e.g.*, at least pH 5.0, but less than pH 8.0. In some embodiments, a physiologically acceptable pH is between pH 5.0 and pH 8.0. In some embodiments, a physiologically acceptable pH is between pH 5.5 and pH 7.5. In some embodiments, a physiologically acceptable pH is, *e.g.*, pH 6. In some embodiments, a physiologically acceptable pH is, *e.g.*, pH 7.4. In some embodiments, the pH of an antibody formulation described herein is between approximately 5.0 and 8.0, inclusive (*e.g.*, approximately 5.0, 5.1, 5.2, 5.3, 5.4, 5.5, 5.6, 5.7, 5.8, 5.9, 6.0, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, 7.0, 7.1, 7.2, 7.3, 7.4, 7.5, 7.6, 7.7, 7.8, 7.9, and 8.0).

In some embodiments, the formulation of the disclosure has a pH of about 5.0 to about 7.0. In some embodiments, the formulation of the disclosure has a pH of about 5.5 to about 7.0. In some embodiments, the formulation of the disclosure has a pH of about 6.0 to about 7.0. In some embodiments, the formulation of the disclosure has a pH of about 6.5 to about 7.0. In some embodiments, the formulation of the disclosure has a pH of about 5.0 to about 6.5. In some embodiments, the formulation of the disclosure has a pH of about 5.5 to about 6.5. In some embodiments, the formulation of the disclosure has a pH of about 6.0 to about 6.5. In some embodiments, the formulation of the disclosure has a pH of about 5.0 to about 6.0. In some embodiments, the formulation of the disclosure has a pH of about 5.5 to about 6.0. In some embodiments, the formulation of the disclosure has a pH of about 5.0 to about 5.5. In some embodiments, the formulation of the disclosure has a pH of about 5.8 to about 6.2.

In some embodiments, the formulation of the disclosure has a pH of about 5.0. In some embodiments, the formulation of the disclosure has a pH of about 5.1. In some embodiments, the formulation of the disclosure has a pH of about 5.2. In some embodiments, the formulation of the disclosure has a pH of about 5.3. In some embodiments, the formulation of the disclosure has a pH of about 5.4. In some embodiments, the formulation of the disclosure has a pH of about 5.5. In some embodiments, the formulation of the disclosure has a pH of about 5.6. In some embodiments, the formulation of the disclosure has a pH of about 5.7. In some embodiments, the formulation of the disclosure has a pH of about 5.8. In some embodiments, the formulation of the disclosure has a pH of about 5.9. In some embodiments, the formulation of the disclosure has a pH of about 6.0. In some embodiments, the formulation of the disclosure has a pH of about 6.1. In some embodiments, the formulation of the disclosure has a pH of about 6.2. In some embodiments, the formulation of the disclosure has a pH of about 6.3. In some embodiments, the formulation of the disclosure has a pH of about 6.4. In some embodiments, the formulation of the disclosure has a pH of about 6.5. In some embodiments, the formulation of the disclosure has a pH of about 6.6. In some embodiments, the formulation of the disclosure has a pH of about 6.7. In some embodiments, the formulation of the disclosure has a pH of about 6.8. In some embodiments, the formulation of the disclosure has a pH of about 6.9. In some embodiments, the formulation of the disclosure has a pH of about 7.0.

In some embodiments, the formulation of the disclosure has a pH of about 5.0 to about 8.0. In some embodiments, the formulation of the disclosure has a pH of about 6.5 to about 8.0.

In some embodiments, the formulation of the disclosure has a pH of about 6.0 to about 8.0. In some embodiments, the formulation of the disclosure has a pH of about 6.5 to about 8.0. In some embodiments, the formulation of the disclosure has a pH of about 5.0 to about 7.5. In some embodiments, the formulation of the disclosure has a pH of about 5.5 to about 7.5. In some embodiments, the formulation of the disclosure has a pH of about 6.0 to about 7.5. In some embodiments, the formulation of the disclosure has a pH of about 5.0 to about 7.0. In some embodiments, the formulation of the disclosure has a pH of about 5.5 to about 7.0. In some embodiments, the formulation of the disclosure has a pH of about 5.0 to about 7.5. In some embodiments, the formulation of the disclosure has a pH of about 5.8 to about 6.2. In some embodiments, the formulation of the disclosure has a pH of about 5.8 to about 7.4.

In some embodiments, the formulation of the disclosure has a pH of about 5.0. In some embodiments, the formulation of the disclosure has a pH of about 5.1. In some embodiments, the formulation of the disclosure has a pH of about 5.2. In some embodiments, the formulation of the disclosure has a pH of about 5.3. In some embodiments, the formulation of the disclosure has a pH of about 5.4. In some embodiments, the formulation of the disclosure has a pH of about 5.5. In some embodiments, the formulation of the disclosure has a pH of about 5.6. In some embodiments, the formulation of the disclosure has a pH of about 5.7. In some embodiments, the formulation of the disclosure has a pH of about 5.8. In some embodiments, the formulation of the disclosure has a pH of about 5.9. In some embodiments, the formulation of the disclosure has a pH of about 6.0. In some embodiments, the formulation of the disclosure has a pH of about 6.1. In some embodiments, the formulation of the disclosure has a pH of about 6.2. In some embodiments, the formulation of the disclosure has a pH of about 6.3. In some embodiments, the formulation of the disclosure has a pH of about 6.4. In some embodiments, the formulation of the disclosure has a pH of about 6.5. In some embodiments, the formulation of the disclosure has a pH of about 6.6. In some embodiments, the formulation of the disclosure has a pH of about 6.7. In some embodiments, the formulation of the disclosure has a pH of about 6.8. In some embodiments, the formulation of the disclosure has a pH of about 6.9. In some embodiments, the formulation of the disclosure has a pH of about 7.0. In some embodiments, the formulation of the disclosure has a pH of about 7.1. In some embodiments, the formulation of the disclosure has a pH of about 7.2. In some embodiments, the formulation of the disclosure has a pH of about 7.3. In some embodiments, the formulation of the disclosure has a pH of about 7.4. In some

embodiments, the formulation of the disclosure has a pH of about 7.5. In some embodiments, the formulation of the disclosure has a pH of about 7.6. In some embodiments, the formulation of the disclosure has a pH of about 7.7. In some embodiments, the formulation of the disclosure has a pH of about 7.8. In some embodiments, the formulation of the disclosure has a pH of about 7.9. In some embodiments, the formulation of the disclosure has a pH of about 8.0.

(vi) Concentration of Anti-CD137 Antibody

In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation of the disclosure at a concentration of about 1 mg/ml to about 100 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 5 mg/ml to about 15 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 15 mg/ml to about 30 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 30 mg/ml to about 45 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 45 mg/ml to about 60 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 60 mg/ml to about 75 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 75 mg/ml to about 90 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 85 mg/ml to about 100 mg/ml.

In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation of the disclosure at a concentration of about 1 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 2 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 3 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 4 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 5 mg/ml. In some embodiments, the anti-CD137 antibody or antigen

binding fragment thereof is present in the formulation at a concentration of about 6 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 7 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 8 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 9 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 10 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 11 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 12 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 13 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 14 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 15 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 16 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 17 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 18 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 19 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 20 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 21 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 22 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 23 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 24 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a

concentration of about 25 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 30 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 35 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 40 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 45 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 50 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 55 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 60 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 65 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 70 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 75 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 80 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 85 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 90 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 95 mg/ml. In some embodiments, the anti-CD137 antibody or antigen binding fragment thereof is present in the formulation at a concentration of about 100 mg/ml.

(vii) Exemplary formulations

In some embodiments, a formulation of the disclosure comprises the following elements: a buffer comprising histidine and an anti-CD137 antibody or antigen binding fragment thereof. In some embodiments, the formulation comprises about 10 mM histidine to about 100 mM

histidine. In some embodiments, the formulation includes an anti-CD137 antibody or antigen binding fragment thereof at a concentration of about 1 mg/ml to about 100 mg/ml.

In some embodiments, the formulation of the disclosure comprises the following elements: a buffer comprising histidine, a disaccharide sugar, and an anti-CD137 antibody or antigen binding fragment thereof. In some embodiments, the formulation comprises about 10 mM histidine to about 100 mM histidine. In some embodiments, the disaccharide sugar is sucrose. In some embodiments, the formulation comprises the disaccharide sugar at about 5-15% (w/v). In some embodiments, the formulation includes an anti-CD137 antibody or antigen binding fragment thereof at a concentration of about 1 mg/ml to about 100 mg/ml.

In some embodiments, a formulation of the disclosure comprises the following elements: a buffer comprising histidine and an anti-CD137 antibody or antigen binding fragment thereof. In some embodiments, the formulation has a pH of about 5.0 to 7.0. In some embodiments, the formulation comprises about 10 mM histidine to about 100 mM histidine. In some embodiments, the formulation includes an anti-CD137 antibody or antigen binding fragment thereof at a concentration of about 1 mg/ml to about 100 mg/ml.

In some embodiments, the formulation of the disclosure comprises the following elements: a buffer comprising histidine, a disaccharide sugar, a non-ionic surfactant, a salt, and an anti-CD137 antibody or antigen binding fragment thereof. In some embodiments, the formulation has a pH of about 5.0 to 7.0. In some embodiments, the formulation comprises about 10 mM histidine to about 100 mM histidine. In some embodiments, the disaccharide sugar of the formulation is sucrose. In some embodiments, the formulation comprises the disaccharide sugar at about 5-15% (w/v). In some embodiments, the non-ionic surfactant of the formulation is polysorbate. In some embodiments, the polysorbate is polysorbate 80. In some embodiments, the formulation comprises the non-ionic surfactant at about 0.01% to about 0.1% (w/v). In some embodiments, the salt of the formulation is NaCl. In some embodiments, the formulation comprises salt at a concentration of about 50 mM to about 200 mM. In some embodiments, the formulation includes an anti-CD137 antibody or antigen binding fragment thereof at a concentration of about 1 mg/ml to about 100 mg/ml.

In some embodiments, the formulation of the disclosure comprises the following elements: a buffer comprising histidine, a disaccharide sugar at about 5% to about 15 % (w/v), a non-ionic surfactant at about 0.01% to about 0.1% w/v, a salt at about 50 mM to about 200 mM,

and an anti-CD137 antibody or antigen binding fragment thereof. In some embodiments, the formulation has a pH of about 5.0 to 7.0. In some embodiments, the formulation comprises about 10 mM histidine to about 100 mM histidine. In some embodiments, the disaccharide sugar of the formulation is sucrose. In some embodiments, the disaccharide sugar of the formulation is lactose. In some embodiments, the disaccharide sugar of the formulation is maltose. In some embodiments, the disaccharide sugar of the formulation is trehalose. In some embodiments, the non-ionic surfactant of the formulation is polysorbate. In some embodiments, the polysorbate is polysorbate 80. In some embodiments, the salt of the formulation is NaCl. In some embodiments, the formulation includes an anti-CD137 antibody or antigen binding fragment thereof at a concentration of about 1 mg/mlto about 100 mg/ml.

In some embodiments, the formulation of the disclosure comprises the following elements: a buffer comprising about 10 mM to about 100 mM histidine, sucrose at about 5% to about 15 % (w/v), polysorbate 80 at about 0.01% to about 0.1% w/v, NaCl at about 50 mM to about 200 mM, and an anti-CD137 antibody or antigen binding fragment thereof. In some embodiments, the formulation has a pH of about 5.0 to 7.0. In some embodiments, the formulation has a pH of about 5.0 to 7.4. In some embodiments, the formulation includes an anti-CD137 antibody or antigen binding fragment thereof at a concentration of about 1 mg/ml to about 100 mg/ml.

In some embodiments, the formulation of the disclosure comprises the following elements: a buffer comprising about 20 mM histidine, sucrose at about 10% (w/v), polysorbate 80 at about 0.03% w/v, NaCl at about 100 mM, and an anti-CD137 antibody or antigen binding fragment thereof. In some embodiments, the formulation has a pH of about 6.0. In some embodiments, the formulation includes an anti-CD137 antibody or antigen binding fragment thereof at a concentration of about 1 mg/ml to about 100 mg/ml. In some embodiments, the formulation includes an anti-CD137 antibody or antigen binding fragment thereof at a concentration of about 5 mg/ml to about 15 mg/ml. In some embodiments, the formulation includes an anti-CD137 antibody or antigen binding fragment thereof at a concentration of about 15 mg/ml to about 30 mg/ml. In some embodiments, the formulation includes an anti-CD137 antibody or antigen binding fragment thereof at a concentration of about 30 mg/ml to about 45 mg/ml. In some embodiments, the formulation includes an anti-CD137 antibody or antigen binding fragment thereof at a concentration of about 45 mg/ml to about 60 mg/ml. In some

embodiments, the formulation includes an anti-CD137 antibody or antigen binding fragment thereof at a concentration of about 60 mg/ml to about 75 mg/ml. In some embodiments, the formulation includes an anti-CD137 antibody or antigen binding fragment thereof at a concentration of about 75 mg/ml to about 90 mg/ml. In some embodiments, the formulation includes an anti-CD137 antibody or antigen binding fragment thereof at a concentration of about 85 mg/ml to about 100 mg/ml. In some embodiments, the formulation includes an anti-CD137 antibody or antigen binding fragment thereof at a concentration of about 5 mg/ml. In some embodiments, the formulation includes an anti-CD137 antibody or antigen binding fragment thereof at a concentration of about 10 mg/ml. In some embodiments, the formulation includes an anti-CD137 antibody or antigen binding fragment thereof at a concentration of about 15 mg/ml. In some embodiments, the formulation includes an anti-CD137 antibody or antigen binding fragment thereof at a concentration of about 20 mg/ml.

The formulations of the disclosure as described herein provide the anti-CD137 antibody or antigen binding fragments thereof with marked stability, minimize the formation of antibody aggregates (high molecular weight species) and particulates, minimize charge variants, and maintain the structural integrity of the antibody.

(viii) Stability of Anti-CD137 Formulations

In some embodiments, the formulations described herein are capable of maintaining the structural integrity of an anti-CD137 antibody or antigen binding fragment thereof in a solution for an extended period of time. In some embodiments, an anti-CD137 antibody in a formulation of the disclosure remains stable after storage for at least four weeks (*e.g.*, at least five weeks, six weeks, seven weeks, eight weeks, nine weeks, 10 weeks, 11 weeks, 12 weeks, 13 weeks, 14 weeks, 15 weeks, 16 weeks, 17 weeks, 18 weeks, 19 weeks, 20 weeks, 21 weeks, 22 weeks, 23 weeks, or 24 weeks, or at least one month, two months, three months, four months, five months, six months, seven months, eight months, nine months, 10 months, 11 months, 12 months, 13 months, 14 months, 15 months, 16 months, 17 months, 18 months, 19 months, 20 months, 21 months, 22 months, 23 months, 24 months, or more) at approximately 2°C to 40°C (*e.g.*, storage at, *e.g.*, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40°C). In some embodiments, an anti-CD137 antibody in a formulation of the disclosure remains stable after storage for at least four weeks at

approximately 2°C to 9°C. In some embodiments, an anti-CD137 antibody in a formulation of the disclosure remains stable after storage for at least four weeks at approximately 10°C to 19°C. In some embodiments, an anti-CD137 antibody in a formulation of the disclosure remains stable after storage for at least four weeks at approximately 20°C to 29°C. In some embodiments, an anti-CD137 antibody in a formulation of the disclosure remains stable after storage for at least four weeks at approximately 30°C to 40°C. In some embodiments, an anti-CD137 antibody in a formulation of the disclosure remains stable after storage for at least four weeks at approximately 4°C. In some embodiments, an anti-CD137 antibody in a formulation of the disclosure remains stable after storage for at least four weeks at approximately 25°C. In some embodiments, an anti-CD137 antibody in a formulation of the disclosure remains stable after storage for at least four weeks at approximately 40°C.

As exemplified in the working examples described herein, the inventors provide formulations suitable for maintaining an anti-CD137 antibody or antigen binding fragments thereof at approximately 10 mg/mL in predominantly monomeric form for at least 24 weeks at 4°C, at least 12 weeks at 25°C, and at least four weeks at 40°C. As used herein, an anti-CD137 antibody or antigen binding fragment thereof in a formulation of the disclosure is "predominantly monomeric," or in "predominantly monomeric form," if the antibody present in the solution is at least 95 (*e.g.*, at least 95.1, 95.2, 95.3, 95.4, 95.5, 95.6, 95.7, 95.8, 95.9, 96, 96.1, 96.2, 96.3, 96.4, 96.5, 96.6, 96.7, 96.8, 96.9, 97, 97.1, 97.2, 97.3, 97.4, 97.5, 97.6, 97.7, 97.8, 97.9, 98, 98.1, 98.2, 98.3, 98.4, 98.5, 98.6, 98.7, 98.8, 98.9, 99, 99.1, 99.2, 99.3, 99.4, 99.5, 99.6, 99.7, 99.8, or 99.9 or greater) % monomeric, *e.g.*, as determined using size exclusion chromatography (SEC). That is: less than 5 (*e.g.*, less than 4.9. 4.8, 4.7, 4.6, 4.5, 4.4, 4.3, 4.2, 4.1, 4.0, 3.9, 3.8, 3.7, 3.6, 3.5, 3.4, 3.3, 3.2, 3.1, 3.0, 2.9, 2.8, 2.7, 2.6, 2.5, 2.4, 2.3, 2.2, 2.1, 2, 1.9, 1.8, 1.7, 1.6, 1.5, 1.4, 1.3, 1.2, 1.1, 1, 0.9, 0.8, 0.7, 0.6, 0.5, 0.4, 0.3, 0.2, or 0.1) % of the antibody in the solution is oligomeric, aggregated, and/or fragmented. As used herein, antibody fragmentation refers to improperly assembled constituents or degradation products of a whole antibody having a lower molecular weight than the whole antibody. Such fragmentation forms include, but are not limited to, a free monomeric heavy chain polypeptide, a dimeric heavy chain polypeptide (*e.g.*, disulfide-linked heavy chain polypeptide), a dimeric heavy chain polypeptide bound to one light chain polypeptide, a monomeric heavy chain polypeptide bound to one light chain polypeptide, or further degradation product(s) or fragment(s) of a light chain or heavy

chain polypeptide. In some embodiments, less than 2 (*e.g.*, less than 1.9, 1.8, 1.7, 1.6, 1.5, 1.4, 1.3, 1.2, 1.1, 1, 0.9, 0.8, 0.7, 0.6, 0.5, 0.4, 0.3, 0.2, or 0.1) % of the antibody is aggregated after storage for at least four weeks (*e.g.*, at least five weeks, six weeks, seven weeks, eight weeks, nine weeks, 10 weeks, 11 weeks, 12 weeks, 13 weeks, 14 weeks, 15 weeks, 16 weeks, 17 weeks, 18 weeks, 19 weeks, 20 weeks, 21 weeks, 22 weeks, 23 weeks, or 24 weeks, or at least one month two months, three months, four months, five months, six months, seven months, eight months, nine months, 10 months, 11 months, 12 months, 13 months, 14 months, 15 months, 16 months, 17 months, 18 months, 19 months, 20 months, 21 months, 22 months, 23 months, 24 months, or more) at 2°C to 8°C. Methods for determining the amount of monomeric antibody, as well as the amount of oligomeric, aggregated, or fragmented forms of the anti-CD137 antibody or antigen binding fragment thereof present in solution are described herein and exemplified in the working examples. For example, a skilled artisan can determine the percentage of whole, fragmented, unfolded intermediates, and/or aggregated antibody species present in a given solution using, *e.g.*, size exclusion chromatography (SEC), size exclusion chromatography high-performance liquid chromatography (SEC-HPLC), static light scattering (SLS), Fourier transform infrared spectroscopy (FTIR), circular dichroism (CD), urea-induced protein unfolding techniques, intrinsic tryptophan fluorescence, non-reducing sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE), and differential scanning calorimetry (DSC).

Anti-CD137 Antibodies and Antigen-binding Fragments Thereof

The present disclosure provides formulations comprising antibodies and antigen binding fragments thereof that specifically bind to and agonize CD137. In some embodiments, the formulations of the disclosure comprise any of the anti-CD137 antibodies or antigen binding fragments thereof that are described herein.

In some aspects, the disclosure provides formulations comprising anti-CD137 agonist antibodies and antigen binding fragments thereof that are useful for the treatment of cancer. In some embodiments, the formulations of the disclosure comprise anti-CD137 agonist antibodies an antigen binding fragments thereof that induce cytokine production. In some embodiments, the formulations of the disclosure comprise anti-CD137 agonist antibodies that increase the number of CD8+ T cells in the tumor microenvironment. In some embodiments, the formulations of the disclosure comprise anti-CD137 agonist antibodies and antigen binding fragments thereof that

induce protective anti-tumor immunity. The disclosure also provides formulations comprising anti-CD137 agonist antibodies and antigen binding fragments thereof that, upon administration *in vivo*, do not substantially increase intrasplenic or intrahepatic CD4+ and/or CD8+ T cell populations.

Human CD137 is a 255 amino acid transmembrane polypeptide (SEQ ID NO: 3; Accession No. NM_001561; NP_001552) and a member of the phylogenetically-conserved tumor necrosis factor receptor (TNFR) superfamily. CD137 (alternatively 4-1BB, TNFR superfamily 9) and its ligand (CD137L) are involved in the regulation of a wide range of immune activities. CD137 ligand cross-links its receptor, CD137, which is expressed on activated T cells, and co-stimulates T cell activities. CD137 is an activation-induced co-stimulatory molecule. Recent studies have revealed that CD137-mediated anti-cancer effects are largely based on its ability to activate T cells, in particular, to induce a cytotoxic T lymphocyte (CTL) response, and induce cytokine production, in particular, high amounts of IFN-γ (Ye et al., (2014) Clin Cancer Res 20(1):44-55). CD137 ligand is a transmembrane protein on the cell surface and transmit signals into the cells on which it is expressed, a phenomenon referred to as "reverse signaling" or "back signaling"). CD137 ligand expression is found on most types of leukocytes and on some nonimmune cells. In monocytic cells (monocytes, macrophages, and DCs), CD137 ligand signaling induces activation, migration, survival, and differentiation.

Accordingly, in some embodiments, an isolated anti-CD137 agonist antibody, or antigen-binding fragment thereof, described herein, binds to and agonizes CD137 and allows or promotes CD137L binding. In some embodiments, an isolated anti-CD137 agonist antibody, or antigen-binding fragment thereof, described herein, binds to and agonizes CD137. In some embodiments, the anti-CD137 antibodies provided by the disclosure bind to and agonize CD137 and co-stimulate activation of T cells.

In some embodiments, the formulations of the disclosure comprise an isolated anti-CD137 agonist antibody, or antigen-binding fragment thereof, described herein, that has one or more of the following properties or characteristics:

a) specifically binds to human CD137;

b) binds to human and cynomolgus CD137; and

c) binds to human and mouse CD137.

In some embodiments, an anti-CD137 agonist antibody, or antigen-binding fragment thereof, described herein, binds to CD137 and co-stimulates T cell activities. In some embodiments, an anti-CD137 agonist antibody, or antigen-binding fragment thereof, described herein, binds to CD137 and induces or enhances T cell activation, a cytotoxic T lymphocyte (CTL) response, T cell proliferation, cytokine production, or a combination thereof. In some embodiments, an anti-CD137 agonist antibody, or antigen-binding fragment thereof, described herein, binds to CD137 and induces or enhances T cell activation, a cytotoxic T lymphocyte (CTL) response, T cell proliferation, cytokine production, or a combination thereof, in a tumor microenvironment. In some embodiments, an anti-CD137 antibody, or antigen-binding fragment thereof, described herein, does not significantly induce or enhance intrahepatic and/or intrasplenic T cell activation and/or T cell proliferation. In some embodiments, an anti-CD137 antibody, described herein, binds to CD137 and induces the production of IFN-γ. In some embodiments, the antibodies provided by the disclosure bind to CD137 and induce the production of IL-2, TNF-α, IL-13, or a combination thereof.

In some embodiments, the formulations of the disclosure comprise anti-CD137 antibodies described herein that specifically bind to and agonize CD137. In some embodiments, agonism of CD137 is measured by determining the concentration of cytokines produced by immune cells. Methods for analyzing cytokine production are known in the art and utilized in the Examples. In some embodiments, an increase in cytokine production by immune cells indicates CD137 agonism. In some embodiments, agonism of CD137 is measured by analyzing T cell proliferation. In some embodiments, an increase in T cell proliferation indicates CD137 agonism. In some embodiments, agonism of CD137 is measured by measuring the level of cell signaling either through quantitation of phosphorylation of relevant molecules or expression of a gene reporter after a relevant promoter. In some embodiments, an increase in cell signaling indicates CD137 agonism. In some embodiments, agonism of CD137 is measured by measuring the volume of a tumor. In some embodiments, a decrease in the volume of a tumor indicates CD137 agonism.

In some embodiments, the formulations of the disclosure comprise anti-CD137 antibodies described herein that induce, increase or stabilize oligomerization, multimerization, or other higher order clustering of CD137. In some embodiments, the clustering of CD137 on the cell surface is observed via fluorescence microscopy.

Provided herein are formulations comprising isolated monoclonal antibodies or antigen binding fragments thereof, that bind to and agonize CD137. In some embodiments, the antibodies or antigen binding fragments thereof, (i) bind human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM); (ii) bind an epitope on human CD137 described herein; and/or (iii) comprise a heavy chain CDR3 comprising the amino acid sequence DXXXXLXXXXYXYYX (SEQ ID NO: 126).

Affinity for CD137

In some embodiments, the formulations of the disclosure comprise an isolated anti-CD137 agonist antibody, or antigen binding fragment thereof, described herein, that binds human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM or between about 40 nM and about 100 nM). In some embodiments, the affinity of the anti-CD137 antibody to human CD137 is at least two (*e.g.*, at least three, four, five, six, seven, eight, nine, or 10) fold higher than the affinity of mAb10 for mouse CD137. In some embodiments, the affinity of the anti-CD137 antibody is no greater than 500, 450, 400, 350, 300, 250, 200, 250, 200, 175, 150, 125, 110, or 100 nM. In some embodiments, the affinity of the anti-CD137 antibody to human CD137 is at least two (*e.g.*, at least three, four, five, six, seven, eight, nine, or 10) fold higher than the affinity of mAb10 for mouse CD137, but no greater than 500, 450, 400, 350, 300, 250, 200, 250, 200, 175, 150, 125, 110, or 100 nM. The affinity of the antibody is the strength of binding to a single CD137 polypeptide. In some embodiments, affinity is indicated by the equilibrium dissociation constant (K_D). The value of K_D is inversely related to the binding affinity of an antibody to an antigen. Accordingly, the smaller the K_D value, the greater the affinity of the antibody for its antigen.

Methods for determining the affinity of an antibody for its antigen are known in the art. An exemplary method for determining binding affinity employs surface plasmon resonance. Surface plasmon resonance is an optical phenomenon that allows for the analysis of real time biospecific interactions by detection of alterations in protein concentrations within a biosensor matrix, for example using the BIAcore system (Pharmacia Biosensor AB, Uppsala, Sweden and Piscataway, N.J.). For further descriptions, see Jonsson, U., et al. (1993) Ann. Biol. Clin. 51: 19-26; Jonsson, U., i (1991) Biotechniques 11 :620-627; Johnsson, B., et al. (1995) J. Mol. Recognit. 8: 125-131; and Johnsson, B., et al. (1991) Anal. Biochem. 198:268-277.

In some embodiments, the anti-CD137 antibodies described herein bind human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM). In some embodiments, the anti-CD137 antibodies described herein bind human CD137 with an affinity (K_D) of about 40-100 nM. In some embodiments, the anti-CD137 antibodies described herein bind human CD137 with an affinity (K_D) of about 30-40 nM, 40-50 nM, 50-60 nM, 60-70 nM, 70-80 nM, 80-90 nM, 90-100 nM, 45-55 nM, 55-65 nM, 75-85 nM, 85-95 nM, 45-95 nM, 50-90 nM, 55-85 nM, 60-80 nM, 65-75 nM, 55-75 nM, 40-70 nM, 50-80 nM, or 60-90 nM. In some embodiments, the anti-CD137 antibodies described herein bind human CD137 with an affinity (K_D) of about 60-80 nM. In some embodiments, the anti-CD137 antibodies described herein bind human CD137 with an affinity (K_D) of about 60-75 nM.

In some embodiments, the anti-CD137 antibodies described herein bind human CD137 with an affinity (K_D) of about 60-90 nM. In some embodiments, the anti-CD137 antibodies described herein bind human CD137 with an affinity (K_D) of about 50-80 nM. In some embodiments, the anti-CD137 antibodies described herein bind human CD137 with an affinity (K_D) of about 40-70 nM. In some embodiments, the anti-CD137 antibodies described herein bind human CD137 with an affinity (K_D) of about 55-75 nM. In some embodiments, the anti-CD137 antibodies described herein bind human CD137 with an affinity (K_D) of about 65-75 nM. In some embodiments, the anti-CD137 antibodies described herein bind human CD137 with an affinity (K_D) of about 60-80 nM. In some embodiments, the anti-CD137 antibodies described herein bind human CD137 with an affinity (K_D) of about 55-85 nM. In some embodiments, the anti-CD137 antibodies described herein bind human CD137 with an affinity (K_D) of about 50-90 nM. In some embodiments, the anti-CD137 antibodies described herein bind human CD137 with an affinity (K_D) of about 45-95 nM. In some embodiments, the anti-CD137 antibodies described herein bind human CD137 with an affinity (K_D) of about 85-95 nM. In some embodiments, the anti-CD137 antibodies described herein bind human CD137 with an affinity (K_D) of about 75-85 nM. In some embodiments, the anti-CD137 antibodies described herein bind human CD137 with an affinity (K_D) of about 75-85 nM. In some embodiments, the anti-CD137 antibodies described herein bind human CD137 with an affinity (K_D) of about 55-65 nM. In some embodiments, the anti-CD137 antibodies described herein bind human CD137 with an affinity (K_D) of about 45-55 nM. In some embodiments, the anti-CD137 antibodies described herein bind human CD137 with an affinity (K_D) of about 80-90 nM. In some embodiments, the anti-

CD137 antibodies described herein bind human CD137 with an affinity (K_D) of about 70-80 nM. In some embodiments, the anti-CD137 antibodies described herein bind human CD137 with an affinity (K_D) of about 60-70 nM. In some embodiments, the anti-CD137 antibodies described herein bind human CD137 with an affinity (K_D) of about 50-60 nM. In some embodiments, the anti-CD137 antibodies described herein bind human CD137 with an affinity (K_D) of about 40-50 nM. In some embodiments, the anti-CD137 antibodies described herein bind human CD137 with an affinity (K_D) of about 30-40 nM. In some embodiments, the anti-CD137 antibodies described herein bind human CD137 with an affinity (K_D) of about 30 nM, about 31 nM, about 32 nM, about 33 nM, about 34 nM, about 35 nM, about 36 nM, about 37 nM, about 38 nM, about 39 nM, about 40 nM, about 41 nM, about 42 nM, about 43 nM, about 44 nM, about 45 nM, about 46 nM, about 47 nM, about 48 nM, about 49 nM, about 50 nM, about 51 nM, about 52 nM, about 53 nM, about 54 nM, about 55 nM, about 56 nM, about 57 nM, about 58 nM, about 59 nM, about 60 nM, about 61 nM, about 62 nM, about 63 nM, about 64 nM, about 65 nM, about 66 nM, about 67 nM, about 68 nM, about 69 nM, about 70 nM, about 71 nM, about 72 nM, about 73 nM, about 74 nM, about 75 nM, about 76 nM, about 77 nM, about 78 nM, about 79 nM, about 80 nM, about 81 nM, about 82 nM, about 83 nM, about 84 nM, about 85 nM, about 86 nM, about 87 nM, about 88 nM, about 89 nM, about 90 nM, about 91 nM, about 92 nM, about 93 nM, about 94 nM, about 95 nM, about 96 nM, about 97 nM, about 98 nM, about 99 nM, about 100 nM, about 101 nM, about 102 nM, about 103 nM, about 104 nM, about 105 nM, about 106 nM, about 107 nM, about 108 nM, about 109 nM or about 110 nM.

In some embodiments, the anti-CD137 antibodies described herein bind human CD137 with an affinity (K_D) of at least 30 nM but less than about 110 nM, at least 31 nM but less than about 109 nM, at least 32 nM but less than about 108 nM, at least 33 nM but less than about 107 nM, at least 34 nM but less than about 106 nM, at least 35 nM but less than about 105 nM, at least 36 nM but less than about 104 nM, at least 37 nM but less than about 103 nM at least 38 nM but less than about 102 nM, at least 39 nM but less than about 101 nM, at least 40 nM but less than about 100 nM; at least 41 nM but less than about 99 nM; least 42 nM but less than about 98 nM; least 43 nM but less than about 97 nM; at least 44 nM but less than about 96 nM; at least 45 nM but less than about 95 nM; at least 46 nM but less than about 94 nM; at least 47 nM but less than about 93 nM; at least 48 nM but less than about 92 nM; at least 49 nM but less than about 91 nM; at least 50 nM but less than about 90 nM; at least 51 nM but less than about

89 nM; at least 52 nM but less than about 88 nM; at least 53 nM but less than about 87 nM; at least 54 nM but less than about 86 nM; at least 55 nM but less than about 85 nM; at least 56 nM but less than about 84 nM; at least 57 nM but less than about 83 nM; at least 58 nM but less than about 82 nM; at least 59 nM but less than about 81 nM; at least 60 nM but less than about 80 nM; at least 61 nM but less than about 79 nM; at least 62 nM but less than about 78 nM; at least 63 nM but less than about 77 nM; at least 64 nM but less than about 76 nM; or at least 65 nM but less than about 75 nM. In some embodiments, the anti-CD137 antibodies described herein bind human CD137 with an affinity (K_D) of at least 40 nM but less than about 100 nM.

In some embodiments, the anti-CD137 antibodies described herein cross-react with CD137 polypeptides from more than one species. In some embodiments, the anti-CD137 antibodies described herein bind cynomolgus CD137 and human CD137. In some embodiments, the anti-CD137 antibodies described herein bind mouse CD137 and human CD137. In some embodiments, the anti-CD137 antibodies described herein bind human CD137, mouse CD137 and cynomolgus CD137.

CD137 Epitope Binding

In some embodiments, the formulations of the disclosure comprise an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds to human CD137. In some embodiments, the formulations of the disclosure comprise an isolated monoclonal antibody, or antigen binding portion thereof, that binds to an epitope on human CD137. In some embodiments, the isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds to human CD137, binds to an epitope on human CD137 comprising one or more (*e.g.*, one, two, three, four, five, six, seven, eight, nine, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or all 25) of amino acids 111-132 of SEQ ID NO:3. In some embodiments, the isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds to human CD137, binds to an epitope within amino acids 111-132 of SEQ ID NO:3. In some aspects, the disclosure provides an isolated monoclonal antibody, or antigen binding portion thereof, that specifically binds to human CD137, binds to all or a portion of amino acids 111-132 of SEQ ID NO:3. In some embodiments, an isolated anti-CD137 agonist antibody, or antigen binding fragment thereof, described herein, binds to an epitope of human CD137 comprising residue K114 of SEQ ID NO: 3. In some embodiments, an isolated anti-CD137 agonist antibody, or antigen binding fragment thereof,

described herein, binds to an epitope of human CD137 comprising residues E111, T113 and K114 of SEQ ID NO: 3. In some embodiments, an isolated anti-CD137 agonist antibody, or antigen binding fragment thereof, described herein, binds to an epitope of human CD137 comprising residues E111, T113, K114, N126 and I132 of SEQ ID NO: 3. In some embodiments, an isolated anti-CD137 agonist antibody, or antigen binding fragment thereof, described herein, binds to an epitope of human CD137 comprising E111, T113, K114, N126, I132 and P135 of SEQ ID NO: 3. In some embodiments, an isolated anti-CD137 agonist antibody, or antigen binding fragment thereof, described herein, binds to an epitope of human CD137 comprising one or more residues E111, T113, K114, N126, I132 and P135 of SEQ ID NO: 3.

In some embodiments, an isolated anti-CD137 agonist antibody, or antigen binding fragment thereof, described herein, binds to an epitope of human CD137 comprising a sequence of one or more amino acid residues corresponding to amino acid positions 100 to 135, 101 to 135, 102 to 135, 103 to 135, 104 to 135, 105 to 135, 106 to 135, 107 to 135, 108 to 135, 109 to 135, 110 to 135, or 111 to 135 of SEQ ID NO: 3. In some embodiments, an isolated anti-CD137 agonist antibody, or antigen binding fragment thereof, described herein, binds to an epitope of human CD137 comprising a sequence of one or more amino acid residues corresponding to amino acid positions 111 to 135 of SEQ ID NO: 3. In some embodiments, the epitope comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 amino acid residues corresponding to amino acid positions 111 to 135 of SEQ ID NO: 3.

In some embodiments, an isolated anti-CD137 agonist antibody, or antigen binding fragment thereof, described herein, binds to an epitope of human CD137 within amino acid positions 100 to 135, 101 to 135, 102 to 135, 103 to 135, 104 to 135, 105 to 135, 106 to 135, 107 to 135, 108 to 135, 109 to 135, 110 to 135, or 111 to 135 of SEQ ID NO: 3. In some embodiments, an isolated anti-CD137 agonist antibody, or antigen binding fragment thereof, described herein, binds to an epitope of human CD137 within amino acid positions 111 to 135 of SEQ ID NO: 3. In some embodiments, the epitope comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 amino acid residues corresponding to amino acid positions 111 to 135 of SEQ ID NO: 3.

In some embodiments, an isolated anti-CD137 agonist antibody, or antigen binding fragment thereof, described herein, binds to an epitope of human CD137 comprising ELTK

(corresponding to amino acid residues 111-114 of SEQ ID NO: 3). In some embodiments, amino acid residue L112 can be another amino acid residue.

In some embodiments, the epitope is a non-linear epitope. In some embodiments, mutation of amino acid residue K114 abrogates bindings of an isolated anti-CD137 agonist antibody, or antigen binding fragment thereof, described herein, to human CD137.

In some embodiments, isolated anti-CD137 agonist antibody, or antigen binding fragment thereof, described herein, binds to an epitope of human CD137 comprising a sequence of one or more amino acid residues corresponding to amino acid positions 111 to 135 of SEQ ID NO: 3, wherein the epitope comprises at least amino acid K114, and wherein the antibody or antigen binding portion thereof binds mouse CD137 and does not bind rat CD137. In some embodiments, the epitope is a non-linear epitope. In some embodiments, the antibody or antigen binding portion thereof binds mouse CD137 and cynomolgus CD137 and does not bind rat CD137. In some embodiments, binding of an isolated anti-CD137 agonist antibody, or antigen binding fragment thereof, described herein, to human, mouse, rat and cynomolgus CD137 is determined by surface plasmon resonance (SPR).

In some embodiments, the antibody or antigen binding portion thereof binds to mouse, cynomolgus or human CD137 with an affinity that is at least 10, 20, 30, 40, 50, 100, 200, 500 or 1000 times greater than the antibody's affinity for rat CD137. In some embodiments, the antibody or antigen binding portion thereof binds to mouse, cynomolgus or human CD137 with an affinity that is at least 10, 20, 30, 40, 50, 100, 200, 500 or 1000 times greater than the antibody's affinity for a CD137 polypeptide that does not comprise a lysine at position 114 relative to human CD137 of SEQ ID NO: 3.

In some embodiments, an isolated anti-CD137 agonist antibody, or antigen-binding fragment thereof, described herein, binds to an epitope of human CD137 and competes with mAb1 for binding to the epitope of human CD137. In some embodiments, an isolated anti-CD137 agonist antibody, or antigen-binding fragment thereof, described herein, binds to and agonizes CD137. In some embodiments, the anti-CD137 antibodies provided by the disclosure bind to and agonize CD137 and co-stimulate activation of T cells.

The present disclosure provides formulations comprising antibodies that compete for binding to an epitope on CD137 which comprises all or a portion of an epitope recognized by one or more particular reference antibodies described herein (*e.g.*, mAb1). In some embodiments, the

anti-CD137 antibodies bind to an epitope of human CD137 and compete with a reference antibody (*e.g.*, mAb1) for binding to the epitope of human CD137 and wherein the antibody, or antigen binding fragment thereof, binds human CD137 with an equilibrium dissociation constant K_D of 1 x 10^{-6} or less. In some embodiments, the anti-CD137 antibodies bind to an epitope on CD137, wherein one or more mutations to the epitope inhibit, reduce, or block binding to both the antibodies and a reference antibody (*e.g.*, mAb1). In some embodiments, the reference antibody is the mAb1 antibody, described herein. In some embodiments, the reference antibody is any one antibody provided in any one of Tables 22-27.

Accordingly, the anti-CD137 antibodies provided by the disclosure may be assessed through x-ray crystallographic analysis of a crystal structure comprising an antibody bound to CD137, or a fragment or portion thereof. In some aspects, the epitopes that bound by the antibodies provided by the disclosure are identified by determining the residues on the human CD137 antigen that reside or are located within 4 angstroms (Å) of an antibody paratope residue, *e.g.*, mAb1.

In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is at least 3 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is at least 4 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is at least 5 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is at least 6 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is at least 7 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is at least 8 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is at least 9 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is at least 10 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is at least 12 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is at least 3 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is at least 13 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is at least 14 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is at least 15 amino acid residues.

In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is fewer than 25 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is fewer than 24 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is fewer than 23 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is fewer than 22 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is fewer than 21 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is fewer than 20 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is fewer than 19 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is fewer than 18 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is fewer than 17 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is fewer than 16 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is fewer than 15 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is fewer than 14 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is fewer than 13 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is fewer than 12 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is fewer than 11 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is fewer than 10 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is fewer than 9 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is fewer than 8 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is fewer than 7 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is fewer than 6 amino acid residues. In some embodiments, the epitope bound by the anti-CD137 antibodies described herein is fewer than 5 amino acid residues.

In some embodiments, the anti-CD137 antibodies described herein bind to an epitope of fewer than 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6 or 5 amino acids and comprises amino acid residue K114 of SEQ ID NO: 3.

Variable Regions

In some embodiments, provided herein are formulations comprising isolated monoclonal antibodies or antigen binding fragments thereof, comprising heavy and light chain variable sequences as set forth in any one of Tables 22-27.

In some embodiments, the anti-CD137 antibodies described herein comprise heavy and light chain CDRs selected from the group consisting of:

(a) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 56 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively;

(b) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 56 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 70, 79 and 90, respectively;

(c) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 56 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 71, 80 and 91, respectively;

(d) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 56 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 72, 81 and 92, respectively;

(e) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 56 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 73, 82 and 91, respectively;

(f) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 56 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 74, 83 and 93, respectively;

(g) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 56 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 75, 84 and 91, respectively;

(h) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 56 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 74, 85 and 94, respectively;

(i) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 56 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 76, 86 and 95, respectively;

(j) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 56 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 77, 87 and 93, respectively;

(k) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 56 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 88 and 90, respectively;

(l) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 49, 57 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively;

(m) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 49, 58 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively;

(n) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 49, 59 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively;

(o) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 49, 60 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively;

(p) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 50, 61 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively;

(q) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 50, 58 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively;

(r) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 51, 62 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively;

(s) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 52, 63 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively;

(t) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 50, 64 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively;

(u) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 50, 65 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively;

(v) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 51, 108 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively;

(w) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 107, 56 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively;

(x) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 56 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 109, 110 and 92, respectively;

(y) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 135, 139 and 143, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 144, 147 and 150, respectively;

(z) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 135, 139 and 143, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 145, 148 and 151, respectively;

(aa) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 135, 139 and 143, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 146, 149 and 152, respectively;

(bb) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 136, 140 and 143, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 144, 147 and 150, respectively;

(cc) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 136, 140 and 143, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 145, 148 and 151, respectively;

(dd) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 136, 140 and 143, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 146, 149 and 152, respectively;

(ee) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 137, 141 and 143, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 144, 147 and 150, respectively;

(ff) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 137, 141 and 143, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 145, 148 and 151, respectively;

(gg) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 137, 141 and 143, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 146, 149 and 152, respectively;

(hh) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 138, 142 and 143, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 144, 147 and 150, respectively;

(ii) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 138, 142 and 143, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 145, 148 and 151, respectively;

(jj) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 138, 142 and 143, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 146, 149 and 152, respectively;

(kk) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 135, 139 and 143, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 144, 147 and 150, respectively;

(ll) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 135, 139 and 143, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 145, 148 and 151, respectively;

(mm) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 135, 139 and 143, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 146, 149 and 152, respectively;

(nn) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 154 and 159, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 144, 147 and 150, respectively;

(oo) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 154 and 159, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 145, 148 and 151, respectively;

(pp) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 154 and 159, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 146, 149 and 152, respectively;

(qq) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 49, 155 and 159, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 144, 147 and 150, respectively;

(rr) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 49, 155 and 159, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 145, 148 and 151, respectively;

(ss) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 49, 155 and 159, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 146, 149 and 152, respectively;

(tt) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 51, 156 and 159, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 144, 147 and 150, respectively;

(uu) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 51, 156 and 159, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 145, 148 and 151, respectively;

(vv) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 51, 156 and 159, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 146, 149 and 152, respectively;

(ww) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 50, 158 and 159, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 144, 147 and 150, respectively;

(xx) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 50, 158 and 159, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 145, 148 and 151, respectively;

(yy) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 50, 158 and 159, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 146, 149 and 152, respectively;

(zz) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 153, 157 and 159, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 144, 147 and 150, respectively;

(aaa) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 153, 157 and 159, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 145, 148 and 151, respectively; and

(bbb) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 153, 157 and 159, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 146, 149 and 152, respectively.

