

**PHARMACEUTICAL FORMULATIONS OF ANTIBODIES THAT BIND
INTERLEUKIN 13**

Related Applications

[0001] This application claims priority to, and the benefit to U.S. Provisional Application Patent No. 63/612,892, filed December 20, 2023, the entire disclosure of which is hereby incorporated by reference in its entirety for all purposes.

Background

[0002] The interleukin (IL)-13 is a T helper cell subclass 2 (Th2) cytokine, and belongs to the family of type I cytokines. However, IL-13 is involved in the differentiation of naïve T cells into Th2 cells. IL-13 promotes B-cell proliferation and induces class switching to IgG4 and IgE in combination with CD40/CD40L co-stimulation (IL-13 up-regulates FcεRI and thus helps in IgE priming of mast cells). In monocytes/macrophages, IL-13 up-regulates expression of CD23 and MHC class I and class II antigens; down-regulates the expression of CD14; inhibits antibody-dependent cytotoxicity IL-13; and promotes eosinophil survival, activation, and recruitment. IL-13 also manifests important functions on nonhematopoietic cells, such as smooth muscle cells, epithelial cells, endothelial cells, and fibroblast cells. IL-13 enhances proliferation and cholinergic-induced contractions of smooth muscles. In epithelial cells, IL-13 potently induces chemokine production, alters mucociliary differentiation, decreases ciliary beat frequency of ciliated epithelial cells, and results in goblet cell metaplasia. In endothelial cells, IL-13 is a potent inducer of vascular cell adhesion molecule 1 (VCAM-1), which is important for recruitment of eosinophils. In human dermal fibroblasts, IL-13 induces type 1 collagen synthesis in human dermal fibroblasts.

[0003] The inhibition of IL-13 may be used to treat or prevent inflammatory diseases and conditions, such as those related to elevated levels of IgE, including but not limited to: asthma, allergic rhinitis, urticaria, asthma, allergic rhinitis, urticaria, and allergic or atopic dermatitis. Thus, the development of potent and specific inhibitors of IL-13, for example, inhibitors that remain active for longer terms when administered to subjects, are needed for the prevention and/or treatment of IL-13 and IgE-mediated diseases or conditions. Furthermore, formulations comprising IL-13 antibodies sufficiently stable and suitable for administration to patients remains an unmet need.

Summary

[0004] In certain aspects, described herein is a formulation comprising: (a) an interleukin 13 (IL-13) antibody present at a concentration between 140 mg/mL and 290 mg/mL; (b) a histidine buffer, an acetate buffer, or a succinate buffer; (c) arginine and/or methionine or a salt solution thereof; and (d) a polysorbate or a poloxamer, wherein the formulation is at pH 5.0 to 7.0. In embodiments, the formulation further comprises a metal ion chelator, such as EDTA or a salt thereof (e.g., EDTA-2Na).

[0005] In certain aspects, described herein is a formulation comprising: (a) an IL-13 antibody present at a concentration between 140 mg/mL and 290 mg/mL; (b) a histidine buffer, an acetate buffer, or a succinate buffer; (c) arginine and/or methionine or a salt solution thereof; and (d) a polysorbate or a poloxamer, wherein the formulation is at pH 5.0 to 7.0, and wherein the IL-13 antibody comprises: (i) a variable heavy (VH) chain sequence comprising three heavy chain CDR sequences, CDR-H1, CDR-H2, and CDR-H3; and (ii) a variable light (VL) chain sequence comprising three light chain CDR sequences, CDR-L1, CDR-L2, and CDR-L3; wherein: (a) CDR-H1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 58-99 and 121; (b) CDR-H2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 100-111; (c) CDR-H3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 112-120 and 130-140, (d) CDR-L1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 141-144 and 149-152, (e) CDR-L2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 153-158 and the amino acid sequence LAS; and (f) CDR-L3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 165-172.