In some embodiments, the anti-CD137 antibodies described herein comprise 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: 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 101 and 103; and wherein the light chain variable region comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 6, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46 and 105.

In some embodiments, the anti-CD137 antibodies described herein comprise heavy and light chain CDRs, wherein heavy chain CDR3 comprises the amino acid sequence set forth in SEQ ID NO: 68.

In some embodiments, the anti-CD137 antibodies described herein comprise heavy and light chain variable regions comprising amino acid sequences selected from the group consisting of:

(a) SEQ ID NO: 4 and 6, respectively;

(b) SEQ ID NO: 4 and 28, respectively;

(c) SEQ ID NO: 4 and 30, respectively;

(d) SEQ ID NO: 4 and 32, respectively;

(e) SEQ ID NO: 4 and 34, respectively;

(f) SEQ ID NO: 4 and 36, respectively;

(g) SEQ ID NO: 4 and 38, respectively;

(h) SEQ ID NO: 4 and 40, respectively;

(i) SEQ ID NO: 4 and 42, respectively;

(j) SEQ ID NO: 4 and 44, respectively;

(k) SEQ ID NO: 4 and 46, respectively;

(l) SEQ ID NO: 8 and 6, respectively;

(m) SEQ ID NO: 10 and 6, respectively;

(n) SEQ ID NO: 12 and 6, respectively;

(o) SEQ ID NO: 14 and 6, respectively;

(p) SEQ ID NO: 16 and 6, respectively;

(q) SEQ ID NO: 18 and 6, respectively;

(r) SEQ ID NO: 20 and 6, respectively;

(s) SEQ ID NO: 22 and 6, respectively;

(t) SEQ ID NO: 24 and 6, respectively;

(u) SEQ ID NO: 26 and 6, respectively;

(v) SEQ ID NO: 101 and 6, respectively;

(w) SEQ ID NO: 103 and 6, respectively; and

(x) SEQ ID NO: 4 and 105, respectively.

In some embodiments, the anti-CD137 antibodies described herein comprise heavy and light chain variable regions, wherein the heavy chain variable region comprises an amino acid sequence which is at least 90% identical to the amino acid sequence selected from the group consisting of SEQ ID NOs: 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 101 and 103; and wherein the light chain variable region comprises an amino acid sequence which is at least 90% identical to the amino acid sequence selected from the group consisting of SEQ ID NOs: 6, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46 and 105.

In some embodiments, the anti-CD137 antibodies described herein comprise heavy and light chain variable regions comprising amino acid sequences at least 90% identical to the amino acid sequences selected from the group consisting of:

(a) SEQ ID NO: 4 and 6, respectively;

(b) SEQ ID NO: 4 and 28, respectively;

(c) SEQ ID NO: 4 and 30, respectively;

(d) SEQ ID NO: 4 and 32, respectively;

(e) SEQ ID NO: 4 and 34, respectively;

(f) SEQ ID NO: 4 and 36, respectively;

(g) SEQ ID NO: 4 and 38, respectively;

(h) SEQ ID NO: 4 and 40, respectively;

(i) SEQ ID NO: 4 and 42, respectively;

(j) SEQ ID NO: 4 and 44, respectively;

(k) SEQ ID NO: 4 and 46, respectively;

(l) SEQ ID NO: 8 and 6, respectively;

(m) SEQ ID NO: 10 and 6, respectively;

(n) SEQ ID NO: 12 and 6, respectively;

(o) SEQ ID NO: 14 and 6, respectively;

(p) SEQ ID NO: 16 and 6, respectively;

(q) SEQ ID NO: 18 and 6, respectively;

(r) SEQ ID NO: 20 and 6, respectively;

(s) SEQ ID NO: 22 and 6, respectively;

(t) SEQ ID NO: 24 and 6, respectively;

(u) SEQ ID NO: 26 and 6, respectively;

(v) SEQ ID NO: 101 and 6, respectively;

(w) SEQ ID NO: 103 and 6, respectively; and

(x) SEQ ID NO: 4 and 105, respectively.

In some embodiments, provided herein are antibodies that specifically bind human CD137 comprising heavy chain and light chain variable regions encoded by nucleotide sequences selected from the group consisting of:

(a) SEQ ID NO: 5 and 7, respectively;

(b) SEQ ID NO: 5 and 29, respectively;

(c) SEQ ID NO: 5 and 31, respectively;

(d) SEQ ID NO: 5 and 33, respectively;

(e) SEQ ID NO: 5 and 35, respectively;

(f) SEQ ID NO: 5 and 37, respectively;

(g) SEQ ID NO: 5 and 39, respectively;

(h) SEQ ID NO: 5 and 41, respectively;

(i) SEQ ID NO: 5 and 43, respectively;

(j) SEQ ID NO: 5 and 45, respectively;

(k) SEQ ID NO: 5 and 47, respectively;

(l) SEQ ID NO: 9 and 7, respectively;

(m) SEQ ID NO: 11 and 7, respectively;

(n) SEQ ID NO: 13 and 7, respectively;

(o) SEQ ID NO: 15 and 7, respectively;

(p) SEQ ID NO: 17 and 7, respectively;

(q) SEQ ID NO: 19 and 7, respectively;

(r) SEQ ID NO: 21 and 7, respectively;

(s) SEQ ID NO: 23 and 7, respectively;

(t) SEQ ID NO: 25 and 7, respectively;

(u) SEQ ID NO: 27 and 7, respectively;

(v) SEQ ID NO: 102 and 7, respectively;

(w) SEQ ID NO: 104 and 7, respectively; and

(x) SEQ ID NO: 5 and 106, respectively.

In some embodiments, provided herein are antibodies that specifically bind human CD137 comprising heavy chain and light chain variable regions encoded by nucleotide sequences having at least 90% identity to the nucleotide sequences selected from the group consisting of:

(a) SEQ ID NO: 5 and 7, respectively;

(b) SEQ ID NO: 5 and 29, respectively;

(c) SEQ ID NO: 5 and 31, respectively;

(d) SEQ ID NO: 5 and 33, respectively;

(e) SEQ ID NO: 5 and 35, respectively;

(f) SEQ ID NO: 5 and 37, respectively;

(g) SEQ ID NO: 5 and 39, respectively;

(h) SEQ ID NO: 5 and 41, respectively;

(i) SEQ ID NO: 5 and 43, respectively;

(j) SEQ ID NO: 5 and 45, respectively;

(k) SEQ ID NO: 5 and 47, respectively;

(l) SEQ ID NO: 9 and 7, respectively;

(m) SEQ ID NO: 11 and 7, respectively;

(n) SEQ ID NO: 13 and 7, respectively;

(o) SEQ ID NO: 15 and 7, respectively;

(p) SEQ ID NO: 17 and 7, respectively;

(q) SEQ ID NO: 19 and 7, respectively;

(r) SEQ ID NO: 21 and 7, respectively;

(s) SEQ ID NO: 23 and 7, respectively;

(t) SEQ ID NO: 25 and 7, respectively;

(u) SEQ ID NO: 27 and 7, respectively;

(v) SEQ ID NO: 102 and 7, respectively;

(w) SEQ ID NO: 104 and 7, respectively; and

(x) SEQ ID NO: 5 and 106, respectively.

In some embodiments, the anti-CD137 antibodies described herein comprise heavy and light chain variable regions, wherein the heavy chain variable region is encoded by a nucleotide sequence selected from the group consisting of SEQ ID NOs: 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 102 and 104; and wherein the light chain variable region is encoded by a nucleotide sequence selected from the group consisting of SEQ ID NOs: 7, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47 and 106.

In some embodiments, the anti-CD137 antibodies described herein comprise heavy and light chain variable regions, wherein the heavy chain variable region is encoded by a nucleotide sequence having at least 90% identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 102 and 104; and wherein the light chain variable region is encoded by a nucleotide sequence having at least 90% identity to a nucleotide

sequence selected from the group consisting of SEQ ID NOs: 7, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47 and 106.

In some embodiments, provided herein are anti-CD137 antibodies that specifically bind to human CD137 and comprise a heavy chain CDR3 having the amino acid sequence DXXXXLXXXXYXYYX (SEQ ID NO: 126), wherein X is any amino acid. In some embodiments, X is any amino acid except for alanine. In some embodiments, mutation of residues D95, L100, Y100E, Y100G, and/or Y100H of SEQ ID NO: 126, results in loss of binding to human CD137.

In some embodiments, provided herein are anti-CD137 antibodies that specifically bind to human CD137 and comprise a heavy chain CDR3 having the amino acid sequence DXPFXLDXXYYYYYX (SEQ ID NO: 127), wherein X is any amino acid. In some embodiments, mutation of residues F98, D100A, Y100D, and/or Y100F, and/or Y100H of SEQ ID NO: 126, to alanine results in loss of binding to human CD137. In some embodiments, mutation of residues F98, D100A, Y100D, and/or Y100F, and/or Y100H of SEQ ID NO: 126, to any residue except for alanine, results in an increase in binding to human CD137.

In some embodiments, provided herein are anti-CD137 antibodies that specifically bind to human CD137 and comprise a heavy chain CDR3 having the amino acid sequence $DX_1X_2X_3X_4LX_5X_6X_7X_8YX_9YYX_{10}$ (SEQ ID NO: 128), wherein X_1 is any amino acid, wherein X_2 is a non-polar amino acid, wherein X_3 is a non-polar amino acid, wherein X_4 is any amino acid, wherein X_5 is a polar amino acid, wherein X_6 is any amino acid, wherein X_7 is any amino acid, wherein X_8 is a polar amino acid, wherein X_9 is a polar amino acid, and wherein X_{10} is any amino acid. In some embodiments, X_2 is proline, wherein X_3 is phenylalanine or tryptophan, wherein X_5 is aspartic acid or glutamic acid, wherein X_8 is tyrosine, and wherein X_9 is tyrosine.

The role of an amino acid residue within the heavy chain CDR3 of an antibody or antigen binding portion thereof, in binding to a specified target (*e.g.*, CD137) can be determined by methods known to one of skill in the art. In some embodiments, an initial analysis using alanine scanning is completed to determine the critical residues for antigen binding. As described herein, alanine scanning is a technique used to determine the contribution of a specific wild-type residue to the stability or function(s) (*e.g.*, binding affinity) of given protein or polypeptide. The technique involves the substitution of an alanine residue for a wild-type residue in a polypeptide, followed by an assessment of the stability or function(s) (*e.g.*, binding affinity) of the alanine-substituted

derivative or mutant polypeptide and comparison to the wild-type polypeptide. In some embodiments, the residues identified as not critical are further evaluated to modulate the binding of the antibody to the antigen (*e.g.*, increase or decrease binding). A non-limiting example of such analysis is deep mutational scanning. This method allows for the evaluation of large numbers of mutations. In some embodiments, each amino acid residue within the heavy chain CDR3 is mutated to every amino acid residue (except for alanine), and binding is assessed. Other methods for analyzing the effect of amino acid residue mutations are known in the art. In some embodiments, these methods are utilized to assess the role of residues in all of the heavy chain and light chain CDRs in binding to human CD137.

Exemplary CD137 Binding Antibodies

In some embodiments, the formulations of the disclosure comprise anti-CD137 antibodies described herein that bind human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM). In some embodiments, the formulations of the disclosure comprise anti-CD137 antibodies described that herein bind human CD137 with an affinity (K_D) of about 40-100 nM (*e.g.*, between about 40 nM and about 100 nM). In some embodiments, the formulations of the disclosure comprise anti-CD137 antibodies described herein that bind an epitope on human CD137 described *supra* (*e.g.*, comprising K114). In some embodiments, the formulations of the disclosure comprise anti-CD137 antibodies described herein that comprise a heavy chain CDR3 comprising the amino acid sequence DXXXXLXXXXYXYYX (SEQ ID NO: 126). In some embodiments, the formulations of the disclosure comprise anti-CD137 antibodies described herein that bind human CD137 with an affinity (K_D) of 30-100 nM (*e.g.*, between about 30 nM and about 100 nM) and bind an epitope on human CD137 described *supra* (*e.g.*, comprising K114). In some embodiments, the formulations of the disclosure comprise anti-CD137 antibodies described herein that bind human CD137 with an affinity (K_D) of 30-100 nM (*e.g.*, between about 30 nM and about 100 nM) and comprise a heavy chain CDR3 comprising the amino acid sequence DXXXXLXXXXYXYYX (SEQ ID NO: 126). In some embodiments, the formulations of the disclosure comprise anti-CD137 antibodies described herein that bind an epitope on human CD137 described *supra* (*e.g.*, comprising K114) and comprise a heavy chain CDR3 comprising the amino acid sequence DXXXXLXXXXYXYYX (SEQ ID NO: 126). In some embodiments, the formulations of the disclosure comprise anti-CD137 antibodies described herein that bind human

CD137 with an affinity (K_D) of 30-100nM (*e.g.*, between about 30 nM and about 100 nM), bind an epitope on human CD137 described *supra* (*e.g.*, comprising K114), and comprise a heavy chain CDR3 comprising the amino acid sequence DXXXXLXXXXYXYYX (SEQ ID NO: 126).

In some embodiments, the anti-CD137 antibodies

(i) bind human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM); and

(ii) comprise a heavy chain CDR3 comprising the amino acid sequence $DX_1X_2X_3X_4LX_5X_6X_7X_8YX_9YYX_{10}$, wherein X_1 is any amino acid, wherein X_2 is a non-polar amino acid, wherein X_3 is a non-polar amino acid, wherein X_4 is any amino acid, wherein X_5 is a polar amino acid, wherein X_6 is any amino acid, wherein X_7 is any amino acid, wherein X_8 is a polar amino acid, wherein X_9 is a polar amino acid, and wherein X_{10} is any amino acid.

In some embodiments, the anti-CD137 antibodies

(i) bind human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM); and

(ii) bind to an epitope on human CD137 comprising one or more residues E111, T113, K114, N126, I132 and P135 of SEQ ID NO: 3.

In some embodiments, the anti-CD137 antibodies

(i) bind human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM);

(ii) bind to an epitope on human CD137 comprising one or more residues E111, T113, K114, N126, I132 and P135 of SEQ ID NO: 3;

(iii) comprise a heavy chain CDR3 comprising the amino acid sequence DXXXXLXXXXYXYYX, wherein X is any amino acid; or

(iv) combinations thereof.

In some embodiments, the anti-CD137 antibodies

(i) bind human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM);

(ii) bind to an epitope on human CD137 comprising one or more residues E111, T113, K114, N126, I132 and P135 of SEQ ID NO: 3;

(iii) comprise a heavy chain CDR3 comprising the amino acid sequence $DX_1X_2X_3X_4LX_5X_6X_7X_8YX_9YYX_{10}$, wherein X_1 is any amino acid, wherein X_2 is a non-polar

amino acid, wherein X_3 is a non-polar amino acid, wherein X_4 is any amino acid, wherein X_5 is a polar amino acid, wherein X_6 is any amino acid, wherein X_7 is any amino acid, wherein X_8 is a polar amino acid, wherein X_9 is a polar amino acid, and wherein X_{10} is any amino acid.; or

(iv) combinations thereof.

In some embodiments, the anti-CD137 antibodies

(i) bind human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM);

(ii) specifically bind to an epitope on human CD137 comprising one or more residues E111, T113, K114, N126, I132 and P135 of SEQ ID NO: 3; and

(iii) comprise a heavy chain CDR3 comprising the amino acid sequence DXXXXLXXXXYXYYX, wherein X is any amino acid.

In some embodiments, the anti-CD137 antibodies

(i) bind human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM);

(ii) bind to an epitope on human CD137 comprising one or more residues E111, T113, K114, N126, I132 and P135 of SEQ ID NO: 3; and

(iii) comprise a heavy chain CDR3 comprising the amino acid sequence $DX_1X_2X_3X_4LX_5X_6X_7X_8YX_9YYX_{10}$, wherein X_1 is any amino acid, wherein X_2 is a non-polar amino acid, wherein X_3 is a non-polar amino acid, wherein X_4 is any amino acid, wherein X_5 is a polar amino acid, wherein X_6 is any amino acid, wherein X_7 is any amino acid, wherein X_8 is a polar amino acid, wherein X_9 is a polar amino acid, and wherein X_{10} is any amino acid.

In some embodiments, the anti-CD137 antibodies

(i) bind human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM); and

(ii) bind to an epitope comprising a sequence of one or more amino acid residues corresponding to amino acid positions 111 to 135 of SEQ ID NO: 3.

In some embodiments, the anti-CD137 antibodies

(i) bind human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM);

(ii) bind to an epitope comprising a sequence of one or more amino acid residues corresponding to amino acid positions 111 to 135 of SEQ ID NO: 3;

(iii) comprise a heavy chain CDR3 comprising the amino acid sequence DXXXXLXXXXYXYYX, wherein X is any amino acid; or

(iv) combinations thereof.

In some embodiments, the anti-CD137 antibodies

(i) bind human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM);

(ii) bind to an epitope comprising a sequence of one or more amino acid residues corresponding to amino acid positions 111 to 135 of SEQ ID NO: 3;

(iii) comprise a heavy chain CDR3 comprising the amino acid sequence $DX_1X_2X_3X_4LX_5X_6X_7X_8YX_9YYX_{10}$, wherein X_1 is any amino acid, wherein X_2 is a non-polar amino acid, wherein X_3 is a non-polar amino acid, wherein X_4 is any amino acid, wherein X_5 is a polar amino acid, wherein X_6 is any amino acid, wherein X_7 is any amino acid, wherein X_8 is a polar amino acid, wherein X_9 is a polar amino acid, and wherein X_{10} is any amino acid; or

(iv) combinations thereof.

In some embodiments, the anti-CD137 antibodies

(i) bind human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM);

(ii) bind to an epitope comprising a sequence of one or more amino acid residues corresponding to amino acid positions 111 to 135 of SEQ ID NO: 3; and

(iii) comprise a heavy chain CDR3 comprising the amino acid sequence DXXXXLXXXXYXYYX, wherein X is any amino acid.

In some embodiments, the anti-CD137 antibodies

(i) bind human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM);

(ii) bind to an epitope comprising a sequence of one or more amino acid residues corresponding to amino acid positions 111 to 135 of SEQ ID NO: 3; and

(iii) comprise a heavy chain CDR3 comprising the amino acid sequence $DX_1X_2X_3X_4LX_5X_6X_7X_8YX_9YYX_{10}$, wherein X_1 is any amino acid, wherein X_2 is a non-polar amino acid, wherein X_3 is a non-polar amino acid, wherein X_4 is any amino acid, wherein X_5 is a polar amino acid, wherein X_6 is any amino acid, wherein X_7 is any amino acid, wherein X_8 is a polar amino acid, wherein X_9 is a polar amino acid, and wherein X_{10} is any amino acid.

In some embodiments, the anti-CD137 antibodies

(i) bind human CD137 with an affinity of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM); and

(ii) bind to an epitope comprising ELTK (corresponding to amino acid residues 111-114 of SEQ ID NO: 3).

In some embodiments, the anti-CD137 antibodies

(i) bind human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM);

(ii) bind to an epitope comprising ELTK (corresponding to amino acid residues 111-114 of SEQ ID NO: 3);

(iii) comprise a heavy chain CDR3 comprising the amino acid sequence DXXXXLXXXXYXYYX, wherein X is any amino acid; or

(iv) combinations thereof.

In some embodiments, the anti-CD137 antibodies

(i) bind human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM);

(ii) bind to an epitope comprising ELTK (corresponding to amino acid residues 111-114 of SEQ ID NO: 3);

(iii) comprise a heavy chain CDR3 comprising the amino acid sequence $DX_1X_2X_3X_4LX_5X_6X_7X_8YX_9YYX_{10}$, wherein X_1 is any amino acid, wherein X_2 is a non-polar amino acid, wherein X_3 is a non-polar amino acid, wherein X_4 is any amino acid, wherein X_5 is a polar amino acid, wherein X_6 is any amino acid, wherein X_7 is any amino acid, wherein X_8 is a polar amino acid, wherein X_9 is a polar amino acid, and wherein X_{10} is any amino acid; or

(iv) combinations thereof.

In some embodiments, the anti-CD137 antibodies

(i) bind human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM);

(ii) bind to an epitope comprising ELTK (corresponding to amino acid residues 111-114 of SEQ ID NO: 3); and

(iii) comprise a heavy chain CDR3 comprising the amino acid sequence DXXXXLXXXXYXYYX, wherein X is any amino acid.

In some embodiments, the anti-CD137 antibodies

(i) bind human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM);

(ii) bind to an epitope comprising ELTK (corresponding to amino acid residues 111-114 of SEQ ID NO: 3); and

(iii) comprise a heavy chain CDR3 comprising the amino acid sequence $DX_1X_2X_3X_4LX_5X_6X_7X_8YX_9YYX_{10}$, wherein X_1 is any amino acid, wherein X_2 is a non-polar amino acid, wherein X_3 is a non-polar amino acid, wherein X_4 is any amino acid, wherein X_5 is a polar amino acid, wherein X_6 is any amino acid, wherein X_7 is any amino acid, wherein X_8 is a polar amino acid, wherein X_9 is a polar amino acid, and wherein X_{10} is any amino acid.

In some embodiments, the anti-CD137 antibodies described *supra* comprise heavy and light chain CDRs selected from the group consisting of:

(a) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 56 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively; and

(b) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 51, 108 and 68, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 69, 78 and 89, respectively.

In some embodiments, the anti-CD137 antibodies described *supra* comprise heavy and light chain CDRs selected from the group consisting of:

(a) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 135, 139, and 143, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 144, 147, and 150, respectively; and

(b) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 137, 141, and 143, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 144, 147, and 150, respectively.

In some embodiments, the anti-CD137 antibodies described *supra* comprise heavy and light chain CDRs selected from the group consisting of:

(a) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 48, 154, and 159, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 144, 147, and 150, respectively; and

(b) heavy chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 51, 156, and 159, respectively, and light chain CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NOs: 144, 147, and 150, respectively.

In some embodiments, the formulations of the disclosure comprise anti-CD137 antibodies that comprise 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: 4 and 101; and wherein the light chain variable region comprises an amino acid sequence of SEQ ID NO: 6.

In some embodiments, the anti-CD137 antibodies comprise heavy and light chain variable regions comprising amino acid sequences selected from the group consisting of:

(a) SEQ ID NOs: 4 and 6, respectively; and

(b) SEQ ID NOs: 101 and 6, respectively.

In some embodiments, the anti-CD137 antibodies comprise heavy and light chain variable regions comprising amino acid sequences selected from the group consisting of:

(a) SEQ ID NOs: 4 and 6, respectively;

(b) SEQ ID NOs: 101 and 6, respectively; and

(c) SEQ ID NOs: 26 and 6, respectively.

In some embodiments, the anti-CD137 antibodies comprise heavy and light chain variable regions encoded by nucleotide sequences selected from the group consisting of:

(a) SEQ ID NOs: 5 and 7, respectively; and

(b) SEQ ID NOs: 102 and 7, respectively.

In some embodiments, the anti-CD137 antibodies comprise heavy and light chain variable regions encoded by nucleotide sequences selected from the group consisting of:

(a) SEQ ID NOs: 5 and 7, respectively;

(b) SEQ ID NOs: 102 and 7, respectively; and

(c) SEQ ID NOs: 27 and 7, respectively.

In some embodiments, the formulations of the disclosure comprise anti-CD137 antibodies that comprise heavy and light chain variable regions, wherein the heavy chain variable region comprises an amino acid sequence which is at least 90% identical to the amino acid sequence selected from the group consisting of SEQ ID NOs: 4 and 101; and wherein the light chain variable region comprises an amino acid sequence which is at least 90% identical to the amino acid sequence of SEQ ID NO: 6.

In some embodiments, the formulations of the disclosure comprise anti-CD137 antibodies that comprise heavy and light chain variable regions, wherein the heavy chain variable region comprises an amino acid sequence which is at least 90% identical to the amino acid sequence selected from the group consisting of SEQ ID NOs: 4, 26 and 101; and wherein the light chain variable region comprises an amino acid sequence which is at least 90% identical to the amino acid sequence of SEQ ID NO: 6.

In some embodiments, the formulations of the disclosure comprise anti-CD137 antibodies that comprise heavy and light chain variable regions, wherein the heavy chain variable region is encoded by a nucleotide sequence which is least 90% identical to the nucleotide sequence selected from the group consisting of SEQ ID NOs: 5 and 102; and wherein the light chain variable region is encoded by a nucleotide sequence which is at least 90% identical to the nucleotide sequence of SEQ ID NO: 7.

In some embodiments, the formulations of the disclosure comprise anti-CD137 antibodies that comprise heavy and light chain variable regions, wherein the heavy chain variable region is encoded by a nucleotide sequence which is least 90% identical to the nucleotide sequence selected from the group consisting of SEQ ID NOs: 5, 27 and 102; and wherein the light chain variable region is encoded by a nucleotide sequence which is at least 90% identical to the nucleotide sequence of SEQ ID NO: 7.

In some embodiments, the anti-CD137 antibodies comprise heavy and light chain variable regions comprising amino acid sequences at least 90% identical to the amino acid sequences selected from the group consisting of:

(a) SEQ ID NOs: 4 and 6, respectively; and

(b) SEQ ID NOs: 101 and 6, respectively.

In some embodiments, the anti-CD137 antibodies comprise heavy and light chain variable regions comprising amino acid sequences at least 90% identical to the amino acid sequences selected from the group consisting of:

(a) SEQ ID NOs: 4 and 6, respectively;

(b) SEQ ID NOs: 101 and 6, respectively; and

(c) SEQ ID NOs: 26 and 6, respectively.

In some embodiments, the anti-CD137 antibodies comprise heavy and light chain variable regions encoded by nucleotide sequences at least 90% identical to the nucleotide sequences selected from the group consisting of:

(a) SEQ ID NOs: 5 and 7, respectively; and

(b) SEQ ID NOs: 102 and 7, respectively.

In some embodiments, the anti-CD137 antibodies comprise heavy and light chain variable regions encoded by nucleotide sequences at least 90% identical to the nucleotide sequences selected from the group consisting of:

(a) SEQ ID NOs: 5 and 7, respectively;

(b) SEQ ID NOs: 102 and 7, respectively; and

(c) SEQ ID NOs: 27 and 7, respectively.

In some embodiments, the anti-CD137 antibodies described herein have at least the functional properties of mAb1 (*i.e.*, an antibody comprising the heavy and light chain variable sequences of SEQ ID NOs: 4 and 6, respectively), mab8 (*i.e.*, an antibody comprising the heavy and light chain variable sequences of SEQ ID NOs: 101 and 6, respectively) or mAb10 (*i.e.*, an antibody comprising the heavy and light chain variable sequences of SEQ ID NOs: 26 and 6, respectively). In some embodiments, the functional properties of an antibody described herein include but are not limited to: induction or enhancement of dimerization of CD137; induction or enhancement of multimerization of CD137; induction or enhancement of CD137-mediated T cell activation; induction or enhancement of CD137-mediated cytotoxic T cell response; induction or enhancement of CD137-mediated T cell proliferation; induction or enhancement of CD137-mediated cytokine production; lack of induction or enhancement of intrahepatic and/or intrasplenic T cell activation and/or T cell proliferation; and reduction or inhibition of tumor growth.

In some embodiments, the anti-CD137 antibodies described herein bind human CD137 with an equilibrium dissociation constant K_D at least equivalent to that of mAb1 (*i.e.*, an antibody comprising the heavy and light chain variable sequences of SEQ ID NOs: 4 and 6, respectively), mab8 (*i.e.*, an antibody comprising the heavy and light chain variable sequences of SEQ ID NOs: 101 and 6, respectively) or mAb10 (*i.e.*, an antibody comprising the heavy and light chain variable sequences of SEQ ID NOs: 26 and 6, respectively).

In some embodiments, the anti-CD137 antibodies described herein comprise a human IgG1 heavy chain constant region or a human IgG4 heavy chain constant region. In some embodiments,

the anti-CD137 antibodies described herein comprise a human wild-type IgG1 heavy chain constant region or a human wild-type IgG4 heavy chain constant region. In some embodiments, the anti-CD137 antibodies described herein comprise a human wild-type IgG1 heavy chain constant region as set forth in SEQ ID NO: 1. In some embodiments, the anti-CD137 antibodies described herein comprise a mutant IgG1 heavy chain constant region or a mutant IgG4 heavy chain constant region. In some embodiments, the anti-CD137 antibodies described herein comprise a mutant IgG4 heavy chain constant region, wherein the mutant IgG4 heavy chain constant region comprises an amino acid substitution at residue Ser228. In some embodiments, the amino acid substitution at residue Ser228 is S228P. In some embodiments, the anti-CD137 antibodies described herein comprise an IgG4 heavy chain constant region, wherein the c-terminal lysine residue is removed. In some embodiments, the anti-CD137 antibodies described herein comprise an IgG4 heavy chain constant region wherein the c-terminal lysine residue is removed and comprises the S228P amino acid substitution. In some embodiments, the anti-CD137 antibodies described herein comprise an IgG4 heavy chain constant region as set forth in SEQ ID NO: 2.

In some embodiments, the anti-CD137 antibodies described herein comprise heavy and light chains comprising the amino acid sequences set forth in SEQ ID NOs: 129 and 133, respectively. In some embodiments, the anti-CD137 antibodies described herein comprise heavy and light chains comprising the amino acid sequences set forth in SEQ ID NOs: 130 and 133, respectively. In some embodiments, the anti-CD137 antibodies described herein comprise heavy and light chains comprising the amino acid sequences set forth in SEQ ID NOs: 131 and 133, respectively. In some embodiments, the anti-CD137 antibodies described herein comprise heavy and light chains comprising the amino acid sequences set forth in SEQ ID NOs: 132 and 133, respectively.

In some embodiments, the anti-CD137 antibodies described herein comprise heavy and light chains comprising amino acid sequences having at least 80%, at least 85%, at least 90%, at least 95%, at least, 96%, at least 97%, at least 98%, or at least 99% identity to SEQ ID NOs: 129 and 133, respectively. In some embodiments, the anti-CD137 antibodies described herein comprise heavy and light chains comprising amino acid sequences having at least 80%, at least 85%, at least 90%, at least 95%, at least, 96%, at least 97%, at least 98%, or at least 99% identity to SEQ ID NOs: 130 and 133, respectively. In some embodiments, the anti-CD137 antibodies described herein comprise heavy and light chains comprising amino acid sequences having at least 80%, at

least 85%, at least 90%, at least 95%, at least, 96%, at least 97%, at least 98%, or at least 99% identity to SEQ ID NOs: 131 and 133, respectively. In some embodiments, the anti-CD137 antibodies described herein comprise heavy and light chains comprising amino acid sequences having at least 80%, at least 85%, at least 90%, at least 95%, at least, 96%, at least 97%, at least 98%, or at least 99% identity to SEQ ID NOs: 132 and 133, respectively.

CDR Numbering Systems

The system described by Kabat, also referred to as "numbered according to Kabat," "Kabat numbering", "Kabat definitions", and "Kabat labeling," provides an unambiguous residue numbering system applicable to any variable domain of an antibody, and provides precise residue boundaries defining the three CDRs of each chain. (Kabat et al., Sequences of Proteins of Immunological Interest, National Institutes of Health, Bethesda, Md. (1987) and (1991), the contents of which are incorporated by reference in their entirety. These CDRs are referred to as Kabat CDRs and comprise about residues 24-34 (CDR1), 50-56 (CDR2), and 89-97 (CDR3) in the light chain variable domain, and 31-35 (CDR1), 50-65 (CDR2), and 95-102 (CDR3) in the heavy chain variable domain. When the CDRs are defined according to Kabat, the light chain FR residues are positioned at about residues 1-23 (LCFR1), 35-49 (LCFR2), 57-88 (LCFR3), and 98-107 (LCFR4), and the heavy chain FR residues are positioned about at residues 1-30 (HCFR1), 36-49 (HCFR2), 66-94 (HCFR3), and 103-113 (HCFR4) in the heavy chain residues. The "EU index as in Kabat" refers to the residue numbering of the human IgG1 EU antibody.

Other CDR numbering systems are also used in the art (see, for example, **Table A**). Chothia and coworkers found that certain sub-portions within Kabat CDRs adopt nearly identical peptide backbone conformations, despite having great diversity at the level of amino acid sequence. (Chothia et al. (1987) J. Mol. Biol. 196: 901-917; and Chothia et al. (1989) Nature 342: 877-883). These sub-portions were designated as L1, L2, and L3 or H1, H2, and H3 where the "L" and the "H" designates the light chain and the heavy chains regions, respectively. These CDRs can be referred to as "Chothia CDRs," "Chothia numbering," or "numbered according to Chothia," and comprise about residues 24-34 (CDR1), 50-56 (CDR2), and 89-97 (CDR3) in the light chain variable domain, and 26-32 (CDR1), 50-56 or 52-56 (CDR2), and 95-102 (CDR3) in the heavy chain variable domain. Mol. Biol. 196:901-917 (1987).

The system described by MacCallum, also referred to as “numbered according to MacCallum,” or “MacCallum numbering” comprises about residues 30-36 (CDR1), 46-55 (CDR2), and 89-96 (CDR3) in the light chain variable domain, and 30-35 (CDR1), 47-58 (CDR2), and 93-101 (CDR3) in the heavy chain variable domain. MacCallum et al. ((1996) J. Mol. Biol. 262(5):732-745).

The system described by AbM, also referred to as “numbering according to AbM,” or “AbM numbering" comprises about residues 24-34 (CDR1), 50-56 (CDR2) and 89-97 (CDR3) in the light chain variable domain, and 26-35 (CDR1), 50-58 (CDR2), and 95-102 (CDR3) in the heavy chain variable domain.

The IMGT (INTERNATIONAL IMMUNOGENETICS INFORMATION SYSTEM) numbering of variable regions can also be used, which is the numbering of the residues in an immunoglobulin variable heavy or light chain according to the methods of the IMGT, as described in Lefranc, M.-P., "The IMGT unique numbering for immunoglobulins, T cell Receptors and Ig-like domains", The Immunologist, 7, 132-136 (1999), and is expressly incorporated herein in its entirety by reference. As used herein, "IMGT sequence numbering" or “numbered according to IMTG,” refers to numbering of the sequence encoding a variable region according to the IMGT. For the heavy chain variable domain, when numbered according to IMGT, the hypervariable region ranges from amino acid positions 27 to 38 for CDR1, amino acid positions 56 to 65 for CDR2, and amino acid positions 105 to 117 for CDR3. For the light chain variable domain, when numbered according to IMGT, the hypervariable region ranges from amino acid positions 27 to 38 for CDR1, amino acid positions 56 to 65 for CDR2, and amino acid positions 105 to 117 for CDR3.

In some embodiments of the anti-CD137 antibodies described herein, the CDRs recited herein comprise about residues 24-34 (CDR1), 50-56 (CDR2), and 89-97 (CDR3) in the light chain variable domain, and 27-35 (CDR1), 49-60 (CDR2), and 93-102 (CDR3) in the heavy chain variable domain, when numbered according to Chothia numbering. In some embodiments, CDR2 in the light chain variable domain can comprise amino acids 49-56, when numbered according to Chothia numbering.

Table A: CDR Definitions

	CDRH1	CDRH2	CDRH3	CDRL1	CDRL2	CDRL3
Kabat	31-35	50-65	95-102	24-34	50-56	89-97

Alternative CDRs numbered according to Chothia	27-35	49-60	93-102	24-34	50-56	89-97
Chothia	26-32	52-56 or 50-56	95-102	24-34	50-56	89-97
MacCallum	30-35	47-58	93-101	30-36	46-55	89-96
AbM	26-35	50-58	95-102	24-34	50-56	89-97
IMGT	27-38	56-65	105-117	27-38	56-65	105-117

In some aspects and embodiments of the anti-CD137 antibodies described herein, the antibody or antigen-binding portion thereof comprises a heavy chain variable region comprising an amino acid sequence that is at least 90% identical (*e.g.*, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95, at least 96%, at least 97%, at least 98%, or at least 99% identical) to SEQ ID NO: 4 and/or a light chain variable region comprising an amino acid sequence that is at least 90% identical (*e.g.*, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical) to SEQ ID NO: 6. In some such embodiments, the heavy chain variable region comprises an amino acid sequence that differs by 15 amino acids or less, 14 amino acids or less, 13 amino acids or less, 12 amino acids or less, 11 amino acids or less, 10 amino acids or less, 9 amino acids or less, 8 amino acids or less, 7 amino acids or less, 6 amino acids or less, 5 amino acids or less, 4 amino acids or less, 3 amino acids or less, 2 amino acids or less, or 1 amino acid from SEQ ID NO: 4. In some such embodiments, the light chain variable region comprises an amino acid sequence that differs by 15 amino acids or less, 14 amino acids or less, 13 amino acids or less, 12 amino acids or less, 11 amino acids or less, 10 amino acids or less, 9 amino acids or less, 8 amino acids or less, 7 amino acids or less, 6 amino acids or less, 5 amino acids or less, 4 amino acids or less, 3 amino acids or less, 2 amino acids or less, or 1 amino acid from SEQ ID NO: 6.

In some embodiments, the CDRs of the antibody or antigen-binding portion thereof comprise about residues 24-34 (CDR1), 50-56 (CDR2), and 89-97 (CDR3) in the light chain variable domain of SEQ ID NO: 6, and 27-35 (CDR1), 49-60 (CDR2), and 93-102 (CDR3) in the heavy chain variable domain of SEQ ID NO: 4, when numbered according to Chothia

numbering. In some embodiments, CDR2 in the light chain variable domain of SEQ ID NO: 6 can comprise amino acids 49-56, when numbered according to Chothia numbering.

The disclosure also provides, in some embodiments, an antibody or antigen-binding portion thereof that comprises heavy chain CDRs of the heavy chain variable region of SEQ ID NO: 4, and light chain CDRs of the light chain variable region of SEQ ID NO: 6, wherein the heavy and light chain CDR residues are numbered according to Kabat.

The disclosure also provides, in some embodiments, an antibody or antigen-binding portion thereof that comprises heavy chain CDRs of the heavy chain variable region of SEQ ID NO: 4, and light chain CDRs of the light chain variable region of SEQ ID NO: 6, wherein the heavy and light chain CDR residues are numbered according to Chothia.

The disclosure also provides, in some embodiments, an antibody or antigen-binding portion thereof that comprises heavy chain CDRs of the heavy chain variable regions of SEQ ID NO: 4, and light chain CDRs of the light chain variable region of SEQ ID NO: 6, wherein the heavy and light chain CDR residues are numbered according to MacCallum.

The disclosure also provides, in some embodiments, an antibody or antigen-binding portion thereof that comprises heavy chain CDRs of the heavy chain variable regions of SEQ ID NO: 4, and light chain CDRs of the light chain variable region of SEQ ID NO: 6, wherein the heavy and light chain CDR residues are numbered according to AbM.

The disclosure also provides, in some embodiments, an antibody or antigen-binding portion thereof that comprises heavy chain CDRs of the heavy chain variable regions of SEQ ID NO: 4, and light chain CDRs of the light chain variable region of SEQ ID NO: 6, wherein the heavy and light chain CDR residues are numbered according to IMGT.

Characterization and Functions of CD137 Binding Antibodies

I. Affinity

In some embodiments, the formulations of the disclosure comprise an anti-CD137 antibody described herein that binds human CD137 with an affinity (KD) of about 40-100 nM (*e.g.*, between about 40 nM and about 100 nM) as determined by an antigen-binding assay. In some embodiments, the formulations of the disclosure comprise an anti-CD137 antibody described herein that binds human CD137 with an affinity (KD) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM) as determined by an antigen-binding assay. In some embodiments, the formulations of

the disclosure comprise an anti-CD137 antibody described herein that binds human CD137 with an affinity (KD) of about 45-95 nM, 50-90 nM, 55-85 nM, 60-80 nM, 65-75 nM, 55-75 nM, 40-70 nM, 50-80 nM, or 60-90 nM as determined by an antigen-binding assay.

In some embodiments, the antigen-binding assay determines a binding affinity of the anti-CD137 antibody for a CD137 polypeptide. In some embodiments, the antigen binding assay is surface plasmon resonance. Accordingly, in some embodiments an anti-CD137 antibody described herein binds human CD137 with an affinity (KD) of about 40-100 nM (*e.g.*, between about 40 nM and about 100 nM) as determined using surface plasmon resonance. In some embodiments, an anti-CD137 antibody described herein binds human CD137 with an affinity (KD) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM) as determined using surface plasmon resonance. In some embodiments, an anti-CD137 antibody described herein binds human CD137 with an affinity (KD) of about 45-95 nM, 50-90 nM, 55-85 nM, 60-80 nM, 65-75 nM, 55-75 nM, 40-70 nM, 50-80 nM, or 60-90 nM as determined using surface plasmon resonance.

The phrase "surface plasmon resonance" includes an optical phenomenon that allows for the analysis of real-time biospecific interactions by detection of alterations in protein concentrations within a biosensor matrix, for example using the BIAcore system (Pharmacia Biosensor AB, Uppsala, Sweden and Piscataway, NJ). For further descriptions, see Jönsson, U., et al. (1993) Ann. Biol. Clin. 51:19-26; Jönsson, U., et al. (1991) Biotechniques 11:620-627; Johnsson, B., et al. (1995) J. Mol. Recognit. 8:125-131; and Johnnson, B., et al. (1991) Anal. Biochem. 198:268-277.In some embodiments, the antigen binding assay is biolayer interferometry (BLI). Accordingly, in some embodiments an anti-CD137 antibody described herein binds human CD137 with an affinity (KD) of about 40-100 nM (*e.g.*, between about 40 nM and about 100 nM) as determined using biolayer interferometry. In some embodiments, an anti-CD137 antibody described herein binds human CD137 with an affinity (KD) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM) as determined using biolayer interferometry. In some embodiments, an anti-CD137 antibody described herein binds human CD137 with an affinity (KD) of about 45-95 nM, 50-90 nM, 55-85 nM, 60-80 nM, 65-75 nM, 55-75 nM, 40-70 nM, 50-80 nM, or 60-90 nM as determined using biolayer interferometry.

The phrase “biolayer interferometry” or “BLI” includes an optical phenomenon that allows for the measurement of sub-nanometer changes in the thickness of its optical layer detection surface. In some embodiments, biomolecules binds at a sensor surface and change the optical

layer thickness. The magnitude of the optical layer thickness change is proportional to the mass or molecular weight of the binding molecule. In some embodiments, CD137 is immobilized to the sensor surface to measure binding by an antibody, wherein binding creates a changes in the molecular weight to produce a corresponding change in the optical layer thickness. In some embodiments, BLI is performed with an OCTET system (FORTE BIO®).

II. Immune Cell Effects

In some embodiments, the formulations of the disclosure comprise an anti-CD137 antibody described herein that induces or enhances cytokine production by an immune cell as determined by a cytokine assay. In some embodiments, the cytokine assay determines an amount of at least one cytokine secreted from an immune cell contacted with the anti-CD137 antibody, wherein an increase in the amount of the at least one cytokine indicates induction or enhancement of cytokine production by the anti-CD137 antibody. In some embodiments, an increase in cytokine production is at least 1 fold, 2 fold, 3 fold, 4 fold or 5 fold more compared to a control antibody (*e.g.*, an antibody that does not bind to CD137 and does not induce cytokine production).

In some embodiments, an anti-CD137 antibody described herein induces or enhances cytokine production by an immune cell as determined by a cytokine assay, wherein the cytokine assay comprises the following steps:

(i) contacting the immune cell with the anti-CD137 antibody; and

(ii) determining an amount of at least one cytokine produced by the immune cell,

wherein an increase in the amount of the at least one cytokine indicates the anti-CD137 antibody induces or enhances cytokine production by the immune cell.

In some embodiments, an anti-CD137 antibody described herein induces or enhances cytokine production by an immune cell as determined by a cytokine assay, wherein the cytokine assay comprises the following steps:

(i) contacting the immune cell with an anti-CD137 antibody; and

(ii) determining an amount of at least one cytokine produced by the immune cell, and

(iii) comparing the amount of the at least one cytokine produced by the immune cell to an amount secreted from a reference immune cell,

wherein the reference immune cell is contacted with a control antibody, and wherein an increase in the amount of the at least one cytokine produced from the immune cell relative to the

reference immune cell indicates induction or enhancement of human CD137-mediated cytokine production.

In some embodiments, an anti-CD137 antibody described herein induces or enhances cytokine production by an immune cell as determined by a cytokine assay, wherein the cytokine assay comprises the following steps:

(i) contacting an immune cell with an anti-CD137 antibody;

(ii) determining an amount of at least one cytokine produced by the immune cell, and

(iii) comparing the amount of the at least one cytokine produced by the immune cell to an amount or level secreted from a reference immune cell,

wherein the reference immune cell is not contacted with the anti-CD137 antibody, and wherein an increase in the amount of the at least one cytokine produced from the immune cell relative to the reference immune cell indicates induction or enhancement of human CD137-mediated cytokine production by the immune cell.

In some embodiments, the at least one cytokine is selected from a group consisting of IL-2, IFN-γ, TNFα, IL-13, and combinations thereof. In some embodiments, the cytokine is IL-2. In some embodiments, the cytokine is IFN-γ. In some embodiments, the cytokine is TNFα. In some embodiments, the cytokine is IL-13. In some embodiments, an anti-CD137 antibody induces or enhances IL-2 production. In some embodiments, an anti-CD137 antibody induces or enhances TNFα production. In some embodiments, an anti-CD137 antibody induces or enhances IL-13 production. In some aspects, the cytokine produced is IL-2. In some aspects, the cytokine produced is TNFα. In some aspects, the cytokine produced is IL-13. In some aspects, the cytokine produced is IFN-γ. In some aspects, the cytokine produced is IL-2 and TNFα. In some aspects, the cytokine produced is IL-2 and IL-13. In some aspects, the cytokine produced is IL-2 and IFN-γ. In some aspects, the cytokine produced is TNFα and IL-13. In some aspects, the cytokine produced is TNFα and IFN-γ. In some aspects, the cytokine produced is IL-13 and IFN-γ. In some aspects, the cytokine produced is IL-2, TNFα and IL-13. In some aspects, the cytokine produced is IL-2, TNFα and IFN-γ. In some aspects, the cytokine produced is IFN-γ, TNFα and IL-13.

In some embodiments, the immune cell is a T cell. In some embodiments, the reference immune cell is a T cell. In some embodiments the T cell is a CD8+ T cell.

In some embodiments, the cytokine assay is a cytokine bead array assay. A cytokine bead array assay is a bead-based immunoassay that allows for multianalyte flow cytometric determination of multiple cytokines in a sample. The use of microspheres of different size or color is the basis of a cytokine bead array assay, wherein each microsphere (or "bead") is coated with an antibody that specifically binds to an antigen (*e.g.*, a cytokine). Antibody-coated beads are then introduced to a sample in combination with detector antibodies. The bead:antigen:detector antibody complexes are then analyzed by flow cytometry. Commercially available cytokine bead array assays include, but are not limited to, BD™ Cytometric Bead Array Systems (BD Biosciences) and LUMINEX® Assays (R&D Systems). In some embodiments, induction or enhancement of human CD137-mediated cytokine production is determined by a cytokine bead array assay. In some embodiments, induction or enhancement of human CD137-mediated cytokine production is determined by a Luminex® Assay.

In some embodiments, the cytokine assay is a Meso Scale Discovery (MSD) assay (Meso Scale Diagnostics; Rockville, MD). An MSD assay is a commercially available assay based on detection of electrochemiluminescent-labeled antibodies that specifically bind to an antigen (*e.g.*, a cytokine) of interest. An MSD assay comprises high binding carbon electrodes in the bottom of microplate wells that allow for attachment of biological reagents (*e.g.*, capture antibodies specific for a cytokine). MSD assays use electrochemiluminescent labels that are conjugated to detection antibodies. A sample is added to the microplate wells and electricity is applied to the plate electrodes by an MSD instrument leading to light emission by the electrochemiluminescent labels. Light intensity is measured to quantify analytes (*e.g.*, cytokines) in the sample. In some embodiments, induction or enhancement of human CD137-mediated cytokine production is determined by a Meso Scale Discovery (MSD) assay.

In some embodiments, an anti-CD137 antibody described herein induces or enhances T cell activation as determined by a T cell activation assay. In some embodiments, the T cell activation assay determines an amount of at least one cytokine secreted from T cells contacted with an anti-CD137 antibody described herein, wherein an increase in the amount of the at least one cytokine indicates induction or enhancement of T cell activation. In some embodiments, an increase in cytokine production is at least 1 fold, 2 fold, 3 fold, 4 fold or 5 fold more compared to a control antibody (*e.g.*, an antibody that does not bind to CD137 and does not induce cytokine production).

In some embodiments, an anti-CD137 antibody described herein induces or enhances T cell activation as determined by a T cell activation assay, wherein the T cell activation assay comprises the following steps:

(i) isolating T cells from a subject;

(ii) contacting the T cells with an anti-CD137 antibody; and

(iii) determining an amount of at least one cytokine secreted by the T cells after (ii),

wherein an increase in the level of the at least one cytokine indicates the anti-CD137 antibody induces or enhances T cell activation.

In some embodiments, an anti-CD137 antibody described herein induces or enhances T cell activation as determined by a T cell activation assay, wherein the T cell activation assay comprises the following steps:

(i) isolating T cells from a subject;

(ii) contacting the T cells with an anti-CD137 antibody;

(iii) determining an amount of at least one cytokine secreted by the T cells; and

(iv) comparing the amount of the at least one cytokines produced by the T cells to an amount or level secreted from reference T cells,

wherein the reference T cells are not contacted with the anti-CD137 antibody, and wherein an increase in the amount of the at least one cytokine produced from the T cells relative to the reference T cells indicates the anti-CD137 antibody induces or enhances T cell activation.

In some embodiments, an anti-CD137 antibody described herein induces or enhances T cell activation as determined by a T cell activation assay, wherein the T cell activation assay comprises the following steps:

(i) isolating T cells from a subject;

(ii) contacting the T cells with an anti-CD137 antibody;

(iii) determining an amount of at least one cytokine secreted by the T cells; and

(iv) comparing the amount of the at least one cytokine produced by the T cells to an amount secreted from reference T cells,

wherein the reference T cells are contacted with a control antibody, and wherein an increase in the amount of the at least one cytokine produced from the T cells relative to the reference T cells indicates the anti-CD137 antibody induces or enhances T cell activation.

In some embodiments, the T cell activation assay comprises determining the level of at least one cytokine secreted by the T cells after contact with an anti-CD137 antibody described herein, wherein the at least one cytokine is selected from the group consisting of IL-2, IFN-γ, TNFα and IL-13. In some embodiments, the cytokine is IL-2. In some embodiments, the cytokine is IFN-γ. In some embodiments, the cytokine is TNFα. In some embodiments, the cytokine is IL-13. In some embodiments, the T cell activation assay comprises a cytokine assay, such as those described herein, to determine the amount of the at least one cytokine. In some embodiments, the cytokine produced is IL-2. In some embodiments, the cytokine produced is TNFα. In some embodiments, the cytokine produced is IL-13. In some embodiments, the cytokine produced is IFN-γ. In some embodiments, the cytokine produced is IL-2 and TNFα. In some embodiments, the cytokine produced is IL-2 and IL-13. In some embodiments, the cytokine produced is IL-2 and IFN-γ. In some embodiments, the cytokine produced is TNFα and IL-13. In some embodiments, the cytokine produced is TNFα and IFN-γ. In some embodiments, the cytokine produced is IL-13 and IFN-γ. In some embodiments, the cytokine produced is IL-2, TNFα and IL-13. In some embodiments, the cytokine produced is IL-2, TNFα and IFN-γ. In some embodiments, the cytokine produced is IFN-γ, TNFα and IL-13.

In some embodiments, an anti-CD137 antibody described herein induces or enhances T cell activation as determined by a T cell activation assay, wherein the T cell activation assay comprises detecting surface expression of at least one activation marker on T cells, and wherein an increase in the expression level of the at least one activation marker indicates induction or enhancement of T cell activation. In some embodiments, "increase in surface expression" refers to at least a 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or 100% increase in surface expression relative to surface expression in the presence of a control antibody or in the absence of an antibody.

In some embodiments, an anti-CD137 antibody described herein induces or enhances T cell activation as determined by a T cell activation assay *in vitro*, wherein the T cell activation assay comprises the following steps:

(i) isolating T cells from a subject;

(ii) contacting the T cells with an anti-CD137 antibody; and

(iii) detecting surface expression of at least one activation marker on the T cells,

wherein an increase in surface expression of at least one activation marker indicates the anti-CD137 antibody induces or enhances T cell activation.

In some embodiments, an anti-CD137 antibody described herein induces or enhances T cell activation as determined by a T cell activation assay, wherein the T cell activation assay comprises the following steps:

(i) isolating T cells from a subject;

(ii) contacting the T cells with an anti-CD137 antibody;

(iii) determining surface expression of at least one activation marker on the T cells; and

(iv) comparing surface expression of at least one activation marker on the T cells to surface expression of the at least one activation marker on reference T cells,

wherein the reference T cells are not contacted with the anti-CD137 antibody, and wherein an increase in surface expression of at least one activation marker on the T cells relative to the reference T cells indicates the anti-CD137 antibody induces or enhances T cell activation.

In some embodiments, an anti-CD137 antibody described herein induces or enhances T cell activation as determined by a T cell activation assay, wherein the T cell activation assay comprises the following steps:

(i) isolating T cells from a subject;

(ii) contacting the T cells with an anti-CD137 antibody;

(iii) determining surface expression of at least one activation marker on the T cells,

(iv) comparing the surface expression of the at least one activation marker on the T cells to surface expression of the at least one activation marker on reference T cells,

wherein the reference T cells are contacted with a control antibody, and wherein an increase in surface expression of the at least one activation marker on the T cells relative to surface expression of the at least one activation marker on the reference T cells indicates the anti-CD137 antibody induces or enhances T cell activation.

In some embodiments, an anti-CD137 antibody described herein induces or enhances T cell activation as determined by a T cell activation assay *in vivo*, wherein the T cell activation assay comprises the following steps:

(i) administering the anti-CD137 antibody to a subject;

(ii) isolating T cells from the subject; and

(iii) detecting surface expression of at least one activation marker on the T cells,

wherein an increase in surface expression of at least one activation marker indicates the anti-CD137 antibody induces or enhances CD137-mediated T cell activation.

In some embodiments, an anti-CD137 antibody described herein induces or enhances T cell activation as determined by a T cell activation assay, wherein the T cell activation assay comprises the following steps:

(i) administering the anti-CD137 antibody to a subject;

(ii) isolating T cells from the subject;

(iii) determining surface expression of at least one activation marker on the T cells after; and

(iv) comparing surface expression of the at least one activation marker on the T cells to surface expression of the at least one activation marker on reference T cells,

wherein the reference T cells are isolated from a subject not administered the anti-CD137 antibody, and wherein an increase in surface expression of the at least one activation marker on the T cells relative to the reference T cells indicates the anti-CD137 antibody induces or enhances T cell activation.

In some embodiments, an anti-CD137 antibody described herein induces or enhances T cell activation as determined by a T cell activation assay, wherein the T cell activation assay comprises the following steps:

(i) administering the anti-CD137 antibody to a subject;

(ii) isolating T cells from the subject;

(iii) determining surface expression of at least one activation marker on the T cells; and

(iv) comparing surface expression of the at least one activation marker on the T cells to surface expression of the at least one activation marker on reference T cells,

wherein the reference T cells are isolated from a subject contacted with a control antibody, and wherein an increase in surface expression of the at least one activation marker on the T cells relative to surface expression of the at least one activation marker on the reference T cells indicates the anti-CD137 antibody induces or enhances T cell activation.

In some embodiments, an anti-CD137 antibody described herein does not induce or enhance intrahepatic T cell activation as determined by a T cell activation assay *in vivo*, wherein the T cell activation assay comprises the following steps:

(i) administering the anti-CD137 to a subject;

(ii) isolating T cells from the liver of the subject;

(iii) detecting surface expression of at least one activation marker on the T cells; and

(iv) comparing the surface expression of the at least one activation marker on the T cells to surface expression of the at least one activation marker on reference T cells,

wherein the reference T cells are isolated from a subject not administered the anti-CD137 antibody, optionally, wherein the reference T cells are isolated from a subject administered a control antibody, and wherein an absence of an increase in surface expression of the at least one activation marker on the T cells relative to surface expression of the at least one activation marker on the reference T cells indicates the anti-CD137 antibody induces or enhances T cell activation.

In some embodiments, an anti-CD137 antibody described herein does not induce or enhance intrasplenic T cell activation as determined by a T cell activation assay *in vivo*, wherein the T cell activation assay comprises the following steps:

(i) administering the anti-CD137 to a subject;

(ii) isolating T cells from the spleen of the subject;

(iii) detecting surface expression of at least one activation marker on the T cells; and

(iv) comparing surface expression of the at least one activation marker on the T cells to surface expression of the at least one activation marker on reference T cells,

wherein the reference T cells are isolated from a subject not administered the anti-CD137 antibody, optionally, wherein the reference T cells are isolated from a subject administered a control antibody, and wherein an absence in an increase in surface expression of the at least one activation marker on the T cells relative to surface expression of the at least one activation marker on the reference T cells indicates the anti-CD137 antibody induces or enhances T cell activation.

In some embodiments "does not induce or enhance" is intended to refer to the absence of an activity (*e.g.*, T cell activation) or a lack of increase of an activity relative to an increase by a reference antibody.

In some embodiments, a surface expression of a T cell activation marker is equivalent to the surface expression in the absence of an antibody. In some embodiments a surface expression of a T cell activation marker is less than the surface expression in the presence of a reference antibody that induces or enhance surface expression at least 1 fold, 5 fold, 10 fold, 50 fold, or 100 fold higher compared to surface expression in the absence of an antibody.

In some embodiments, the at least one activation marker is selected from the group consisting of CD25, CD69 and CD40L. In some embodiments, the one or more activation markers is CD25.

In some embodiments, T cells are isolated from a subject having a tumor. In some embodiments, the T cells are isolated from the tumor. In some embodiments, the control antibody is an isotype control antibody.

In some embodiments, an anti-CD137 antibody described herein induces or enhances infiltration of one or more immune cells into a tumor microenvironment as determined by an immune cell infiltration assay. In some embodiments, an anti-CD137 antibody described herein decreases infiltration of one or more immune cells into a tumor microenvironment as determined by an immune cell infiltration assay.

In some embodiments, the immune cell infiltration assay determines a quantity of immune cells expressing one or more immune cell markers in a tumor. In some embodiments, the one or more immune cell markers is labeled with an antibody. In some embodiments, the one or more immune cell markers is selected from the group consisting of CD45, CD25, FOXP3, CD4, CD8, F4/80, CD11b, TIGIT and PD-1. In some embodiments, the quantity of immune cells expressing the one or more immune cell markers in a tumor is determined by flow cytometry. Methods of quantifying immune cells expressing one or more immune cell markers by flow cytometry are known in the art.

In some embodiments, the anti-CD137 antibody induces or enhances infiltration of one or more immune cells into a tumor microenvironment relative to a reference antibody, as determined by an immune cell infiltration assay. In some embodiments, the reference antibody is an antibody comprising the same isotype as the anti-CD137 antibody and does not specifically bind to CD137. In some embodiments, the reference antibody is an antibody comprising the same isotype as the anti-CD137 antibody and specifically binds to CD137. In some embodiments, the reference antibody is an antibody comprising the different isotype as the anti-CD137 antibody and does not specifically bind to CD137. In some embodiments, the reference antibody is an antibody comprising a different isotype as the anti-CD137 antibody and specifically binds to CD137.

In some embodiments, an anti-CD137 antibody described herein increases infiltration of immune cells expressing CD45 into a tumor microenvironment in a subject as determined by an immune cell infiltration assay, wherein the assay comprises the following steps:

(i) administering the anti-CD137 antibody to a subject having a tumor;

(ii) obtaining a sample of the tumor;

(iii) contacting the sample with an fluorescently-labeled detection antibody that specifically binds to CD45, wherein the detection antibody fluorescently-labels the immune cells expressing CD45; and

(iv) determining a quantity of the fluorescently-labeled immune cells expressing CD45 by flow cytometry,

wherein an increase in the quantity of fluorescently-immune cells expressing CD45 in the tumor indicates the anti-CD137 antibody induces or enhances infiltration of immune cells into the tumor microenvironment. In some embodiments, an increase in the quantity of immune cells expressing CD45 is at least 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, or 80% of total cells in the tumor microenvironment.

In some embodiments, an anti-CD137 antibody described herein reduces or inhibits infiltration of one or more immune cells into a tumor microenvironment as determined by an immune cell infiltration assay. In some embodiments, the anti-CD137 antibody decreases infiltration of one or more immune cells into a tumor microenvironment relative to a reference antibody, as determined by an immune cell infiltration assay. In some embodiments, the reference antibody is an antibody comprising the same isotype as the anti-CD137 antibody and does not specifically bind to CD137. In some embodiments, the reference antibody is an antibody comprising the same isotype as the anti-CD137 antibody and specifically binds to CD137. In some embodiments, the reference antibody is an antibody comprising the different isotype as the anti-CD137 antibody and does not specifically bind to CD137. In some embodiments, the reference antibody is an antibody comprising a different isotype as the anti-CD137 antibody and specifically binds to CD137. In some embodiments, a decrease in immune cells is less than 40%, 35%, 30%, 25%, 20%, 15%, 10%, or 5% of total cells in a tumor microenvironment.

In some embodiments, an anti-CD137 antibody described herein decreases infiltration of tumor associated macrophages into a tumor microenvironment in a subject as determined by an immune cell infiltration assay, wherein the assay comprises the following steps:

(i) obtaining a sample of the tumor;

(ii) contacting the sample with one or more antibodies that label the tumor associated macrophage, wherein the one or more antibodies specifically bind to an immune cell marker selected from the group consisting of F4/80, CD11b, CD45 and a combination thereof; and

(iii) determining a quantity of the labeled tumor associated macrophages by flow cytometry. In some embodiments, tumor-associated macrophages are less than 40%, 35%, 30%, 25%, 20%, 15%, 10%, or 5% of immune cells in the tumor microenvironment. In some embodiments, tumor-associated macrophages express F4/80, CD11b and CD45.

In some embodiments, an anti-CD137 antibody described herein decreases infiltration of T regulatory cells (Tregs) into a tumor microenvironment in a subject as determined by an immune cell infiltration assay, wherein the assay comprises the following steps:

(i) obtaining a sample of the tumor;

(ii) contacting the sample with one or more antibodies that label the tumor associated macrophage, wherein the one or more antibodies specifically bind to an immune cell marker selected from the group consisting of CD25, FOXP-3, CD4 and a combination thereof; and

(iii) determining a quantity of the labeled Treg cells by flow cytometry. In some embodiments, Treg cells are less than 35%, 30%, 25%, 20%, 15%, 10%, or 5% of CD4+ T cells in the tumor microenvironment. In some embodiments, Treg cells express CD4, FOXP-3 and CD25.

In some embodiments, an anti-CD137 antibody described herein protects T cells from T cell exhaustion and/or reverses T cell exhaustion as determined by a T cell exhaustion assay. Exhausted T cells can be distinguished from other T cell dysfunctions such as anergy and senescence based on their underlying molecular mechanisms (Crespo et al., (2013) Curr Opin Immunol 25(2):241-221). Whereas anergy occurs during priming due to the absence of costimulatory signals and senescence is growth arrest after extensive proliferation, exhausted T cells arise from T cells which initially gained and provided T cell effector function, but that exhibit a gradual deterioration of T cell effector function due to continuous T cell receptor (TCR) stimulation from persistent antigen and inflammatory mediators, both of which commonly occur in tumors (Wherry & Kurachi (2015) Nat Rev Immunol 15(8):486–99). Hallmarks of T cell exhaustion include, but are not limited to, continuous deterioration of *in vivo* and/or *ex vivo* T cell function, an increased expression of multiple inhibitory receptors (IRs) (*e.g.*, PD-1, CTLA-4, LAG-3, TIM-3, CD244, CD160, TIGIT), progressive loss or decrease of effector cytokine

secretion (*e.g.*, IL-2, interferon gamma (IFN-γ), tumor necrosis factor alpha (TNFα)), loss or decrease of CC chemokine (β-chemokine) production, poor responsiveness to IL-7 and IL-15, loss or decrease of proliferative capacity, loss or decrease of *in vivo* and/or *ex vivo* cytolytic activity, altered cell metabolism and a different transcriptional profile relative to non-exhausted T cells. Severely exhausted T cells can succumb to deletion (Yi et al., (2010) Immunology 129(4):474-481).

In some embodiments, an anti-CD137 antibody described herein protects T cells from T cell exhaustion and/or reverses T cell exhaustion as determined by a T cell exhaustion assay wherein the T cell exhaustion assay determines an amount or level of one or more effector cytokines secreted from T cells treated with an anti-CD137 antibody described herein, wherein the amount or level of the one or more effector cytokines indicates protection from or reversion of T cell exhaustion. In some embodiments, the T cell exhaustion assay comprises the following steps:

(i) isolating of T cells from a subject (*e.g.*, a human subject);

(ii) contacting the T cells with an antigen that induces T cell exhaustion;

(iii) contacting the T cells with the anti-CD137 antibody;

(iv) determining an amount of one or more effector cytokines secreted from the T cells; and;

(v) comparing the amount or level of the one or more effector cytokines secreted from the T cells to an amount or level secreted from reference T cells,

wherein the reference T cells are not contacted with the antigen that induces T cell exhaustion, and wherein the difference in the amount or level of the one or more effector cytokines secreted from the T cells and reference T cells indicates protection from or reversion of T cell exhaustion.

In some embodiments, the one or more effector cytokines is selected from IL-2, IFN-γ, and TNFα. In some embodiments, the amount or level of the one or more effector cytokines is determined by ELISA. ELISAs suitable for the determination of the amount or level of the one or more effector cytokines are known in the art. In some embodiments, the amount or level of the one or more effector cytokines is determined by Meso Scale Discovery. In some embodiments, the amount or level of the one or more effector cytokines is determined by any one of the cytokine production assays described herein.

The gradual dysfunction of exhausted T cells is accompanied by the expression of IRs, which transmit inhibitory signals to the nucleus upon interaction with ligands on target cells. Accordingly, in some embodiments, an anti-CD137 antibody described herein protects T cells from T cell exhaustion and/or reverses T cell exhaustion as determined by a T cell exhaustion assay wherein the T cell exhaustion assay determines an expression level of one or more inhibitory receptors on T cells treated with an anti-CD137 antibody described herein, wherein the expression level of the one or more inhibitory receptors indicates protection from or reversion of T cell exhaustion. In some embodiments, the T cell exhaustion assay comprises the following steps:

(i) isolating of T cells from a subject (*e.g.*, a human subject);

(ii) contacting the T cells with an antigen that induces T cell exhaustion;

(iii) contacting the T cells with the anti-CD137 antibody;

(iv) determining an expression level of one or more inhibitory receptors on T cells; and

(v) comparing the expression level of one or more inhibitory receptors on T cells to an amount or level secreted from reference T cells, wherein the reference T cells are not contacted with the antigen that induces T cell exhaustion, and wherein the difference in the expression level of one or more inhibitory receptors on T cells and reference T cells indicates protection from or reversion of T cell exhaustion.

In some embodiments, the one or more inhibitory receptors is selected from TIGIT and PD-1 In some embodiments, the expression level of the one or more inhibitory receptors is determined by flow cytometry. Methods to determine expression levels of inhibitory receptors on immune cells (*e.g.* T cells) by flow cytometry are known in the art.

In some embodiments, the amount of exhausted T cells is less than 20%, 15%, 10% or 5% of total CD8+ or CD4+ T cells in a tumor microenvironment.

Where the assays described herein refer to 'isolating T cells from a subject'; it is to be understood that the assay may suitably be performed on T cells previously isolated from a subject.

Where the assays described herein refer to (i) administering the anti-CD137 antibody to a subject and (ii) isolating T cells from the subject; it is to be understood that the assay may suitably be performed on T cells previously isolated from a subject to whom the anti-CD137 antibody has been administered.

Where the assays described herein refer to 'obtaining a sample of the tumor'; it is to be understood that the assay may suitably be performed on a sample of a tumor previously isolated from a subject.

Where the assays described herein refer to (i) administering the anti-CD137 antibody to a subject having a tumor and (ii) obtaining a sample of the tumor; it is to be understood that the assay may suitably be performed a sample of a tumor previously isolated from a subject to whom the anti-CD137 antibody has been administered.

III. Non-Ligand Binding

In some embodiments, the formulations of the disclosure comprise an anti-CD137 antibody described herein that binds to a non-ligand binding region of CD137, as determined by a ligand binding assay. A ligand binding assay (LBA) is an assay, or an analytic procedure, that provides a measure of the interactions that occur between two reactant molecules (*e.g.*, a receptor and ligand polypeptides). Suitably, the LBA provides a measure of the degree of affinity between the two reactant molecules (*e.g.*, a receptor and ligand polypeptides). For example, in some embodiments a ligand binding assay is used to determine the presence, rate, extent of binding, or combinations thereof, of a ligand molecule (*e.g.*, CD137L) to a receptor (*e.g.*, CD137). In some embodiments, to determine the presence, rate and/or extent of ligand binding to a receptor, a ligand binding assay comprises detecting the formation of a ligand:receptor complex. In some embodiments, to determine the presence, rate and/or extent of ligand binding to a receptor, a ligand binding assay comprises determining the dissociation of a ligand:receptor complex.

In some embodiments, the formation and/or dissociation of a ligand:receptor complex is determined by detection of a fluorescently-labeled ligand in complex with a receptor. In some embodiments, the formation and/or dissociation of a ligand:receptor complex is determined by detection and/or quantification of an amount of fluorescently-labeled receptor in complex with a ligand. In some embodiments, the formation and/or dissociation of a ligand:receptor complex is determined by detection and/or quantification of an amount of a fluorescently-labeled antibody that specifically binds to the ligand:receptor complex. Methods of detecting and quantifying fluorescence are known in the art and include, but are not limited to, fluorescence polarization (FP) and fluorescence anisotropy (FA).

In some embodiments, the formation and/or dissociation of a ligand:receptor complex is determined by detection and/or quantification of an amount of a radioactively-labeled ligand in complex with a receptor. In some embodiments, the formation and/or dissociation of a ligand:receptor complex is determined by detection and/or quantification of an amount of radioactively-labeled receptor in complex with a ligand. In some embodiments, the formation and/or dissociation of a ligand:receptor complex is determined by detection and/or quantification of an amount of a radioactively-labeled antibody that specifically binds to the ligand:receptor complex. Methods of detecting and quantifying radioactivity are known in the art and include, but are not limited to, quantitative autoradiography and scintillation counting.

In some embodiments, the formation and/or dissociation of a ligand:receptor complex is determined by detection and/or quantification of an amount of a bioluminescently-labeled ligand in complex with a receptor. In some embodiments, the formation and/or dissociation of a ligand:receptor complex is determined by detection and/or quantification of an amount of bioluminescently-labeled receptor in complex with a ligand. In some embodiments, the formation and/or dissociation of a ligand:receptor complex is determined by detection and/or quantification of an amount of a bioluminescently-labeled antibody that specifically binds to the ligand:receptor complex. Methods of detecting and quantifying bioluminescence are known in the art and include, but are not limited to, luminometry.

In some embodiment, formation and/or dissociation of the ligand:receptor complex is determined by surface plasmon resonance (SPR) as described *supra*.

In some embodiments, a ligand binding assay determines if an antibody that specifically binds to a receptor (*e.g.*, an anti-CD137 antibody) affects the formation of a ligand:receptor complex by determining the presence, rate and/or extent of ligand binding to the receptor in the presence of the antibody. In some embodiments, an antibody (*e.g.*, an anti-CD137 antibody) that specifically binds to a receptor (*e.g.*, CD137) and decreases, disrupts or blocks the formation of a ligand:receptor complex (*e.g.*, a CD137:CD137L complex) is known as a "ligand blocking antibody". In some embodiments, a "ligand blocking antibody" may decrease the formation of a ligand:receptor complex (*e.g.*, a CD137:CD137L complex) by at least 10%, at least 20%, at least 30%, at least 40% or at least 50% compared to the formation of the ligand:receptor complex (*e.g.*, the CD137:CD137L complex) which occurs in the absence of the ligand blocking antibody. In some embodiments, an antibody (*e.g.*, an anti-CD137 antibody) that specifically binds to a receptor

(*e.g.*, CD137) and does not decrease, disrupt or block the formation of a ligand:receptor complex (*e.g.*, a CD137:CD137L complex) is referred to as a "non-ligand blocking antibody". In some embodiments, a "non-ligand blocking antibody" may decrease the formation of a ligand:receptor complex (*e.g.*, a CD137:CD137L complex) by less than 10%, less than 5%, less than 2% or less than 1% compared to the formation of the ligand:receptor complex (*e.g.*, the CD137:CD137L complex) which occurs in the absence of the non-ligand blocking antibody. Accordingly, in some embodiments a ligand binding assay characterizes an antibody that binds to a receptor as a "ligand blocking antibody" or a "non-ligand blocking antibody".

In some embodiments, a ligand binding assay characterizes an antibody that specifically binds to a receptor and promotes the formation of a ligand:receptor complex. In some embodiments, a ligand binding assay characterizes an antibody that specifically binds to a receptor and stabilizes the formation of a ligand:receptor complex. In some embodiments, the induction and/or stabilization of the formation of a ligand:receptor complex by an antibody contributes to the antibody's agonistic effect. In some embodiments, an anti-CD137 antibody described herein agonizes CD137, as determined by a ligand binding assay.

In some embodiments, the formulations of the disclosure comprise an isolated anti-CD137 antibody, or antigen-binding fragment thereof, described herein, that binds to CD137 and induces CD137L binding as determined by a ligand binding assay (LBA).

In some embodiments, an isolated anti-CD137 antibody, or antigen-binding fragment thereof, described herein, binds to CD137 and induces CD137L binding as determined by a ligand binding assay, wherein the ligand binding assay comprises the following steps:

(i) combining an anti-CD137 antibody with CD137 and CD137L at various concentrations, wherein CD137 and CD137L form a CD137:CD137L complex, and

(ii) detecting the CD137:CD137L complex in the presence of the anti-CD137 antibody over time,

wherein an increase in CD137:CD137L complex in the presence of the anti-CD137 antibody indicates the anti-CD137 antibody induces CD137L binding to CD137. The increase in CD137:CD137L complex in the presence of the anti-CD137 antibody may be at least 1.5-fold, at least 2-fold, at least 5-fold, at least 10-fold, or at least 20-fold greater that the amount CD137:CD137L complex in the absence of the anti-CD137 antibody.

In some embodiments, an isolated anti-CD137 antibody, or antigen-binding fragment thereof, described herein, binds to a non-ligand binding region of CD137 as determined by a ligand binding assay, wherein the ligand binding assay comprises the following steps:

(i) combining an anti-CD137 antibody with CD137 and CD137L at various concentrations, wherein CD137 and CD137L form a CD137:CD137L complex, and

(ii) detecting the CD137:CD137L complex in the presence of the anti-CD137 antibody over time,

wherein no change in the CD137:CD137L complex in the presence of the anti-CD137 antibody indicates the anti-CD137 antibody binds to a non-ligand binding region of CD137. In some embodiments, less than a 2% change in CD137:CD137L complex indicates the anti-CD137 antibody binds to a non-ligand binding region of CD137. In some embodiments, less than a 5% change in CD137:CD137L complex indicates the anti-CD137 antibody binds to a non-ligand binding region of CD137. In some embodiments, less than a 10% change in CD137:CD137L complex indicates the anti-CD137 antibody binds to a non-ligand binding region of CD137.

In some embodiments, an anti-CD137 antibody described herein binds to a non-ligand binding region of CD137, as determined by biolayer interferometry. In some embodiments, an anti-CD137 antibody described herein binds to a non-ligand binding region of CD137, as determined by surface plasmon resonance imaging (SPRi). In some embodiments, CD137 and CD137L is sequentially applied to a sensor pre-loaded with an anti-CD137 antibody (i.e., the antibody is captured on a sensor). In some embodiments, the binding of an anti-CD137 antibody to a non-ligand binding region is indicated by an increase in response upon exposure to CD137L.

IV. Functions of CD137 Binding Antibodies

In some embodiments, the formulations of the disclosure comprise the anti-CD137 antibodies or antigen binding fragments thereof described herein that bind to human CD137. In some embodiments, the anti-CD137 agonist antibodies described herein bind to human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM) and inhibit or reduce T cell exhaustion. In some embodiments, the anti-CD137 agonist antibodies described herein bind to human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM) and induce or enhance T cell activation. In some embodiments, the anti-CD137 agonist antibodies described herein bind to human CD137 with an affinity (K_D) of

about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM) and induce or enhance cytokine production by immune cells. In some embodiments, the anti-CD137 agonist antibodies described herein bind to human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM) and induce or enhance T cell proliferation. In some embodiments, the anti-CD137 agonist antibodies described herein bind to human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM) and exhibit anti-tumor efficacy. In some embodiments, the anti-CD137 agonist antibodies described herein bind to human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM) and inhibit or reduce macrophage differentiation and/or activation. In some embodiments, the anti-CD137 agonist antibodies described herein bind to human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM) and induce or enhance NFκβ signaling. In some embodiments, the anti-CD137 agonist antibodies described herein bind to human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM) and induce or enhance immune cell infiltration into a tumor microenvironment. In some embodiments, the anti-CD137 agonist antibodies described herein bind to human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM) and do not induce hepatotoxicity. In some embodiments, the anti-CD137 agonist antibodies described herein bind to human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM) and bind to a non-ligand binding domain on extracellular CD137. In some embodiments, the anti-CD137 agonist antibodies described herein bind to human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM) and do not inhibit CD137 and CD137L interaction. In some embodiments, the anti-CD137 agonist antibodies described herein bind to human CD137 with an affinity (K_D) of about 30-100 nM (*e.g.*, between about 30 nM and about 100 nM) and bind to an epitope comprising K114 of SEQ ID NO: 3.

In some embodiments, the anti-CD137 agonist antibodies described herein inhibit or reduce T cell exhaustion and induce or enhance T cell activation. In some embodiments, the anti-CD137 agonist antibodies described herein inhibit or reduce T cell exhaustion and induce or enhance cytokine production by immune cells. In some embodiments, the anti-CD137 agonist antibodies described herein inhibit or reduce T cell exhaustion and induce or enhance T cell proliferation. In some embodiments, the anti-CD137 agonist antibodies described herein inhibit or reduce T cell exhaustion and exhibit anti-tumor efficacy. In some embodiments, the anti-

CD137 agonist antibodies described herein inhibit or reduce T cell exhaustion and inhibit or reduce macrophage differentiation and/or activation. In some embodiments, the anti-CD137 agonist antibodies described herein inhibit or reduce T cell exhaustion and induce or enhance NFκβ signaling. In some embodiments, the anti-CD137 agonist antibodies described herein inhibit or reduce T cell exhaustion and induce or enhance immune cell infiltration into a tumor microenvironment. In some embodiments, the anti-CD137 agonist antibodies described herein inhibit or reduce T cell exhaustion and do not induce hepatotoxicity. In some embodiments, the anti-CD137 agonist antibodies described herein inhibit or reduce T cell exhaustion and bind to a non-ligand binding domain on extracellular CD137. In some embodiments, the anti-CD137 agonist antibodies described herein inhibit or reduce T cell exhaustion and do not inhibit CD137 and CD137L interaction. In some embodiments, the anti-CD137 agonist antibodies described herein inhibit or reduce T cell exhaustion and bind to an epitope comprising K114 of SEQ ID NO: 3.

In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance T cell activation and induce or enhance cytokine production by immune cells. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance T cell activation and induce or enhance T cell proliferation. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance T cell activation and exhibit anti-tumor efficacy. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance T cell activation and inhibit or reduce macrophage differentiation and/or activation. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance T cell activation and induce or enhance NFκβ signaling. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance T cell activation and induce or enhance immune cell infiltration into a tumor microenvironment. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance T cell activation and do not induce hepatotoxicity. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance T cell activation and bind to a non-ligand binding domain on extracellular CD137. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance T cell activation and do not inhibit CD137 and CD137L interaction. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance T cell activation and bind to an epitope comprising K114 of SEQ ID NO: 3.

In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance cytokine production by immune cells and induce or enhance T cell proliferation. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance cytokine production by immune cells and exhibit anti-tumor efficacy. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance cytokine production by immune cells and inhibit or reduce macrophage differentiation and/or activation. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance cytokine production by immune cells and induce or enhance NFκβ signaling. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance cytokine production by immune cells and induce or enhance immune cell infiltration into a tumor microenvironment. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance cytokine production by immune cells and do not induce hepatotoxicity. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance cytokine production by immune cells and bind to a non-ligand binding domain on extracellular CD137. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance cytokine production by immune cells and do not inhibit CD137 and CD137L interaction. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance cytokine production by immune cells and bind to an epitope comprising K114 of SEQ ID NO: 3.

In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance T cell proliferation and exhibit anti-tumor efficacy. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance T cell proliferation and inhibit or reduce macrophage differentiation and/or activation. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance T cell proliferation and induce or enhance NFκβ signaling. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance T cell proliferation and induce or enhance immune cell infiltration into a tumor microenvironment. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance T cell proliferation and do not induce hepatotoxicity. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance T cell proliferation and bind to a non-ligand binding domain on extracellular CD137. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance T cell proliferation and do not inhibit CD137 and CD137L interaction. In some embodiments, the anti-

CD137 agonist antibodies described herein induce or enhance T cell proliferation and bind to an epitope comprising K114 of SEQ ID NO: 3.

In some embodiments, the anti-CD137 agonist antibodies described herein exhibit anti-tumor efficacy and inhibit or reduce macrophage differentiation and/or activation. In some embodiments, the anti-CD137 agonist antibodies described herein exhibit anti-tumor efficacy and induce or enhance NFκβ signaling. In some embodiments, the anti-CD137 agonist antibodies described herein exhibit anti-tumor efficacy and induce or enhance immune cell infiltration into a tumor microenvironment. In some embodiments, the anti-CD137 agonist antibodies described herein exhibit anti-tumor efficacy and do not induce hepatotoxicity. In some embodiments, the anti-CD137 agonist antibodies described herein exhibit anti-tumor efficacy and bind to a non-ligand binding domain on extracellular CD137. In some embodiments, the anti-CD137 agonist antibodies described herein exhibit anti-tumor efficacy and do not inhibit CD137 and CD137L interaction. In some embodiments, the anti-CD137 agonist antibodies described herein exhibit anti-tumor efficacy and bind to an epitope comprising K114 of SEQ ID NO: 3.

In some embodiments, the anti-CD137 agonist antibodies described herein inhibit or reduce macrophage differentiation and/or activation and induce or enhance NFκβ signaling. In some embodiments, the anti-CD137 agonist antibodies described herein inhibit or reduce macrophage differentiation and/or activation and induce or enhance immune cell infiltration into a tumor microenvironment. In some embodiments, the anti-CD137 agonist antibodies described herein inhibit or reduce macrophage differentiation and/or activation and do not induce hepatotoxicity. In some embodiments, the anti-CD137 agonist antibodies described herein inhibit or reduce macrophage differentiation and/or activation and bind to a non-ligand binding domain on extracellular CD137. In some embodiments, the anti-CD137 agonist antibodies described herein inhibit or reduce macrophage differentiation and/or activation and do not inhibit CD137 and CD137L interaction. In some embodiments, the anti-CD137 agonist antibodies described herein inhibit or reduce macrophage differentiation and/or activation and bind to an epitope comprising K114 of SEQ ID NO: 3.

In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance NFκβ signaling and induce or enhance immune cell infiltration into a tumor microenvironment. In some embodiments, the anti-CD137 agonist antibodies described herein

induce or enhance NFκβ signaling and do not induce hepatotoxicity. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance NFκβ signaling and bind to a non-ligand binding domain on extracellular CD137. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance NFκβ signaling and do not inhibit CD137 and CD137L interaction. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance NFκβ signaling and bind to an epitope comprising K114 of SEQ ID NO: 3.

In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance immune cell infiltration into a tumor microenvironment and do not induce hepatotoxicity. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance immune cell infiltration into a tumor microenvironment and bind to a non-ligand binding domain on extracellular CD137. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance immune cell infiltration into a tumor microenvironment and do not inhibit CD137 and CD137L interaction. In some embodiments, the anti-CD137 agonist antibodies described herein induce or enhance immune cell infiltration into a tumor microenvironment and bind to an epitope comprising K114 of SEQ ID NO: 3. In some embodiments, the anti-CD137 agonist antibodies described herein do not induce hepatotoxicity and bind to a non-ligand binding domain on extracellular CD137. In some embodiments, the anti-CD137 agonist antibodies described herein do not induce hepatotoxicity and do not inhibit CD137 and CD137L interaction. In some embodiments, the anti-CD137 agonist antibodies described herein do not induce hepatotoxicity and bind to an epitope comprising K114 of SEQ ID NO: 3.

In some embodiments, the anti-CD137 agonist antibodies described herein bind to a non-ligand binding domain on extracellular CD137 and do not inhibit CD137 and CD137L interaction. In some embodiments, the anti-CD137 agonist antibodies described herein bind to a non-ligand binding domain on extracellular CD137 and bind to an epitope comprising K114 of SEQ ID NO: 3. In some embodiments, the anti-CD137 agonist antibodies described herein do not inhibit CD137 and CD137L interaction and bind to an epitope comprising K114 of SEQ ID NO: 3.

Epitope Mapping

The disclosure provides formulations comprising anti-CD137 antibodies, or antigen binding fragments thereof, that specifically bind to an epitope of human CD137 and compete with a reference mAb (*e.g.*, mAb1) for binding to the epitope of human CD137. Methods to characterize, map, or otherwise elucidate the epitope of an anti-CD137 antibody can be grouped into structural, functional, or computational methods. A particularly suitable structural method to determine the precise molecular architecture of the interaction between an antibody and the corresponding antigen to which it binds is x-ray crystallography (alternatively "x-ray co-crystallography). A crystal structure of a bonded antibody-antigen pair enables very accurate determination of key interactions between individual amino acids from both side chains and main chain atoms in both the epitope of the antigen and the paratope of the antibody. Amino acids that are within 4 angstroms (Å) of each other are generally considered to be contacting residues. The methodology typically involves purification of antibody and antigen, formation and purification of the complex, followed by successive rounds of crystallization screens and optimization to obtain diffraction-quality crystals. Structural solution is obtained following x-ray crystallography frequently at a synchrotron source. Other structural methods for epitope mapping include, but are not limited to, hydrogen-deuterium exchange coupled to mass spectrometry, crosslinking-coupled mass spectrometry, and nuclear magnetic resonance (NMR) (see, *e.g.*, Epitope Mapping Protocols in Methods in Molecular Biology, Vol. 66, G. E. Morris, Ed. (1996); Abbott et al., (2014) Immunology 142(4):526-535).

Functional methods for epitope mapping are well known in the art and typically involve an assessment or quantification of antibody binding to whole proteins, protein fragments or peptides. Functional methods for epitope mapping can be used, for example, to identify linear or conformational epitopes and/or can be used to infer when two or more distinct antibodies bind to the same or similar epitopes. Functional methods for epitope mapping include, for example, immunoblotting and immunoprecipitation assays, wherein overlapping or contiguous peptides from CD137 are tested for reactivity with an anti-CD137 antibody, *e.g.*, mAb1. Other functional methods for epitope mapping include array-based oligopeptide scanning (alternatively known as "overlapping peptide scanning" or "pepscan analysis"), site-directed mutagenesis (*e.g.*, alanine-scanning mutagenesis), and high-throughput mutagenesis mapping (*e.g.*, shotgun mutagenesis mapping).