[0006] In certain aspects, described herein is a formulation comprising: (a) an IL-13 antibody present at a concentration between 140 mg/mL and 290 mg/mL; (b) a histidine buffer, an acetate buffer, or a succinate buffer; (c) arginine and/or methionine or a salt solution thereof; and (d) a polysorbate or a poloxamer, wherein the formulation is at pH 5.0 to 7.0, wherein the IL-13 antibody comprises: (i) a variable heavy (VH) chain sequence comprising three heavy chain CDR sequences, CDR-H1, CDR-H2, and CDR-H3; and (ii) a variable light (VL) chain sequence comprising three light chain CDR sequences, CDR-L1, CDR-L2, and CDR-L3; wherein: (a) CDR-H1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 58, SEQ ID NO: 68, and SEQ ID NO: 85; (b) CDR-H2 comprises a sequence selected from the sequences set forth in any one of SEQ ID

NO: 100, SEQ ID NO: 104, and SEQ ID NO: 108; (c) CDR-H3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 112 and SEQ ID NO: 130, (d) CDR-L1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 141 and SEQ ID NO: 149, (e) CDR-L2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 153 and SEQ ID NO: 164; and (f) CDR-L3 comprises the sequence set forth in SEQ ID NO: 165.

[0007] In other embodiments, the formulation comprises:

- (a) an IL-13 antibody present at a concentration between 140 mg/mL and 290 mg/mL;
- (b) a histidine buffer, an acetate buffer, or a succinate buffer;
- (c) arginine and/or methionine or a salt solution thereof; and
- (d) a polysorbate or a poloxamer,

wherein the formulation is at pH 5.0 to 7.0,

wherein the IL-13 antibody comprises:

- (i) a variable heavy (VH) chain sequence comprising three heavy chain CDR sequences, CDR-H1, CDR-H2, and CDR-H3; and
- (ii) a variable light (VL) chain sequence comprising three light chain CDR sequences, CDR-L1, CDR-L2, and CDR-L3; wherein:
 - a. CDR-H1 comprises the sequence set forth in SEQ ID NO: 58 or 67;
 - b. CDR-H2 comprises the sequence set forth in SEQ ID NO: 100 or 104;
 - c. CDR-H3 comprises the sequence set forth in SEQ ID NO: 112;
 - d. CDR-L1 comprises the sequence set forth in SEQ ID NO: 141 or 149;
 - e. CDR-L2 comprises the sequence set forth in SEQ ID NO: 153 or 596; and
 - f. CDR-L3 comprises the sequence set forth in SEQ ID NO: 165.

[0008] In embodiments, the formulation further comprises a metal ion chelator. In embodiments, the metal ion chelator is EDTA or salt thereof. Other metal ion chelators are described herein.

[0009] In embodiments, the IL-13 antibody comprises a means for extending the half-life of the IL-13 antibody. In embodiments, the means comprises at least one amino acid modification in the IL-13 antibody, as described further herein.

[0010] In certain embodiments, the formulation further comprises: (e) a sugar or sugar alcohol.

[0011] In certain embodiments, the IL-13 antibody is at a concentration between 160 mg/mL and 250 mg/mL. In certain embodiments, the IL-13 antibody is at a concentration of about 180 mg/mL. In certain embodiments, the IL-13 antibody is at a concentration of about 200 mg/mL. In certain embodiments, the antibody is at a concentration of about 160-200 mg/mL.

[0012] In certain embodiments, the histidine buffer, acetate buffer, or succinate buffer is at a concentration between 5 mM and 20 mM. In certain embodiments, the histidine buffer, acetate buffer, or succinate buffer is at a concentration of about 10 mM.

[0013] In certain embodiments, the histidine buffer comprises a histidine and a histidine salt. In certain embodiments, the histidine is L-histidine. In certain embodiments, the histidine salt is L-histidine HCl monohydrate.

[0014] In certain embodiments, the formulation comprises methionine, and wherein the methionine is L-methionine. In certain embodiments, the L-methionine is at a concentration between 1 mM and 20 mM. In certain embodiments, the L-methionine is at a concentration of about 10 mM.

[0015] In certain embodiments, the formulation comprises arginine, and wherein the arginine is L-arginine. In certain embodiments, the formulation comprises an L-arginine salt solution. In certain embodiments, the L-arginine salt solution comprises HCl monohydrate. In certain embodiments, wherein the L-arginine salt solution is at a concentration between 40 mM and 250 mM. In certain embodiments, the L-arginine salt solution is at a concentration of about 80 mM. In certain embodiments, the L-arginine salt solution is at a concentration of about 120 mM.

[0016] In certain embodiments, the formulation further comprises a surfactant.

[0017] In certain embodiments, the formulation comprises a polysorbate. In certain embodiments the polysorbate is at a concentration between 0.005% w/v and 0.15% w/v, e.g., 0.01% w/v-0.10% w/v. In certain embodiments, the polysorbate is at a concentration of about 0.05% w/v. In certain embodiments, the polysorbate is polysorbate 20, polysorbate 40, polysorbate 60, or polysorbate 80. In certain embodiments, the polysorbate is polysorbate 80.

In certain embodiments, polysorbate 80 is at a concentration of about 0.05% w/v or at 0.05% w/v.

[0018] In certain embodiments, the formulation comprises a poloxamer. In certain embodiments, the poloxamer is poloxamer 188. In certain embodiments, poloxamer 188 is at a concentration between 0.5-1.0 mg/ml.

[0019] In certain embodiments, the pH is between 5.5 and 7.0. In certain embodiments, the pH is between 5.6 and 5.9. In certain embodiments, the pH is about 5.8. In certain embodiments, the pH is between 5.5 and 6.5, such as at about 6.0. In certain embodiments, the pH is 5.8. In certain embodiments, the pH is 6.0.

[0020] In certain aspects, described herein is a formulation comprising: (a) an IL-13 antibody at a concentration of about 180 mg/mL; (b) a histidine buffer at a concentration of about 10 mM, wherein the histidine buffer comprises L-histidine and L-histidine HCl monohydrate; (c) an L-arginine salt solution at a concentration of about 120 mM; (d) L-methionine at a concentration of about 10 mM; and (e) polysorbate 80 at a concentration of about 0.05% w/v, at pH of about 5.8.

[0021] In certain aspects, described herein is a formulation comprising: (a) an IL-13 antibody present at a concentration of about 180 mg/mL; (b) a histidine buffer at a concentration of about 10 mM, wherein the histidine buffer comprises L-histidine and L-histidine HCl monohydrate; (c) an L-arginine salt solution at a concentration of about 80 mM; (d) L-methionine at a concentration of about 10 mM; and (e) polysorbate 80 at a concentration of about 0.05% w/v, at pH of about 5.8.

[0022] In certain aspects, described herein is a formulation comprising: (a) an IL-13 antibody present at a concentration of about 200 mg/mL; (b) a histidine buffer at a concentration of about 10 mM, wherein the histidine buffer comprises L-histidine and L-histidine HCl monohydrate; (c) an L-arginine salt solution at a concentration of about 120 mM; (d) L-methionine at a concentration of about 10 mM; and (e) polysorbate 80 at a concentration of about 0.05% w/v, at pH of about 5.8.

[0023] In certain aspects, described herein is a formulation comprising: (a) an IL-13 antibody at a concentration of about 180-200 mg/mL (e.g., at 180 mg/mL or 200 mg/mL); (b) a histidine buffer at a concentration of about 10 mM (e.g., at 10 mM), wherein the histidine buffer comprises L-histidine and L-histidine HCl monohydrate; (c) an L-arginine salt solution at a concentration of about 120 mM (e.g., at 120 mM); (d) L-methionine at a concentration of about 10 mM (e.g., at 10 mM); (e) polysorbate 80 at a concentration of about 0.05% w/v

(e.g., at 0.05% polysorbate 80), (f) EDTA or a salt thereof (e.g., EDTA-2Na) at a concentration of about 0.05 mM (e.g., at 0.05 mM), at pH of about 5.8-6.0 (e.g., at a pH of 5.8 or a pH of 6.0).