Numerous types of competitive binding assays are known, for example: 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)). Typically, such assays involve the use of purified antigen bound to a solid surface or cells and either 1) an unlabeled test antigen-binding protein and a labeled reference antigen-binding protein, or 2) a labeled test antigen-binding protein and an unlabeled reference antigen-binding protein. Competitive inhibition is measured by determining the amount of label bound to the solid surface or cells in the presence of the test antigen-binding protein. Usually the test antigen-binding protein is present in excess. Antigen-binding proteins identified by competition assay (competing antigen-binding proteins) include antigen-binding proteins binding to the same epitope as the reference antigen-binding proteins (*e.g.*, mAb1) and antigen-binding proteins binding to an adjacent epitope sufficiently proximal to the epitope bound by the reference antigen-binding protein (*e.g.*, mAb1) for steric hindrance to occur. Additional details regarding methods for determining competitive binding are provided in the examples herein. Usually, when a competing antigen- binding protein is present in excess (*e.g.*, about 1-, about 5-, about 10-, about 20- about 50-, or about 100-fold excess), it will inhibit (*e.g.*, reduce or block) specific binding of a reference antigen-binding protein to a common antigen by at least about 40-45%, about 45-50%, about 50-55%, about 55-60%, about 60-65%, about 65-70%, about 70-75% or about 75% or more. In some instances, binding is inhibited by at least about 80-85%, about 85-90%, about 90-95%, about 95-97%, or about 97% or more.

The site-directed mutagenesis method involves targeted site-directed mutagenesis where critical amino acids are identified by systematically introducing substitutions along the protein sequence and then determining the effects of each substitution on antibody binding. This may be done by "alanine scanning mutagenesis" (Cunningham and Wells (1989) Science 244:1081-085), or some other form of point mutagenesis of amino acid residues in CD137. Without being bound by theory, two or more antibodies (*e.g.*, a test antibody and a reference antibody, *e.g.*, mAb1) have

the same epitope if essentially all amino acid mutations in the antigen that reduce or eliminate binding of the first antibody reduce or eliminate binding of the second or more antibodies.

Shotgun mutagenesis mapping utilizes a comprehensive plasmid-mutation library for the target gene, with each clone in the library bearing a unique amino acid mutation and the entire library covering every amino acid in the target protein. The clones that constitute the mutation library are individually arranged in microplates, expressed within living mammalian cells, and tested for immunoreactivity with antibodies of interest. Amino acids critical for antibody epitopes are identified by a loss of reactivity and are then mapped onto a protein structure to visualize epitopes. Expression of the target protein antigen within mammalian cells often provides the native structure of the target protein antigen, which allows both linear and conformational epitope structures to be mapped on complex proteins. (Paes et al., J. Am. Chem. Soc. 131 (20): 6952-6954 (2009); Banik and Doranz, Genetic Engineering and Biotechnology News 3(2): 25-28 (2010)).

The epitope bound by an anti-CD137 antibody may also be determined using peptide scanning methods. In peptide scanning, libraries of short peptide sequences from overlapping segments of the target protein, CD137 are tested for their ability to bind antibodies of interest. The peptides are synthesized and screened for binding, *e.g.* using ELISA or BIACORE, or on a chip, by any of the multiple methods for solid-phase screening (Reineke et al, Curr. Opin. Biotechnol. 12: 59-64, 2001) as in the "pepscan" methodology (WO 84/03564; WO 93/09872).

A recently developed technology termed CLIPS (chemical linkage of peptides onto scaffolds) may be used to map conformational epitopes. The loose ends of the peptides are affixed onto synthetic scaffolds, so that the scaffolded peptide may be able to adopt the same spatial structure as the corresponding sequence in the intact protein. CLIPS technology is used to fix linear peptides into cyclic structures ('single-loop' format), and to bring together different parts of a protein binding site ('double- loop', 'triple-loop', etc. format), so as to create conformational epitopes that may be assayed for antibody binding. (US Pat. No. 7,972,993).

The epitopes bound by antibodies provided by the disclosure may also be mapped using computational methods. In these methods, for example, libraries of peptide fragments are displayed on the surface of the phage or cell. Epitopes are then mapped by screening antibodies against these fragments using selective binding assays. A number of computational tools have been developed which allow the prediction of conformational epitopes based upon linear affinity-selected peptides obtained using phage display (Mayrose et al., (2007) Bioinformatics 23:3244-

3246). Methods are also available for the detection of conformational epitopes by phage display. Microbial display systems may also be used to express properly folded antigenic fragments on the cell surface for identification of conformational epitopes (Cochran et al., J. Immunol. Meth. 287: 147-158, 2004; Rockberg et al., Nature Methods 5: 1039-1045, 2008).

Methods involving proteolysis and mass spectroscopy may also be used to determine antibody epitopes (Baerga-Ortiz et al., Protein Sci. 2002 June; 1 1 (6): 1300-1308). In limited proteolysis, the antigen is cleaved by different proteases, in the presence and in the absence of the antibody, and the fragments are identified by mass spectrometry. The epitope is the region of the antigen that becomes protected from proteolysis upon binding of the antibody (Suckau et al., Proc. Natl. Acad. Sci. USA 87: 9848-9852, 1990). Additional proteolysis based methods include, for example, selective chemical modification (Fiedler et al., Bioconjugate Chemistry 1998, 9(2): 236-234, 1998), epitope excision (Van de Water et al., Clin. Immunol. Immunopathol. 1997, 85(3): 229-235, 1997), and the recently developed method of hydrogen-deuterium (H/D) exchange (Flanagan, N., Genetic Engineering and Biotechnology News 3(2): 25-28, 2010).

In some embodiments, the anti-CD137 antibodies described herein bind to an epitope located within amino acid residues 111-135 of SEQ ID NO: 3 as determined by mutagenesis and mammalian display. In some embodiments, the anti-CD137 antibodies described herein bind to an epitope comprising K114 of SEQ ID NO: 3 as determined by mutagenesis and mammalian display. In some embodiments, the anti-CD137 antibodies described herein bind to an epitope comprising E111, T113 and K114 of SEQ ID NO: 3 as determined by mutagenesis and mammalian display. In some embodiments, the anti-CD137 antibodies described herein bind to an epitope comprising E111, T113, K114 and P135 of SEQ ID NO: 3 as determined by mutagenesis and mammalian display. In some embodiments, the anti-CD137 antibodies described herein bind to an epitope comprising E111, T113, K114, N126, I132 and P135 of SEQ ID NO: 3 as determined by mutagenesis and mammalian display.

Methods for Producing the Anti-CD137 Antibodies and Antigen-binding Fragments Thereof

The disclosure also features methods for producing any of the anti-CD137 antibodies or antigen-binding fragments thereof described herein. In some embodiments, methods for preparing an antibody described herein can include immunizing a subject (*e.g.*, a non-human mammal) with an appropriate immunogen. Suitable immunogens for generating any of the antibodies described

herein are set forth herein. For example, to generate an antibody that binds to CD137, a skilled artisan can immunize a suitable subject (*e.g.*, a non-human mammal such as a rat, a mouse, a gerbil, a hamster, a dog, a cat, a pig, a goat, a horse, or a non-human primate) with a full-length CD137 polypeptide such as a full-length human CD137 polypeptide comprising the amino acid sequence depicted in SEQ ID NO. 3.

A suitable subject (*e.g.*, a non-human mammal) can be immunized with the appropriate antigen along with subsequent booster immunizations a number of times sufficient to elicit the production of an antibody by the mammal. The immunogen can be administered to a subject (*e.g.*, a non-human mammal) with an adjuvant. Adjuvants useful in producing an antibody in a subject include, but are not limited to, protein adjuvants; bacterial adjuvants, *e.g.*, whole bacteria (BCG, *Corynebacterium parvum* or *Salmonella minnesota*) and bacterial components including cell wall skeleton, trehalose dimycolate, monophosphoryl lipid A, methanol extractable residue (MER) of tubercle *bacillus*, complete or incomplete Freund's adjuvant; viral adjuvants; chemical adjuvants, *e.g.*, aluminum hydroxide, and iodoacetate and cholesteryl hemisuccinate. Other adjuvants that can be used in the methods for inducing an immune response include, *e.g.*, cholera toxin and parapoxvirus proteins. See also Bieg et al. (1999) *Autoimmunity* 31(1):15-24. See also, *e.g.*, Lodmell et al. (2000) *Vaccine* 18:1059-1066; Johnson et al. (1999) *J Med Chem* 42:4640-4649; Baldridge et al. (1999) *Methods* 19:103-107; and Gupta et al. (1995) *Vaccine* 13(14): 1263-1276.

In some embodiments, the methods include preparing a hybridoma cell line that secretes a monoclonal antibody that binds to the immunogen. For example, a suitable mammal such as a laboratory mouse is immunized with a CD137 polypeptide as described above. Antibody-producing cells (*e.g.*, B cells of the spleen) of the immunized mammal can be isolated two to four days after at least one booster immunization of the immunogen and then grown briefly in culture before fusion with cells of a suitable myeloma cell line. The cells can be fused in the presence of a fusion promoter such as, *e.g.*, vaccinia virus or polyethylene glycol. The hybrid cells obtained in the fusion are cloned, and cell clones secreting the desired antibodies are selected. For example, spleen cells of Balb/c mice immunized with a suitable immunogen can be fused with cells of the myeloma cell line PAI or the myeloma cell line Sp2/0-Ag 14. After the fusion, the cells are expanded in suitable culture medium, which is supplemented with a selection medium, for example HAT medium, at regular intervals in order to prevent normal myeloma cells from overgrowing the

desired hybridoma cells. The obtained hybridoma cells are then screened for secretion of the desired antibodies, *e.g.*, an antibody that binds to CD137.

In some embodiments, a skilled artisan can identify an anti-CD137 antibody from a non-immune biased library as described in, *e.g.*, U.S. patent no. 6,300,064 (to Knappik et al.; Morphosys AG) and Schoonbroodt et al. (2005) *Nucleic Acids Res* 33(9):e81.

In some embodiments, the methods described herein can involve, or be used in conjunction with, *e.g.*, phage display technologies, bacterial display, yeast surface display, eukaryotic viral display, mammalian cell display, and cell-free (*e.g.*, ribosomal display) antibody screening techniques (see, *e.g.*, Etz et al. (2001) *J Bacteriol* 183:6924-6935; Cornelis (2000) *Curr Opin Biotechnol* 11:450-454; Klemm et al. (2000) *Microbiology* 146:3025-3032; Kieke et al. (1997) *Protein Eng* 10:1303-1310; Yeung et al. (2002) *Biotechnol Prog* 18:212-220; Boder et al. (2000) *Methods Enzymology* 328:430-444; Grabherr et al. (2001) *Comb Chem High Throughput Screen* 4:185-192; Michael et al. (1995) *Gene Ther* 2:660-668; Pereboev et al. (2001) *J Virol* 75:7107-7113; Schaffitzel et al. (1999) *J Immunol Methods* 231:119-135; and Hanes et al. (2000) *Nat Biotechnol* 18:1287-1292).

Methods for identifying antibodies using various phage display methods are known in the art. In phage display methods, functional antibody domains are displayed on the surface of phage particles which carry the polynucleotide sequences encoding them. Such phage can be utilized to display antigen-binding domains of antibodies, such as Fab, Fv, or disulfide-bond stabilized Fv antibody fragments, expressed from a repertoire or combinatorial antibody library (*e.g.*, human or murine). Phage used in these methods are typically filamentous phage such as fd and M13. The antigen binding domains are expressed as a recombinantly-fused protein to any of the phage coat proteins pIII, pVIII, or pIX. See, *e.g.*, Shi et al. (2010) *JMB* 397:385-396. Examples of phage display methods that can be used to make the immunoglobulins, or fragments thereof, described herein include those disclosed in Brinkman et al. (1995) *J Immunol Methods* 182:41-50; Ames et al. (1995) *J Immunol Methods* 184:177-186; Kettleborough et al. (1994) *Eur J Immunol* 24:952-958; Persic et al. (1997) *Gene* 187:9-18; Burton et al. (1994) *Advances in Immunology* 57:191-280; and PCT publication nos. WO 90/02809, WO 91/10737, WO 92/01047, WO 92/18619, WO 93/11236, WO 95/15982, and WO 95/20401. Suitable methods are also described in, *e.g.*, U.S. patent nos. 5,698,426; 5,223,409; 5,403,484; 5,580,717; 5,427,908; 5,750,753; 5,821,047; 5,571,698; 5,427,908; 5,516,637; 5,780,225; 5,658,727; 5,733,743 and 5,969,108.

In some embodiments, the phage display antibody libraries can be generated using mRNA collected from B cells from the immunized mammals. For example, a splenic cell sample comprising B cells can be isolated from mice immunized with CD137 polypeptide as described above. mRNA can be isolated from the cells and converted to cDNA using standard molecular biology techniques. See, *e.g.*, Sambrook et al. (1989) "Molecular Cloning: A Laboratory Manual, 2nd Edition," Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.; Harlow and Lane (1988), *supra*; Benny K. C. Lo (2004), *supra*; and Borrebaek (1995), *supra*. The cDNA coding for the variable regions of the heavy chain and light chain polypeptides of immunoglobulins are used to construct the phage display library. Methods for generating such a library are described in, *e.g.*, Merz et al. (1995) *J Neurosci Methods* 62(1-2):213-9; Di Niro et al. (2005) *Biochem J* 388(Pt 3):889–894; and Engberg et al. (1995) *Methods Mol Biol* 51:355-376.

In some embodiments, a combination of selection and screening can be employed to identify an antibody of interest from, *e.g.*, a population of hybridoma-derived antibodies or a phage display antibody library. Suitable methods are known in the art and are described in, *e.g.*, Hoogenboom (1997) *Trends in Biotechnology* 15:62-70; Brinkman et al. (1995), *supra*; Ames et al. (1995), *supra*; Kettleborough et al. (1994), *supra*; Persic et al. (1997), *supra*; and Burton et al. (1994), *supra*. For example, a plurality of phagemid vectors, each encoding a fusion protein of a bacteriophage coat protein (*e.g.*, pIII, pVIII, or pIX of M13 phage) and a different antigen-combining region are produced using standard molecular biology techniques and then introduced into a population of bacteria (*e.g.*, *E. coli*). Expression of the bacteriophage in bacteria can, in some embodiments, require use of a helper phage. In some embodiments, no helper phage is required (see, *e.g.*, Chasteen et al., (2006) *Nucleic Acids Res* 34(21):e145). Phage produced from the bacteria are recovered and then contacted to, *e.g.*, a target antigen bound to a solid support (immobilized). Phage may also be contacted to antigen in solution, and the complex is subsequently bound to a solid support.

A subpopulation of antibodies screened using the above methods can be characterized for their specificity and binding affinity for a particular antigen (*e.g.*, human CD137) using any immunological or biochemical based method known in the art. For example, specific binding of an antibody to CD137, may be determined for example using immunological or biochemical based methods such as, but not limited to, an ELISA assay, SPR assays, immunoprecipitation assay, affinity chromatography, and equilibrium dialysis as described above. Immunoassays which can

be used to analyze immunospecific binding and cross-reactivity of the antibodies include, but are not limited to, competitive and non-competitive assay systems using techniques such as Western blots, RIA, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoprecipitation assays, immunodiffusion assays, agglutination assays, complement-fixation assays, immunoradiometric assays, fluorescent immunoassays, and protein A immunoassays. Such assays are routine and well known in the art.

It is understood that the above methods can also be used to determine if, *e.g.*, an anti-CD137 antibody does not bind to full-length, human CD137 and/or CD137 proteins.

In embodiments where the selected CDR amino acid sequences are short sequences (*e.g.*, fewer than 10-15 amino acids in length), nucleic acids encoding the CDRs can be chemically synthesized as described in, *e.g.*, Shiraishi et al. (2007) *Nucleic Acids Symposium Series* 51(1):129-130 and U.S. Patent No. 6,995,259. For a given nucleic acid sequence encoding an acceptor antibody, the region of the nucleic acid sequence encoding the CDRs can be replaced with the chemically synthesized nucleic acids using standard molecular biology techniques. The 5' and 3' ends of the chemically synthesized nucleic acids can be synthesized to comprise sticky end restriction enzyme sites for use in cloning the nucleic acids into the nucleic acid encoding the variable region of the donor antibody. Alternatively, fragments of chemically synthesized nucleic acids, together capable of encoding an antibody, can be joined together using DNA assembly techniques known in the art (*e.g.* Gibson Assembly).

In some embodiments, the anti-CD137 antibodies described herein comprise an altered heavy chain constant region that has reduced (or no) effector function relative to its corresponding unaltered constant region. Effector functions involving the constant region of the anti-CD137 antibody may be modulated by altering properties of the constant or Fc region. Altered effector functions include, for example, a modulation in one or more of the following activities: antibody-dependent cellular cytotoxicity (ADCC), complement-dependent cytotoxicity (CDC), apoptosis, binding to one or more Fc-receptors, and pro-inflammatory responses. Modulation refers to an increase, decrease, or elimination of an effector function activity exhibited by a subject antibody containing an altered constant region as compared to the activity of the unaltered form of the constant region. In particular embodiments, modulation includes situations in which an activity is abolished or completely absent.

An altered constant region with altered FcR binding affinity and/or ADCC activity and/or altered CDC activity is a polypeptide which has either an enhanced or diminished FcR binding activity and/or ADCC activity and/or CDC activity compared to the unaltered form of the constant region. An altered constant region which displays increased binding to an FcR binds at least one FcR with greater affinity than the unaltered polypeptide. An altered constant region which displays decreased binding to an FcR binds at least one FcR with lower affinity than the unaltered form of the constant region. Such variants which display decreased binding to an FcR may possess little or no appreciable binding to an FcR, *e.g.*, 0 to 50% (*e.g.*, less than 50, 49, 48, 47, 46, 45, 44, 43, 42, 41, 40, 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1%) of the binding to the FcR as compared to the level of binding of a native sequence immunoglobulin constant or Fc region to the FcR. Similarly, an altered constant region that displays modulated ADCC and/or CDC activity may exhibit either increased or reduced ADCC and/or CDC activity compared to the unaltered constant region. For example, in some embodiments, the anti-CD137 antibody comprising an altered constant region can exhibit approximately 0 to 50% (*e.g.*, less than 50, 49, 48, 47, 46, 45, 44, 43, 42, 41, 40, 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1%) of the ADCC and/or CDC activity of the unaltered form of the constant region. An anti-CD137 antibody described herein comprising an altered constant region displaying reduced ADCC and/or CDC may exhibit reduced or no ADCC and/or CDC activity.

In some embodiments, an anti-CD137 antibody described herein exhibits reduced or no effector function. In some embodiments, an anti-CD137 antibody comprises a hybrid constant region, or a portion thereof, such as a G2/G4 hybrid constant region (see *e.g.*, Burton et al. (1992) *Adv Immun* 51:1-18; Canfield et al. (1991) *J Exp Med* 173:1483-1491; and Mueller et al. (1997) *Mol Immunol* 34(6):441-452). See above.

In some embodiments, an anti-CD137 antibody may contain an altered constant region exhibiting enhanced or reduced complement dependent cytotoxicity (CDC). Modulated CDC activity may be achieved by introducing one or more amino acid substitutions, insertions, or deletions in an Fc region of the antibody. See, *e.g.*, U.S. patent no. 6,194,551. Alternatively or additionally, cysteine residue(s) may be introduced in the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated may have

improved or reduced internalization capability and/or increased or decreased complement-mediated cell killing. See, *e.g.*, Caron et al. (1992) *J Exp Med* 176:1191-1195 and Shopes (1992) *Immunol* 148:2918-2922; PCT publication nos. WO 99/51642 and WO 94/29351; Duncan and Winter (1988) *Nature* 322:738-40; and U.S. Patent Nos. 5,648,260 and 5,624,821.

Recombinant Antibody Expression and Purification

The antibodies or antigen-binding fragments thereof described herein for use in any of the formulations of the disclosure can be produced using a variety of techniques known in the art of molecular biology and protein chemistry. For example, a nucleic acid encoding one or both of the heavy and light chain polypeptides of an antibody can be inserted into an expression vector that contains transcriptional and translational regulatory sequences, which include, *e.g.*, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, transcription terminator signals, polyadenylation signals, and enhancer or activator sequences. The regulatory sequences include a promoter and transcriptional start and stop sequences. In addition, the expression vector can include more than one replication system such that it can be maintained in two different organisms, for example in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification.

Several possible vector systems are available for the expression of cloned heavy chain and light chain polypeptides from nucleic acids in mammalian cells. One class of vectors relies upon the integration of the desired gene sequences into the host cell genome. Cells which have stably integrated DNA can be selected by simultaneously introducing drug resistance genes such as *E. coli* gpt (Mulligan and Berg (1981) *Proc Natl Acad Sci USA* 78:2072) or *Tn*5 neo (Southern and Berg (1982) *Mol Appl Genet* 1:327). The selectable marker gene can be either linked to the DNA gene sequences to be expressed, or introduced into the same cell by co-transfection (Wigler et al. (1979) *Cell* 16:77). A second class of vectors utilizes DNA elements which confer autonomously replicating capabilities to an extrachromosomal plasmid. These vectors can be derived from animal viruses, such as bovine papillomavirus (Sarver et al. (1982) *Proc Natl Acad Sci USA*, 79:7147), cytomegalovirus, polyoma virus (Deans et al. (1984) *Proc Natl Acad Sci USA* 81:1292), or SV40 virus (Lusky and Botchan (1981) *Nature* 293:79).

The expression vectors can be introduced into cells in a manner suitable for subsequent expression of the nucleic acid. The method of introduction is largely dictated by the targeted cell

type, discussed below. Exemplary methods include $CaPO_4$ precipitation, liposome fusion, cationic liposomes, electroporation, viral infection, dextran-mediated transfection, polybrene-mediated transfection, protoplast fusion, and direct microinjection.

Appropriate host cells for the expression of antibodies or antigen-binding fragments thereof include yeast, bacteria, insect, plant, and mammalian cells. Of particular interest are bacteria such as *E. coli*, fungi such as *Saccharomyces cerevisiae* and *Pichia pastoris*, insect cells such as SF9, mammalian cell lines (*e.g.*, human cell lines), as well as primary cell lines.

In some embodiments, an antibody or fragment thereof can be expressed in, and purified from, transgenic animals (*e.g.*, transgenic mammals). For example, an antibody can be produced in transgenic non-human mammals (*e.g.*, rodents) and isolated from milk as described in, *e.g.*, Houdebine (2002) *Curr Opin Biotechnol* 13(6):625-629; van Kuik-Romeijn et al. (2000) *Transgenic Res* 9(2):155-159; and Pollock et al. (1999) *J Immunol Methods* 231(1-2):147-157.

The antibodies and fragments thereof can be produced from the cells by culturing a host cell transformed with the expression vector containing nucleic acid encoding the antibodies or fragments, under conditions, and for an amount of time, sufficient to allow expression of the proteins. Such conditions for protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation. For example, antibodies expressed in *E. coli* can be refolded from inclusion bodies (see, *e.g.*, Hou et al. (1998) *Cytokine* 10:319-30). Bacterial expression systems and methods for their use are well known in the art (see Current Protocols in Molecular Biology, Wiley & Sons, and Molecular Cloning--A Laboratory Manual --3rd Ed., Cold Spring Harbor Laboratory Press, New York (2001)). The choice of codons, suitable expression vectors and suitable host cells will vary depending on a number of factors, and may be easily optimized as needed. An antibody (or fragment thereof) described herein can be expressed in mammalian cells or in other expression systems including but not limited to yeast, baculovirus, and *in vitro* expression systems (see, *e.g.*, Kaszubska et al. (2000) *Protein Expression and Purification* 18:213-220).

Following expression, the antibodies and fragments thereof can be isolated. An antibody or fragment thereof can be isolated or purified in a variety of ways known to those skilled in the art depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological, and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography. For example, an

antibody can be purified using a standard anti-antibody column (*e.g.*, a protein-A or protein-G column). Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. See, *e.g.*, Scopes (1994) "Protein Purification, 3rd edition," Springer-Verlag, New York City, New York. The degree of purification necessary will vary depending on the desired use. In some instances, no purification of the expressed antibody or fragments thereof will be necessary.

Methods for determining the yield or purity of a purified antibody or fragment thereof are known in the art and include, *e.g.*, Bradford assay, UV spectroscopy, Biuret protein assay, Lowry protein assay, amido black protein assay, high pressure liquid chromatography (HPLC), mass spectrometry (MS), and gel electrophoretic methods (*e.g.*, using a protein stain such as Coomassie Blue or colloidal silver stain).

Modification of the Antibodies or Antigen-Binding Fragments Thereof

The antibodies or antigen-binding fragments thereof for use in any of the formulations of the disclosure can be modified following their expression and purification. The modifications can be covalent or non-covalent modifications. Such modifications can be introduced into the antibodies or fragments by, *e.g.*, reacting targeted amino acid residues of the polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or terminal residues. Suitable sites for modification can be chosen using any of a variety of criteria including, *e.g.*, structural analysis or amino acid sequence analysis of the antibodies or fragments.

In some embodiments, the antibodies or antigen-binding fragments thereof can be conjugated to a heterologous moiety. The heterologous moiety can be, *e.g.*, a heterologous polypeptide, a therapeutic agent (*e.g.*, a toxin or a drug), or a detectable label such as, but not limited to, a radioactive label, an enzymatic label, a fluorescent label, a heavy metal label, a luminescent label, or an affinity tag such as biotin or streptavidin. Suitable heterologous polypeptides include, *e.g.*, an antigenic tag (*e.g.*, FLAG (DYKDDDDK; SEQ ID NO: 98), polyhistidine (6-His; HHHHHH; SEQ ID NO: 99), hemagglutinin (HA; YPYDVPDYA; SEQ ID NO: 100), glutathione-S-transferase (GST), or maltose-binding protein (MBP)) for use in purifying the antibodies or fragments. Heterologous polypeptides also include polypeptides (*e.g.*, enzymes) that are useful as diagnostic or detectable markers, for example, luciferase, a fluorescent protein (*e.g.*, green fluorescent protein (GFP)), or chloramphenicol acetyl transferase (CAT). Suitable

radioactive labels include, *e.g.*, ^{32}P, ^{33}P, ^{14}C, ^{125}I, ^{131}I, ^{35}S, and ^{3}H. Suitable fluorescent labels include, without limitation, fluorescein, fluorescein isothiocyanate (FITC), green fluorescent protein (GFP), DYLIGHT™ 488, phycoerythrin (PE), propidium iodide (PI), PerCP, PE-ALEXA FLUOR® 700, Cy5, allophycocyanin, and Cy7. Luminescent labels include, *e.g.*, any of a variety of luminescent lanthanide (*e.g.*, europium or terbium) chelates. For example, suitable europium chelates include the europium chelate of diethylene triamine pentaacetic acid (DTPA) or tetraazacyclododecane-1,4,7,10-tetraacetic acid (DOTA). Enzymatic labels include, *e.g.*, alkaline phosphatase, CAT, luciferase, and horseradish peroxidase.

Two proteins (*e.g.*, an antibody and a heterologous moiety) can be cross-linked using any of a number of known chemical cross linkers. Examples of such cross linkers are those which link two amino acid residues via a linkage that includes a "hindered" disulfide bond. In these linkages, a disulfide bond within the cross-linking unit is protected (by hindering groups on either side of the disulfide bond) from reduction by the action, for example, of reduced glutathione or the enzyme disulfide reductase. One suitable reagent, 4-succinimidyloxycarbonyl-α-methyl-α(2-pyridyldithio) toluene (SMPT), forms such a linkage between two proteins utilizing a terminal lysine on one of the proteins and a terminal cysteine on the other. Heterobifunctional reagents that cross-link by a different coupling moiety on each protein can also be used. Other useful cross-linkers include, without limitation, reagents which link two amino groups (*e.g.*, N-5-azido-2-nitrobenzoyloxysuccinimide), two sulfhydryl groups (*e.g.*, 1,4-bis-maleimidobutane), an amino group and a sulfhydryl group (*e.g.*, m-maleimidobenzoyl-N-hydroxysuccinimide ester), an amino group and a carboxyl group (*e.g.*, 4-[p-azidosalicylamido]butylamine), and an amino group and a guanidinium group that is present in the side chain of arginine (*e.g.*, p-azidophenyl glyoxal monohydrate).

In some embodiments, a radioactive label can be directly conjugated to the amino acid backbone of the antibody. Alternatively, the radioactive label can be included as part of a larger molecule (*e.g.*, ^{125}I in meta-[^{125}I]iodophenyl-N-hydroxysuccinimide ([^{125}I]mIPNHS) which binds to free amino groups to form meta-iodophenyl (mIP) derivatives of relevant proteins (see, *e.g.*, Rogers et al. (1997) *J Nucl Med* 38:1221-1229) or chelate (*e.g.*, to DOTA or DTPA) which is in turn bound to the protein backbone. Methods of conjugating the radioactive labels or larger molecules/chelates containing them to the antibodies or antigen-binding fragments described herein are known in the art. Such methods involve incubating the proteins with the radioactive

label under conditions (*e.g.*, pH, salt concentration, and/or temperature) that facilitate binding of the radioactive label or chelate to the protein (see, *e.g.*, U.S. Patent No. 6,001,329).

Methods for conjugating a fluorescent label (sometimes referred to as a "fluorophore") to a protein (*e.g.*, an antibody) are known in the art of protein chemistry. For example, fluorophores can be conjugated to free amino groups (*e.g.*, of lysines) or sulfhydryl groups (*e.g.*, cysteines) of proteins using succinimidyl (NHS) ester or tetrafluorophenyl (TFP) ester moieties attached to the fluorophores. In some embodiments, the fluorophores can be conjugated to a heterobifunctional cross-linker moiety such as sulfo-SMCC. Suitable conjugation methods involve incubating an antibody protein, or fragment thereof, with the fluorophore under conditions that facilitate binding of the fluorophore to the protein. See, *e.g.*, Welch and Redvanly (2003) "Handbook of Radiopharmaceuticals: Radiochemistry and Applications," John Wiley and Sons (ISBN 0471495603).

In some embodiments, the antibodies or fragments can be modified, *e.g.*, with a moiety that improves the stabilization and/or retention of the antibodies in circulation, *e.g.*, in blood, serum, or other tissues. For example, the antibody or fragment can be PEGylated as described in, *e.g.*, Lee et al. (1999) *Bioconjug Chem* 10(6): 973-8; Kinstler et al. (2002) *Advanced Drug Deliveries Reviews* 54:477-485; and Roberts et al. (2002) *Advanced Drug Delivery Reviews* 54:459-476 or HESylated (Fresenius Kabi, Germany; see, *e.g.*, Pavisić et al. (2010) *Int J Pharm* 387(1-2):110-119). The stabilization moiety can improve the stability, or retention of, the antibody (or fragment) by at least 1.5 (*e.g.*, at least 2, 5, 10, 15, 20, 25, 30, 40, or 50 or more) fold.

In some embodiments, the antibodies or antigen-binding fragments thereof described herein can be glycosylated. In some embodiments, an antibody or antigen-binding fragment thereof described herein can be subjected to enzymatic or chemical treatment, or produced from a cell, such that the antibody or fragment has reduced or absent glycosylation. Methods for producing antibodies with reduced glycosylation are known in the art and described in, *e.g.*, U.S. patent no. 6,933,368; Wright et al. (1991) *EMBO J* 10(10):2717-2723; and Co et al. (1993) *Mol Immunol* 30:1361.

Applications

The formulations described herein can be used in diagnostic and therapeutic applications. For example, detectably-labeled antigen-binding molecules can be used in assays to detect the

presence or amount of the target antigens in a sample (*e.g.*, a biological sample). The compositions can be used in *in vitro* assays for studying inhibition of target antigen function (*e.g.* CD137-mediated cellular signaling or response). In some embodiments, *e.g.*, in which the compositions bind to and activate a target antigen (*e.g.* a protein or polypeptide), the compositions can be used as positive controls in assays designed to identify additional novel compounds that also induce activity of the target protein or polypeptide and/or are otherwise are useful for treating a disorder associated with the target protein or polypeptide. For example, a CD137-activating composition can be used as a positive control in an assay to identify additional compounds (*e.g.*, small molecules, aptamers, or antibodies) that induce, increase, or stimulate CD137 function. The compositions can also be used in therapeutic methods as elaborated on below.

Kits

In some embodiments, the disclosure provides a kit comprising any of the formulations described herein. In some embodiments, a kit includes a formulation comprising an anti-CD137 antibody as disclosed herein, and instructions for use. The kits may comprise, in a suitable container, an anti-CD137 antibody, one or more controls, and various buffers, reagents, enzymes and other standard ingredients well known in the art.

The container can include at least one vial, well, test tube, flask, bottle, syringe, or other container means, into which any of the formulations of the disclosure may be placed, and in some instances, suitably aliquoted. Where an additional component is provided, the kit can contain additional containers into which this component may be placed. The kits can also include a means for containing a formulation comprising an anti-CD137 antibody and any other reagent containers in close confinement for commercial sale. Such containers may include injection or blow-molded plastic containers into which the desired vials are retained. Containers and/or kits can include labeling with instructions for use and/or warnings.

In some embodiments, a kit comprises a formulation comprising an anti-CD137 antibody and a buffer, or a formulation comprising the anti-CD137 antibody, and instructions for treating or delaying progression of cancer or reducing or inhibiting tumor growth in a subject in need thereof. In some embodiments, a kit comprises a formulation comprising an anti-CD137 antibody and a buffer, or a formulation comprising the anti-CD137 antibody, and instructions for administering the anti-CD137 antibody to a subject in need thereof, alone or in combination with

another agent, for treating or delaying progression of cancer or reducing or inhibiting tumor growth in the subject.

Methods of Use

The formulations of the present invention have numerous *in vitro* and *in vivo* utilities involving the detection and/or quantification of CD137 and/or the agonism of CD137 function.

The above-described formulations are useful in, *inter alia*, methods for treating or preventing a variety of cancers in a subject. The fromulations can be administered to a subject, *e.g.*, a human subject, using a variety of methods that depend, in part, on the route of administration. The route can be, *e.g.*, intravenous injection or infusion (IV), subcutaneous injection (SC), intraperitoneal (IP) injection, intramuscular injection (IM), or intrathecal injection (IT). The injection can be in a bolus or a continuous infusion.

Administration can be achieved by, *e.g.*, local infusion, injection, or by means of an implant. The implant can be of a porous, non-porous, or gelatinous material, including membranes, such as sialastic membranes, or fibers. The implant can be configured for sustained or periodic release of the composition to the subject. See, *e.g.*, U.S. Patent Application Publication No. 20080241223; U.S. Patent Nos. 5,501,856; 4,863,457; and 3,710,795; EP488401; and EP 430539, the disclosures of each of which are incorporated herein by reference in their entirety. The composition can be delivered to the subject by way of an implantable device based on, *e.g.*, diffusive, erodible, or convective systems, *e.g.*, osmotic pumps, biodegradable implants, electrodiffusion systems, electroosmosis systems, vapor pressure pumps, electrolytic pumps, effervescent pumps, piezoelectric pumps, erosion-based systems, or electromechanical systems.

In some embodiments, a formulation comprising an anti-CD137 antibody or antigen-binding fragment thereof is therapeutically delivered to a subject by way of local administration.

A suitable dose of a formulation described herein, which dose is capable of treating or preventing cancer in a subject, can depend on a variety of factors including, *e.g.*, the age, sex, and weight of a subject to be treated and the particular inhibitor compound used. For example, a different dose of a formulation comprising a whole anti-CD137 antibody may be required to treat a subject with cancer as compared to the dose of a formulation comprising a CD137-binding Fab' antibody fragment required to treat the same subject. Other factors affecting the dose administered to the subject include, *e.g.*, the type or severity of the cancer. For example, a subject having

metastatic melanoma may require administration of a different dosage of a formulation comprising an anti-CD137 antibody than a subject with glioblastoma. Other factors can include, *e.g.*, other medical disorders concurrently or previously affecting the subject, the general health of the subject, the genetic disposition of the subject, diet, time of administration, rate of excretion, drug combination, and any other additional therapeutics that are administered to the subject. It should also be understood that a specific dosage and treatment regimen for any particular subject will also depend upon the judgment of the treating medical practitioner (*e.g.*, doctor or nurse). Suitable dosages are described herein. In some embodiments, the formulations comprising the anti-CD137 antibodies described herein are effective at both high and low doses.

A pharmaceutical formulation can include a therapeutically effective amount of an anti-CD137 antibody or antigen-binding fragment thereof described herein. Such effective amounts can be readily determined by one of ordinary skill in the art based, in part, on the effect of the administered antibody, or the combinatorial effect of the antibody and one or more additional active agents, if more than one agent is used. A therapeutically effective amount of an antibody or fragment thereof described herein can also vary according to factors such as the disease state, age, sex, and weight of the individual, and the ability of the antibody (and one or more additional active agents) to elicit a desired response in the individual, *e.g.*, reduction in tumor growth. For example, a therapeutically effective amount of an anti-CD137 antibody can inhibit (lessen the severity of or eliminate the occurrence of) and/or prevent a particular disorder, and/or any one of the symptoms of the particular disorder known in the art or described herein. A therapeutically effective amount is also one in which any toxic or detrimental effects of the formulation are outweighed by the therapeutically beneficial effects.

Suitable human doses of any of the antibodies or fragments thereof described herein can further be evaluated in, *e.g.*, Phase I dose escalation studies. See, *e.g.*, van Gurp et al. (2008) *Am J Transplantation* 8(8):1711-1718; Hanouska et al. (2007) *Clin Cancer Res* 13(2, part 1):523-531; and Hetherington et al. (2006) *Antimicrobial Agents and Chemotherapy* 50(10): 3499-3500.

In some embodiments, the formulation contains any of the antibodies or antigen-binding fragments thereof described herein and one or more (*e.g.*, two, three, four, five, six, seven, eight, nine, 10, or 11 or more) additional therapeutic agents such that the formulation as a whole is therapeutically effective. For example, a formulation can contain an anti-CD137 antibody described herein and an alkylating agent, wherein the antibody and agent are each at a

concentration that when combined are therapeutically effective for treating or preventing a cancer (*e.g.*, melanoma) in a subject.

Toxicity and therapeutic efficacy of such formulations can be determined by known pharmaceutical procedures in cell cultures or experimental animals (*e.g.*, animal models of any of the cancers described herein). These procedures can be used, *e.g.*, for determining the LD_{50} (the dose lethal to 50% of the population) and the ED_{50} (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD_{50}/ED_{50}. An antibody or antigen-binding fragment thereof that exhibits a high therapeutic index is preferred. While formulations that exhibit toxic side effects may be used, care should be taken to design a delivery system that targets such compounds to the site of affected tissue and to minimize potential damage to normal cells and, thereby, reduce side effects.

The data obtained from the cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such antibodies or antigen-binding fragments thereof lies generally within a range of circulating concentrations of the antibodies or fragments that include the ED_{50} with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For a formulation comprising an anti-CD137 antibody described herein, the therapeutically effective dose can be estimated initially from cell culture assays. A dose can be formulated in animal models to achieve a circulating plasma concentration range that includes the EC_{50} (i.e., the concentration of the antibody which achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by high performance liquid chromatography. In some embodiments, *e.g.*, where local administration (*e.g.*, to the eye or a joint) is desired, cell culture or animal modeling can be used to determine a dose required to achieve a therapeutically effective concentration within the local site.

The pharmaceutical composition comprising a formulation as described herein to be used for *in vivo* administration typically is sterile. In certain embodiments, this can be accomplished by filtration through sterile filtration membranes. In certain embodiments, where the composition is lyophilized, sterilization using this method can be conducted either prior to or following lyophilization and reconstitution. In certain embodiments, the composition for parenteral

administration can be stored in lyophilized form or in a solution. In certain embodiments, parenteral compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

In certain embodiments, once the pharmaceutical composition has been formulated, it can be stored in sterile vials as a solution, suspension, gel, emulsion, solid, or as a dehydrated or lyophilized powder. In certain embodiments, such formulations can be stored either in a ready-to-use form or in a form (*e.g.*, lyophilized) that is reconstituted according to a formulations as described herein prior to administration.

In certain embodiments, kits are provided for producing a single-dose administration unit. In certain embodiments, the kit can contain both a first container having a dried protein and a second container having an aqueous formulation. In certain embodiments, kits containing single and multi-chambered pre-filled syringes (*e.g.*, liquid syringes and lyosyringes) are included.

In certain embodiments, the effective amount of a pharmaceutical composition comprising an anti-CD137 antibody to be employed therapeutically will depend, for example, upon the therapeutic context and objectives. One skilled in the art will appreciate that the appropriate dosage levels for treatment, according to certain embodiments, will thus vary depending, in part, upon the molecule delivered, the indication for which an anti-CD137 antibody is being used, the route of administration, and the size (body weight, body surface or organ size) and/or condition (the age and general health) of the patient. In certain embodiments, the clinician can titer the dosage and modify the route of administration to obtain the optimal therapeutic effect.

In certain embodiments, the frequency of dosing will take into account the pharmacokinetic parameters of an anti-CD137 antibody in the formulation used. In certain embodiments, a clinician will administer the composition until a dosage is reached that achieves the desired effect. In certain embodiments, the composition can therefore be administered as a single dose or as two or more doses (which may or may not contain the same amount of the desired molecule) over time, or as a continuous infusion via an implantation device or catheter. Further refinement of the appropriate dosage is routinely made by those of ordinary skill in the art and is within the ambit of tasks routinely performed by them. In certain embodiments, appropriate dosages can be ascertained through use of appropriate dose-response data.

In certain embodiments, the route of administration of the pharmaceutical composition is in accord with known methods, *e.g.* orally, through injection by intravenous, intraperitoneal, intracerebral (intra-parenchymal), intracerebroventricular, intramuscular, subcutaneously, intra-ocular, intraarterial, intraportal, or intralesional routes; by sustained release systems or by implantation devices. In certain embodiments, the compositions can be administered by bolus injection or continuously by infusion, or by implantation device. In certain embodiments, individual elements of a combination therapy can be administered by different routes.

In some embodiments, the methods can be performed in conjunction with other therapies for cancer. For example, the formulation can be administered to a subject at the same time, prior to, or after, radiation, surgery, targeted or cytotoxic chemotherapy, chemoradiotherapy, hormone therapy, immunotherapy, gene therapy, cell transplant therapy, precision medicine, genome editing therapy, or other pharmacotherapy.

As described above, the formulations described herein (*e.g.*, formulations comprising an anti-CD137 antibody or antigen binding fragment thereof) can be used to treat a variety of cancers such as but not limited to: Kaposi's sarcoma, leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, myeloblasts promyelocyte myelomonocytic monocytic erythroleukemia, chronic leukemia, chronic myelocytic (granulocytic) leukemia, chronic lymphocytic leukemia, mantle cell lymphoma, primary central nervous system lymphoma, Burkitt's lymphoma and marginal zone B cell lymphoma, Polycythemia vera Lymphoma, Hodgkin's disease, non-Hodgkin's disease, multiple myeloma, Waldenstrom's macroglobulinemia, heavy chain disease, solid tumors, sarcomas, and carcinomas, fibrosarcoma, myxosarcoma, liposarcoma, chrondrosarcoma, osteogenic sarcoma, osteosarcoma, chordoma, angiosarcoma, endotheliosarcoma, lymphangiosarcoma, lymphangioendotheliosarcoma, synovioma, mesothelioma, Ewing's tumor, leiomyosarcoma, rhabdomyosarcoma, colon sarcoma, colorectal carcinoma, pancreatic cancer, breast cancer, ovarian cancer, prostate cancer, squamous cell carcinoma, basal cell carcinoma, adenocarcinoma, sweat gland carcinoma, sebaceous gland carcinoma, papillary carcinoma, papillary adenocarcinomas, cystadenocarcinoma, medullary carcinoma, bronchogenic carcinoma, renal cell carcinoma, hepatoma, bile duct carcinoma, choriocarcinoma, seminoma, embryonal carcinoma, Wilm's tumor, cervical cancer, uterine cancer, testicular tumor, lung carcinoma, small cell lung carcinoma, non-small cell lung carcinoma, bladder carcinoma, epithelial carcinoma, glioma, astrocytoma, medulloblastoma, craniopharyngioma, ependymoma, pinealoma,

hemangioblastoma, acoustic neuroma, oligodendroglioma, menangioma, melanoma, neuroblastoma, retinoblastoma, nasopharyngeal carcinoma, esophageal carcinoma, basal cell carcinoma, biliary tract cancer, bladder cancer, bone cancer, brain and central nervous system (CNS) cancer, cervical cancer, choriocarcinoma, colorectal cancers, connective tissue cancer, cancer of the digestive system, endometrial cancer, esophageal cancer, eye cancer, head and neck cancer, gastric cancer, intraepithelial neoplasm, kidney cancer, larynx cancer, liver cancer, lung cancer (small cell, large cell), melanoma, neuroblastoma; oral cavity cancer (for example lip, tongue, mouth and pharynx), ovarian cancer, pancreatic cancer, retinoblastoma, rhabdomyosarcoma, rectal cancer; cancer of the respiratory system, sarcoma, skin cancer, stomach cancer, testicular cancer, thyroid cancer, uterine cancer, and cancer of the urinary system.

In some embodiments, a formulation comprising an anti-CD137 antibody or an antigen-binding fragment thereof described herein can be administered to a subject as a monotherapy. Alternatively, as described above, the formulation comprising an antibody or fragment thereof can be administered to a subject as a combination therapy with another treatment, *e.g.*, another treatment for a cancer. For example, the combination therapy can include administering to the subject (*e.g.*, a human patient) one or more additional agents that provide a therapeutic benefit to a subject who has, or is at risk of developing, cancer. Chemotherapeutic agents suitable for co-administration with compositions of the present invention include, for example: taxol, cytochalasin B, gramicidin D, ethidium bromide, emetine, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicin, doxorubicin, daunorubicin, dihydroxyanthrancindione, mitoxantrone, mithramycin, actinomycin D, 1-dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and puromycin and analogs or homologs thereof. Further agents include, for example, antimetabolites (*e.g.*, methotrexate, 6-mercaptopurine, 6-thioguanine, cytarabine, 5-fluorouracil decarbazine), alkylating agents (*e.g.* mechlorethamine, thioTEPA, chlorambucil, melphalan, carmustine (BSNU), lomustine (CCNU), cyclophosphamide, busulfan, dibromomannitol, streptozotocin, mitomycin C, cis-dichlordiamine platinum (II)(DDP), procarbazine, altretamine, cisplatin, carboplatin, oxaliplatin, nedaplatin, satraplatin, or triplatin tetranitrate), anthracycline (*e.g.* daunorubicin (formerly daunomycin) and doxorubicin), antibiotics (*e.g.* dactinomcin (formerly actinomycin), bleomycin, mithramycin, and anthramycin (AMC)), and anti-mitotic agents (*e.g.* vincristine and vinblastine) and temozolomide. In some embodiments, the formulation comprising an anti-CD137 antibody and the one or more additional active agents

are administered at the same time. In other embodiments, the formulation comprising an anti-CD137 antibody is administered first in time and the one or more additional active agents are administered second in time. In some embodiments, the one or more additional active agents are administered first in time and the formulation comprising an anti-CD137 antibody is administered second in time.

A formulation comprising an anti-CD137 antibody or an antigen-binding fragment thereof described herein can replace or augment a previously or currently administered therapy. For example, upon treating with a formulation comprising an anti-CD137 antibody or antigen-binding fragment thereof, administration of the one or more additional active agents can cease or diminish, *e.g.*, be administered at lower levels or dosages. In some embodiments, administration of the previous therapy can be maintained. In some embodiments, a previous therapy will be maintained until the level of the anti-CD137 antibody reaches a level sufficient to provide a therapeutic effect. The two therapies can be administered in combination.

Monitoring a subject (*e.g.*, a human patient) for an improvement in a cancer, as defined herein, means evaluating the subject for a change in a disease parameter, *e.g.*, a reduction in tumor growth. In some embodiments, the evaluation is performed at least one (1) hour, *e.g.*, at least 2, 4, 6, 8, 12, 24, or 48 hours, or at least 1 day, 2 days, 4 days, 10 days, 13 days, 20 days or more, or at least 1 week, 2 weeks, 4 weeks, 10 weeks, 13 weeks, 20 weeks or more, after an administration. The subject can be evaluated in one or more of the following periods: prior to beginning of treatment; during the treatment; or after one or more elements of the treatment have been administered. Evaluation can include evaluating the need for further treatment, *e.g.*, evaluating whether a dosage, frequency of administration, or duration of treatment should be altered. It can also include evaluating the need to add or drop a selected therapeutic modality, *e.g.*, adding or dropping any of the treatments for a cancer described herein.

In some embodiments, a formulation comprising an anti-CD137 antibody or an antigen-binding fragment thereof described herein is administered to modulate a T-cell response in a patient, for example, by increasing T-cell activation and/or proliferation. Crosslinking of CD137 strongly enhances T cell proliferation, IFN-γ production and secretion, and the cytolytic activity of T cells. Accordingly, in some embodiments, a formulation comprising an anti-CD137 agonist antibody, or an antigen-binding fragment thereof, of the present disclosure is administered to a

patent in need thereof to induce or increase T-cell activation, enhance T cell proliferation, induce the production and/or secretion of IFN-γ, and/or induce a cytolytic T cell response.

In some embodiments, a formulation comprising an anti-CD137 antibody or an antigen-binding fragment thereof described herein is useful to modulate or shift the T-cell population in a patient from a T_H2/T_{reg} T cell population to a T_H1/T_H17 T cell population to thereby improve or enhance an anti-tumor response in the patient. Studies have shown that while CD137 is expressed in both T-cell subsets, Th1 and Th2 T cells, CD137 is expressed at higher levels on CD8+ T cells than on CD4+ T cells. Accordingly, CD137 mainly co-stimulates CD8+ T cells. Accordingly, a formulation comprising an anti-CD137 antibody, or an antigen-binding fragment thereof, as described herein, is administered to a patient to enhance an anti-tumor response, for example, by modulating or shifting the T-cell response and/or T cell population in the patient from a T_H2/T_{reg} T cell response and or T cell population to a T_H1/T_H17 T cell response and/or T cell population in the patient.

In some cancers (*e.g.* melanoma and ovarian cancer), natural tumor-infiltrating lymphocytes (TILs) can be enriched through optimized cell culture methods and provide a source of tumor-reactive lymphocytes useful for adoptive immunotherapy. Adoptive TIL therapy can result in durable tumor regression for some types of cancer, which warrants the development and optimization of TIL-based approaches for cancer. Currently, the identification and expansion of natural tumor-reactive TILs remains challenging due to low level and/or rarity of antigen-specific CD8+ T cells. CD137 expression by T cells is activation dependent, which provides an opportunity to capture CD137-expressing activated T cells from circulation or from tumor samples. Accordingly, a formulation comprising an anti-CD137 antibody, or an antigen-binding fragment thereof, as described herein, can be employed for the selective enrichment of activated, antigen-specific T cells.

In some embodiments, the efficacy of the formulations comprising the anti-CD137 antibodies described herein is dependent on a competent immune system. Specifically, in some embodiments, depletion of CD4+ T cells, CD8+ T cells and/or Natural Killer cells reduces the efficacy of the anti-CD137 antibodies. In some embodiments, depletion of CD4+ T cells, CD8+ T cells and/or Natural Killer cells reduces the inhibition or reduction of tumor growth by the anti-CD137 antibodies described herein. In some embodiments, depletion of CD4+ T cells, CD8+ T cells and/or Natural Killer cells reduces the inhibition or reduction of tumor growth by the anti-

CD137 antibodies described herein. In some embodiments, the efficacy of a formulation comprising the anti-CD137 antibodies described herein is dependent on an infiltration of immune cells into a tumor microenvironment. In some embodiments, the infiltration of immune cells into a tumor microenvironment is coupled with a lack of infiltration into the spleen and/or liver.

In some embodiments, the formulations comprising the anti-CD137 antibodies described herein induce a protective anti-tumor memory immune response. Memory T cells are a subset of antigen-specific T cells that persist long-term after having encountered and responded to their cognate antigen. Such cells quickly expand to large numbers of effector cells upon re-exposure to their cognate antigen. Accordingly, in some embodiments the formulations comprising the anti-CD137 antibodies described herein stimulate the production of memory T cells to a cancer antigen. In some embodiments, a subject that has received a formulation comprising an anti-CD137 antibody described herein to treat or cure a cancer, develops memory T cells specific to the cancer. In some embodiments, a subject that has received a formulation comprising an anti-CD137 antibody described herein to treat or cure a cancer, develops an anti-tumor memory immune response upon re-exposure to the cancer. In some embodiments, the anti-tumor memory immune response comprises stimulating memory T cells to become effector cells. In some embodiments, a subject that has received a formulation comprising an anti-CD137 antibody described herein to treat or cure a cancer, develops an anti-tumor memory immune response to a cancer antigen.

In some embodiments, the formulations comprising anti-CD137 antibodies described herein induce immune re-programming with a tumor microenvironment. Specifically, in some embodiments, the formulations comprising anti-CD137 antibodies induce immune infiltration; reduce, inhibit or prevent Treg proliferation; reduce, inhibit or prevent tumor-associated macrophage proliferation; and protect or reverse T cell exhaustion.

In some embodiments, the formulations comprising anti-CD137 antibodies induce infiltration of immune cells into a tumor microenvironment relative. In some embodiments, the formulations comprising anti-CD137 antibodies increase immune cell infiltration by at least 5%, at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 100%, at least 105%, at least 110%, at least 115%, at least 120%, at least 125%, at least 130%, at least 135%, at least 140%, at least 145%, or at least 150%. In some embodiments, immune cell infiltration is determined by measuring the

level of CD45 expression on cells isolated from a tumor microenvironment. Methods for measuring protein expression are known to those of skill in the art and described herein.

In some embodiments, the formulations comprising anti-CD137 antibodies prevent or inhibit an increase in Treg cells in a tumor microenvironment. In some embodiments, prevention or inhibition is relative to the amount of Treg cells in a tumor microenvironment in the absence of an anti-CD137 antibody. In some embodiments, prevention or inhibition of an increase in Treg cells is relative to a reference antibody. In some embodiments, Treg cells are detected by expression of CD25 and FOX-3P on CD4+ T cells isolated from a tumor microenvironment. Methods for measuring protein expression are known to those of skill in the art and described herein.

In some embodiments, the formulations comprising anti-CD137 antibodies prevent or inhibit an increase in tumor-associated macrophages in a tumor microenvironment. In some embodiments, prevention or inhibition is relative to the amount of tumor-associated macrophages in a tumor microenvironment in the absence of an anti-CD137 antibody. In some embodiments, prevention or inhibition of an increase in tumor-associated macrophages is relative to a reference antibody. In some embodiments, tumor-associated macrophages are detected by expression of CD11b and F4/80 on CD45+ immune cells isolated from a tumor microenvironment. Methods for measuring protein expression are known to those of skill in the art and described herein.

In some embodiments, the formulations comprising anti-CD137 antibodies protect T cells from T cell exhaustion in a tumor microenvironment. In some embodiments, the formulations comprising anti-CD137 antibodies reverse T cell exhaustion in a tumor microenvironment. In some embodiments, T cell exhaustion in a tumor microenvironment is reduced in the presence of a formulation comprising an anti-CD137 antibody described herein, relative to a tumor microenvironment in the absence of the anti-CD137 antibody. In some embodiments, T cell exhaustion is determined by analyzing CD8+ T cells or CD4+ T cells for expression of co-inhibitory receptors (*e.g.*, PD-1, TIGIT or LAG-3). In some embodiments, T cell exhaustion is detected by expression of PD-1 and TIGIT on CD4+ or CD8+ T cells isolated from a tumor microenvironment.

In some embodiments, a formulation comprising an anti-CD137 antibody, or an antigen-binding fragment thereof, described herein, can be employed in methods of detection and/or quantification of human CD137 in a biological sample. Accordingly, formulations comprising an

anti-CD137 antibodies, or an antigen-binding fragment thereof, as described herein, are used to diagnose, prognose, and/or determine progression of disease (*e.g.*, cancer) in a patient.

Other Embodiments

The disclosure relates to the following embodiments. Throughout this section, the term embodiment is abbreviated as 'E' followed by an ordinal. For example, E1 is equivalent to Embodiment 1.

E1. A formulation comprising:

(a) an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises a heavy chain CDR3 of SEQ ID NO: 126, wherein X is any amino acid, and

(b) a buffer comprising histidine.

E2. A formulation comprising:

(a) an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises a heavy chain CDR3 of SEQ ID NO: 126, wherein X is any amino acid,

(b) a buffer comprising histidine; and

(c) a disaccharide sugar.

E3. A formulation comprising:

(a) an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises a heavy chain CDR3 of SEQ ID NO: 126, wherein X is any amino acid, and

(b) a buffer comprising histidine;

wherein the formulation has a pH of about 5.0-7.0.

E4. A formulation comprising:

(a) an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises a heavy chain CDR3 of SEQ ID NO: 126, wherein X is any amino acid,

(b) a buffer comprising histidine,

(c) a disaccharide sugar,

(d) a non-ionic surfactant, and

(e) a salt,

wherein the pH of the formulation is about 5.0 to about 7.0.

E5. A formulation comprising:

(a) an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises a heavy chain CDR3 of SEQ ID NO: 126, wherein X is any amino acid,

(b) a buffer comprising histidine,

(c) a disaccharide sugar at about 5%-about 15% weight/volume,

(d) a non-ionic surfactant at about 0.01%-about 0.1% weight/volume (w/v), and

(e) a salt at about 50 mM – 200 mM,

wherein the pH of the formulation is about 5.0 to about 7.0

E6. A formulation comprising:

(a) an anti-CD137 antibody at a concentration of about 1mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises a heavy chain CDR3 of SEQ ID NO: 126, wherein X is any amino acid,

(b) a buffer comprising about 10 mM to about 100 mM histidine,

(c) sucrose at about 5%-about 15% weight/volume,

(d) polysorbate-80 at about 0.01%-about 0.1% weight/volume (w/v), and

(e) NaCl at about 50 mM – 200 mM,

wherein the pH of the formulation is about 5.0 to about 7.0.

E7. A formulation comprising:

(a) an anti-CD137 antibody at a concentration of about 1 mg/ml to about 100 mg/ml, wherein the anti-CD137 antibody comprises a heavy chain CDR3 of SEQ ID NO: 126, wherein X is any amino acid,

(b) a buffer comprising about 20 mM histidine,

(c) sucrose at about 10% weight/volume (w/v),

(d) polysorbate-80 at about 0.03% weight/volume (w/v), and

(e) NaCl at about 100mM,

wherein the pH of the formulation is about 6.0.

E8. The formulation of any one of embodiments 1-7, wherein the anti-CD137 antibody comprises a heavy chain CDR3 of DXPFXLDXXYYYYYX (SEQ ID NO: 127), wherein X is any amino acid.

E9. The formulation of any one of embodiments 1-7, wherein the anti-CD137 antibody comprises a heavy chain CDR3 of $DX_1X_2X_3X_4LX_5X_6X_7X_8YX_9YYX_{10}$ (SEQ ID NO: 128), wherein X_1 is any amino acid, wherein X_2 is a non-polar amino acid, wherein X_3 is a non-polar amino acid, wherein X_4 is any amino acid, wherein X_5 is a polar amino acid, wherein X_6 is any amino acid, wherein X_7 is any amino acid, wherein X_8 is a polar amino acid, wherein X_9 is a polar amino acid, and wherein X_{10} is any amino acid.

E10. The formulation of embodiment 9, wherein X_2 is proline, X_3 is phenylalanine or tryptophan, X_5 is aspartic acid or glutamic acid, X_8 is tyrosine, and X_9 is tyrosine.

E11. The formulation of any one of embodiments 1-10, wherein the anti-CD137 antibody comprises a heavy chain CDR3 of SEQ ID NO: 68.

E12. The formulation of any one of embodiments 1-11, wherein the anti-CD137 antibody comprises a comprises a heavy chain CDR1 of SEQ ID NO: 48, a heavy chain CDR2 of SEQ ID NO: 56, and a heavy chain CDR3 of SEQ ID NO: 68, and a light chain CDR1 of SEQ ID NO: 69, a light chain CDR2 of SEQ ID NO: 78, and a light chain CDR3 of SEQ ID NO: 89.

E13. The formulation of any one of embodiments 1-11, wherein the anti-CD137 antibody comprises a comprises a heavy chain CDR1 of SEQ ID NO: 51, a heavy chain CDR2 of SEQ ID NO: 108, and a heavy chain CDR3 of SEQ ID NO: 68, and a light chain CDR1 of SEQ ID NO: 69, a light chain CDR2 of SEQ ID NO: 78, and a light chain CDR3 of SEQ ID NO: 89.

E14. The formulation of any one of embodiments 1-12, wherein the anti-CD137 antibody comprises heavy and light chain sequences comprising amino acid sequences having at least 90% identity to SEQ ID NOs: 4 and 6, respectively.

E15. The formulation of embodiment 14, wherein the anti-CD137 antibody comprises heavy and light chain sequences having amino acid sequences set forth in SEQ ID NOs: 4 and 6, respectively.

E16. The formulation of any one of embodiments 1-11 and 13, wherein the anti-CD137 antibody comprises heavy and light chain sequences comprising amino acid sequences having at least 90% identity to SEQ ID NOs: 101 and 6, respectively.

E17. The formulation of embodiment 16, wherein the anti-CD137 antibody comprises heavy and light chain sequences having amino acid sequences set forth in SEQ ID NOs: 101 and 6, respectively.

E18. The formulation of any one of embodiments 1-15, wherein the antibody comprises an IgG1 heavy chain constant region.

E19. The formulation of embodiment 18, wherein the IgG1 heavy chain constant region is a wild-type human IgG1 heavy chain constant region

E20. The formulation of embodiment 18, wherein the IgG1 heavy chain constant region comprises an amino acid substitution relative to a wild-type human IgG1 heavy chain constant region.

E21. The formulation of any one of embodiment 1-15, wherein the antibody comprises an IgG4 heavy chain constant region.

E22. The formulation of embodiment 21, wherein the IgG4 heavy chain constant region is a wild-type human IgG4 heavy chain constant region

E23. The formulation of embodiment 21, wherein the IgG4 heavy chain constant region comprises an amino acid substitution relative to a wild-type human IgG4 heavy chain constant region.

E24. The formulation of any one of embodiments 1-23, comprising about 10 mM histidine to about 100 mM histidine.

E25. The formulation of any one of embodiments 1-24, comprising about 20 mM histidine.

E26. The formulation of any one of embodiments 1, 3, 6, and 8-24, further comprising a disaccharide sugar.

E27. The formulation of any one of embodiments 2, 4, 5, and 26, wherein the disaccharide sugar is selected from sucrose, lactose, and maltose.

E28. The formulation of embodiment 27, wherein the disaccharide sugar is sucrose.

E29. The formulation of any one of embodiments 2, 4, and 26-28, wherein the disaccharide sugar is at about 5%-about 15% weight/volume.

E30. The formulation of any one of embodiments 2, 4, 5, and 26-28, wherein the disaccharide sugar is at about 10% weight/volume.

E31. The formulation of any one of embodiments 1-3 and 8-24, further comprising a salt.

E32. The formulation of any one of embodiments 4, 5, and 31, wherein the salt is NaCl.

E33. The formulation of any one of embodiments 4 and 31-32, wherein the salt is at a concentration of about 50 mM - 200 mM.

E34. The formulation of any one of embodiments 4-6 and 31-32, wherein the salt is at a concentration of about 100 mM.

E35. The formulation of any one of embodiments 1, 2, and 8-24, wherein the formulation has a pH of about 5.0-7.0.

E36. The formulation of any one of embodiments 3, 5, 6, and 35 wherein the pH is about 6.0.

E37. The formulation of any one of embodiments 1-3 and 8-36, further comprising a non-ionic surfactant.

E38. The formulation of any one of embodiments 4, 5, and 37, wherein the non-ionic surfactant is a polysorbate.

E39. The formulation of embodiment 38, wherein the polysorbate is polysorbate-80.

E40. The formulation of any one of embodiments 4 and 37-38, wherein the non-ionic surfactant is at about 0.01%-about 0.1% weight/volume (w/v).

E41. The formulation of any one of embodiments 4, 5, and 37-38, wherein the non-ionic surfactant is at about 0.03% weight/volume (w/v).

E42. The formulation of any one of embodiments 1-41, comprising the anti-CD137 antibody at a concentration of about 5 mg/ml to about 15 mg/ml.

E43. The formulation of any one of embodiments 1-41, comprising the anti-CD137 antibody at a concentration of about 15 mg/ml to about 30 mg/ml.

E44. The formulation of any one of embodiments 1-41, comprising the anti-CD137 antibody at a concentration of about 30 mg/ml to about 45 mg/ml.

E45. The formulation of any one of embodiments 1-41, comprising the anti-CD137 antibody at a concentration of about 45 mg/ml to about 60 mg/ml.

E46. The formulation of any one of embodiments 1-41, comprising the anti-CD137 antibody at a concentration of about 60 mg/ml to about 75 mg/ml.

E47. The formulation of any one of embodiments 1-41, comprising the anti-CD137 antibody at a concentration of about 75 mg/ml to about 90 mg/ml.

E48. The formulation of any one of embodiments 1-41, comprising the anti-CD137 antibody at a concentration of about 85 mg/ml to about 100 mg/ml.

E49. The formulation of any one of embodiments 1-41, comprising the anti-CD137 antibody at a concentration of about 5 mg/ml.

E50. The formulation of any one of embodiments 1-41, comprising the anti-CD137 antibody at a concentration of about 10 mg/ml.

E51. The formulation of any one of embodiments 1-41, comprising the anti-CD137 antibody at a concentration of about 15 mg/ml.

E52. The formulation of any one of embodiments 1-41, comprising the anti-CD137 antibody at a concentration of about 20 mg/ml.

E53. A method for inducing or enhancing dimerization of human CD137 trimers in a subject, comprising administering to a subject in need thereof, an effective amount of the formulation of any one of embodiments 1-52.

E54. A method for inducing or enhancing multimerization of human CD137 trimers in a subject, comprising administering to a subject in need thereof, an effective amount of the formulation of any one of embodiments 1-52.

E55. A method for inducing or enhancing T cell activation in a subject, comprising administering to a subject in need thereof, an effective amount of the formulation of any one of embodiments 1-52.

E56. The method of embodiment 55, wherein the T cell activation occurs in a tumor microenvironment.

E57. A method for inducing or enhancing a cytotoxic T cell response in a subject, comprising administering to a subject in need thereof, an effective amount of the formulation of any one of embodiments 1-52.

E58. The method of embodiment 57, wherein the cytotoxic T cell response occurs in a tumor microenvironment.

E59. A method for inducing or enhancing cytokine production of an immune cell in a subject, comprising administering to a subject in need thereof, an effective amount of the formulation of any one of embodiments 1-52.

E60. The method of embodiment 59, wherein the cytokine produced is IL-2, TNFα, IL-13, IFN-γ, or combinations thereof.

E61. The method of embodiment 59 or embodiment 60, wherein the cytokine production occurs in a tumor microenvironment.

E62. A method for inducing or enhancing T cell proliferation in a subject, comprising administering to a subject in need thereof, an effective amount of the formulation of any one of embodiments 1-52.

E63. The method of embodiment 62, wherein the T cell proliferation occurs in a tumor microenvironment.

E64. A method for reducing or inhibiting tumor growth, comprising administering to a subject in need thereof, an effective amount of the formulation of any one of embodiments 1-52.

E65. A method for treating a disorder mediated by human CD137 in a subject, comprising administering to a subject in need thereof, an effective amount of the formulation of any one of embodiments 1-52.

E66. A method for treating cancer in a subject, comprising administering to a subject in need thereof, an effective amount of the formulation of any one of embodiments 1-52.

E67. The method of any one of embodiments 64-66, wherein infiltration of immune cells into a tumor microenvironment is increased after administration of the formulation.

E68. The method of embodiment 67, wherein the immune cells express CD45.

E69. The method of any one of embodiments 64-68, wherein the quantity of T regulatory (Treg) cells is reduced in a tumor microenvironment after administration of the formulation.

E70. The method of embodiment 69, wherein the Treg cells express CD4, FOXP-3 and CD25.

E71. The method of any one of embodiments 64-70, wherein the quantity of macrophages is reduced in a tumor microenvironment after administration of the isolated monoclonal antibody or antigen binding portion.

E72. The method of embodiment 71, wherein the macrophages express CD45 and CD11b.

E73. The method of any one of embodiments 64-72, wherein T cell exhaustion is reduced in a tumor microenvironment after administration of the isolated monoclonal antibody or antigen binding portion, optionally wherein reduction of T cell exhaustion comprises a decrease in expression of TIGIT, PD-1, LAG-3, or combinations thereof.

E74. The method of any one of embodiments 66-73, wherein the cancer is selected from the group consisting of melanoma, glioma, renal, breast, hematological, and head and neck cancer.

E75. The method of embodiment 74, wherein the hematological cancer is a B cell lymphoma.

E76. A method of inducing an anti-tumor memory immune response, comprising administering to a subject in need thereof, an effective amount of the formulation of embodiments 1-52.

E77. The method of any one of embodiments 53-76, wherein the anti-CD137 antibody binds Fc gamma receptor.

E78. The method of any one of embodiments 53-77, wherein depletion of CD4+ T cells, CD8+ T cells, Natural Killer cells, or combinations thereof, reduces the efficacy of the formulation.

E79. A kit comprising a container comprising the formulation of any one of embodiments 1-52, and a package insert comprising instructions for administration of the formulation, for treating or delaying progression of cancer or reducing or inhibiting tumor growth in a subject in need thereof.

E80. A kit comprising a container comprising the formulation of any one of embodiments 1-52, and a package insert comprising instructions for administration of the formulation alone or in combination with another agent, for treating or delaying progression of cancer or reducing or inhibiting tumor growth in a subject in need thereof.

E81. The use of the formulation of any one of embodiments 1-52, for the manufacture of a medicament for treating or delaying progression of cancer or reducing or inhibiting tumor growth in a subject in need thereof.

E82. A formulation according to any one of embodiments 1-52, in the manufacture of a medicament for treating or delaying progression of cancer or reducing or inhibiting tumor growth in a subject in need thereof.

E83. A formulation according to any one of embodiments 1-52, for use as a medicament.

EXAMPLES

While the present disclosure has been described with reference to the specific embodiments thereof, it should be understood by those skilled in the art that various changes may be made and equivalents may be substituted without departing from the true spirit and scope of the disclosure. In addition, many modifications may be made to adapt a particular situation, material, composition of matter, process, process step or steps, to the objective, spirit and scope of the present disclosure. All such modifications are intended to be within the scope of the disclosure.

Example 1: Synthetic Human Monoclonal Antibodies Produced in Yeast Exhibit Binding To Recombinant Human CD137

Purified CD137 protein antigen was biotinylated using the EZ-Link Sulfo-NHS-Biotinylation Kit (Thermo Scientific). CD137 antigens were concentrated to ~1mg/mL and buffer exchanged into PBS before addition of 1:7.5 molar ratio biotinylation reagent (EZ-Link Sulfo-NHS-Biotinylation Kit, Thermo Scientific, Cat #21425.). The mixture was held at 4°C overnight prior to another buffer exchange to remove free biotin in the solution. Biotinylation was confirmed through Streptavidin sensor binding of the labeled proteins on a FORTE BIO®. Successful biotinylation of the CD137 protein antigen was confirmed via detectable binding to a streptavidin-linked biosensor installed on FORTEBIO OCTET™ Red384 Interferometer (Pall ForteBio, Menlo Park, CA) according to the manufacturer's guidelines (data not shown).

Eight naïve human synthetic yeast-based antibody libraries each of ~10^9 diversity were designed, generated, and propagated as described previously (see, *e.g.*, WO2009036379; WO2010105256; WO2012009568; Xu et al., Protein Eng Des Sel. 2013 Oct;26(10):663-70). Eight parallel selections were performed, using the eight naïve libraries against biotinylated human CD137-Fc fusion.

For the first two rounds of selection, a magnetic bead sorting technique utilizing the Miltenyi MACS system was performed, essentially as described (Siegel *et al.*, J Immunol Methods. 2004 Mar;286(1-2):141-53). Briefly, yeast cells (~10^{10} cells/library) were incubated with 10 mL of 10 nM biotinylated human CD137-Fc fusion antigen for 15 minutes at room temperature in FACS wash buffer PBS with 0.1% BSA. After washing once with 50 mL ice-cold wash buffer, the cell pellet was resuspended in 40 mL wash buffer, and 500 µl Streptavidin MicroBeads (Miltenyi Biotec, Bergisch Gladbach, Germany. Cat # 130-048-101) were added to the yeast and incubated for 15 minutes at 4°C. Next, the yeast were pelleted, resuspended in 5 mL wash buffer, and loaded onto a MACS LS column (Miltenyi Biotec, Bergisch Gladbach, Germany. Cat.# 130-042-401). After the 5 mL was loaded, the column was washed three times with 3 mL FACS wash buffer. The column was then removed from the magnetic field, and the yeast were eluted with 5 mL of growth media and then grown overnight.

Subsequent to the two rounds of MACS, three rounds of sorting were performed using flow cytometry (FACS), which are described in the following three paragraphs.

Selection strategy employing 8 parallel selections with Fc antigen

The eight libraries from the MACS selections were taken through three rounds of FACS selections. Approximately 1×10^8 yeast per library were pelleted, washed three times with wash buffer, and incubated with 10 nM of biotinylated human CD137-Fc fusion and 10 nM of biotinylated murine CD137-Fc fusion antigen separately for 10 minutes at room temperature. Yeast were then washed twice and stained with goat anti-human $F(ab')_2$ kappa-FITC diluted 1:100 (Southern Biotech, Birmingham, Alabama, Cat# 2062-02) and either streptavidin-Alexa Fluor 633 (Life Technologies, Grand Island, NY, Cat # S21375) diluted 1:500, or Extravidin-phycoerthyrin (Sigma-Aldrich, St Louis, Cat # E4011) diluted 1:50, secondary reagents for 15 minutes at 4°C. After washing twice with ice-cold wash buffer, the cell pellets were resuspended in 0.4 mL wash buffer and transferred to strainer-capped sort tubes. Sorting was performed using a FACS ARIA sorter (BD Biosciences) and sort gates were determined to select only CD137 binding. The murine- and human-selected populations from the first round of FACS were brought forward into the next round.

The second and third round of FACS for the above selected populations involved positive sorts for binders to human and/or murine CD137 reagents; or negative sorts to decrease polyspecific reagent binders (Xu *et al.*, PEDS. 2013 Oct;26(10):663-70). Depending on the amount of polyspecific binding or target binding of a specific selection output, a positive sort followed a negative sort or vice versa, to enrich for a full binding population with limited amount of polyspecific binding. Competition selections were also performed with control mAbs from the literature. For competition selections, mAb4 (urelumab; Bristol-Myers Squibb; CAS Number: 934823-49-1) and mAb5 (utomilumab; Pfizer; CAS Number: 1417318-27-4) were pre-complexed to biotinylated human CD137-Fc fusion. Antibodies that bind and do not bind in the presence of the control mAbs were selected for on FACS. The outputs of these rounds were plated and isolates were picked for sequencing and characterization.

Affinity maturation of clones identified in naïve selections

Heavy chains from the first FACS sorting round against biotinylated human CD137 Fc fusion outputs were used to prepare light chain diversification libraries used for four additional selection rounds. The first of these selection rounds utilized Miltenyi MACs beads conjugated with 10 nM biotinylated human CD137-Fc fusion as antigen.

Subsequent to the MACs bead selections, three rounds of FACS sorting were performed. The first of these rounds used biotinylated human CD137-Fc fusion at 10nM. The second FACS round for the above involved positive sorts for binders to mouse CD137 reagents, competition sorts with previously mentioned control mAbs or negative sorts to decrease polyspecific reagent binders as described above. The third and final round of FACS selection was done using either biotinylated murine CD137 Fc fusion at 10 nM or biotinylated human monomeric CD137 at 50 nM. Individual colonies from each FACS selection round described above were picked for sequencing characterization.

IgG and Fab production and purification

Yeast clones were grown to saturation and then induced for 48 hours at 30°C with shaking. After induction, yeast cells were pelleted and the supernatants were harvested for purification. IgGs were purified using a Protein A column and eluted with acetic acid, pH 2.0. Fab fragments were generated by papain digestion and purified over CaptureSelect IgG-CH1 affinity matrix (LifeTechnologies, Cat # 1943200250).

Example 2: Epitope Binning and Determination of Human Anti-CD137 Antibody Affinity to Recombinant CD137

Epitope binning of the antibodies isolated in Example 1 was performed on a Forte Bio Octet Red384 system (Pall Forte Bio Corporation, Menlo Park, CA) using a standard sandwich format binning assay. CD137 control antibody IgGs were loaded onto AHQ sensors and unoccupied Fc-binding sites on the sensor were blocked with a non-relevant human IgG1 antibody. The sensors were then exposed to 100 nM target antigen followed by exposure to the isolated antibodies identified as described in Example 1. Data were processed using ForteBio's Data Analysis Software 7.0. Additional binding by the second antibody after antigen association indicates an unoccupied epitope (non-competitor), while no binding indicates epitope blocking (competitor) (data not shown).

Affinity of the CD137 antibodies was determined by measuring their kinetic constants (k_a, k_d, K_D) on ForteBio Octet. ForteBio affinity measurements were performed generally as previously described (Estep *et al.*, MAbs. 2013 5(2):270-8). Briefly, ForteBio affinity measurements were performed by loading antibodies (IgGs) on-line onto AHQ sensors. Sensors

were equilibrated off-line in assay buffer for 30 minutes and then monitored on-line for 60 seconds for baseline establishment. For avid binding measurement, sensors with loaded IgGs were exposed to 100 nM antigen (human, cyno, or murine CD137) for 3 minutes, afterwards they were transferred to assay buffer for 3 minutes for off-rate measurement. Monovalent binding measurements were obtained by loading human CD137-Fc fusion on AHQ sensors followed by exposure to 200 nM antibody Fab in solution. Kinetics data were fit using a 1:1 binding model in the data analysis software provided by ForteBio (data not shown).

Determination of whether antibodies were ligand blocking was also assessed. Specifically, ligand blocking experiments were performed both on Octet HTX (ForteBio) and on label-free MX96 SPRi (Caterra). mAb1 was captured on Octet sensor or MX96 chip sensor. CD137 and CD137L were sequentially applied to the sensors pre-loaded with mAb1. An increase in response upon exposure to CD137L indicated non-competition between mAb1 and CD137L for binding to CD137. On the other hand, a lack of change in the signal indicated competition, which was the case for control antibody mAb5. mAb1 did not inhibit binding of CD137L to CD137 (data not show), and therefore was considered a non-ligand blocking antibody.

Example 3: Distribution of Binding Affinities of Affinity-Matured Anti-CD137 Antibodies

Affinity matured anti-CD137 antibodies were generated using 2 mutant libraries. The first library contained mutations in the heavy chain and the second library contained mutations in the light chain, wherein donor diversity in light chain CDR1, CDR2 and CDR3 was created. The mutant libraries went through 3 rounds of phage panning aimed at increasing affinity and maintaining cross-reactivity with mouse CD137. In each round, an off-rate competition step was employed after initial binding to biotinylated antigens (i.e., 1 hour incubation with excess unlabeled antigen or parental IgG at 37°C).

The resulting anti-CD137 antibodies from different selection rounds were plotted on k_d/k_a double log plots. Apparent association and dissociation kinetic rate constants (k_a and k_d values) were determined on an SPRi reader (MX96, Carterra) in a running buffer of PBS-T 0.01%. Anti-human CD137 antibodies were covalently printed on a Carboxymethyldextran hydrogel 50L chip (Xantec bioanalytics) on a CFM (Carterra). Freshly mixed activating reagents (150 ml 0.4 M EDC and 150 ml 0.1 M sulfo-NHS in H2O) were used to activate the surface of the SPR substrate for 7 minutes. Antibodies at 10 mg/ml in acetic acid buffer pH 4.5 were used for printing for 15 minutes.

The printed chip was then quenched on SPRi reader (MX96, Carterra) with 1 M ethanolamine for 15 minutes. For kinetics analysis, purified recombinant his tagged human CD137 (0, 2.05, 5.12, 12.8, 32, 80, 200, 500 nM) was injected sequentially. For each concentration, there was 5 minutes of association followed by 10 minutes of dissociation. Data were processed and analyzed in SPR Inspection Tool and Scrubber softwares. The kinetic data were referenced with the interstitial reference spots and double-referenced to a buffer cycle, and then fit globally to a 1:1 binding model to determine their apparent association and dissociation kinetic rate constants (k_a and k_d values). The ratio k_d/k_a was used to derive the K_D value of each antigen/mAb interaction, i.e. $K_D=k_d/k_a$.

Antibodies with K_D (k_d/k_a) between 10-20 nM are shown as upright triangles, while the ones with K_D lower than 10 nM are shown as upside down triangles (**FIG. 1**). Affinity maturation of only the heavy chains (top panels) or only the light chains (bottom panels) both resulted in the isolation of anti-CD137 antibodies with higher binding affinities than the parental antibody (mAb1) (**FIG. 1**). The heavy chain and light chain variable regions of mAb1 are set forth in SEQ ID NOs: 4 and 6, respectively.

Example 4: Identification of Critical Binding Residues Comprising Heavy Chain CDR3 (CDRH3) of Anti-CD137 Antibodies

To determine which amino acid residues within CDRH3 are critical for the binding of mAb1 to mouse and human CD137 polypeptides, alanine scanning was performed. A set of polynucleotides encoding derivatives of the mAb1 open reading frame was generated, wherein each derivative contained a single alanine residue substitution at a wild-type amino acid residue position comprising CDRH3. Positions D95 through M100I of SEQ ID NO: 4 were each mutated to alanine by replacing the wild-type codon with the alanine codon GCC. The amino acid sequences of each CDRH3 of each mAb1 alanine-substituted derivative are set forth in SEQ ID NOs: 111-125. The polynucleotides encoding each of the 15 mAb1 alanine-substituted derivatives were individually cloned into an expression vector (aglyco-IgG1, DID-2600) via Gibson Assembly. Each mAb1 alanine-substituted derivative was expressed and purified using standard techniques known in the art. Binding affinities of each mAb1 alanine-substituted derivative for human and mouse CD137 were determined via Wasatch SPR kinetics measurements for human CD137 (huCD137) or equilibrium cell-binding assays for mouse CD137 (mCD137).

Table 1 provides the calculated dissociation constants (K_D) for each mutant. When "*Weak*" is noted in the table there was measurable binding above background but not enough confidence in the curve fitting to assign an accurate K_D value. In Table 1, "**NB**" signifies that no binding was observed during the determination of binding affinities and indicates which alanine substitutions in CDRH3 resulted in an antibody that did not bind to CD137.

Table 1: Binding affinity (K_D) of alanine scanning clones for human and mouse CD137

Substitution	huCD137	mCD137	Substitution	huCD137	mCD137
D95A	**NB**	**NB**	Y(100C)A	1nM	25nM
S96A	1.8nM	40nM	Y(100D)A	*Weak*	170nM
P97A	*Weak*	*Weak*	Y(100E)A	**NB**	**NB**
F98A	*Weak*	*Weak*	Y(100F)A	*Weak*	*Weak*
L99A	2.7nM	33nM	Y(100G)A	**NB**	**NB**
L100A	**NB**	**NB**	Y(100H)A	**NB**	**NB**
D(100A)A	*Weak*	*Weak*	M(100I)A	1.8nM	21nM
D(100B)A	1.3nM	54nM	WT K_D	1nM	11nM

The retention, weakening, or loss of binding affinity resulting from mutations to alanine informed the determination of which residues were required for CD137 binding and which residues tolerated mutations. **FIG. 2** summarizes the binding data for alanine scanning of CDRH3 with wild-type amino acid identity indicated at each position. CDRH3 positions are color-coded based on the effects of mutating the position to alanine, as shown. This analysis resulted in the following consensus sequence: **D**X*PF*X**L***D*XX*Y***YY**X. When **bolded** residues in the consensus sequence were mutated to alanine there was a complete loss of binding and these residues were therefore necessary for mAb1 binding to CD137. When *italicized* residues in the consensus sequence were mutated to alanine the antibody was still able to bind CD137 but with a weaker affinity indicating these residues played a partial role in binding but were not absolutely required. When residue positions denoted with an X in the consensus sequence were mutated to alanine there was little to no change in binding affinity. Thus, these residues tolerated mutations and were not critical to the binding interaction.

Example 5: Epitope Mapping by Scanning Saturation Mutagenesis and Homolog Comparison

Functional mapping of the CD137 epitope by scanning saturation mutagenesis library and homology comparison were performed to identify residues important for antibody binding to CD137. Combinatorial libraries of CD137 mutants with single point mutations at all residue positions to every possible amino acid substitution except cysteine were generated and tested for their ability to bind to mAb1, mAb4, and mAb5. A library consisting of genes encoding each point mutant of CD137 were synthesized from a commercial supplier and cloned into a mammalian display expression vector. Mammalian display was used to present a library of variant human CD137 extracellular domains, with each variant having at least one point mutation relative to wild type human CD137.

The library of cells displaying CD137 variants was stained with non-overlapping antibodies (i) mAb4 and mAb1 or (ii) mAb4 and mAb5. Populations of cells with reduced binding to one antibody but not the other were enriched by FACS. Each population was sequenced by Illumina sequencing to identify mutations in positions that specifically disrupted binding to each antibody but did not affect correct folding of CD137 or binding to the non-overlapping antibody.

For mAb1, K114 was identified as the most important residue important for binding to CD137, with 34% of all mutations observed occurring in that position, and all amino acid substitutions observed. E111, T113, and P135 are also important for binding, with 10% of mutations observed in each of those positions. Additionally, N126 and I132 was observed in the population that had partial decrease in binding for mAb1. **FIG. 3A** shows the residues comprising the epitope for mAb1, mAb4 and mAb5. mAb4 and mAb5 had binding epitopes that were distinct from mAb1. For mAb4, N42 was the most important residue with 50% of all mutations observed in that position, followed by R41 and D38. For mAb5, I132 was the most important with 32% of all mutations occurring in that position, followed by N126, G96, K114, and L95.

Point mutants isolated from the library screen were expressed as soluble proteins and tested for binding to mAb1. All 4 mutations tested at K114 (R, E, N, T) abolished binding to mAb1. Mutations at T113 and P135 also disrupted binding. 1/2 point mutants at E111, 1/3 mutants at N126, and 1/4 mutants at I132 showed no binding. Likewise, 3/3 mutants at N42 did not bind to mAb4, and 3/4 mutants at I132 did not bind to mAb5.

Additionally, CD137 homologs were tested for their binding to mAb1. mAb1 was able to bind to mouse CD137, but not to rat CD137, as shown in **FIG. 3B**. To determine if there was a difference in the residues comprising the epitope for mAb1 between mouse CD137 and rat CD137, the amino acid sequences of CD137 homologs from human, cynomolgus monkey, rat, and mouse were aligned for comparison. All of the amino acid residues comprising the mAb1 epitope are present in human, cynomolgus monkey, and mouse, but not in rat. Lysine 114 (K114) of the human CD137 sequence, as well as the corresponding lysine in the cynomolgus monkey and mouse CD137 sequences, is glutamic acid (E) in the rat CD137 sequence, further indicating that K114 of the human CD137 sequence is at least one of the critical binding residues for mAb1.

FIGs. 3C and 3D show the crystal structure of human CD137 bound to CD137L (Bitra A et al., J Biol Chem 2018, 293(26):9958-9969), wherein residues E111, T113, K114 and P135 are shown as spheres. As can be seen, these residues are located away from the CD137 ligand (CD137L) binding domain, shown in grey.

Example 6: Effect of Anti-CD137 Antibodies on Immune Regulators and CD8+ T Cells in Mice

Three anti-CD137 antibodies generated in Example 1, mAb1, mAb2 and mAb3, were further analyzed for their efficacy. These antibodies were mouse cross-reactive and comprised the constant regions of the human IgG4 isotype containing the S228P mutation to prevent Fab shuffling. The 3H3 monoclonal antibody, known to stimulate mouse CD137 signaling *in vivo* and elicit anti-tumor immunity (Melero et al. (1997) Nature Medicine 3(6):682-685; Uno et al. (2006) Nature Medicine 12(6):693-696), was used as a comparator (BioXcell cat# BE0239; lot number 5926/1115). Notably, antibody 3H3 has similar properties to that of urelumab (Bristol-Myers Squibb; CAS Number: 934823-49-1), a fully human IgG4-S228P agonistic antibody that targets the extracellular domain of CD137, but does not block ligand binding. In addition, anti-Rat IgG4 was used as an isotype control (BioXcell cat# BE0089; lot number 5533/5679-316J1). Dilutions were made in PBS to achieve desired dose per mice, as indicated, in 100 µL injection volume.

The antibodies (100 µg) were administered intraperitoneally on days 0, 3, 6 to non-tumor bearing female Balb/c mice and spleens were harvested on day 9. Levels of PD-1 and TIGIT expression on CD8+CD44+ T cells were measured by flow cytometry. Specifically, single cell suspensions from the spleens were obtained by mechanical disruption and passing through a 40

μm cell strainer. Red blood cells were lysed using ACK buffer. The cell suspensions were stained with the following antibodies: CD45 (clone 30-F11, eBioscience), CD8 (clone 53-6.7, BD Biosciences), CD4 (clone RM-45, BD Biosciences), CD44 (clone IM7, eBioscience), PD-1 (RMP1-30, eBioscience) and TIGIT (GIGD7, eBioscience). Data acquisition was carried out on the MACSQuant Analyzer flow cytometer (Miltenyi) and data were analyzed using the FlowJo software, version 10.