[0024] In certain aspects, described herein is a formulation comprising: (a) an IL-13 antibody at a concentration of about 180-200 mg/mL (e.g., at 180 mg/mL or 200 mg/mL); (b) a histidine buffer at a concentration of about 10 mM (e.g., at 10 mM), wherein the histidine buffer comprises L-histidine and L-histidine HCl monohydrate; (c) an L-arginine salt solution at a concentration of about 120 mM (e.g., at 120 mM); (d) L-methionine at a concentration of about 10 mM (e.g., at 10 mM); and (e) poloxamer 188 at a concentration of about 0.5 mg/ml (e.g., at 0.5 mg/ml), at pH of about 5.8-6.0 (e.g., at a pH of 5.8 or a pH of 6.0).

[0025] In certain embodiments, the formulation further comprises: (f) a sugar or sugar alcohol. In certain embodiments, the sugar or sugar alcohol is at a concentration between 1% w/v and 8% w/v. In certain embodiments, the sugar or sugar alcohol is at a concentration of about 3% w/v. In certain embodiments, the sugar or sugar alcohol is a disaccharide. In certain embodiments, the disaccharide is sucrose.

[0026] In certain embodiments, the IL-13 antibody comprises: (a) a variable heavy (VH) chain sequence comprising three heavy chain CDR sequences, CDR-H1, CDR-H2, and CDR-H3; and (b) a variable light (VL) chain sequence comprising three light chain CDR sequences, CDR-L1, CDR-L2, and CDR-L3; wherein: (i) CDR-H1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 58-99 and 121; (ii) CDR-H2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 100-111; (iii) CDR-H3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 112-120 and 130-140, (iv) CDR-L1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 141-144 and 149-152, (v) CDR-L2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 153-158 and the amino acid sequence LAS; and (vi) CDR-L3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 165-172.

[0027] In certain embodiments, the (a) CDR-H1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 58, SEQ ID NO: 68, and SEQ ID NO: 85; (b) CDR-H2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 100, SEQ ID NO: 104, and SEQ ID NO: 108; (c) CDR-H3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 112 and SEQ ID NO: 130, (d) CDR-L1 comprises a sequence selected from the sequences set forth in any one of SEQ

ID NO: 141 and SEQ ID NO: 149, (e) CDR-L2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 153 and SEQ ID NO: 164; and (f) CDR-L3 comprises the sequence set forth in SEQ ID NO: 165.

[0028] In certain embodiments, the IL-13 antibody comprises: (a) CDR-H1 comprising a sequence selected from the sequences set forth in any one of SEQ ID NOs: 58-66; (b) CDR-H2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 100-103; (c) CDR-H3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 112-120, (d) CDR-L1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 141-144, (e) CDR-L2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 153-158; and (f) CDR-L3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 165-172.

[0029] In certain embodiments, the IL-13 antibody comprises: (a) CDR-H1 comprising a sequence selected from the sequences set forth in any one of SEQ ID NOs: 67-83; (b) CDR-H2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 104-107; (c) CDR-H3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 112-120, (d) CDR-L1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 141-144, (e) CDR-L2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 153-158; and (f) CDR-L3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 165-172.

[0030] In certain embodiments, the IL-13 antibody comprises: (a) CDR-H1 comprising a sequence selected from the sequences set forth in any one of SEQ ID NOs: 84-99 and 121; (b) CDR-H2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 108-111; (c) CDR-H3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 130-140, (d) CDR-L1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 149-152, (e) CDR-L2 comprises the amino acid sequence LAS; and (f) CDR-L3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 165-172.