Antibody 3H3 caused a significant increase in expression of both PD-1 and TIGIT, whereas only antibody mAb1 increased expression compared to mAb2 and mAb3 (**FIGs. 4A and 4B).** In addition, expansion of CD8+ T cells was assessed by analyzing the percentage of splenic CD45+ cells or number of CD8+ T cells per spleen. Similarly, antibody 3H3 caused the highest expansion of CD8+ T cells, with mAb1 resulting in the highest levels of CD8+ T cell expansion relative to mAb2 and mAb3 (**FIG. 4C**). Accordingly, mAb1 was selected for further testing.

Example 7: Efficacy of Anti-CD137 Antibodies in Tumor-Bearing Mice

Given the ability of mAb1 to enhance CD8+ T cell expansion, as shown in Example 6, mAb1 was further analyzed for anti-tumor activity using a subcutaneous model of syngeneic colon cancer. Specifically, CT26 tumor cells (passage 3) were maintained under aseptic conditions in DMEM Medium (Gibco cat#11965-092), containing 10% 56ºC –heat inactivated FBS (Gibco 10438-034), 1 mM sodium pyruvate (Gibco cat. # 11360-070), 1X NEAA (Gibco cat# 11140-050) and 1X MEM Vitamin solution (Gibco cat#11120-052). Cells were maintained at 37ºC and 5% CO_2. Upon reaching 50-70 % confluence, cells were passaged at a ratio of 1:10, for a total of two passages, prior to *in vivo* implantation. Cells were harvested and counted using a Hemacytometer (Hausser Scientific Bright-Line #1492).

Balb/c female mice were purchased from Charles River Laboratories and were nine weeks old at the start of study. CT26 tumor cells (1 $x10^5$ cells per mouse in 0.1 mL PBS) were injected subcutaneously into the right flank of each mouse, and tumor volume was calculated twice weekly (Length*(Width^2)/2) using dial calipers. On day 7 post-tumor inoculation, animals were sorted into groups of eight, and treatments were initiated. Body weights were recorded three times per week for the duration of the study.

mAb1 was administered at three different dosages (100, 50 or 25 μg/mouse), 3H3 at two different dosages (50 or 10 μg/mouse) and the isotype control antibody at a dosage of 50 μg/mouse. All mice were dosed intraperitoneally at days 0, 3, 6 and 9.

Expansion of CD8+ T cells in the tumors was confirmed *in vivo* for both mAb1 and 3H3 antibodies (data not shown). Individual tumor volumes are shown in **FIG. 5A** and mean tumor volumes are shown in **FIG. 5B**. mAb1 treatment resulted in inhibition of tumor growth compared to the control group at all three dosages. Moreover, treatment with mAb1 resulted in the complete regressions in 6 out of 8 mice at the 25 μg dose level, 5 out of 8 mice at the 50 μg dose level and 3 out of 8 mice at the 100 μg dose level.

Overall survival in each treatment group is shown in **FIG. 5C**. Strong anti-tumor activity of mAb1 against CT26 tumors was reflected as extended overall survival. Long term survival (>60 days) were observed in 80% of the mice at the 25 μg dose level, 62% of the mice at the 50 μg dose level and 38% of the mice at the 100 μg dose level.

Mice with no palpable tumor at day 70 were considered cured and re-challenged with subcutaneous injection of CT26 cells in the opposite flank. Specifically, mice with eradicated tumors were injected again with 1×10^5 CT26 cells in the left flank and tumor volume was calculated twice weekly (Length*(Width^2)/2) using dial calipers. Five non-immunized (naïve) mice were injected in the same manner as a control, respectively. Results of the re-challenge experiment are shown in **FIG. 5D**. Twenty-two days after the subcutaneous injection of CT26 cells, none of the re-challenged mice formed tumors. In contrast, all of the naïve mice that were injected with the same cells formed tumors. Therefore, all mice that were considered cured rejected CT26 tumors suggesting that mAb1 can induce long-term protective memory.

Example 8: Efficacy of Affinity-Matured Anti-CD137 Antibodies in Tumor-Bearing Mice

The affinity-matured monoclonal antibodies generated in Example 4 were analyzed for anti-tumor activity using the same subcutaneous model of syngeneic colon cancer (CT26) essentially as described in Example 7. Specifically, 6 affinity-matured clones (mAb7-mAb12) were generated with IgG4 constant regions and tested accordingly. The sequences of the heavy chain and light chain variable regions are provided in the chart below, along with their K_D values to mouse CD137 (determined by ForteBio Octet, described in Example 2) and human CD137 (determined by Carterra, described in Example 4).

Table A

Antibody	V_H Chain	V_L Chain	Binding to Mouse CD137 K_D (nM)	Binding to Human CD137 K_D (nM)
mAb7	SEQ ID NO: 8	SEQ ID NO: 6	1.2	6.8
mAb8	SEQ ID NO: 101	SEQ ID NO: 6	72	3.2
mAb9	SEQ ID NO: 103	SEQ ID NO: 6	6.9	41.4
mAb10	SEQ ID NO: 26	SEQ ID NO: 6	8.4	20
mAb11	SEQ ID NO: 4	SEQ ID NO: 28	4.8	4.1
mAb12	SEQ ID NO: 4	SEQ ID NO: 105	25.8	12.1

Parental mAb1, the 3H3 antibody (data not shown), and an IgG4 isotype antibody were used as controls. All mice were dosed with 50µg of mAb/mouse intraperitoneally at days 0, 3, 7 and 10. Spleens and livers were harvested on day 13 after therapy initiation.

Individual tumor volumes are shown in **FIG. 6A** and mean tumor volumes are shown in **FIG. 6B**. Consistent with the results from Example 7, treatment with parental mAb1 resulted in a reduction in tumor volume. Further, administration of all affinity-matured clones derived from mAb1 (mAb7-mAb12) to tumor-bearing mice resulted in an inhibition of tumor growth compared to mice treated with the isotype control antibody.

Example 9: Effect of Anti-CD137 Antibodies on T Cells in Tumor-Bearing Mice

To determine the effect of anti-CD137 antibodies (i.e., 3H3 and mAb1) on the level of T cells in tumor-bearing mice, Balb/c mice with CT26 tumors, as described in Example 7, were intraperitoneally injected with antibodies on days 0 and 3, and tissues were harvested on day 7. mAb1 was administered at three different dosages (100, 50 or 25 µg/mouse), 3H3 at two different dosages (50 or 10 µg/mouse) and the isotype control antibody at a dosage of 50 µg/mouse.

Single cell suspensions from the spleen were obtained as described in Example 6 and tumor cell suspensions were obtained by enzymatic and mechanical digestion using tumor dissociation kit (Miltenyi cat# 130-096-730). Cell suspensions were treated with complete medium to inactivate the enzymes and then passed through a 40 µm cell strainer. Red blood cells were lysed

using ACK buffer. Cells were stained with antibodies against CD45, CD8 and CD4, and analyzed as described in Example 6.

FIG. 7 shows the number of CD4+ and CD8+ T cells, as a percentage of CD45+ cells, found in the spleen and tumor. These results indicated that mAb1 selectively expands tumor-infiltrating CD8+ T cells as compared to splenic CD8+ T cells.

Example 10: Effect of CD4+, CD8+, or NK lymphocytes Depletion on Anti-Tumor Efficacy of Anti-CD137 Antibodies *In Vivo*

To assess the mechanism of action of anti-CD137 antibodies, Balb/c mice with CT26 tumors, as described in Example 7, were intraperitoneally injected with mAb1 alone or in combination with anti-CD4 (GK1.5), anti-CD8 (YTS169.4), or anti-asialo-GM1 (targets NK cells) antibodies to deplete these specific lymphocyte subsets from the animals. Mice treated only with the mAb1 antibody were administered 150µg of antibody on days 6, 9, 12, 19, and 26. The mice treated with 150µg mAb1 in combination with 500µg anti-CD4, anti-CD8, or 50uL of anti-asialo-GM1 antibodies administered on days -1, 0, 5, 10, 15, and 20. Effective depletion was confirmed by FACS analysis (data not shown).

Individual tumor volumes are shown in **FIG. 8**. Consistent with the results from Example 7, treatment with parental mAb1 resulted in a reduction in tumor volume. Further, administration of mAb1 in combination with lymphocyte-depleting anti-CD4, anti-CD8, or anti-asialo-GM1 antibodies reduced the anti-tumor activity of the mAb1 antibody. These results indicated cooperation between innate and adaptive immunity for anti-tumor efficacy of the anti-CD137 antibodies described herein.

Example 11: Anti-Tumor Efficacy of Anti-CD137 Antibodies in Various Tumor Models

To determine whether an anti-CD137 antibody had anti-tumor efficacy in different tumor models, mAb8 was administered to mice having either CT26 tumors (colon carcinoma; as described above), EMT-6 tumors (breast carcinoma), A20 tumors (B cell lymphoma) or MC38 tumors (colon carcinoma).

For all tumor models, female mice were purchased from Charles River Laboratories and were 7-9 weeks old at the start of study. For each tumor type appropriate syngeneic mouse strain was used (Balb/c for CT26, EMT-6 and A20; C57BL/6 for MC38). EMT6 tumor cells (5×10^4)

cells per mouse in 0.05 mL PBS) were injected into the right mammary fat pad of each mouse. CT26 tumor cells (1 x10^5 cells per mouse), A20 tumor cells (5 x10^6 cells per mouse) and MC38 tumor cells (5 x10^5 cells per mouse) were injected subcutaneously into the right flank of each mouse, and tumor volume was calculated twice weekly (Length*(Width^2)/2) using dial calipers. Upon reaching 50-100 mm^3 sized tumors, the mice were randomized to receive mAb8 or isotype control (day 0). Mice with orthoptic EMT6 tumors received 12.5 µg on days 0, 3, 6 and 9. Mice with A20 (200 µg/mouse) and MC38 (12.5 µg/mouse) tumors received 5 doses once a week. All mice were dosed intraperitoneally.

As shown in **FIG. 9**, mAb8 was effective in all four tumor models tested, indicating a wide range of efficacy for varying cancer types. Treatment with mAb8 resulted in tumor regressions in mice carrying 8/8 CT26, 3/8 EMT6, 5/8 A20 tumors and delayed growth in majority of the remaining mice carrying EMT6, A20 and MC38.

Example 12: Effect of Dosage of Anti-CD137 Antibodies

To further characterize the anti-tumor efficacy of the anti-CD137 antibodies, a dosage study was performed using the same subcutaneous model of syngeneic colon cancer (CT26) essentially as described in Example 7. Specifically, parental mAb1 and affinity matured antibodies mAb8 and mAb10 were administered intraperitoneally at doses of either 150µg (high dose) or 20µg (low dose) per mouse on days 0, 3, 6 and 9, with 8 mice per treatment group. One group of mice (n=8) was administered an IgG4 isotype control at a dose of 150µg.

Individual tumor volumes, mean tumor volume and percent survival of mice treated at the 150µg are shown in **FIG. 10A, FIG. 10B, and FIG. 10C,** respectively. Individual tumor volumes, mean tumor volume and percent survival of mice treated at the 20µg are shown in **FIG. 11A, FIG. 11B, and FIG. 11C,** respectively. These results indicated that treatment with the parental mAb1 and the affinity-matured mAb8 and mAb10 antibodies resulted in a reduction in tumor volume and an increase in mouse survival at both high and low doses.

In a separate dosage study utilizing the CT26 tumor model, additional doses of parental mAb1 were tested. Specifically, mAb1 was administered intraperitoneally at the following doses: 12.5µg, 25µg, 50µg, 100µg and 200µg. **FIG. 12** shows the results of the dosage study, indicating efficacy over a wide dose range. Treatment with mAb1 resulted in tumor regressions in at least 3/8

mice in each dose level with optimum dose range (50-100 μg/mouse) leading to 7/8 mice with eradicated tumors.

Example 13: Effect of Fc-Receptor Binding on Anti-Tumor Efficacy of Anti-CD137 Antibodies

To determine the contribution of Fc-receptor binding on the anti-tumor activity of anti-CD137 antibodies, aglycosylated IgG1 and IgG4 versions of mAb1 were generated. CT26 tumors were established in mice as described in Example 7. Mice received 150ug of either (a) isotype control; (b) mAb1 as IgG4; (c) aglycosylated mAb1 as IgG4; or (d) aglycosylated mAb1 as IgG1.

As shown in **FIGs. 13A and 13B**, aglycosylated IgG4 and IgG1 isotypes of the parental mAb1 antibody had reduced effect on tumor volume in comparison to mAb1. However, efficacy was not completely abolished. Accordingly, these results indicated that while the anti-tumor efficacy of mAb1 is not entirely Fc-dependent, it is enhanced by Fc receptor binding.

Example 14: Cross-Species Affinity of Anti-CD137 Antibodies

The anti-CD137 antibodies were further tested for their binding to CD137 from multiple species. Specifically, mAb1, mAb8 and mAb10 were analyzed for binding to human, mouse, cynomolgus and canine CD137. Kinetic experiments were performed on Octet HTX (ForteBio) in kinetics buffer (1x PBS, pH 7.4, 0.1 mg/ml BSA, and 0.002% Tween 20). Fc-, mouse IgG2a-, or His- tagged CD137 (human, mouse, cyno or canine) were loaded for 5 minutes on pre-hydrated biosensors, AHC, AMC or NTA respectively. The sensors were then dipped into Fabs (0, 5.12, 12.8, 32, 80, 200 and 500 nM) for 5 minutes of association, following by 15 minutes of dissociation. Results were analyzed with ForteBio Data Analysis 9.0 and fit globally to a 1:1 binding model to determine the apparent K_D. K_D for human and mouse CD137 binding were confirmed by using antigens from different sources (ACRO Biosystems, Sino Biological and internal). The results are shown in Table 2 below.

Table 2: Cross-Species Affinity

Species of CD137	mAb1	mAb8	mAb10
Human	50-70 nM	3-5 nM	0.9 nM
Mouse	300-500 nM	50-90 nM	10-30 nM

Cynomolgus	30-100 nM	3-7 nM	1.8 nM
Canine	Poor fit	Poor fit	Poor fit

Example 15: Effect of Size of Tumor on Anti-Tumor Efficacy of Anti-CD137 Antibodies

To further characterize the anti-tumor efficacy of the anti-CD137 antibodies, the anti-tumor efficacy against large tumors was assessed. CT26 tumors were allowed to grow to approximately 500mm^3 prior to treatment. Parental mAb1, and affinity matured mAb8 and mAb10 antibodies were administered at 150µg/mouse (n=6 mice/treatment group) on days 0, 3, 6 and 9 post tumor-establishment. The IgG4 isotype control antibody was used as a comparator.

As shown in **FIGs. 14A-14C**, the parental mAb1 as well as the affinity-matured mAb8 and mAb10 reduced tumor volume (**FIGs. 14A-14B**) and increased mouse survival (**FIG. 14C**) relative to the isotype control. mAb8 resulted in significantly greater anti-tumor efficacy compared to mAb1 and mAb10. A separate study was conducted comparing the efficacy of mAb8 and 3H3 against large tumors using the same study design, except 25µg of the antibodies were administered on days 0, 7 and 14. **FIG. 14D** provides the results, showing 3H3 had no efficacy against large tumors, whereas mAb8 induced tumor regression.

As described in Example 14, mAb8 has an affinity for mouse CD137 that is comparable with the affinity of mAb1 for human CD137. While the disclosure is not bound by any particular theory or mechanism of action, it is believed that agonist anti-CD137 antibodies with intermediate affinity may be even more useful for treating cancer.

Mice with no palpable tumor at day 70 were considered cured and re-challenged with subcutaneous injection of CT26 cells in the opposite flank. Specifically, mice with eradicated tumors were injected again with 1×10^5 CT26 cells in the left flank and tumor volume was calculated twice weekly (Length*(Width^2)/2) using dial calipers. Five non-immunized (naïve) mice were injected in the same manner as a control, respectively. Results of the re-challenge experiment are shown in **FIG. 15**. Eighty days after the subcutaneous injection of CT26 cells, none of the re-challenged mice formed tumors. In contrast, all of the naïve mice that were injected with the same cells formed tumors. Therefore, all mice that were considered cured rejected CT26 tumors suggesting that mAb1 can induce long-term protective memory immunity.

Example 16: Toxicity of Anti-CD137 Antibodies in Tumor-Bearing Mice

To determine the effect of anti-CD137 antibodies (i.e., 3H3 and mAb1) on the level of intrahepatic T cells in tumor-bearing mice, mice from Example 7 were analyzed. Liver lymphocytes were collected and analyzed via flow cytometry. Specifically, single cell suspensions from the liver were obtained using the liver dissociation kit (Miltenyi cat# 130-105-807) and the gentle MACS Dissociator (Miltenyi). Cell suspensions were treated with complete medium to inactivate the enzymes and then passed through a 40 μm cell strainer. Red blood cells were lysed using ACK buffer. Cells were stained with antibodies against CD45, CD8 and CD4, and analyzed as described in Example 3.

FIGs. 16A and 16B show the number of CD4+ and CD8+ T cells, as a percentage of CD45+ cells, found in the livers of treated mice. The results indicated mAb1 did not induce infiltration of intrahepatic T cells, demonstrating lower toxicity relative to antibody 3H3.

Example 17: Toxicity of Affinity-Matured Anti-CD137 Antibodies in Tumor-Bearing Mice

To assess toxicity-related effects mediated by anti-CD137 antibodies (i.e., 3H3, mAb1, and mAb7-mAb12), the cellular composition of spleens and livers of tumor-bearing mice from Example 8 were analyzed following antibody administration.

Intrahepatic (liver) and intrasplenic (spleen) T cells in tumor-bearing mice from Example 8 were collected and analyzed via flow cytometry. CD45+ cells from livers and spleens were assessed for CD3+, CD4+, or CD8+ expression following administration of anti-CD137 antibodies or the isotype control antibody, as indicated. Results are shown in **FIGs. 17A** (splenic) and **17B** (liver). The results indicated that the administration of parental mAb1 as well as the affinity-matured antibodies (mAb7-mAb12) had little to no effect on the percentage of intrahepatic or intrasplenic T cells relative to administration of the isotype control antibody. In contrast, administration of the 3H3 antibody resulted in elevated T cells in both the spleens and livers relative to the isotype control antibody, particularly CD3+ T cells and CD8+ T cells.

Further, CD45+ CD8+ T cells and CD45+CD4+ T cells from the livers and spleens of treated mice were assessed for expression of TIGIT, PD-1, or LAG-3 co-inhibitory receptors, as indicators of T cell activation or exhaustion, following administration of anti-CD137 antibodies or the isotype control antibody. Levels of TIGIT, PD-1, and LAG-3 expression on CD8+ T cells and CD4+ T cells were measured by flow cytometry as described in previous Examples. **FIGs. 18A-**

18B and 19A-19B show that administration of the 3H3 antibody caused a significant increase in expression of these co-inhibitory receptor in both CD8+ T cells and CD4+ T cells, whereas administration of the parental mAb1 or affinity-matured mAb7-mAb12 antibodies resulted in expression of TIGIT, PD-1, or LAG-3 to a similar extent as seen after administration of the isotype control antibody. These results indicated the affinity matured antibodies did not induce systemic CD8+ T cell or CD4+ T cell activation.

Taken together, these results indicate that the parental mAb1 and affinity-matured mAb7-mAb12 antibodies exhibit lower potential for *in vivo* toxicity relative to the 3H3 comparator antibody. Absence of systemic T cell activation and expansion, particularly in the liver, after treatment with mAb1 and affinity-matured mAb7-mAb12 antibodies might translate into lower possibility of hepatotoxicity (transaminitis) in patients.

Example 18: Toxicity of Multiple Doses of Anti-CD137 Antibodies in Tumor-Bearing Mice

To confirm the lack of toxicity induced by mAb1, a repeated-dose toxicity study was conducted. Specifically, mice were administered anti-CD137 antibodies mAb1, mAb8, or 3H3 weekly, for 4 weeks. mAb1 and mAb8 were administered at either 10, 20, 40 or 80 mg/kg, whereas 3H3 was administered at either 10 or 80 mg/kg. On day 35, alanine aminotransaminase (ALT) levels in the plasma was determined using a fluorometric activity assay (Sigma, cat# MAK052), CD8+ T cells in the liver was determined using flowcytometry (as described above), and concentration of TNFα in the plasma was determined using an electrochemiluminscence assay (Meso Scale Discovery, custom kit) according to manufacturer's instructions.

FIG. 20A shows low levels of CD8+ T cells in the livers of mice administered mAb1 and mAb8 at all 4 doses, whereas 3H3 induced high levels of CD8+ T cells at both the low (10 mg/kg) and high (80 mg/kg) doses. **FIG. 20B** shows low levels of ALT activity in the plasma of mice administered mAb1 and mAb8 at all 4 doses, whereas 3H3 induced high levels of ALT at the 80 mg/kg dose. **FIG. 20C** shows low levels of TNFα in the plasma of mice administered mAb1 mAb8 at both low (10 mg/kg) and high (80 mg/kg) doses, whereas 3H3 induced high levels of TNFα at both low (10 mg/kg) and high (80 mg/kg) doses.

In addition, livers from treated mice that received 80 mg/kg of the anti-CD137 agonistic antibodies were sectioned and stained with H&E. From each animal, half of a liver lobe was embedded in OCT and fresh frozen in liquid nitrogen. Sectioning and H&E staining was

performed by a histopathology laboratory (Mass Histology Service, Inc) according to standard procedures. **FIG. 21** provides the results, which show inflammatory centrilobular foci in mice that received 3H3 (see arrows), but not mAb1 or affinity-matured mAb1.

Example 19: Immune Reprogramming with Anti-CD137 Antibodies

To determine the role of anti-CD137 antibodies on immune cells in the tumor microenvironment, the CT26 tumor model was utilized. Specifically, CT26 tumors were established as described in Example 7. mAb8 was administered to mice on days 0, 3, 6 and 9 at a dose of 25ug. Tumors were analyzed on day 11 as described in Example 16.

Overall infiltration of immune cells into the tumor microenvironment was determined by measuring the quantity of CD45+ live cells. As shown in **FIG. 22A**, mAb8 significantly increased infiltration of immune cells into the tumor microenvironment.

The level of Treg cells in the tumor microenvironment was determined by measuring the quantity of CD25+ FOXP-3+ CD4+ tumor infiltrating lymphocytes. As shown in **FIG. 22B**, mAb8 significantly reduced the level of Tregs in the tumor microenvironment.

The effect of mAb8 on T-cell exhaustion was determined by measuring the level of PD-1+TIGIT+ expression on CD8+ or CD4+ tumor infiltrating lymphocytes (TILs). **FIG. 22C** shows the results for CD8+ TILs, wherein PD-1+TIGIT+ cells were reduced in the tumor microenvironment when mAb8 was administered. Similar results were observed for CD4+ TILs (data not shown). These results indicate mAb8 protects and/or reverses T-cell exhaustion.

In addition, the effect of mAb8 on tumor-associated macrophages was analyzed. Specifically, F4/80+CD11b+CD45+ cells were measured and a reduction in tumor-associated macrophages was observed with treatment of mAb8.

In a separate study, the effect of anti-CD137 antibodies (*i.e.,* mAb1 and 3H3) on peripheral immune cells was assessed. Specifically, spleens from CT26 tumor-bearing mice treated with mAb1 or 3H3 on days 0 and 3 at a dose of 150ug, were analyzed on day 7. As shown in **FIG. 23**, anti-CD137 antibody 3H3 induced TIGIT and PD-1 expression on CD8+ and CD4+ T cells, as well as increased CD8+CD25+ and CD4+Foxp3+ cells. In addition, 3H3 induced both CD8+ and CD4+ effector memory cells. In contrast, anti-CD137 antibody mAb1 did not significantly induce CD8+TIGIT+PD-1+, CD8+CD25+, and CD4+Foxp3+ T cells. Further, mAb1 did not induce CD8+ or CD4+ effector memory cells.

Overall, these results indicate anti-CD137 antibodies mAb1 and mAb8 induce dramatic immune reprogramming within the tumor microenvironment and has less of an effect, if any, on peripheral immune cells.

Example 20: Enhancement of Murine T Cell Activation by Anti-CD137 Antibodies

The agonistic activity of the anti-CD137 antibodies was further analyzed by assessing the stimulation of IL-2 production in a murine ovalbumin stimulation assay. In a 96-well plate, JAWS-II dendritic cell-like cells were plated at 10^4 cells/well and incubated overnight in the presence of murine IFN-γ (10ng/mL). Cells were incubated with 2μg/mL OVA/A2 peptide and incubated for 2 hours at 37^0C, followed by incubation with 10^5 CD8+ T cells isolated from OT-I mouse spleen, which express OVA. Antibodies were added simultaneously. Atezolizumab (anti-PD-L1 antibody) and a mouse anti-PD-1 antibody (RMP1-14), along with an IgG4 isotype control, were used as comparators. IL-2 concentration was determined by Meso Scale Discovery (MSD).

As shown in **FIG. 24**, mAb8 and mAb10 significantly enhanced IL-2 production.

In addition to measuring IL-2 production, the percentages of CD25+CD8+ T cells and TIGIT+CD8+ T cells were analyzed using the same murine ovalbumin stimulation assay. Antibody 3H3 was included as a comparator. **FIGs. 25A and 25B** show that mAb8 and mAb10 enhanced the expression of CD25, an activation marker, and spared the induction of TIGIT, an exhaustion marker. In contrast, 3H3 enhanced the expression of TIGIT.

Example 21: Effect of Anti-CD137 Antibodies on Cytokine Induction

To determine the effect of anti-CD137 antibodies on cytokine induction by T cells, plate-bound antibodies were utilized. Three antibodies were used as comparators: mAb4, corresponding to urelumab (Bristol-Myers Squibb; CAS Number: 934823-49-1), a fully human IgG4-S228P agonistic antibody that targets the extracellular domain of CD137, but does not block ligand binding; mAb5, corresponding to utomilumab (Pfizer; CAS Number: 1417318-27-4), a fully human IgG2-S228P agonistic antibody that targets the extracellular domain of CD137 and blocks ligand binding; and mAb6, a fully human IgG4-S228P agonistic antibody selected from the same library as mAb1 and targets the extracellular domain of CD137. The mAb6 antibody does not block ligand binding.

Human CD3+ T cells were isolated via negative selection and added to plates bound with anti-CD137 antibodies and 1μg/ml of anti-CD3. Anti-CD137 antibodies were added at either 1nM, 10nM, 50nM or 100nM. Antibodies were coated overnight at 4°C.

72 hours after addition of the T cells, levels of IL-2, IFN-γ, TNFα and IL-13 were assessed by Luminex kits (Luminex Corporation, Austin, TX) following the manufacturer's instructions. Soluble anti-CD28 (2μg/mL) was used as a T cell activation control and the activation baseline was set using the plate bound anti-CD3. **FIG. 26** shows the fold change in each cytokine level as it relates to the activation baseline. mAb4 (urelumab) showed the highest level of induction of each cytokine, with mAb1 showing a lower level of induction but higher relative to mAb5 (utomilumab) and mAb6. These results indicate mAb1 agonizes CD137 less than mAb4 (urelumab) at the same concentrations.

Example 22: Induction of Interferon-gamma (IFN-γ) by Anti-CD137 Antibodies

To further assess the agonistic activity of the anti-CD137 antibodies, IFN-γ production was analyzed in a mixed lymphocyte reaction (MLR). mAb2, mAb4 (urelumab), mAb5 (utomilumab) and Keytruda, a humanized antibody that blocks PD-1 (Merck) and is known to induce IFN-γ production, were used as comparators.

Peripheral blood mononuclear cells (PBMCs) were isolated from leukopaks (HemaCare, Van Nuys, CA) derived from three independent human donors (D985, D7603, and D5004). Total T cells were enriched from PBMC by negative selection using immunomagnetic cell separation (EasySep™; Stemcell Technologies, Vancouver BC). Monocytes were isolated from PBMCs using immunomagnetic cell separation (EasySep™; Stemcell Technologies, Vancouver BC). T cells were resuspended in complete RPMI at $1x10^6$ cells/ml concentration and monocytes were adjusted to $5x10^5$ cells/ml respectively. In a 96-well plate, 100μl of media containing T cells were plated at $1x10^5$ cells/well density followed by adding 100μl of monocyte cell suspension (E:T ratio 2:1). Next, 50 μl of media containing various dilutions of CD137 antibodies was added. Plates were incubated at 37°C in a CO_2 incubator for five days. At the end of incubation period, culture supernatants were collected and IFN-γ levels were analyzed by MSD assay (Mesoscale Diagnostics, Rockville, MD). **FIGs. 27A-27C** show the concentration of IFN-γ as pg/mL at the final concentrations of antibodies tested, as indicated. These results indicated mAb1 agonizes

CD137 less than mAb4 (urelumab), but to a similar extent as mAb5 (utomilumab) at the same concentrations.

In a separate study, IFN-γ induction was measured by utilizing CHO cells engineered to express CD32 (FCyRIIb) (CHO-CD32 cells). Specifically, CHO-CD32 cells were co-cultured with human T cells in the presence of soluble anti-CD3 and anti-CD137 antibodies mAb1, mAb8, mAb4 and mAb5.

Frozen PBMCs were thawed and rested overnight in T cell media (TCM) in a humidified 37°C 5% CO2 incubator. The following day, CD3+ T cells were isolated with an untouched CD3 T cell isolation kit (Stemcell # 17951) before being mixed together with CHO cells (Gibco # A29127) transduced to express human CD32 (CHO-CD32), 250 ng/ml anti-CD3 (clone OKT3), and the anti-CD137 or control antibodies. 100,000 T cells were mixed together with 50,000 CHO-CD32 cells. After incubation at 37°C for 3 days, supernatants were collected for analysis of secreted interferon-gamma (IFN-γ) via MesoScale Discovery (MSD).

FIG. 28 provides the results, showing mAb4 induced IFN-γ to the highest level and at low doses. In contrast, mAb5 induced almost no product of IFN-γ. Notably, mAb1 and mAb8 provided a dose-dependent response and induced IFN-γ production between the levels induced by mAb4 and mAb5. Overall, these results indicate that mAb4 has superagonist activity, mAb5 has weaker activity, and mAb1 and mAb8 have an intermediate activity compared to mAb4 and mAb5.

Example 23: Effect of Anti-CD137 Antibodies on Treg Cells

To further characterize the mechanism of action for anti-CD137 antibodies, the effect of the antibodies on Treg cells was determined. Human Tregs were isolated using EasySep™ Human CD4+CD127lowCD25+ Regulatory T Cell Isolation Kit (Stemcell Technologies, Cat #18063) and expanded for 13 days by immunocult anti-CD3/28 (Stemcell # 10971) in complete T cell media with 10% FBS. Specifically, the CHO-CD32 cells described in Example 21 were co-cultured with expanded human Treg cells, which were labeled with Cell-trace violet dye (Thermo Fisher, Cat #C34557) in the presence of soluble anti-CD3 (clone OKT3) and anti-CD137 antibodies mAb1, mAb8, mAb4, mAb5 and isotype control. Proliferation of Treg cells was determined on Day 4.

FIG. 29 provides the results, showing mAb4 strongly induced Treg proliferation, even at low concentrations. In contrast, mAb5 had a very weak effect on Treg proliferation. Notably, mAb1 and mAb8 showed moderate increases in Treg proliferation. Overall, these results confirm

that mAb4 has superagonist activity, mAb5 has weak activity, and mAb1 and mAb8 have an intermediate activity.

Example 24: Effect of Anti-CD137 Antibodies on Intracellular Signaling

To further assess the differences between anti-CD137 agonistic antibodies, intracellular signaling was assessed *in vitro*. Specifically, CCL-119 T cells (ATCC; Cat# ATCC CCL-119) lentifected with NFkβ (Qiagen; Cat# CLS-013L-1) or SRF (Qiagen; Cat# CLS-010L-1) were stimulated with 250 ng/mL of plate-bound anti-CD3 (clone OKT3) in conjunction with varying concentrations of plate-bound mAb1, mAb8, mAb4, mAb5 and isotype control. After stimulation for 16 hours in RPMI media without additives, cells were lysed in luciferase buffer (Promega; Cat# E263B) and relative light units (RLUs) were acquired on a BioTek Synergy H1 microplate reader (Cat# 11-120-533). Raw RLU data was then exported to Microsoft Excel and fold-induction was calculated by dividing RLUs from stimulated conditions over unstimulated controls.

FIG. 30 provides the results, showing minimal NFkβ and SRF activity of mAb4 and mAb5 relative to mAb1 and its affinity-matured variant, mAb8. Overall, these results indicate mAb1 induces intracellular signaling differently than mAb4 and mAb5.

Example 25: Effect of Anti-CD137 Antibodies on Macrophage Activation and Differentiation

It has previously been shown the hepatotoxicity induced by anti-mCD137 agonistic antibody 3H3 was associated with expansion of macrophages and CD8+ T cells in the livers, and increased cytokine levels and ALT activity in the serum. Further, antibody 3H3 has been characterized as having similar properties as urelumab. As described herein, mAb1 does not induce hepatotoxicity. Accordingly, anti-CD137 agonistic antibodies were analyzed for their effect on macrophage activation *in vitro*.

Specifically, murine bone marrow-derived mouse macrophages were established from 10-week old female C57BL/6 mice (Charles River Laboratories). The femur and tibia bones were extracted from the musculature of the mice and bone marrow was flushed with PBS into 15 mL conical tubes on ice. The cells were centrifuged at 1500 rpm for 5 minutes and the supernatant was discarded. The cell pellet was broken and culture media (RPMI, 20% FBS, 50

μg/mL M-CSF (Shenandoah Biotechnology, Inc.; Cat# 200-08-100), and pen/strep) was added. Cells were filtered on 40-micron mesh filter and plated into non-tissue culture treated petri dishes. After 3 days 10 mL of media was added to each petri dish. On day 7 of culture, media was removed and cells were washed with PBS (10 mL) twice. MACS buffer (PBS, 2 μM EDTA, and 0.5% FBS) was added to each dish and incubated at 37^0C for 10 minutes. Cells were collected from the petri dishes and centrifuged at 1500 rpm for 5 minutes. These bone marrow derived macrophages were then stimulated with TLR9 agonist CpG in the presence of 50nm of anti-CD137 antibodies mAb1, 3H3, or LOB12.3 (mouse specific CD137 agonist antibody). Production of IL-6, TNFα and IL-27 by murine bone marrow-derived macrophages was assessed from culture supernatants after 48 hours using an electrochemiluminscence assay (Meso Scale Discovery, custom kit) according to manufacturer's instructions. **FIG. 31** provides the results, which indicate mAb1 did not induce secretion of proinflammatory cytokines by macrophages, whereas antibodies 3H3 and LOB12.3 did.

The human monocyte-derived macrophages were generated by magnetically separating $CD14^+$ cells using anti-CD14 microbeads (Miltenyi Biotech, Cat# 130-050-201) and maturing 7 days in the presence of 50ng/mL m-CSF. Human monocyte-derived macrophages were than stimulated with 10ng/mL LPS in the presence of 5nm of anti-CD137 antibodies mAb1, mAb4 or mAb5. Production of TNFα was assessed after 48 hours using an electrochemiluminscence assay (Meso Scale Discovery, custom kit) according to manufacturer's instructions. **FIG. 32** provides the results, which indicate mAb4 and mAb5 induced macrophage activation significantly more than mAb1.

Further, THP1 monocytes were differentiated to macrophages with 2 μM phorbol 12-myristate 13-acetate (PMA; Sigma; P1585) overnight. The macrophages were than cultured in the presence of 50nm of anti-CD137 antibodies mAb1, mAb4 or mAb5 and CD64 expression was measured 48 hours later using flow cytometry (APC anti-human CD64 antibody clone 10.1; BioLegend; Cat#305013). **FIG. 33** provides the results, which indicate mAb4 and mAb5 induced macrophage differentiation significantly more than mAb1.

While the disclosure is not bound by any particular theory or mechanism of action, overall, these results suggest mAb1 spares hepatic toxicity due to reduced potential for macrophage activation.

Example 26: Expansion of human CD8+ T cells *in vivo* by anti-CD137 agonistic antibodies

To test the effect of CD137 agonistic antibodies on human cells *in vivo*, human PBMCs ($7x10^6$) were intravenously injected to immunocompromised NSG mice (NOD.Cg-*Prkdc*^{scid} *Il2rg*^{tm1Wjl}/SzJ; Jackson Laboratory; Cat# 005557). The mice were randomized to groups of 8 and received CD137 antibodies (200 µg/mouse) or vehicle control on days 0, 7 and 14. Peripheral blood from each mouse was collected on days 10, 20 and 29 for determination of human $CD45^+$ (FITC anti-human CD45 clone HI30; BioLegend; Cat# 304038), $CD8^+$ (Alexa Fluor® 647 anti-human CD8a clone HIT8a; BioLegend; Cat#300918), and $CD4^+$ (APC-Cy7 anti-human CD4 clone RPA-T4; Bd; Cat# 557871) engraftment using flow cytometry.

FIGs. 34A-34C show overall increase in numbers of $hCD45^+$ cells and systemic hyper expansion of human CD8+ T cells in mice that received mAb4 at the expense of human CD4+ T cells. Notably, mAb1 did not induce over activation of human T cells. Reduced potential of mAb1 to activate human T cells in the periphery might contribute to reduced potential for toxicity.

Example 27: Formulations Materials and Methods

Size Exclusion Chromatography

Size exclusion chromatography (SEC) was performed with a YMC Diol-200 8 x 300 mm column (Cat.no # DL20S05-3008WT) on an Agilent 1200 series HPLC instrument. The running buffer was 20mM sodium phosphate, 400mM NaCl pH 7.0 at a flow rate of 1 mL/min and running time of 15 min per sample.

Capillary Isoelectric Focusing

Capillary isoelectric focusing (cIEF) was performed on a Maurice C. instrument (ProteinSimple) with Maurice cIEF Cartridge (Cat. No# PS-MC02-C). The final assay composition consisted of 0.5 mg/mL antibody, 4% Pharmalyte 3-10, and 0.35% methylcellulose. PI markers 5.85 and 8.4 were used. The focusing conditions were: 1500 V for 1 min followed by 3000 V for 4 min. Native fluorescence signal with 3 second exposure time was used for peak integration using the dropline method.

Capillary Electrophoresis Sodium Dodecyl Sulfate

Capillary electrophoresis sodium dodecyl sulfate (CE-SDS) was performed on a LapChip GX II instrument using HT Protein Express Chip (Perkin Elmer, #760528) and Protein Express Assay Reagent Kit (Perkin Elmer, # CLS960008). The reagents and chip were prepared according to the manufacturer's instruction. The samples were diluted with PBS to 0.5 mg/mL immediately before the assay. For non-reducing condition, 2μL of diluted samples were mixed with 7μL of sample buffer containing 25mM iodoacetamide (Sigma-Aldrich #A3221-10VL) in a 96-well plate; for reducing condition, 2μL of diluted samples were mixed with 7μL of sample buffer containing 25 mM DTT. After denaturation at 75°C for 10 min on a thermocycler (Eppendorf Mastercycler pro), 35μL of water was added to each well and mixed by pipetting up and own. The plate was then centrifuged at 2,000 g for 1min to remove air bubbles before placing in the LapChip GXII instrument for analysis.

Micro-flow imaging (MFI)

Micro-flow imaging (MFI) was performed on a FlowCam PV-100 instrument (Fluid Imaging Technologies). The samples were flown at a rate of 0.15 mL/min for a total volume of 200~300 μL. Each sample was run twice, and the particle counts in the range of 2-10 μm, 10-25 μm and >25 μm were averaged respectively.

Example 28: Stability of an Anti-CD137 Antibody at a High Concentration and Forced Degradation in Buffers with Different pH

The stability of an anti-CD137 antibody, mAb1, at high concentration and two different temperatures was assessed in three buffers with different pH. mAb1 is an anti-CD137 antibody comprising the heavy and light chain variable sequences of SEQ ID NOs: 4 and 6, respectively.

Specifically, 100 mg/mL of mAb1 was buffer exchanged to each of the following buffers: (1) 20 mM Tris, 8.5% sucrose, at pH 7.5; (2) 20 mM Histidine, 8.5% sucrose, 0.005% EDTA, at pH 5.8; and (3) 20 mM Glutamic acid, 8.5% trehalose, at pH 4.5. Half of each sample was stored at 4°C and half was stored at 25°C. The stability of each of the formulations (1)-(3) were analyzed at weeks 0, 1, 2, 4, and 6 by SEC, CE-SDS, and cIEF.

The results of cIEF demonstrated that at high concentration, histidine buffer at pH 5.8 provided mAB1 with the highest stability. As shown in **Table 3** and **FIG. 35**, there was gradual

increase of acidic species at pH 4.5 at 25˚C; while there was more significant increase of basic species at pH 7.5 at 25°C with concomitant decrease of the main peak. There was no noticeable change when the samples were analyzed by SEC and CE-SDS.

Table 3: cIEF charge variant analysis of mAb1 at high concentration in three different buffers following storage at either 4°C or 25°C.

Temperature	Buffer	Species	Time				
			W0	W1	W2	W4	W6
4 °C	Glu pH4.5	Acidic	15.6	16	16.8	16.6	17.5
		Main	78.4	77.6	80.8	77.6	75.8
		Basic	6	6.4	2.4	5.9	6.7
	His pH5.8	Acidic	15.3	14.1	14.4	15.2	14.4
		Main	77.6	78.9	82.8	82	78.9
		Basic	7.2	7	2.8	2.9	6.7
	Tri pH7.5	Acidic	13.4	13.6	13.5	13.7	13.9
		Main	78.8	81.8	81.3	80.8	79.5
		Basic	7.8	4.6	5.3	5.4	6.6
25 °C	Glu pH4.5	Acidic	15.4	18.2	20	24	23.1
		Main	81.9	74.7	72.9	72.7	71
		Basic	2.7	7.2	7	3.3	5.9
	His pH5.8	Acidic	14.4	14.9	15.1	15.4	15.9
		Main	82.4	80.7	79.5	77.5	72.2
		Basic	3.2	4.4	5.3	7.2	11.9
	Tri pH7.5	Acidic	13.9	13.6	13.5	12.2	12.6
		Main	78.6	75.2	68.2	61.2	57
		Basic	**7.5**	**11.2**	**18.3**	**26.7**	**30.5**

The stability of mAb1 was also assessed under forced degradation conditions in three formulations at different pH. Specifically, 5 mg/mL of mAb1 prepared in each of the following three buffers (1) 20 mM Tris at pH 7.5 (2) 20 mM Histidine at pH 5.8 (3) 20 mM Glutamic acid at pH 4.5. The samples were stored at 40°C for up to four weeks and stability was assessed by SEC, CE-SDS, and cIEF at week 0, 2, and 4.

When mAb1 was subjected to forced degradation conditions, similar but more profound changes were observed by cIEF analysis. The buffer which provided the highest stability under

forced degradation conditions was 20 mM histidine buffer at pH 5.8. As shown in **Table 4** and **FIG. 36**, there was an approximately 30% increase of acidic species when mAb1 was incubated in 20 mM Glutamic acid at pH 4.5 for 4 weeks; and approximately 30% increase of basic species when mAb1 was incubated in 20 mM Tris at pH 7.5 for 4 weeks, with concomitant decrease of the main peak.

Table 4: cIEF charge variant analysis of mAB1 under forced degradation conditions in three different buffers following storage at 40°C.

Temperature	Buffer	Species	Time		
			W0	W2	W4
40 °C	Glu pH4.5	Acidic	15.1	33.4	46.1
		Main	80.5	51.3	37.5
		Basic	4.4	15.4	16.4
	His pH5.8	Acidic	13.7	20.7	27.7
		Main	78.3	59.2	50.9
		Basic	8	20.1	21.5
	Tri pH7.5	Acidic	13.4	13.2	18.2
		Main	78.1	42.7	40
		Basic	8.5	44.2	41.4

Example 29: A Pre-Formulation Study to Determine the Impact of Buffer pH, Salt Concentration, Detergent and Excipients on Stability of an Anti-CD137 Antibody

A pre-formulation study was performed to evaluate the effect of different buffer pH, salt concentration, detergents, and excipients on the stability of anti-CD137 antibodies. The study was performed using an affinity-matured version of mAb1, mAb8, the mouse surrogate molecule for *in vivo* studies because its affinity with mouse CD137 is similar to that of mAb1 with human CD137. Specifically, mAb8 is an anti-CD137 an antibody comprising the heavy and light chain variable sequences of SEQ ID NOs: 101 and 6, respectively

48 different formulations of mAb8 were analyzed. Each of the formulations contained a salt, buffer, detergent and excipient selected from the following groups:

(1) Salt: 50 mM NaCl or 125 mM NaCl,

(2) Buffer: 20 mM Acetate pH 5.5, 20 mM Histidine pH 6.0, 20 mM Histidine pH 6.5, or 20 mM Phosphate pH 7.0

(3) Detergent: 0.1% Polysorbate 80 or 0.1% Poloxamer P188

(4) Excipient: 10% Sucrose, 5% Sorbitol, or 7% Trehalose

mAb8 was buffer exchanged and concentrated to 50 mg/mL in 100 or 250 mM NaCl. 250 µL of the antibody stock was mixed with 50 µL of 10x buffer solutions, 50µL 10x detergent solutions, 125µL of 4x sugar solutions of buffers, and 25 µL water, resulting a total of 48 formulations (2 x 4 x 2 x 3 = 48), each containing 0.5mL of 25 mg/mL mAb8 in 2 mL glass vials with rubber stopper.