[0031] In certain embodiments, the IL-13 antibody does not comprise: (a) CDR-H1 set forth in SEQ ID NO: 58; CDR-H2 set forth in SEQ ID NO: 100; CDR-H3 set forth in SEQ ID NO: 112; CDR-L1 set forth in SEQ ID NO: 141; CDR-L2 set forth in SEQ ID NO: 153; and CDR-L3 set forth in SEQ ID NO: 165; or (b) CDR-H1 set forth in SEQ ID NO: 67; CDR-H2 set forth in SEQ ID NO: 104; CDR-H3 set forth in SEQ ID NO: 112; CDR-L1 set forth in SEQ ID NO: 141; CDR-L2 set forth in SEQ ID NO: 153; and CDR-L3 set forth in

SEQ ID NO: 165; or (c) CDR-H1 set forth in SEQ ID NO: 84; CDR-H2 set forth in SEQ ID NO: 108; CDR-H3 set forth in SEQ ID NO: 130; CDR-L1 set forth in SEQ ID NO: 149; CDR-L2 set forth in the amino acid sequence LAS; and CDR-L3 set forth in SEQ ID NO: 165.

[0032] In certain embodiments, the IL-13 antibody does not comprise any combination of: (a) a CDR-H1 set forth in any of SEQ ID NOs: 58, 67, or 84; (b) a CDR-H2 set forth in any of SEQ ID NOs: 100, 104, or 108; (c) a CDR-H3 set forth in any of SEQ ID NOs: 112 or 130; (d) a CDR-L1 set forth in any of SEQ ID NOs: 141 or 149; (e) a CDR-L2 set forth in any of SEQ ID NOs: 153 or 154; and (f) a CDR-L3 set forth in SEQ ID NO: 165.

[0033] In certain embodiments, the IL-13 antibody comprises a VH sequence having at least 90%, 95%, 96%, 97%, 98%, 99% or 100% identity to an amino acid sequence set forth in SEQ ID NOs: 1-32.

[0034] In certain embodiments, the IL-13 antibody comprises a VL sequence having at least 90%, 95%, 96%, 97%, 98%, 99% or 100% identity to an amino acid sequence set forth in SEQ ID NOs: 33-57.

[0035] In certain embodiments, the IL-13 antibody comprises a VH sequence having at least 90%, 95%, 96%, 97%, 98%, 99% or 100% identity to an amino acid sequence set forth in SEQ ID NOs: 1-32 and a VL sequence having at least 90%, 95%, 96%, 97%, 98%, 99% or 100% identity to an amino acid sequence set forth in of SEQ ID NOs: 33-57.

[0036] The formulation of any one of the above claims, wherein the IL-13 antibody comprises a VH comprising an amino acid sequence having at least 90%, 95%, 96%, 97%, 98%, 99% or 100% identity to an amino acid sequence set forth in SEQ ID NO: 3 and a VL comprising an amino acid sequence having at least 90%, 95%, 96%, 97%, 98%, 99% or 100% identity to an amino acid sequence set forth in SEQ ID NO: 39.

[0037] In certain embodiments, the IL-13 antibody comprises a VH sequence selected from the sequences set forth in any one of SEQ ID NOs: 1-32.

[0038] In certain embodiments, the IL-13 antibody comprises a VL sequence selected from the sequences set forth in any one of SEQ ID NOs: 33-57.

[0039] In certain embodiments, the IL-13 antibody comprises a VH sequence selected from the sequences set forth in any one of SEQ ID NOs: 1-32 and a VL sequence selected from the sequences set forth in any one of SEQ ID NOs: 33-57.

[0040] In certain embodiments, the IL-13 antibody comprises a VH comprising an amino acid sequence as set forth in SEQ ID NO: 3 and a VL comprising an amino acid sequence as set forth in SEQ ID NO: 39.

[0041] In certain embodiments, the isolated antibody comprises a HCDR1 comprising SEQ ID NO: 58, a HCDR2 comprising SEQ ID NO: 100, a HCDR3 comprising SEQ ID NO: 112, a LCDR1 comprising SEQ ID NO: 141, a LCDR2 comprising SEQ ID NO: 153, and a LCDR3 comprising SEQ ID NO: 165. In certain embodiments, the isolated antibody comprises a VH comprising an amino acid sequence set forth in SEQ ID NO:3. In certain embodiments, the isolated antibody comprises a VL comprising an amino acid sequence set forth in SEQ ID NO:39. In certain embodiments, the isolated antibody comprises a VH comprising an amino acid sequence set forth in SEQ ID NO:3 and a VL comprising an amino acid sequence set forth in SEQ ID NO:39. In certain embodiments, the isolated antibody comprises a heavy chain constant (HC) region comprising an amino acid sequence set forth in SEQ ID NO: 439. In certain embodiments, the isolated antibody comprises a heavy chain constant (HC) region comprising an amino acid sequence set forth in SEQ ID NO: 624. In certain embodiments, the isolated antibody comprises a constant light chain (LC) region comprising an amino acid sequence set forth in SEQ ID NO: 469. In certain embodiments, the isolated antibody comprises a heavy chain constant (HC) region comprising an amino acid sequence set forth in SEQ ID NO: 439 or 624 and a constant light chain (LC) region comprising an amino acid sequence set forth in SEQ ID NO: 469.

[0042] In certain embodiments, the isolated antibody comprises the HCDR1, HCDR2, HCDR3, LCDR1, LCDR2 and LCDR3 of Construct 133. In certain embodiments, the isolated antibody comprises the VH of Construct 133. In certain embodiments, the isolated antibody comprises the VL of Construct 133. In certain embodiments, the isolated antibody comprises the VH and VL of Construct 133. In certain embodiments, the isolated antibody comprises the heavy chain constant (HC) region of Construct 133. In certain embodiments, the isolated antibody comprises the constant light chain (LC) region of Construct 133. In certain embodiments, the isolated antibody comprises the heavy chain constant (HC) region and constant light chain (LC) region of Construct 133.

[0043] In certain embodiments, the isolated antibody comprises Construct 133, *i.e.*, comprising a HCDR1 comprising SEQ ID NO: 58, a HCDR2 comprising SEQ ID NO: 100, a HCDR3 comprising SEQ ID NO: 112, a LCDR1 comprising SEQ ID NO: 141, a LCDR2 comprising SEQ ID NO: 153, a LCDR3 comprising SEQ ID NO: 165, a VH comprising SEQ

ID NO:3, a VL comprising SEQ ID NO:39, a heavy chain constant (HC) region comprising an amino acid sequence set forth in SEQ ID NO: 439 or 624 and a constant light chain (LC) region comprising an amino acid sequence set forth in SEQ ID NO: 469.

[0044] In certain embodiments, the IL-13 antibody is a humanized, human, or chimeric antibody. In certain embodiments, the IL-13 antibody is a humanized antibody.

[0045] In certain embodiments, the IL-13 antibody comprises a heavy chain human constant region of a class selected from IgG, IgA, IgD, IgE, and IgM. In certain embodiments, the IL-13 antibody comprises a human Fc region comprising a human heavy chain constant region of the class IgG and a subclass selected from IgG1, IgG2, IgG3, and IgG4.

[0046] In certain embodiments, the human Fc region comprises a human IgG1 Fc. In certain embodiments, the human Fc region comprises a human IgG4 Fc. In certain embodiments, the human Fc region comprises a human IgG2 Fc.

[0047] In certain embodiments, the IL-13 antibody comprises a heavy chain comprising a constant heavy chain sequence selected from the sequences set forth in any one of SEQ ID NOs: 425-468, 484-539, and 610-709. In certain embodiments, the IL-13 antibody comprises a heavy chain comprising a constant heavy chain sequence selected from the sequences set forth in any one of SEQ ID NOs: 610, 615-641, and 654-709.

[0048] In certain embodiments, the IL-13 antibody comprises an Fc region comprising one or more amino acid substitutions, wherein the one or more substitutions result in a change in antibody half-life, ADCC activity, ADCP activity, or CDC activity as compared to an otherwise equivalent antibody comprising an Fc without the one or more substitutions.

[0049] In certain embodiments, the IL-13 antibody comprises an Fc region, and wherein the Fc region binds to Neonatal Fc receptor (FcRn).

[0050] In certain embodiments, the IL-13 antibody is a monoclonal antibody.