The vials were incubated in an incubator at 40°C with 75% humidity, and samples were taken at Day 0, 3, 6, 10, and 14 (40 µL) for analysis by SEC, CE-SDS, and cIEF.

Table 5 shows the abbreviated naming and the final concentrations of the formulation components for each of the 48 different formulations. The key for reading the table is shown below. For example, formulation A1 (S1B1D1E1) comprises (S1) 50 mM Sodium Chloride, (B1) 20 mM Acetate pH 5.5, (D1) 0.1% Polysorbate 80, and (E1) 10% Sucrose.

Table 5: Formulations comprising mAb8

	1	2	3	4	5	6	7	8	9	10	11	12
A	S1B1D1E1	S1B1D1E2	S1B1D1E3	S1B1D2E1	S1B1D2E2	S1B1D2E3	S2B1D1E1	S2B1D1E2	S2B1D1E3	S2B1D2E1	S2B1D2E2	S2B1D2E3
B	S1B2D1E1	S1B2D1E2	S1B2D1E3	S1B2D2E1	S1B2D2E2	S1B2D2E3	S2B2D1E1	S2B2D1E2	S2B2D1E3	S2B2D2E1	S2B2D2E2	S2B2D2E3
C	S1B3D1E1	S1B3D1E2	S1B3D1E3	S1B3D2E1	S1B3D2E2	S1B3D2E3	S2B3D1E1	S2B3D1E2	S2B3D1E3	S2B3D2E1	S2B3D2E2	S2B3D2E3
D	S1B4D1E1	S1B4D1E2	S1B4D1E3	S1B4D2E1	S1B4D2E2	S1B4D2E3	S2B4D1E1	S2B4D1E2	S2B4D1E3	S2B4D2E1	S2B4D2E2	S2B4D2E3

The final concentrations of individual components of the formulations are as follows:

Salt (S)

S1 50 mM Sodium Chloride

S2 125 mM Sodium Chloride

Buffer (B)

B1 20 mM Acetate pH 5.5

B2 20 mM Histidine pH 6.0

B3 20 mM Histidine pH 6.5

B4 20 mM Phosphate pH 7.0

Detergent (D)

D1 0.1% Polysorbate 80

D2 0.1% Poloxamer P188

Excipient (E)

E1 10% Sucrose

E2 5% Sorbitol

E3 7% Trehalose

The results of cIEF analysis of each of the 48 formulations are shown in **Table 6**. Specifically, Table 6 provides the percentage of mAb8 in the main peak in each of the 48 formulations over time, which was sorted by the Main peak% at day 14, from high to low. These data demonstrate that, in general, mAB8 in buffer 2 and 3 (histidine pH 6.0 and 6.5) has the highest percentage of main peak, followed by buffer 1 (acetate buffer pH 5.5) and lastly buffer 4 (Tris pH 7.5).

Table 6: Main peak % for each of the 48 formulations as determined by cIEF analysis.

	Days				
	14	**10**	**6**	**3**	**0**
S2B3D1E1	55.3	57.2	59.4	61.7	61.1
S2B3D1E2	55.1	57.2	59.5	62	59.2
S2B2D1E1	54.2	56.8	59.3	61.7	60.8
S1B3D1E2	54.2	56.3	58.5	61.2	
S2B3D2E2	54.1	56.7	59	61.2	62
S2B3D2E3	54	57.1	59.6	61	60.2
S1B3D1E1	53.9	56.7	58.7	60.9	61.3
S2B2D2E3	53.7	55.7	58.1	60.1	
S2B2D1E3	53.6	57.2	58.5	62.2	62.3
S1B2D1E3	53.3	56.8	58.2	60.3	60.9
S1B3D2E3	53.2	55.6	59	60.5	60.3
S2B3D2E1	53.2	56.5	59	60.9	60.6

S1B3D2E2	53.1	55.7	58.4	60.6	61.4
S2B2D1E2	53	55.8	57.9	60.2	62.2
S1B2D1E1	52.8	54.9	57.4	59.9	
S2B2D2E2	52.7	55.3	57.8	60.4	60.4
S1B2D1E2	52.6	55.9	58.1	60.5	60.1
S1B3D2E1	52.6	55.3	58.5	60.6	61.8
S1B2D2E3	52.1	54.5	57.3	59.9	61.5
S2B2D2E1	52	55.3	57.9	61.2	60.3
S1B2D2E1	51.7	54.3	57.1	59.9	60.7
S1B2D2E2	51.6	53.9	57.1	59.4	60.6
S2B1D2E3	50.6	53	55.7	58.2	59.6
S1B1D2E3	50.2	52.3	54.9	59.2	60.9
S2B1D2E1	50.2	51.4	54.2	58.7	61
S1B1D2E1	49.8	52	54.8	58.8	61
S1B1D1E3	49.7	50.9	54.8	58.1	60.1
S2B1D1E3	49.7	50.7	55.1	58.5	
S2B1D2E2	49.5	53	54.4	58.1	60.1
S2B4D2E2	49	52.2	56	59.3	61.5
S2B1D1E1	48.8	51.1	54.4	58.1	60.9
S1B1D2E2	48.7	50.6	54.4	58.7	60.3
S2B1D1E2	48.7	52.8	55.4	59	60.5
S2B4D1E2	48.7	50.3	54.4	57.4	61
S2B4D1E3	48.6	51.9	56.1	59.5	61
S1B1D1E1	48.4	51.3	54.1	57.9	59.3
S2B4D2E1	48.4	51.3	56	58.4	61
S1B4D1E3	48.2	51.1	55.9	58.7	59.6
S2B4D1E1	48.2	51	55	58.7	
S1B1D1E2	48	51.7	53.8	58.8	60.8
S1B4D2E2	47.5	50.8	55.1	58.1	60.7
S2B3D1E3	47.4	50.9	55.1	58.3	55
S1B4D1E1	47.4	57.5	58.5	61.5	61.6
S1B4D2E3	46.9	50.9	55.1	58.8	60.1
S1B4D2E1	46.3	49.8	54.8	58.4	
S1B4D1E2	46	50.4	54.6	58.1	57.8
S1B3D1E3	44.4	59.1	60.5	61.9	61.4

S2B4D2E3	39.4	51.8	55.4	59.2	60.5

Each of the 48 formulations was also analyzed by CE-SDS and SEC. As shown **Table 7** no significant aggregation or degradation was observed in any of the formulations tested as measured by CE-SDS. No significant change was observed between the different formulations when analyzed by SEC (data not shown).

Table 7: Purity of each of the 48 formulations as determined by CE-SDS analysis

	Purity by day		
Sample name	0	10	14
S1B1D1E1	100.0	99.0	99.7
S1B1D1E2	100.0	98.7	100.0
S1B1D1E3	100.0	98.9	100.0
S1B1D2E1	100.0	98.7	100.0
S1B1D2E2	100.0	98.9	100.0
S1B1D2E3	99.9	98.9	100.0
S2B1D1E1	100.0	98.9	100.0
S2B1D1E2	100.0	99.0	100.0
S2B1D1E3	100.0	98.9	100.0
S2B1D2E1	100.0	98.9	100.0
S2B1D2E2	100.0	98.9	100.0
S2B1D2E3	100.0	98.9	99.9
S1B2D1E1	99.7	99.0	100.0
S1B2D1E2	99.9	99.0	100.0
S1B2D1E3	100.0	99.0	100.0
S1B2D2E1	99.8	98.3	100.0
S1B2D2E2	99.7	98.9	100.0
S1B2D2E3	99.7	97.9	100.0
S2B2D1E1	ND	98.9	100.0
S2B2D1E2	100.0	99.0	100.0
S2B2D1E3	100.0	99.0	100.0
S2B2D2E1	99.7	98.9	100.0
S2B2D2E2	99.7	98.9	100.0
S2B2D2E3	99.8	98.7	100.0
S1B3D1E1	100.0	98.9	100.0
S1B3D1E2	100.0	98.9	100.0
S1B3D1E3	100.0	98.2	100.0
S1B3D2E1	100.0	98.0	100.0

S1B3D2E2	99.7	98.7	100.0
S1B3D2E3	99.8	98.5	100.0
S2B3D1E1	100.0	99.0	100.0
S2B3D1E2	100.0	98.9	100.0
S2B3D1E3	100.0	99.0	100.0
S2B3D2E1	100.0	98.4	100.0
S2B3D2E2	100.0	98.8	99.7
S2B3D2E3	100.0	98.1	100.0
S1B4D1E1	99.9	98.9	100.0
S1B4D1E2	100.0	98.9	99.6
S1B4D1E3	99.9	98.7	100.0
S1B4D2E1	100.0	98.6	99.6
S1B4D2E2	100.0	99.0	99.4
S1B4D2E3	99.9	98.7	99.6
S2B4D1E1	100.0	98.9	100.0
S2B4D1E2	100.0	99.0	100.0
S2B4D1E3	100.0	98.9	99.6
S2B4D2E1	100.0	98.9	100.0
S2B4D2E2	100.0	99.0	99.6
S2B4D2E3	100.0	98.6	99.6

In summary, the pH of the buffer had the greatest effect on the percentage of charge variants observed under accelerated conditions (40˚C). Formulations comprising mAb8 in histidine buffer at pH 6.0 and at pH 6.5 had the lowest percentage of acidic/basic species.

Example 30: Impact of Excipients on Stability of an Anti-CD137 Antibody Formulation at Various Temperatures

The stability of mAB1 was assessed in 100 mM NaCl, 0.03% polysorbate80, 20 mM histidine pH 6.0 without excipient, 10% sucrose, or 5% sorbitol under 4°C, 25°C, or 40˚C.

mAb1 (21.8 mg/mL in 20 mM Histidine 10 mM NaCl, 10% sucrose pH6.0) was thawed from -80˚C stock. 70 mL of the antibody solution was dialyzed in three Slide-A-Lyzer Dialysis Cassette (Thermo Scientific #66830, MWCO=10 kDa, 15-30mL) against 1.5L of 20 mM Histidine, 100 mM NaCl, 0.03% polysorbate 80, pH 6.0 at 4˚C for 4hrs, followed by dialysis against 2.5L of fresh buffer overnight. The next morning, the dialysates were pooled, filter through 0.22um filter, and 20% polysorbate 80 stock solution was added to reach a final concentration of 0.03%.

Formulations comprising no excipient, 10% sucrose, or 5% sorbitol were prepared as follows: (1) 22mL of the antibody solution was dialyzed against 1L of 20 mM Histidine, 100 mM NaCl, 0.03% polysorbate80, pH 6.0; (2) 5 mL of 50% sucrose was added to 20 mL of the antibody solution, and dialyzed against 1L of 20 mM Histidine, 100 mM NaCl, 0.03% polysorbate80, 10% sucrose, pH 6.0; and (3) 1.79 mL of 70% sorbitol was added to 23mL of the antibody solution, dialyzed against 1L of 20 mM Histidine, 100 mM NaCl, 0.03% polysorbate80, 5% sorbitol pH 6.0.

After dialysis, antibody concentrations were measured by A280 on a NanoDrop2000, and adjusted to ~10 mg/mL using respective buffers. All samples were sterilized through 0.22 μm filters (EMD Millipore, #SLGV033RS; BD Luer-Lock 20mL syringe #302830) in biosafety cabinet. 1mL of filtered antibody solutions were transferred to 2 mL glass vials and closed with stoppers and seals.

For each formulation, 4 vials were stored at 4˚C (refrigerator) and sampled at 1, 2, 3, 4, 6, 8, 10, 12, 14, 16, 20, and 24 weeks; 8 vials were stored at 25˚C with 60% humidity and sampled at 1, 2, 3, 4, 6, 8, 10, and 12 weeks; 12 vials were stored at 40˚C with 75% humidity and sampled at 1, 2, 3, and 4 weeks. At each time point, one vial of each formulation was taken for analysis by SEC, cIEF, CE-SDS, and micro-flow imaging.

Table 8: Matrix of mAb1 formulations comprising 100 mM NaCl, 0.03% polysorbate80, 20 mM histidine at pH 6.0, and comprising no excipient, 10% sucrose, or 5% sorbitol, and analyzed at 4°C, 25°C, or 40˚C.

Excipient	Temp (˚C)	Month 1				Month 2		Month 3		Month 4		Month 5	Month 6
		W1	W2	W3	W4	W6	W8	W10	W12	W14	W16	W20	W24
No sugar	40	X	X	X	X								
	25	X	X	X	X	X	X	X	X				
	4	X	X	X	X	X	X	X	X	X	X	X	X
10% Sucrose	40	X	X	X	X								
	25	X	X	X	X	X	X	X	X				

	4	X	X	X	X	X	X	X	X	X	X	X	X
5% Sorbitol	40	X	X	X	X								
	25	X	X	X	X	X	X	X	X				
	4	X	X	X	X	X	X	X	X	X	X	X	X

As shown in **Tables 9-11**, the type and presence of sugar excipient did not show a significant effect on charge variants under various storage temperatures.

Table 9: cIEF Analysis - Acidic Species

	No sugar			**10% sucrose**			**5% sorbitol**		
	4°C	**25°C**	**40°C**	**4°C**	**25°C**	**40°C**	**4°C**	**25°C**	**40°C**
W1	29.01	28.71	26.59	26.68	26.15	25.39	27.89	26.89	26.87
W2	29.35	27.88	28.59	27.13	25.9	28.05	26.42	26.33	28.99
W3	29.85	27.15	31.01	27	25.7	29.4	27.4	25.92	31.66
W4	26.96	26.05	31.84	26.53	25.31	33.04	27.16	25.62	34.21
W6	28.42	26.47		26.75	26.88		27.42	29.02	
W8	28.79	27.69		26.47	27.78		26.66	28.7	
W10	29	28.65		27.23	28.88		27.27	29.4	
W12	27.2	28.1		28.3	29.3		27.5	30.8	
W14	28.9			28.5			29.3		
W16	30.1			28.1			28.8		
W20	26.9			24.8			25.4		
W24	27			27.1			27		

Table 10: cIEF Analysis - Main Species

	No sugar			10% sucrose			5% sorbitol		
	4°C	25°C	40°C	4°C	25°C	40°C	4°C	25°C	40°C
W1	66.74	63.85	59.68	69.21	67.05	61.6	68.05	66.61	59.4
W2	66.61	63.64	56.56	68.16	65.26	57.43	69.15	65.02	55.46
W3	64.57	62.99	54.47	68.7	64.9	55	68.05	64.14	52.67
W4	68.63	64.16	54.28	68.79	64.45	52.43	67.91	64.01	51.04
W6	66.89	63.28		68.42	62.22		67.97	59.1	
W8	66.23	61.19		68.46	60.9		68.13	59.53	
W10	65.42	60.64		67.37	59.41		67.52	58.66	
W12	67.2	60.9		66.1	58.7		67	56.8	
W14	65.2			65.9			64.1		
W16	63.6			65.8			64.7		
W20	67.1			69.2			68.7		
W24	66.9			66.8			67		

Table 11: cIEF Analysis - Basic Species

	No sugar			10% sucrose			5% sorbitol		
	4°C	25°C	40°C	4°C	25°C	40°C	4°C	25°C	40°C
W1	4.26	7.43	13.72	4.1	6.8	13.01	4.06	6.5	13.73
W2	4.05	8.48	14.85	4.71	8.84	14.52	4.43	8.66	15.56
W3	5.59	9.86	14.53	4.3	9.3	14.7	4.55	9.94	15.67
W4	4.42	9.79	13.88	4.68	10.24	14.54	4.93	10.37	14.75
W6	4.69	10.25		4.83	10.9		4.61	11.87	
W8	4.98	11.13		5.08	11.32		5.22	11.77	

W10	5.58	10.71		5.4	11.72		5.21	11.94	
W12	5.6	11		5.7	11.9		5.6	12.4	
W14	5.9			5.6			6.6		
W16	6.3			6.2			6.5		
W20	6.1			6			5.9		
W24	6.1			6.1			6		

As shown in **Table 12**, in all three mAb1 formulations (no sugar, 10% sucrose, 5% sorbitol), there was no significant increase of aggregation over the duration of the study as determined by size-exclusion chromatography.

Table 12: Percentage of monomers as determined by Size Exclusion Chromatography

	mAb1-No sugar			mAb1-10% sucrose			mAb1-5% sorbitol		
Week	4°C	25°C	40°C	4°C	25°C	40°C	4°C	25°C	40°C
0	98.9	98.9	98.9	98.9	98.9	98.9	98.8	98.8	98.8
1	98.9	98.9	98.8	98.9	98.9	98.8	98.8	98.8	98.6
2	98.8	98.9	98.7	98.8	98.9	98.8	98.8	98.7	98.5
3	98.9	98.9	98.6	98.9	98.8	98.8	98.8	98.7	98.6
4	98.8	98.8	98.6	98.9	98.9	98.7	98.8	98.6	98.4
6	98.8	98.7		98.8	98.8		98.7	98.5	
8	98.7	98.6		98.7	98.7		98.6	98.4	
10	98.9	98.7		98.9	98.8		98.6	98.5	
12	98.8	98.5		98.7	98.7		98.5	98.4	
14	98.9			98.8			98.6		
16	98.8			98.9			98.6		
20	98.7			98.7			98.5		
24	98.8			98.6			98.4		

Micro-flow imaging analysis was used to assess the number of sub-visible particles in each of the formulations. As shown in **Tables 13-15**, the number of sub-visible particles increased over time. The mAB1 formulation containing 10% sucrose showed the lowest increase in number of particles, especially under accelerated conditions (40°C). The mAb1 formulation containing 5% sorbitol showed a greater increase in the number of particles. However, the 5% sorbitol formulation had fewer particles than the formulation without sugar.

Table 13: Micro-flow imaging analysis – mAb1 formulation without sugar

No sugar		Week											
	Size range	1	2	3	4	6	8	10	12	14	16	20	24
4°C	2-10 µm	4053	906	2657	1765	2034	1450	1047	2808	3587	6697	1743	2527
	10-25 µm	397	11	315	184	54	185	55	78	163	87	78	170
	> 25 µm	35	0	44	11	11	120	11	11	0	54	12	17
25°C	2-10 µm	611	204	3584	3361	1374	2635	2648	4658				
	10-25 µm	52	37	93	281	44	108	165	389				
	> 25 µm	0	22	0	33	11	22	44	44				
40°C	2-10 µm	20414	26908	7600	11232								
	10-25 µm	81	1977	294	514								
	> 25 µm	0	457	22	66								

Table 14: Micro-flow imaging analysis – mAb1 formulation with 10% sucrose

10 % sucrose		Week											
	Size range	1	2	3	4	6	8	10	12	14	16	20	24
4°C	2-10 µm	498	1487	921	1426	1396	4828	1809	885	1649	1268	1531	1575
	10-25 µm	0	33	87	97	44	226	98	33	76	33	69	12
	> 25 µm	0	0	11	0	11	72	22	11	11	11	35	0
25°C	2-10 µm	427	502	911	6353	678	2266	2933	1108				
	10-25 µm	14	0	87	367	77	113	109	87				
	> 25 µm	0	14	11	86	11	12	0	0				

40˚C	2-10 µm	421	2374	2423	2674								
	10-25 µm	31	132	144	403								
	> 25 µm	0	0	18	39								

Table 15: Micro-flow imaging analysis – mAb1 formulation with 5% sorbitol

5 % sorbitol		Week											
	Size range	1	2	3	4	6	8	10	12	14	16	20	24
4˚C	2-10 µm	329	691	1053	1351	1645	1807	1872	2004	1474	2000	2164	2098
	10-25 µm	13	0	44	33	44	174	152	44	141	184	173	87
	> 25 µm	13	0	0	11	22	35	11	11	33	76	25	15
25˚C	2-10 µm	2415	344	1315	1313	2490	10421	2717	4058				
	10-25 µm	180	11	55	44	291	848	182	251				
	> 25 µm	88	0	0	11	135	259	46	11				
40˚C	2-10 µm	588	116674	2303	2639								
	10-25 µm	24	10010	65	231								
	> 25 µm	0	2054	0	109								

In summary, mAb1 demonstrated excellent stability in all three formulations. There was no significant loss of monomeric antibody, nor degradation. The increase of acidic and basic species with concomitant decrease of main charge species were comparable among each of the three mAb1 formulations (no excipient, 10% sucrose, or 5% sorbitol).

Notably, at elevated temperatures (25°C and 40˚C), the mAb1 formulation without sugar showed a significantly higher level of sub-visible particles than the other two formulations. The formulation comprising 10% sucrose was demonstrated to be superior to the formulation comprising 5% sorbitol at elevated temperature.

Example 31: Impact of Freeze-Thaw Stress on Stability of an Anti-CD137 Antibody Formulation

Aggregation of mAb1 following freeze-thaw stress was assessed and characterized by size exclusion chromatography (SEC). Specifically, mAb1 in 100 mM NaCl, 0.03% polysorbate80, 20 mM histidine pH 6.0, and either without excipient, 10% sucrose, or 5%

sorbitol was subjected to up to 5 cycles of freeze-thaw between -80˚C and room temperature. SEC was then performed on the samples. As shown in **Table 16**, the increase in high molecular weight (HMW) % species was < 0.2% in all three formulations. The formulation comprising 10% sucrose had the lowest increase in HMW species, followed by 5% sorbitol and no sugar.

Table 16: SEC analysis of mAb1 formulations comprising no sugar, 10% sucrose, or 5% sorbitol

	FT cycles	Main %	HMW%	LMW%
No sugar	0	98.54	1.04	0.42
	1	98.53	1.14	0.33
	3	98.44	1.17	0.40
	5	98.29	1.30	0.42
10% sucrose	0	ND	ND	ND
	1	98.60	1.08	0.33
	3	98.50	1.10	0.40
	5	98.49	1.14	0.37
5% sorbitol	0	98.60	1.04	0.36
	1	98.56	1.11	0.33
	3	98.52	1.13	0.34
	5	98.47	1.22	0.31

Freeze-thaw analysis of the mAb1 formulations was also performed at temperatures cycling between -30°C and room temperature. Specifically, mAb1 formulations comprising 100 mM NaCl, 0.03% polysorbate80, 20 mM histidine pH 6.0, and either without excipient or 10% sucrose, were subjected to three-cycles of freeze-thaw between -30˚C and room temperature. The samples were analyzed by SEC and cIEF.

No significant change in the percentage of monomers was observed in either formulation following up to three freeze-thaw cycles (**Table 17**). mAb1 in the formulation without sugar had slightly more acid species after freeze-thaw than in the formulation comprising 10% sucrose (**Table 18**).

Table 17: Percentage of monomers observed by SEC analysis of mAb1 formulations comprising no sugar or 10% sucrose

	No sugar	10% sucrose
0	99.04	99.14
1 X FT	99.04	99.12
3 X FT	99.01	99.15

Table 18: cIEF analysis of mAb1 formulations comprising no sugar or 10% sucrose

	No sugar			**10% sucrose**		
	0 x FT	**1x FT**	**3x FT**	**0 x FT**	**1x FT**	**3x FT**
Acidic Peak %	27.9	28.7	29	27.9	27.9	27.6
Main Peak %	66.6	65.4	65.4	66.5	67	67.5
Basic Peak %	5.5	6	5.7	5.7	5.1	4.9

Thus, freeze-thaw cycles between -80°C and room temperature or -30°C and room temperature did not cause a significant increase in aggregation or charge variants in the mAb1 formulations.

Example 32: **Impact of Dilution on Stability of an Anti-CD137 Antibody Formulation**

Many therapeutic antibodies are administered by intravenous infusion. Typical infusion fluid includes 5% dextrose and 0.9% saline. The stability of an antibody upon dilution into infusion fluids varies. For example, Herceptin undergo rapid aggregation upon dilution into 5% dextrose solution (Luo et al. MAbs. 2015;7(6):1094-103).

The stability of mAb1 upon dilution into 5% dextrose and 0.9% NaCl solutions was studied. 5% dextrose solution (w/v) was prepared with dextrose (D-Glucose, Sigma-Aldrich, #G7021-1KG) in water, and filtered through 0.22 μm filter to sterilize. 0.5% and 0.1% dextrose solutions were prepared by diluting the 5% stock into water. 0.9% (w/v) saline solution was prepared with sodium chloride (JT.Baker #3627-01) in water, and filtered through 0.22 μm filter to sterilize.

mAb1 (Lot0536-07, 20 mM Histidine, 100 mM NaCl, 0.03% polysorbate 80, pH 6.0, 14.5 mg/mL) was diluted 10-fold into 5%, 0.5%, or 0.1% dextrose solutions, 0.9% saline, or pure water and kept at room temperature (18-25˚C) for 3 days before assays. For control, the antibody stock was diluted 10-fold into 20mM sodium phosphate, 150mM NaCl pH 7.0 immediately before the analytical assays.

Size exclusion chromatography (SEC) was performed on each of the samples with a YMC Diol-200 8 x 300 mm column (Cat.no # DL20S05-3008WT) on an Agilent 1200 series HPLC instrument. The running buffer was 20mM sodium phosphate, 400mM NaCl pH 7.0 at a flow rate of 1 mL/min and running time of 15min per sample. As shown in **Fig. 37**, there was no detectable increase of aggregation by SEC, even after 3-day incubation after dilution into respective solutions (the term dextrose is used interchangeably with the term glucose).

Dynamic light scattering (DLS) was performed on a Wyatt Dynapro PlateReader-II instrument with 30 μL sample volume in 384-well clear-bottom plate (Corning #3540) at 25˚C. Each sample was measured with 5 second acquisition time for 10 times. As shown in **Fig. 38**, there was no detectable increase of aggregation by DLS, except for the dilution into pure water.

These data provide evidence that mAb1 is stable upon dilution into two frequently used infusion fluids: 5% dextrose and 0.9% saline.

Example 33: Impact of Freeze-Thaw on Subvisible Particle Formation of an Anti-CD137 Antibody Formulation

During the manufacturing, storage, transportation, and administration, protein therapeutics might go through multiple cycles of freeze-thaw. This process potentially causes the formation of aggregates, which have been associated with anti-drug response and adverse effects.

The effect of freeze-thaw on the biophysical properties of the novel anti-CD137 agonist antibody mAb1 was investigated. Specifically, the formation of subvisible particles and the effectiveness of removing the particles by passing the solution through needles with built-in filters was assessed.

mAb1 was subjected to 3 cycles of freeze-thaw between -30˚C and room temperature (25±3˚C). After each cycle, samples were characterized by size-exclusion chromatography, dynamic light scattering, or microfluidic imaging.

Analytical Methods

For the multiple freeze-thaw test, eight vials of mAb1 were thawed at room temperature (**1 x FT**). One vial was used for the SEC, DLS, and micro-flow imaging assays. The seven remaining vials were re-frozen at -30˚C overnight. On day 2, the seven vials were thawed at room temperature and one vial was used for SEC, DLS and MFI (**2 x FT**). The remaining six vials were re-frozen at -30˚C overnight. On day 3, the six vials were thawed at room temperature and pooled. One aliquot was used for SEC, DLS, and MFI (**3 x FT**). The rest of the antibody solution was split into two halves. One half of the antibody solution was drawn into a 5mL syringe (BD #309646) with a needle containing built-in 5 µm filter (BD # 305211). Then, the needle was detached, and the solution was dispensed into a new vial (**S1**). About 750uL of this solution was saved for assays while the remainder went through another two filtrations (**S2 and S3**) as described above, each time using a new syringe/needle. The other half of the antibody solution was filtered by the same method, except vented needles were used (BD #305201) that contained a built-in 5 µm filter. The resulting fractions were labeled **Sv1, Sv2, and Sv3.** Filtration was performed in a biosafety cabinet. All resulting fractions were analyzed via SEC, DLS, and MFI.

Size exclusion chromatography (SEC) was performed with a YMC Diol-200 8 x 300 mm column (Cat.no # DL20S05-3008WT) on an Agilent 1200 series HPLC instrument. The running buffer was 20mM sodium phosphate, 400mM NaCl pH 7.0 at a flow rate of 1 mL/min and running time of 15min per sample.

Capillary isoelectric focusing (cIEF) was performed on a Maurice C. instrument (ProteinSimple) with Maurice cIEF Cartridge (Cat. No# PS-MC02-C). The final assay composition consisted of 0.5 mg/mL antibody, 4% Pharmalyte 3-10, and 0.35% methylcellulose. PI markers 5.85 and 8.4 were used. The focusing conditions were: 1500 V for 1min followed by 3000 V for 4min. Native fluorescence signal with 3 second exposure time was used for peak integration using the dropline method.

Capillary electrophoresis sodium dodecyl sulfate (CE-SDS) was performed on a LapChip GX II instrument using HT Protein Express Chip (Perkin Elmer, #760528) and Protein Express Assay Reagent Kit (Perkin Elmer, # CLS960008). The reagents and chip were prepared according to the manufacturer's instruction. The samples were diluted with PBS to 0.5 mg/mL immediately before the assay. For non-reducing condition, 2µL of diluted samples were mixed

with 7μL of sample buffer containing 25mM iodoacetamide (Sigma-Aldrich #A3221-10VL) in a 96-well plate; for reducing condition, 2μL of diluted samples were mixed with 7μL of sample buffer containing 25 mM DTT. After denaturation at 75˚C for 10min on a thermocycler (Eppendorf Mastercycler pro), 35μL of water was added to each well and mixed by pipetting up and own. The plate was then centrifuged at 2,000 g for 1 min to remove air bubbles before placing in the LapChip GXII instrument for analysis.

Micro-flow imaging (MFI) was performed on a FlowCam PV-100 instrument (Fluid Imaging Technologies). The samples were flown at a rate of 0.15 mL/min for a total volume of 200~300 μL. Each sample was run twice, and the particle counts in the range of 2-10 μm, 10-25 μm and >25 μm were averaged respectively.

Results

There was no significant change in the percentage of high molecular weight species (HMW%) or the percentage of monomers in the antibody solutions after 3 cycles of freeze-thaw and passes through the needle with built-in filters, as measured by SEC and shown in **Table 19**.

Table 19: Area under curve and percentage of monomers as measured by SEC

	Peak area				
	HMW1	**HMW2**	**Main**	**% Monomer**	**CV% ***
mAb1_1XFT	0.00	61.43	3269.17	98.16	0.097
mAb1_2XFT	0.00	61.04	3238.09	98.15	0.160
mAb1_3XFT	0.00	62.10	3285.09	98.14	0.139
mAb1_3XFT_S1	0.00	62.11	3293.17	98.15	0.215
mAb1_3XFT_S2	0.00	62.47	3294.00	98.14	0.042
mAb1_3XFT_S3	0.00	62.51	3293.13	98.14	0.068
mAb1_3XFT_SV1	0.00	62.11	3298.86	98.15	0.098
mAb1_3XFT_SV2	0.00	62.01	3293.07	98.15	0.057
mAb1_3XFT_SV3	0.00	62.16	3302.52	98.15	0.056

* CV % represent the variation of the main peak area between duplicate injections

DLS is more sensitive than SEC in detecting small amounts of aggregations with hydrodynamic radius of 1-1000 nm. In the present study, the freeze-thaw and needle passage samples were measured by DLS in duplicates. DLS was performed according to the methods described in Example 32. There was no detectable aggregation in most of the samples, with the exception of two samples which may contain subvisible particles, which were beyond the measurable range of DLS (**Table 20**).

Table 20: DLS analysis

	Read1 (nm)	Read2 (nm)
1XFT	6.7	7.4
2XFT	6.2*	5.9
3XFT	6.5	7.3
S1	7	6.6
S2	6.6	6.4
S3	6.9	6.9
Sv1	6.5	6.6
Sv2	6.5	6.4**
Sv3	6	6.9

* A species with the radius of 9233 nm (<10% in Mass%) was found in Read1 but not read 2

** A species with the radius of 6228 nm (<5% in Mass%) was found in Read2 but not read 1

As shown in **Fig. 39** and **Table 21**, micro-flow imaging detected subvisible particles between 2-80 μm, which were hardly detected by SEC and DLS. Upon freeze-thaw, the number of particles in the range of 2-10 μm increased ~ 10-fold; larger size particles increased to a lesser extent. Upon additional freeze-thaw, the 2-25 μm particle numbers decreased while the >25 μm particle numbers increased. It is possible, without being bound or limited by theory, that the smaller particles aggregated to form larger particles.

One pass through the needles with built-in 5 µm filter effectively removed the majority of particles, especially particles > 5 µm. The two types of syringe had comparable performance in removing particles.

Table 21: Subvisible particles detected by micro-flow imaging

	P/ml in different size range (µm)			
	2-5	**5-10**	**10-25**	**>25**
1xFT	1414	285	177	44
2xFT	15271	3453	936	74
3xFT	3632	713	270	106
S1	1595	94	6	0
S2	1513	224	136	34
S3	1307	99	45	10
SV1	1848	159	25	10
SV2	1293	77	7	0
SV3	1163	83	47	0

In summary, freeze-thaw was shown to induce an increase in the number of subvisible particles in the antibody solution comprising mAb1. However, the majority of particles were effectively removed using a needle with a built in 5µm filter or a vented needle with a built in 5µm filter.

TABLE 22: ANTIBODY COMBINATION TABLE I

V_H	**V_L**	**V_H CDR**			**V_L CDR**		
		CDR1	**CDR2**	**CDR3**	**CDR1**	**CDR2**	**CDR3**
4	6	48	56	68	69	78	89
4	28	48	56	68	70	79	90
4	30	48	56	68	71	80	91

4	32	48	56	68	72	81	92
4	34	48	56	68	73	82	91
4	36	48	56	68	74	83	93
4	38	48	56	68	75	84	91
4	40	48	56	68	74	85	94
4	42	48	56	68	76	86	95
4	44	48	56	68	77	87	93
4	46	48	56	68	69	88	90
4	105	48	56	68	109	110	92
8	6	49	57	68	69	78	89
10	6	49	58	68	69	78	89
12	6	49	59	68	69	78	89
14	6	49	60	68	69	78	89
16	6	50	61	68	69	78	89
18	6	50	58	68	69	78	89
20	6	51	62	68	69	78	89
22	6	52	63	68	69	78	89
24	6	50	64	68	69	78	89
26	6	50	65	68	69	78	89
101	6	51	108	68	69	78	89
103	6	107	56	68	69	78	89
8	28	49	57	68	70	79	90
8	30	49	57	68	71	80	91
8	32	49	57	68	72	81	92
8	34	49	57	68	73	82	91
8	36	49	57	68	74	83	93
8	38	49	57	68	75	84	91
8	40	49	57	68	74	85	94
8	42	49	57	68	76	86	95
8	44	49	57	68	77	87	93
8	46	49	57	68	69	88	90
8	105	49	57	68	109	110	92
10	28	49	58	68	70	79	90
10	30	49	58	68	71	80	91
10	32	49	58	68	72	81	92
10	34	49	58	68	73	82	91
10	36	49	58	68	74	83	93
10	38	49	58	68	75	84	91
10	40	49	58	68	74	85	94
10	42	49	58	68	76	86	95

10	44	49	58	68	77	87	93
10	46	49	58	68	69	88	90
10	105	49	58	68	109	110	92
12	28	49	59	68	70	79	90
12	30	49	59	68	71	80	91
12	32	49	59	68	72	81	92
12	34	49	59	68	73	82	91
12	36	49	59	68	74	83	93
12	38	49	59	68	75	84	91
12	40	49	59	68	74	85	94
12	42	49	59	68	76	86	95
12	44	49	59	68	77	87	93
12	46	49	59	68	69	88	90
12	105	49	59	68	109	110	92
14	28	49	60	68	70	79	90
14	30	49	60	68	71	80	91
14	32	49	60	68	72	81	92
14	34	49	60	68	73	82	91
14	36	49	60	68	74	83	93
14	38	49	60	68	75	84	91
14	40	49	60	68	74	85	94
14	42	49	60	68	76	86	95
14	44	49	60	68	77	87	93
14	46	49	60	68	69	88	90
14	105	49	60	68	109	110	92
16	28	50	61	68	70	79	90
16	30	50	61	68	71	80	91
16	32	50	61	68	72	81	92
16	34	50	61	68	73	82	91
16	36	50	61	68	74	83	93
16	38	50	61	68	75	84	91
16	40	50	61	68	74	85	94
16	42	50	61	68	76	86	95
16	44	50	61	68	77	87	93
16	46	50	61	68	69	88	90
16	105	50	61	68	109	110	92
18	28	50	58	68	70	79	90
18	30	50	58	68	71	80	91
18	32	50	58	68	72	81	92
18	34	50	58	68	73	82	91

18	36	50	58	68	74	83	93
18	38	50	58	68	75	84	91
18	40	50	58	68	74	85	94
18	42	50	58	68	76	86	95
18	44	50	58	68	77	87	93
18	46	50	58	68	69	88	90
18	105	50	58	68	109	110	92
20	28	51	62	68	70	79	90
20	30	51	62	68	71	80	91
20	32	51	62	68	72	81	92
20	34	51	62	68	73	82	91
20	36	51	62	68	74	83	93
20	38	51	62	68	75	84	91
20	40	51	62	68	74	85	94
20	42	51	62	68	76	86	95
20	44	51	62	68	77	87	93
20	46	51	62	68	69	88	90
20	105	51	62	68	109	110	92
22	28	52	63	68	70	79	90
22	30	52	63	68	71	80	91
22	32	52	63	68	72	81	92
22	34	52	63	68	73	82	91
22	36	52	63	68	74	83	93
22	38	52	63	68	75	84	91
22	40	52	63	68	74	85	94
22	42	52	63	68	76	86	95
22	44	52	63	68	77	87	93
22	46	52	63	68	69	88	90
22	105	52	63	68	109	110	92
24	28	50	64	68	70	79	90
24	30	50	64	68	71	80	91
24	32	50	64	68	72	81	92
24	34	50	64	68	73	82	91
24	36	50	64	68	74	83	93
24	38	50	64	68	75	84	91
24	40	50	64	68	74	85	94
24	42	50	64	68	76	86	95
24	44	50	64	68	77	87	93
24	46	50	64	68	69	88	90
24	105	50	64	68	109	110	92

26	28	50	65	68	70	79	90
26	30	50	65	68	71	80	91
26	32	50	65	68	72	81	92
26	34	50	65	68	73	82	91
26	36	50	65	68	74	83	93
26	38	50	65	68	75	84	91
26	40	50	65	68	74	85	94
26	42	50	65	68	76	86	95
26	44	50	65	68	77	87	93
26	46	50	65	68	69	88	90
26	105	50	65	68	109	110	92
101	28	51	108	68	70	79	90
101	30	51	108	68	71	80	91
101	32	51	108	68	72	81	92
101	34	51	108	68	73	82	91
101	36	51	108	68	74	83	93
101	38	51	108	68	75	84	91
101	40	51	108	68	74	85	94
101	42	51	108	68	76	86	95
101	44	51	108	68	77	87	93
101	46	51	108	68	69	88	90
101	105	51	108	68	109	110	92
103	28	107	56	68	70	79	90
103	30	107	56	68	71	80	91
103	32	107	56	68	72	81	92
103	34	107	56	68	73	82	91
103	36	107	56	68	74	83	93
103	38	107	56	68	75	84	91
103	40	107	56	68	74	85	94
103	42	107	56	68	76	86	95
103	44	107	56	68	77	87	93
103	46	107	56	68	69	88	90
103	105	107	56	68	109	110	92

TABLE 23: ANTIBODY COMBINATION TABLE II

V_H (SEQ ID NO)	**V_L** (SEQ ID NO)	**V_H CDR** (SEQ ID NO)			**V_L CDR** (SEQ ID NO)		
		CDR1	**CDR2**	**CDR3**	**CDR1**	**CDR2**	**CDR3**
4	6	135	139	143	144	147	150
4	28	135	139	143	145	148	151

4	105	135	139	143	146	149	152
8	6	136	140	143	144	147	150
8	28	136	140	143	145	148	151
8	105	136	140	143	146	149	152
101	6	137	141	143	144	147	150
101	28	137	141	143	145	148	151
101	105	137	141	143	146	149	152
26	6	138	142	143	144	147	150
26	28	138	142	143	145	148	151
26	105	138	142	143	146	149	152
103	6	135	139	143	144	147	150
103	28	135	139	143	145	148	151
103	105	135	139	143	146	149	152

TABLE 24: ANTIBODY COMBINATION TABLE III

V_H (SEQ ID NO)	**V_L** (SEQ ID NO)	**V_H CDR** (SEQ ID NO)			**V_L CDR** (SEQ ID NO)		
		CDR1	**CDR2**	**CDR3**	**CDR1**	**CDR2**	**CDR3**
4	6	48	154	159	144	147	150
4	28	48	154	159	145	148	151
4	105	48	154	159	146	149	152
8	6	49	155	159	144	147	150
8	28	49	155	159	145	148	151
8	105	49	155	159	146	149	152
101	6	51	156	159	144	147	150
101	28	51	156	159	145	148	151
101	105	51	156	159	146	149	152
26	6	50	158	159	144	147	150
26	28	50	158	159	145	148	151
26	105	50	158	159	146	149	152
103	6	153	157	159	144	147	150
103	28	153	157	159	145	148	151
103	105	153	157	159	146	149	152

TABLE 25: SEQUENCE LISTING

SEQ ID NO	Description	Sequence
1	Human IgG1	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT

		TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK
2	Human IgG4 mutant (S228P/C-terminal K truncation)	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCP**P**CPAPEFLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVS VLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLS LSLG
3	Human CD137 (Accession # NP_001552)	MGNSCYNIVATLLLVLNFERTRSLQDPCSNCPAGTFCDNNRNQICS PCPPNSFSSAGGQRTCDICRQCKGVFRTRKECSSTSNAECDCTPGF HCLGAGCSMCEQDCKQGQELTKKGCKDCCFGTFNDQKRGICRPWTN CSLDGKSVLVNGTKERDVVCGPSPADLSPGASSVTPPAPAREPGHS PQIISFFLALTSTALLFLLFFLTLRFSVVKRGRKKLLYIFKQPFMR PVQTTQEEDGCSCRFPEEEEGGCEL
4	V_H1 amino acid sequence	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLE WVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTA VYYCAKDSPFLLDDYYYYYYMDVWGKGTTVTVSS
5	V_H1 nucleic acid sequence	GAAGTGCAATTATTGGAATCCGGCGGCGGTTTAGTTCAGCCAGGTG GCTCTTTGAGGCTGAGTTGCGCAGCCTCTGGATTCACTTTTAGTTC GTATGCAATGTCGTGGGTTCGCCAGGCGCCCGGTAAGGGTCTGGAG TGGGTGAGTGCTATTTCCGGCTCTGGCGGATCTACCTATTACGCCG ACTCTGTGAAAGGTCGTTTTACCATAAGCCGCGACAATTCTAAGAA TACTTTATATCTTCAAATGAATTCGCTGCGGGCAGAAGACACGGCC GTCTATTACTGCGCAAAGGACTCACCTTTTCTATTAGACGACTACT ACTACTACTACTACATGGACGTATGGGGCAAGGGTACAACTGTCAC CGTCTCCTCAGCTAGC
6	V_L1 amino acid sequence	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKL LIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGH LFPITFGGGTKVEIK
7	V_L1 nucleic acid sequence	GATATTCAGATGACACAGAGCCCGTCATCAGTAAGTGCAAGCGTCG GAGATCGGGTTACAATAACATGTCGTGCCTCGCAAGGAATTTCCTC CTGGTTGGCCTGGTATCAGCAGAAACCTGGCAAAGCCCCCAAATTA CTAATTTATGCCGCAAGCTCTCTGCAATCGGGTGTTCCTTCGCGGT TTTCTGGCTCTGGAAGTGGCACCGACTTCACGCTTACTATCTCTAG CCTTCAGCCGGAGGATTTTGCTACCTACTACTGCCAACAAGGCCAT TTATTCCCTATTACCTTTGGGGGCGGTACAAAAGTCGAGATCAAGC GTACG
8	V_H2 amino acid sequence	EVQLLESGGGLVQPGGSLRLSCAASGFTFNYYAMSWVRQAPGKGLE WVSAIDGSGDNTTYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTA VYYCAKDSPFLLDDYYYYYYMDVWGKGTTVTVSS
9	V_H2 nucleic acid sequence	GAAGTGCAATTATTGGAATCCGGCGGCGGTTTAGTTCAGCCAGGTG GCTCTTTGAGGCTGAGTTGCGCAGCCTCTGGATTCACCTTTAACTA TTACGCAATGTCTTGGGTTCGCCAGGCGCCCGGTAAGGGTCTGGAG TGGGTGTCTGCAATCGATGGTTCTGGTGATAACACTACTTACGCCG

		ACTCTGTGAAAGGTCGTTTTACCATAAGCCGCGACAATTCTAAGAA TACTTTATATCTTCAAATGAATTCGCTGCGGGCAGAAGACACGGCC GTCTATTACTGCGCAAAGGACTCACCTTTTCTATTAGACGACTACT ACTACTACTACTACATGGACGTATGGGGCAAGGGTACAACTGTCAC CGTCTCCTCAGCTAGC
10	V_H3 amino acid sequence	EVQLLESGGGLVQPGGSLRLSCAASGFTFNYYAMSWVRQAPGKGLE WVAAISGSGDGTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTA VYYCAKDSPFLLDDYYYYYYMDVWGKGTTVTVSS
11	V_H3 nucleic acid sequence	GAAGTGCAATTATTGGAATCCGGCGGCGGTTTAGTTCAGCCAGGTG GCTCTTTGAGGCTGAGTTGCGCAGCCTCTGGATTCACCTTTAACTA TTACGCAATGTCTTGGGTTCGCCAGGCGCCCGGTAAGGGTCTGGAG TGGGTGGCAGCAATCTCTGGTTCTGGTGATGGTACTTACTACGCCG ACTCTGTGAAAGGTCGTTTTACCATAAGCCGCGACAATTCTAAGAA TACTTTATATCTTCAAATGAATTCGCTGCGGGCAGAAGACACGGCC GTCTATTACTGCGCAAAGGACTCACCTTTTCTATTAGACGACTACT ACTACTACTACTACATGGACGTATGGGGCAAGGGTACAACTGTCAC CGTCTCCTCAGCTAGC
12	V_H4 amino acid sequence	EVQLLESGGGLVQPGGSLRLSCAASGFTFNYYAMSWVRQAPGKGLE WVSAISGSGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTA VYYCAKDSPFLLDDYYYYYYMDVWGKGTTVTVSS
13	V_H4 nucleic acid sequence	GAAGTGCAATTATTGGAATCCGGCGGCGGTTTAGTTCAGCCAGGTG GCTCTTTGAGGCTGAGTTGCGCAGCCTCTGGATTCACCTTTAACTA TTACGCAATGTCTTGGGTTCGCCAGGCGCCCGGTAAGGGTCTGGAG TGGGTGTCTGCAATCTCTGGTTCTGGTGATTCTACTTACTACGCCG ACTCTGTGAAAGGTCGTTTTACCATAAGCCGCGACAATTCTAAGAA TACTTTATATCTTCAAATGAATTCGCTGCGGGCAGAAGACACGGCC GTCTATTACTGCGCAAAGGACTCACCTTTTCTATTAGACGACTACT ACTACTACTACTACATGGACGTATGGGGCAAGGGTACAACTGTCAC CGTCTCCTCAGCTAGC
14	V_H5 amino acid sequence	EVQLLESGGGLVQPGGSLRLSCAASGFTFNYYAMSWVRQAPGKGLE WVAAISGGGDATYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTA VYYCAKDSPFLLDDYYYYYYMDVWGKGTTVTVSS
15	V_H5 nucleic acid sequence	GAAGTGCAATTATTGGAATCCGGCGGCGGTTTAGTTCAGCCAGGTG GCTCTTTGAGGCTGAGTTGCGCAGCCTCTGGATTCACCTTTAACTA TTACGCAATGTCTTGGGTTCGCCAGGCGCCCGGTAAGGGTCTGGAG TGGGTGGCAGCAATCTCTGGTGGTGGTGATGCAACTTACTACGCCG ACTCTGTGAAAGGTCGTTTTACCATAAGCCGCGACAATTCTAAGAA TACTTTATATCTTCAAATGAATTCGCTGCGGGCAGAAGACACGGCC GTCTATTACTGCGCAAAGGACTCACCTTTTCTATTAGACGACTACT ACTACTACTACTACATGGACGTATGGGGCAAGGGTACAACTGTCAC CGTCTCCTCAGCTAGC
16	V_H6 amino acid sequence	EVQLLESGGGLVQPGGSLRLSCAASGFTFYGYAMSWVRQAPGKGLE WVSSISGSGDVTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTA VYYCAKDSPFLLDDYYYYYYMDVWGKGTTVTVSS
17	V_H6	GAAGTGCAATTATTGGAATCCGGCGGCGGTTTAGTTCAGCCAGGTG GCTCTTTGAGGCTGAGTTGCGCAGCCTCTGGATTCACCTTTTATGG

	nucleic acid sequence	TTACGCAATGTCTTGGGTTCGCCAGGCGCCCGGTAAGGGTCTGGAG TGGGTGTCTTCTATCTCTGGTTCTGGTGATGTTACTTACTACGCCG ACTCTGTGAAAGGTCGTTTTACCATAAGCCGCGACAATTCTAAGAA TACTTTATATCTTCAAATGAATTCGCTGCGGGCAGAAGACACGGCC GTCTATTACTGCGCAAAGGACTCACCTTTTCTATTAGACGACTACT ACTACTACTACTACATGGACGTATGGGGCAAGGGTACAACTGTCAC CGTCTCCTCAGCTAGC
18	V_H7 amino acid sequence	EVQLLESGGGLVQPGGSLRLSCAASGFTFYGYAMSWVRQAPGKGLE WVAAISGSGDGTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTA VYYCAKDSPFLLDDYYYYYYMDVWGKGTTVTVSS
19	V_H7 nucleic acid sequence	GAAGTGCAATTATTGGAATCCGGCGGCGGTTTAGTTCAGCCAGGTG GCTCTTTGAGGCTGAGTTGCGCAGCCTCTGGATTCACCTTTTATGG TTACGCAATGTCTTGGGTTCGCCAGGCGCCCGGTAAGGGTCTGGAG TGGGTGGCAGCAATCTCTGGTTCTGGTGATGGTACTTACTACGCCG ACTCTGTGAAAGGTCGTTTTACCATAAGCCGCGACAATTCTAAGAA TACTTTATATCTTCAAATGAATTCGCTGCGGGCAGAAGACACGGCC GTCTATTACTGCGCAAAGGACTCACCTTTTCTATTAGACGACTACT ACTACTACTACTACATGGACGTATGGGGCAAGGGTACAACTGTCAC CGTCTCCTCAGCTAGC
20	V_H8 amino acid sequence	EVQLLESGGGLVQPGGSLRLSCAASGFTFRNYAMSWVRQAPGKGLE WVSAISGFGESTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTA VYYCAKDSPFLLDDYYYYYYMDVWGKGTTVTVSS
21	V_H8 nucleic acid sequence	GAAGTGCAATTATTGGAATCCGGCGGCGGTTTAGTTCAGCCAGGTG GCTCTTTGAGGCTGAGTTGCGCAGCCTCTGGATTCACCTTTAGAAA CTACGCAATGTCTTGGGTTCGCCAGGCGCCCGGTAAGGGTCTGGAG TGGGTGTCTGCAATCTCTGGTTTTGGTGAATCTACTTACTACGCCG ACTCTGTGAAAGGTCGTTTTACCATAAGCCGCGACAATTCTAAGAA TACTTTATATCTTCAAATGAATTCGCTGCGGGCAGAAGACACGGCC GTCTATTACTGCGCAAAGGACTCACCTTTTCTATTAGACGACTACT ACTACTACTACTACATGGACGTATGGGGCAAGGGTACAACTGTCAC CGTCTCCTCAGCTAGC
22	V_H9 amino acid sequence	EVQLLESGGGLVQPGGSLRLSCAASGFTFNYYAMNWVRQAPGKGLE WVAAISGSGGRTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTA VYYCAKDSPFLLDDYYYYYYMDVWGKGTTVTVSS
23	V_H9 nucleic acid sequence	GAAGTGCAATTATTGGAATCCGGCGGCGGTTTAGTTCAGCCAGGTG GCTCTTTGAGGCTGAGTTGCGCAGCCTCTGGATTCACCTTTAACTA TTACGCAATGAACTGGGTTCGCCAGGCGCCCGGTAAGGGTCTGGAG TGGGTGGCAGCAATCTCTGGTTCTGGTGGTAGAACTTACTACGCCG ACTCTGTGAAAGGTCGTTTTACCATAAGCCGCGACAATTCTAAGAA TACTTTATATCTTCAAATGAATTCGCTGCGGGCAGAAGACACGGCC GTCTATTACTGCGCAAAGGACTCACCTTTTCTATTAGACGACTACT ACTACTACTACTACATGGACGTATGGGGCAAGGGTACAACTGTCAC CGTCTCCTCAGCTAGC
24	V_H10 amino acid sequence	EVQLLESGGGLVQPGGSLRLSCAASGFTFYGYAMSWVRQAPGKGLE WVSAISGSGGNTSYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTA VYYCAKDSPFLLDDYYYYYYMDVWGKGTTVTVSS

25	V_H10 nucleic acid sequence	GAAGTGCAATTATTGGAATCCGGCGGCGGTTTAGTTCAGCCAGGTG GCTCTTTGAGGCTGAGTTGCGCAGCCTCTGGATTCACCTTTTATGG TTACGCAATGTCTTGGGTTCGCCAGGCGCCCGGTAAGGGTCTGGAG TGGGTGTCTGCAATCTCTGGTTCTGGTGGTAACACTTCTTACGCCG ACTCTGTGAAAGGTCGTTTTACCATAAGCCGCGACAATTCTAAGAA TACTTTATATCTTCAAATGAATTCGCTGCGGGCAGAAGACACGGCC GTCTATTACTGCGCAAAGGACTCACCTTTTCTATTAGACGACTACT ACTACTACTACTACATGGACGTATGGGGCAAGGGTACAACTGTCAC CGTCTCCTCAGCTAGC
26	V_H11 amino acid sequence	EVQLLESGGGLVQPGGSLRLSCAASGFTFYGYAMSWVRQAPGKGLE WVAAISGSGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTA VYYCAKDSPFLLDDYYYYYYMDVWGKGTTVTVSS
27	V_H11 nucleic acid sequence	GAAGTGCAATTATTGGAATCCGGCGGCGGTTTAGTTCAGCCAGGTG GCTCTTTGAGGCTGAGTTGCGCAGCCTCTGGATTCACCTTTTATGG TTACGCAATGTCTTGGGTTCGCCAGGCGCCCGGTAAGGGTCTGGAG TGGGTGGCAGCAATCTCTGGTTCTGGTGATTCTACTTACTACGCCG ACTCTGTGAAAGGTCGTTTTACCATAAGCCGCGACAATTCTAAGAA TACTTTATATCTTCAAATGAATTCGCTGCGGGCAGAAGACACGGCC GTCTATTACTGCGCAAAGGACTCACCTTTTCTATTAGACGACTACT ACTACTACTACTACATGGACGTATGGGGCAAGGGTACAACTGTCAC CGTCTCCTCAGCTAGC
28	V_L2 amino acid sequence	DIQMTQSPSTLSASVGDRVTITCRASQNIHNWLAWYQQKPGKAPKL LIYKASGLESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQGD RFPLTFGGGTKVEIK
29	V_L2 nucleic acid sequence	GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAG GAGACAGAGTCACCATCACTTGCCGGGCCAGTCAGAATATTCATAA CTGGTTGGCCTGGTATCAGCAAAAACCAGGGAAAGCCCCTAAGCTC CTGATCTATAAGGCGTCTGGTTTGGAAAGTGGGGTCCCATCAAGAT TCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAG CCTGCAACCTGATGATTTTGCAACTTACTACTGTCAACAGGGTGAC AGATTCCCTCTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAAC GTACG
30	V_L3 amino acid sequence	DIQMTQSPSILSASVGDRVTITCRASQSISRWLAWYQQKPGKPPKL LIFKASALESGVPSRFSGSGYGTDFTLTISNLQPEDFATYFCQQGN SFPLTFGGGTKVDIK
31	V_L3 nucleic acid sequence	GACATCCAGATGACCCAGTCTCCTTCCATCCTGTCTGCATCTGTAG GAGACAGAGTCACTATCACTTGCCGGGCCAGTCAGAGTATCAGTAG GTGGTTGGCCTGGTATCAGCAGAAGCCAGGGAAACCCCCTAAACTC CTGATCTTTAAGGCGTCTGCTTTAGAAAGTGGGGTCCCATCGAGGT TCAGCGGCAGTGGATATGGGACAGATTTCACTCTCACCATCAGCAA CCTGCAGCCTGAAGACTTTGCAACTTACTTCTGTCAACAGGGTAAT AGTTTCCCTCTCACTTTCGGCGGAGGGACCAAAGTGGATATCAAAC GTACG
32	V_L4 amino acid sequence	DIQMTQSPSTLSASVGDRVTITCRASQNIDIWLAWYQWKPGKAPKL LIYKASGLETGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQGN QFPLTFGQGTRLEIK

33	V_L4 nucleic acid sequence	GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAG GAGACAGAGTCACCATCACTTGCCGGGCCAGTCAGAATATTGATAT CTGGTTGGCCTGGTATCAGTGGAAACCAGGGAAGGCCCCTAAACTC CTGATCTATAAGGCGTCTGGTTTAGAAACTGGGGTCCCTTCAAGGT TCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACTATCAGCAG CCTGCAGCCAGAGGATTTTGCGACTTACTATTGTCAACAGGGTAAC CAGTTCCCGCTCACCTTCGGCCAAGGGACACGACTGGAGATTAAAC GTACG
34	V_L5 amino acid sequence	DIQMTQSPSSLSASVGDRVTITCRASQSIGRWLAWYQQKPGKAPKL LIFKASALEVGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGN SFPLTFGGGTKVDIK
35	V_L5 nucleic acid sequence	GACATCCAGATGACCCAGTCTCCTTCCTCCCTGTCTGCATCTGTAG GAGACAGAGTCACCATCACTTGCCGGGCCAGTCAGAGTATCGGTAG GTGGTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAACTC CTGATCTTTAAGGCGTCTGCTTTAGAAGTTGGGGTCCCATCAAGGT TCAGCGGCAGTGGGTCTGGGACAGATTTCACTCTCACCATCAGCAG CCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGGTAAC AGTTTCCCGCTCACTTTCGGCGGAGGGACCAAAGTGGATATCAAAC GTACG
36	V_L6 amino acid sequence	DIQLTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKL LIYAASALQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGD SFPLTFGGGTKVEIK
37	V_L6 nucleic acid sequence	GACATCCAGTTGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAG GAGACAGAGTCACCATCACTTGCCGGGCCAGTCAGAGTATTAGTAG CTGGTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAACTC CTGATCTATGCTGCATCCGCTTTGCAAAGTGGGGTCCCATCAAGGT TCAGCGGCAGCGGATCTGGGACAGATTTCACTCTCACTATCAGCAG CCTGCAGCCCGAAGATTTTGCAACTTACTATTGTCAACAGGGTGAC AGTTTCCCTCTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAAC GTACG
38	V_L7 amino acid sequence	DIQMTQSPSTLSASVGDTVTFSCRASQSINTWLAWYQQKPGKAPKL LIYKASALENGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQGN SFPLTFGGGTKVEIK
39	V_L7 nucleic acid sequence	GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAG GAGACACAGTCACCTTCAGTTGCCGGGCCAGTCAGAGTATTAACAC CTGGTTGGCCTGGTATCAGCAAAAGCCAGGGAAAGCCCCTAAACTC CTTATCTATAAGGCGTCTGCTTTAGAAAATGGGGTCCCATCAAGGT TCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACAATCAGCAG CCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGGGAAC AGTTTCCCTCTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAAC GTACG
40	V_L8 amino acid sequence	DIQMTQSPSSLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKL LIYKASALESGVPSRFSGGGSGTEFTLTISSLQPEDFATYYCQQGH SFPLTFGGGTKLEIK
41	V_L8 nucleic	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAG GAGACAGAGTCACCATCACTTGCCGGGCCAGTCAGAGTATTAGTAG

	acid sequence	CTGGTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAACTC CTCATCTATAAGGCGTCTGCTTTAGAAAGTGGGGTCCCATCAAGGT TCAGCGGCGGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAG CCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGGTCAC AGTTTCCCTCTCACTTTCGGCGGAGGGACCAAGCTGGAGATCAAAC GTACG
42	V_L9 amino acid sequence	DIQLTQSPSSLSASVGDRVTITCRASQSISDWLAWYQQKPGKAPKL LIFKASALEGGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGN SFPITFGQGTRLEIK
43	V_L9 nucleic acid sequence	GACATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAG GAGACAGAGTCACCATCACTTGCCGGGCCAGTCAGAGTATTAGTGA CTGGTTGGCCTGGTATCAGCAGAAGCCAGGTAAAGCCCCTAAACTC CTGATCTTTAAGGCTTCTGCTTTAGAAGGTGGGGTCCCATCAAGGT TCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAG CCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGGTAAC AGTTTCCCGATCACCTTCGGCCAAGGGACACGACTGGAGATTAAAC GTACG
44	V_L10 amino acid sequence	DIQMTQSPATLSASVGDRVTITCRASQSVDRWLAWYQQKPGKAPNL LIYEASALQGGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGD SFPLTFGGGTKVEIK
45	V_L10 nucleic acid sequence	GACATCCAGATGACCCAGTCTCCAGCCACCCTGTCTGCATCTGTTG GAGACAGGGTCACCATCACTTGCCGGGCCAGTCAGAGTGTTGATAG GTGGTTGGCCTGGTACCAGCAGAAACCAGGGAAAGCCCCTAACCTC CTAATCTATGAGGCGTCTGCCTTACAAGGTGGGGTCCCGTCAAGGT TCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAG CCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGGTGAT AGTTTCCCTCTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAAC GTACG
46	V_L11 amino acid sequence	DIQLTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKL LIYAASGLQNGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGD RFPLTFGGGTKVEIK
47	V_L11 nucleic acid sequence	GACATCCAGTTGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAG GAGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAG CTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTC CTGATCTATGCTGCATCCGGTTTGCAAAATGGGGTCCCATCAAGGT TCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAG CCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGGTGAC AGGTTCCCGCTCACTTTCGGCGGAGGGACCAAGGTGGAGATCAAAC GTACG
48	V_H CDR1	FTFSSYAMS
49	V_H CDR1.1	FTFNYYAMS
50	V_H CDR1.2	FTFYGYAMS
51	V_H CDR1.3	FTFRNYAMS

52	V_H CDR1.4	FTFNYYAMN
53	V_H CDR1.5	FTFNYYAMXaa$_1$, wherein Xaa$_1$ = S or N
54	V_H CDR1.6	FTFXaa$_1$Xaa$_2$YAMS, wherein Xaa1 = S, N, Y, R; Xaa2 = S, N, Y, G
55	V_H CDR1.7	FTFXaa$_1$Xaa$_2$YAMXaa$_3$, wherein Xaa1 = S, N, Y, R; Xaa2 = S, N, Y, G; Xaa3 = S or N.
56	V_H CDR2	SAISGSGGSTYY
57	V_H CDR2.1	SAIDGSGDNTTY
58	V_H CDR2.2	AAISGSGDGTYY
59	V_H CDR2.3	SAISGSGDSTYY
60	V_H CDR2.4	AAISGGGDATYY
61	V_H CDR2.5	SSISGSGDVTYY
62	V_H CDR2.6	SAISGFGESTYY
63	V_H CDR2.7	AAISGSGGRTYY
64	V_H CDR2.8	SAISGSGGNTSY
65	V_H CDR2.9	AAISGSGDSTYY
66	V_H CDR2.10	AAISGXaa1GXaa2Xaa3TYY, wherein Xaa1 = S or G; Xaa2 = D or G, Xaa3 = S, R, G, A
67	V_H CDR2.11	Xaa$_1$Xaa$_2$IXaa$_3$GXaa$_4$GXaa$_5$Xaa$_6$TXaa$_7$Y
68	V_H CDR3	AKDSPFLLDDYYYYYYMD
69	V_L CDR1	RASQGISSWLAW
70	V_L CDR1.1	RASQNIHNWLAW
71	V_L CDR1.2	RASQSISRWLAW
72	V_L CDR1.3	RASQNIDIWLAW
73	V_L CDR1.4	RASQSIGRWLAW
74	V_L CDR1.5	RASQSISSWLAW
75	V_L CDR1.6	RASQSINTWLAW
76	V_L CDR1.7	RASQSISDWLAW
77	V_L CDR1.8	RASQSVDRWLAW
78	V_L CDR2	YAASSLQS

79	V_L CDR2.1	YKASGLES
80	V_L CDR2.2	FKASALES
81	V_L CDR2.3	YKASGLET
82	V_L CDR2.4	FKASALEV
83	V_L CDR2.5	YAASALQS
84	V_L CDR2.6	YKASALEN
85	V_L CDR2.7	YKASALES
86	V_L CDR2.8	FKASALEG
87	V_L CDR2.9	YEASALQG
88	V_L CDR2.10	YAASGLQN
89	V_L CDR3	QQGHLFPITF
90	V_L CDR3.1	QQGDRFPLTF
91	V_L CDR3.2	QQGNSFPLTF
92	V_L CDR3.3	QQGNQFPLTF
93	V_L CDR3.4	QQGDSFPLTF
94	V_L CDR3.5	QQGHSFPLTF
95	V_L CDR3.6	QQGNSFPITF
96	V_L CDR3.7	QQGXaa$_1$Xaa$_2$FPXaa$_3$TF
97	Human CD137L Uniprot ID – P41273	MEYASDASLDPEAPWPPAPRARACRVLPWALVAGLLLLLLLAAACA VFLACPWAVSGARASPGSAASPRLREGPELSPDDPAGLLDLRQGMF AQLVAQNVLLIDGPLSWYSDPGLAGVSLTGGLSYKEDTKELVVAKA GVYYVFFQLELRRVVAGEGSGSVSLALHLQPLRSAAGAAALALTVD LPPASSEARNSAFGFQGRLLHLSAGQRLGVHLHTEARARHAWQLTQ GATVLGLFRVTPEIPAGLPSPRSE
98	FLAG	DYKDDDDK
99	6-His	HHHHHH
100	HA	YPYDVPDYA
101	V_H12 amino acid sequence	EVQLLESGGGLVQPGGSLRLSCAASGFTFRNYAMSWVRQAPGKGLE WVSAISGSGDTTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTA VYYCAKDSPFLLDDYYYYYYMDVWGKGTTVTVSS
102	V_H12 nucleic acid sequence	GAAGTGCAATTATTGGAATCCGGCGGCGGTTTAGTTCAGCCAGGTG GCTCTTTGAGGCTGAGTTGCGCAGCCTCTGGATTCACCTTTAGAAA CTACGCAATGTCTTGGGTTCGCCAGGCGCCCGGTAAGGGTCTGGAG TGGGTGTCTGCAATCTCTGGTTCTGGTGATACTACTTACTACGCCG ACTCTGTGAAAGGTCGTTTTACCATAAGCCGCGACAATTCTAAGAA TACTTTATATCTTCAAATGAATTCGCTGCGGGCAGAAGACACGGCC GTCTATTACTGCGCAAAGGACTCACCTTTTCTATTAGACGACTACT ACTACTACTACTACATGGACGTATGGGGCAAGGGTACAACTGTCAC CGTCTCCTCAGCTAGC
103	V_H13 amino acid sequence	EVQLLESGGGLVQPGGSLRLSCAASGFTFGSYAMSWVRQAPGKGLE WVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTA VYYCAKDSPFLLDDYYYYYYMDVWGKGTTVTVSS

104	V_H13 nucleic acid sequence	GAAGTGCAATTATTGGAATCCGGCGGCGGTTTAGTTCAGCCAGGTG GCTCTTTGAGGCTGAGTTGCGCAGCCTCTGGATTCACCTTTGGTTC TTACGCAATGTCTTGGGTTCGCCAGGCGCCCGGTAAGGGTCTGGAG TGGGTGTCTGCAATCTCTGGTTCTGGTGGTTCTACTTACTACGCCG ACTCTGTGAAAGGTCGTTTTACCATAAGCCGCGACAATTCTAAGAA TACTTTATATCTTCAAATGAATTCGCTGCGGGCAGAAGACACGGCC GTCTATTACTGCGCAAAGGACTCACCTTTTCTATTAGACGACTACT ACTACTACTACTACATGGACGTATGGGGCAAGGGTACAACTGTCAC CGTCTCCTCAGCTAGC
105	V_L12 amino acid sequence	DIQLTQSPSSLSASVGDRVTITCRASQDIGDWLAWYQQKPGKAPKL LIYKASGLQSGVPSRFSGSGSGTEFTLTISNLQPEDFATYYCQQGN QFPLTFGQGTRLE
106	V_L12 nucleic acid sequence	GACATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAG GAGACAGAGTAACCATCACTTGCCGGGCAAGTCAGGATATTGGTGA CTGGTTGGCCTGGTATCAGCAGAAGCCTGGGAAAGCCCCTAAGCTC CTGATCTATAAGGCGTCTGGTTTACAAAGTGGGGTCCCATCAAGAT TCAGTGGCAGTGGATCTGGGACAGAATTCACTCTCACTATCAGCAA CCTGCAGCCAGAGGATTTTGCGACTTACTATTGTCAACAGGGTAAC CAGTTCCCGCTCACCTTCGGCCAAGGGACACGACTGGAG
107	V_H CDR1.8	FTFGWYAMS
108	V_H CDR2.12	SAISGSGDTTYY
109	V_L CDR1.9	RASQDIGDWLAW
110	V_L CDR2.11	YKASGLQS
111	V_H CDR3.1	AKASPFLLDDYYYYYYMD
112	V_H CDR3.2	AKDAPFLLDDYYYYYYMD
113	V_H CDR3.3	AKDSAFLLDDYYYYYYMD
114	V_H CDR3.4	AKDSPALLDDYYYYYYMD
115	V_H CDR3.5	AKDSPFALDDYYYYYYMD
116	V_H CDR3.6	AKDSPFLADDYYYYYYMD
117	V_H CDR3.7	AKDSPFLLADYYYYYYMD
118	V_H CDR3.8	AKDSPFLLDAYYYYYYMD
119	V_H CDR3.9	AKDSPFLLDDAYYYYYMD

120	V_H CDR3.10	AKDSPFLLDDYAYYYYMD
121	V_H CDR3.11	AKDSPFLLDDYYAYYYMD
122	V_H CDR3.12	AKDSPFLLDDYYYAYYMD
123	V_H CDR3.13	AKDSPFLLDDYYYYAYMD
124	V_H CDR3.14	AKDSPFLLDDYYYYYAMD
125	V_H CDR3.15	AKDSPFLLDDYYYYYYAD
126	V_H CDR3.16	DXXXXLXXXXYXYYX
127	V_H CDR3.17	DXPFXLDXXYYYYYYX
128	V_H CDR3.18	$DX_1X_2X_3X_4LX_5X_6X_7X_8YX_9YYX_{10}$
129	mAb1 heavy chain	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLE WVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTA VYYCAKDSPFLLDDYYYYYYMDVWGKGTTVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGP PCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQED PEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS RLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
130	mAb8 heavy chain V1	GTEVQLLESGGGLVQPGGSLRLSCAASGFTFRNYAMSWVRQAPGKG LEWVSAISGSGDTTYYADSVKGRFTISRDNSKNTLYLQMNSLRAED TAVYYCAKDSPFLLDDYYYYYYMDVWGKGTTVTVSSASTKGPSVFP LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKY GPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQ EDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
131	mAb8 heavy chain V2	EVQLLESGGGLVQPGGSLRLSCAASGFTFRNYAMSWVRQAPGKGLE WVSAISGSGDTTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTA VYYCAKDSPFLLDDYYYYYYMDVWGKGTTVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGP PCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQED PEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNG

		KEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS RLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
132	mAb10 heavy chain	EVQLLESGGGLVQPGGSLRLSCAASGFTFYGYAMSWVRQAPGKGLE WVAAISGSGDSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTA VYYCAKDSPFLLDDYYYYYYMDVWGKGTTVTVSSASTKGPSVFPLA PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGP PCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQED PEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS RLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG
133	mAb1, mAb8 and mAb10 light chain	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKL LIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGH LFPITFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC
134	Human IgG4	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGAL TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNT KVDKRVESKYGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVS VLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYT LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLS LSLGK

Table 26: Sequence Listing II

SEQ ID NO	Description	Sequence
135	V_H CDR1a	SYAMS
136	V_H CDR1a.1	YYAMS
137	V_H CDR1a.2	NYAMS
138	V_H CDR1a.3	GYAMS
139	V_H CDR2a	AISGSGGSTYYADSVKG
140	V_H CDR2a.1	AIDGSGDNTTYADSVKG
141	V_H CDR2a.2	AISGSGDTTYYADSVKG
142	V_H CDR2a.3	AISGSGDSTYYADSVKG
143	V_H CDR3a	DSPFLLDDYYYYYYMDV
144	V_L CDR1a	RASQGISSWLA
145	V_L CDR1a.1	RASQNIHNWLA
146	V_L CDR1a.2	RASQDIGDWLA
147	V_L CDR2a	AASSLQS
148	V_L CDR2a.1	KASGLES

149	V_L CDR2a.2	KASGLQS
150	V_L CDR3a	QQGHLFPIT
151	V_L CDR3a.1	QQGDRFPLT
152	V_L CDR3a.2	QQGNQFPLT

Table 27: Sequence Listing III

SEQ ID NO	Description	Sequence
48	V_H CDR1b	FTFSSYAMS
49	V_H CDR1b.1	FTFNYYAMS
51	V_H CDR1b.2	FTFRNYAMS
153	V_H CDR1b.3	FTFGSYAMS
50	V_H CDR1b.4	FTFYGYAMS
154	V_H CDR2b	SAISGSGGSTYYA
155	V_H CDR2b.1	SAIDGSGDNTTYA
156	V_H CDR2b.2	SAISGSGDTTYYA
157	V_H CDR2b.3	SAISGSGGSTYYA
158	V_H CDR2b.4	AAISGSGDSTYYA
159	V_H CDR3b	AKDSPFLLDDYYYYYYMDV
144	V_L CDR1a	RASQGISSWLA
145	V_L CDR1a.1	RASQNIHNWLA
146	V_L CDR1a.2	RASQDIGDWLA
147	V_L CDR2a	AASSLQS
148	V_L CDR2a.1	KASGLES
149	V_L CDR2a.2	KASGLQS
150	V_L CDR3a	QQGHLFPIT
151	V_L CDR3a.1	QQGDRFPLT
152	V_L CDR3a.2	QQGNQFPLT

CLAIMS

1. A formulation comprising:

(a) an anti-CD137 antibody at a concentration of 1 mg/ml to 100 mg/ml, wherein the anti-CD137 antibody comprises heavy and light chain sequences having amino acid sequences set forth in SEQ ID NOs: 4 and 6, respectively, and

(b) a buffer comprising histidine.

2. A formulation comprising:

(a) an anti-CD137 antibody at a concentration of 1 mg/ml to 100 mg/ml, wherein the anti-CD137 antibody comprises heavy and light chain sequences having amino acid sequences set forth in SEQ ID NOs: 4 and 6, respectively,

(b) a buffer comprising histidine; and

(c) a disaccharide sugar.

3. A formulation comprising:

(a) an anti-CD137 antibody at a concentration of 1 mg/ml to 100 mg/ml, wherein the anti-CD137 antibody comprises heavy and light chain sequences having amino acid sequences set forth in SEQ ID NOs: 4 and 6, respectively, and

(b) a buffer comprising histidine;

wherein the formulation has a pH of 5.0-7.0.

4. A formulation comprising:

(a) an anti-CD137 antibody at a concentration of 1 mg/ml to 100 mg/ml, wherein the anti-CD137 antibody comprises heavy and light chain sequences having amino acid sequences set forth in SEQ ID NOs: 4 and 6, respectively, and

(b) a buffer comprising histidine;

wherein the formulation has a pH of 5.0-7.4.

5. A formulation comprising:

(a) an anti-CD137 antibody at a concentration of 1 mg/ml to 100 mg/ml, wherein the anti-CD137 antibody comprises heavy and light chain sequences having amino acid sequences set forth in SEQ ID NOs: 4 and 6, respectively,

(b) a buffer comprising histidine,

(c) a disaccharide sugar,

(d) a non-ionic surfactant, and

(e) a salt,

wherein the pH of the formulation is 5.0 to 7.0.

6. A formulation comprising:

(a) an anti-CD137 antibody at a concentration of 1 mg/ml to 100 mg/ml, wherein the anti-CD137 antibody comprises heavy and light chain sequences having amino acid sequences set forth in SEQ ID NOs: 4 and 6, respectively,

(b) a buffer comprising histidine,

(c) a disaccharide sugar,

(d) a non-ionic surfactant, and

(e) a salt,

wherein the pH of the formulation is 5.0 to 7.4.

7. A formulation comprising:

(a) an anti-CD137 antibody at a concentration of 1 mg/ml to 100 mg/ml, wherein the anti-CD137 antibody comprises heavy and light chain sequences having amino acid sequences set forth in SEQ ID NOs: 4 and 6, respectively,

(b) a buffer comprising histidine,

(c) a disaccharide sugar at 5%- 15% weight/volume,

(d) a non-ionic surfactant at 0.01%- 0.1% weight/volume (w/v), and

(e) a salt at 50 mM – 200 mM,

wherein the pH of the formulation is 5.0 to 7.0.

8. A formulation comprising:

(a) an anti-CD137 antibody at a concentration of 1 mg/ml to 100 mg/ml, wherein the anti-CD137 antibody comprises heavy and light chain sequences having amino acid sequences set forth in SEQ ID NOs: 4 and 6, respectively,

(b) a buffer comprising histidine,

(c) a disaccharide sugar at 5%- 15% weight/volume,

(d) a non-ionic surfactant at 0.01%- 0.1% weight/volume (w/v), and

(e) a salt at 50 mM – 200 mM,

wherein the pH of the formulation is 5.0 to 7.4.

9. A formulation comprising:

(a) an anti-CD137 antibody at a concentration of 1mg/ml to 100 mg/ml, wherein the anti-CD137 antibody comprises heavy and light chain sequences having amino acid sequences set forth in SEQ ID NOs: 4 and 6, respectively,

(b) a buffer comprising 10 mM to 100 mM histidine,

(c) sucrose at 5%- 15% weight/volume,

(d) polysorbate-80 at 0.01%- 0.1% weight/volume (w/v), and

(e) NaCl at 50 mM – 200 mM,

wherein the pH of the formulation is 5.0 to 7.0.

10. A formulation comprising:

(a) an anti-CD137 antibody at a concentration of 1mg/ml to 100 mg/ml, wherein the anti-CD137 antibody comprises heavy and light chain sequences having amino acid sequences set forth in SEQ ID NOs: 4 and 6, respectively,

(b) a buffer comprising 10 mM to 100 mM histidine,

(c) sucrose at 5%- 15% weight/volume,

(d) polysorbate-80 at 0.01%- 0.1% weight/volume (w/v), and

(e) NaCl at 50 mM – 200 mM,

wherein the pH of the formulation is 5.0 to 7.4.

11. A formulation comprising:

(a) an anti-CD137 antibody at a concentration of 1 mg/ml to 100 mg/ml, wherein the anti-CD137 antibody comprises heavy and light chain sequences having amino acid sequences set forth in SEQ ID NOs: 4 and 6, respectively,

(b) a buffer comprising 20 mM histidine,

(c) sucrose at 10% weight/volume (w/v),

(d) polysorbate-80 at 0.03% weight/volume (w/v), and

(e) NaCl at 100mM,

wherein the pH of the formulation is 6.0.

12. The formulation of any one of claims 1-11, wherein the anti-CD137 antibody comprises a heavy chain CDR3 of SEQ ID NO: 68.

13. The formulation of any one of claims 1-12, wherein the anti-CD137 antibody comprises a comprises a heavy chain CDR1 of SEQ ID NO: 48, a heavy chain CDR2 of SEQ ID NO: 56, and a heavy chain CDR3 of SEQ ID NO: 68, and a light chain CDR1 of SEQ ID NO: 69, a light chain CDR2 of SEQ ID NO: 78, and a light chain CDR3 of SEQ ID NO: 89.

14. The formulation of any one of claims 1-13, wherein the antibody comprises an IgG1 heavy chain constant region.

15. The formulation of claim 14, wherein the IgG1 heavy chain constant region is a wild-type human IgG1 heavy chain constant region.

16. The formulation of claim 14, wherein the IgG1 heavy chain constant region comprises an amino acid substitution relative to a wild-type human IgG1 heavy chain constant region.

17. The formulation of any one of claim 1-13, wherein the antibody comprises an IgG4 heavy chain constant region.

18. The formulation of claim 17, wherein the IgG4 heavy chain constant region is a wild-type human IgG4 heavy chain constant region.

19. The formulation of claim 17, wherein the IgG4 heavy chain constant region comprises an amino acid substitution relative to a wild-type human IgG4 heavy chain constant region.

20. The formulation of any one of claims 1-10 and 12-19, comprising 10 mM histidine to 100 mM histidine.

21. The formulation of any one of claims 1-20, comprising 20 mM histidine.

22. The formulation of any one of claims 1, 3-4, 9-10, and 12-20, further comprising a disaccharide sugar.

23. The formulation of any one of claims 2, 5-8, and 22, wherein the disaccharide sugar is selected from sucrose, lactose, maltose, and trehalose.

24. The formulation of claim 23, wherein the disaccharide sugar is sucrose.

25. The formulation of any one of claims 2, 5-6, and 22-24, wherein the disaccharide sugar is at 5%- 15% weight/volume.

26. The formulation of any one of claims 2, 5-8, and 22-24, wherein the disaccharide sugar is at 10% weight/volume.

27. The formulation of any one of claims 1-4 and 12-20, further comprising a salt.

28. The formulation of any one of claims 5-8, and 27, wherein the salt is NaCl.

29. The formulation of any one of claims 5 and 27-28, wherein the salt is at a concentration of 50 mM - 200 mM.

30. The formulation of any one of claims 5-10 and 27-28, wherein the salt is at a concentration of 100 mM.

31. The formulation of any one of claims 1, 2, and 12-20, wherein the formulation has a pH of 5.0-7.0.

32. The formulation of any one of claims 1, 2, and 12-20, wherein the formulation has a pH of 5.0-7.4.

33. The formulation of any one of claims 3-4, 7-10, and 31-32 wherein the pH is 6.0.

34. The formulation of any one of claims 1-4 and 12-33, further comprising a non-ionic surfactant.

35. The formulation of any one of claims 5-8, and 34, wherein the non-ionic surfactant is a polysorbate.

36. The formulation of claim 35, wherein the polysorbate is polysorbate-80.

37. The formulation of any one of claims 5-6 and 34-35, wherein the non-ionic surfactant is at 0.01%- 0.1% weight/volume (w/v).

38. The formulation of any one of claims 5-8, and 34-35, wherein the non-ionic surfactant is at 0.03% weight/volume (w/v).

39. The formulation of any one of claims 1-38, comprising the anti-CD137 antibody at a concentration of 5 mg/ml to 15 mg/ml.

40. The formulation of any one of claims 1-38, comprising the anti-CD137 antibody at a concentration of 15 mg/ml to 30 mg/ml.

41. The formulation of any one of claims 1-38, comprising the anti-CD137 antibody at a concentration of 30 mg/ml to 45 mg/ml.

42. The formulation of any one of claims 1-38, comprising the anti-CD137 antibody at a concentration of 45 mg/ml to 60 mg/ml.

43. The formulation of any one of claims 1-38, comprising the anti-CD137 antibody at a concentration of 60 mg/ml to 75 mg/ml.

44. The formulation of any one of claims 1-38, comprising the anti-CD137 antibody at a concentration of 75 mg/ml to 90 mg/ml.

45. The formulation of any one of claims 1-38, comprising the anti-CD137 antibody at a concentration of 85 mg/ml to 100 mg/ml.

46. The formulation of any one of claims 1-38, comprising the anti-CD137 antibody at a concentration of 5 mg/ml.

47. The formulation of any one of claims 1-38, comprising the anti-CD137 antibody at a concentration of 10 mg/ml.

48. The formulation of any one of claims 1-38, comprising the anti-CD137 antibody at a concentration of 15 mg/ml.

49. The formulation of any one of claims 1-38, comprising the anti-CD137 antibody at a concentration of 20 mg/ml.

50. Use of the formulation of any one of claims 1-49 in the manufacture of a medicament for inducing or enhancing dimerization of human CD137 trimers in a subject that has cancer or a tumor.

51. Use of the formulation of any one of claims 1-49 in the manufacture of a medicament for inducing or enhancing multimerization of human CD137 trimers in a subject that has cancer or a tumor.

52. Use of the formulation of any one of claims 1-49 in the manufacture of a medicament for inducing or enhancing T cell activation in a subject that has cancer or a tumor.

53. The use of claim 52, wherein the T cell activation occurs in a tumor microenvironment.

54. Use of the formulation of any one of claims 1-49 in the manufacture of a medicament for inducing or enhancing a cytotoxic T cell response in a subject that has cancer or a tumor.

55. The use of claim 54, wherein the cytotoxic T cell response occurs in a tumor microenvironment.

56. Use of the formulation of any one of claims 1-49 in the manufacture of a medicament for inducing or enhancing cytokine production of an immune cell in a subject that has cancer or a tumor.

57. The use of claim 56, wherein the cytokine produced is IL-2, TNFα, IL-13, IFN-γ, or combinations thereof.

58. The use of claim 56 or claim 57, wherein the cytokine production occurs in a tumor microenvironment.

59. Use of any one of claims 1-49 in the manufacture of a medicament for inducing or enhancing T cell proliferation in a subject that has cancer or a tumor.

60. The use of claim 59, wherein the T cell proliferation occurs in a tumor microenvironment.

61. Use of the formulation of any one of claims 1-49 in the manufacture of a medicament for reducing or inhibiting tumor growth.

62. Use of the formulation of any one of claims 1-49 in the manufacture of a medicament for treating a disorder mediated by human CD137 in a subject that has cancer or a tumor.

63. Use of the formulation of any one of claims 1-49 in the manufacture of a medicament for treating cancer in a subject.

64. The use of any one of claims 61-63, wherein infiltration of immune cells into a tumor microenvironment is increased after administration of the formulation.

65. The use of claim 64, wherein the immune cells express CD45.

66. The use of any one of claims 61-65, wherein the quantity of T regulatory (Treg) cells is reduced in a tumor microenvironment after administration of the formulation.

67. The use of claim 66, wherein the Treg cells express CD4, FOXP-3 and CD25.

68. The use of any one of claims 61-67, wherein the quantity of macrophages is reduced in a tumor microenvironment after administration of an isolated monoclonal antibody or antigen binding portion.

69. The use of claim 68, wherein the macrophages express CD45 and CD11b.

70. The use of any one of claims 61-69, wherein T cell exhaustion is reduced in a tumor microenvironment after administration of an isolated monoclonal antibody or antigen binding portion, optionally wherein reduction of T cell exhaustion comprises a decrease in expression of TIGIT, PD-1, LAG-3, or combinations thereof.

71. The use of any one of claims 63-70, wherein the cancer is selected from the group consisting of melanoma, glioma, renal, breast, hematological, and head and neck cancer.

72. The use of claim 71, wherein the hematological cancer is a B cell lymphoma.

73. Use of the formulation of claims 1-49 in the manufacture of a medicament for inducing an anti-tumor memory immune response.

74. The use of any one of claims 50-73, wherein the anti-CD137 antibody binds Fc gamma receptor.

75. The use of any one of claims 50-74, wherein depletion of CD4+ T cells, CD8+ T cells, Natural Killer cells, or combinations thereof, reduces the efficacy of the formulation.

76. A kit comprising a container comprising the formulation of any one of claims 1-49, and a package insert comprising instructions for administration of the formulation, for treating or delaying progression of cancer or reducing or inhibiting tumor growth in a subject in need thereof.

77. A kit comprising a container comprising the formulation of any one of claims 1-49, and a package insert comprising instructions for administration of the formulation alone or in combination with another agent, for treating or delaying progression of cancer or reducing or inhibiting tumor growth in a subject in need thereof.

78. Use of the formulation of any one of claims 1-49 in the manufacture of a medicament for treating or delaying progression of cancer or reducing or inhibiting tumor growth in a subject in need thereof.

79. A formulation according to any one of claims 1-49, for use as a medicament.