[0051] In certain embodiments, the IL-13 antibody binds an IL-13 sequence selected from a sequence set forth in any one of SEQ ID NOs: 472-475.

[0052] In certain embodiments, the IL-13 antibody does not have a heavy chain variable region sequence set forth in SEQ ID NO: 470.

[0053] In certain embodiments, a formulation of the disclosure can be filtered, such as by Ultrafiltration and Diafiltration (UFDF).

[0054] In certain aspects, described herein is a vial, bag, bottle or on-body delivery device comprising the formulation of any one of the above-described aspects and

embodiments. In certain embodiments, the vial is a prefilled syringe. In certain embodiments, the vial is a glass syringe. In certain embodiments, the vial is a prefilled glass syringe. In certain embodiments, the vial is an autoinjector. In certain embodiments, the vial is an injector cartridge. In certain embodiments, the vial is a pre-filled autoinjector cartridge.

In certain embodiments, an extractable volume of the vial is between 1.0 mL and 3.0 mL. In certain embodiments, the extractable volume of the vial is about 2.0 mL. In certain embodiments, an extractable volume of the vial is between 3.0 mL and 10.0 mL, e.g., 5.0 mL. In certain embodiments, the vial has an extractable volume between 1.0 mL and 10.0 mL, such as about 3.0-5.0 mL.

[0055] In certain aspects, described herein is a composition comprising the formulation, vial of any one of the above-described aspects and embodiments for use in the treatment of an inflammatory disorder or disease.

[0056] In certain embodiments, any one of the above-described aspects and embodiments are for use in the treatment of atopic dermatitis. In certain embodiments, the treatment reduces disease severity in a subject, and wherein disease severity is assessed by an Atopic Dermatitis Disease Severity Outcome Measure.

[0057] In certain embodiments, any one of the above described aspects and embodiments are for use in the treatment of an inflammatory disorder or disease selected from the group consisting of asthma, idiopathic pulmonary fibrosis, alopecia areata, chronic sinusitis with nasal polyps, Chronic Rhinosinusitis without Nasal Polyps (CRSsNP), eosinophilic esophagitis (EoE), an Eosinophilic gastrointestinal disorder or disease (ENID) selected from the group consisting of Eosinophilic Gastritis (EoG), Eosinophilic Enteritis (EoN), Eosinophilic Colitis (EoC), and Eosinophilic Gastroenteritis (EGE), Churg-Strauss syndrome/Eosinophilic granulomatosis with polyangiitis (EGPA), Prurigo Nodularis (PN), of Chronic Spontaneous Urticaria (CSU), Chronic Pruritis of Unknown Origin (CPUO), Bullous Pemphigoid (BP), Cold Inducible Urticaria (ColdU), Allergic Fungal Rhinosinusitis (AFRS), Allergic Bronchopulmonary Aspergillosis (ABPA), and Chronic Obstructive Pulmonary Disease (COPD).

[0058] In certain aspects, described herein is a method for treating an inflammatory disorder or disease in a mammalian subject in need thereof, the method comprising administering to the mammalian subject a therapeutically effective amount of the formulation vial of any one of the above-described aspects and embodiments.

[0059] In certain embodiments, the inflammatory disorder or disease is atopic dermatitis. In certain embodiments, the inflammatory disorder or disease is selected from the group consisting of asthma, idiopathic pulmonary fibrosis, alopecia areata, chronic sinusitis with nasal polyps, Chronic Rhinosinusitis without Nasal Polyps (CRSsNP), eosinophilic esophagitis (EoE), an Eosinophilic gastrointestinal disorder or disease (ENID) selected from the group consisting of Eosinophilic Gastritis (EoG), Eosinophilic Enteritis (EoN), Eosinophilic Colitis (EoC), and Eosinophilic Gastroenteritis (EGE), Churg-Strauss syndrome/Eosinophilic granulomatosis with polyangiitis (EGPA), Prurigo Nodularis (PN), of Chronic Spontaneous Urticaria (CSU), Chronic Pruritis of Unknown Origin (CPUO), Bullous Pemphigoid (BP), Cold Inducible Urticaria (ColdU), Allergic Fungal Rhinosinusitis (AFRS), Allergic Bronchopulmonary Aspergillosis (ABPA), and Chronic Obstructive Pulmonary Disease (COPD).

[0060] In certain aspects, described herein is a method for treating a pathology associated with elevated levels of IL-13 in a mammalian subject in need thereof, the method comprising administering to the mammalian subject a therapeutically effective amount of the formulation or vial of any one of the above-described aspects and embodiments.

[0061] In certain aspects, described herein is a diafiltration buffer comprising: (a) a histidine buffer; and (b) arginine or a salt solution thereof, at pH of from 5.4 to 7.0., e.g., from 5.5 to 6.5 or from 5.8 to 6.8.

[0062] In certain embodiments, the histidine buffer comprises a histidine and a histidine salt. In certain embodiments, the histidine is L-histidine. In certain embodiments, the histidine salt is L-histidine HCl monohydrate.

[0063] In certain embodiments, the formulation comprises arginine, and wherein the arginine is L-arginine. In certain embodiments, the formulation comprises an L-arginine salt solution. In certain embodiments, the L-arginine salt solution comprises HCl monohydrate. In certain embodiments, the L-arginine salt solution is at a concentration between 40 mM and 200 mM. In certain embodiments, the L-arginine salt solution is at a concentration of about 50 mM. In certain embodiments, the L-arginine salt solution is at a concentration of about 100 mM. In certain embodiments, the L-arginine salt solution is at a concentration of about 120 mM.

[0064] In certain embodiments, the pH is from about 5.7 to about 7.0., such as from about 5.5 to about 6.5. In certain embodiments, the pH is about 5.8. In certain embodiments, the

pH is 5.8. In certain embodiments, the pH is about 6.0. In certain embodiments, the pH is 6.0.

[0065] In certain aspects, described herein is a method of manufacturing an intermediate preparation of an interleukin 13 (IL-13) antibody comprising: (a) obtaining a purified preparation of the IL-13 antibody; and (b) adjusting the matrix of the purified preparation of step (a), wherein adjusting the matrix of the purified preparation comprises performing Ultrafiltration and Diafiltration (UFDF) with the diafiltration buffer of the above described aspect or any one of the embodiments thereof, thereby obtaining the intermediate preparation of the IL-13 antibody.

[0066] In certain embodiments, the intermediate preparation of the IL-13 antibody has a higher concentration of the IL-13 antibody relative to the purified preparation.

[0067] In certain embodiments, the method of manufacturing further comprises: (c) formulating the intermediate preparation to obtain a formulation of the IL-13 antibody. In certain embodiments, the formulation of the IL-13 antibody comprises the formulation of any one of the above-described aspects or embodiments.

[0068] In certain other embodiments, the formulation comprises:

- (a) an interleukin 13 (IL-13) antibody present at a concentration between 140 mg/mL and 290 mg/mL;
 - (b) a histidine buffer, an acetate buffer, or a succinate buffer;
 - (c) arginine and/or methionine or a salt solution thereof;
 - (d) a polysorbate or a poloxamer; and
 - (e) a metal ion chelator,
- wherein the formulation is at pH 5.0 to 7.0.

[0069] In certain other embodiments, the formulation comprises:

- (a) an interleukin 13 (IL-13) antibody present at a concentration of about 180 mg/mL;
 - (b) a histidine buffer at a concentration of about 10 mM, wherein the histidine buffer comprises L-histidine and L-histidine HCl monohydrate;
 - (c) an L-arginine salt solution at a concentration of about 120 mM;
 - (d) L-methionine at a concentration of about 10 mM;
 - (e) polysorbate 80 at a concentration of about 0.05% w/v; and
 - (f) EDTA or salt thereof at a concentration of about 0.05 mM,
- wherein the formulation is at a pH of about 6.0

[0070] In certain other embodiments, the formulation comprises:

- (a) an interleukin 13 (IL-13) antibody present at a concentration between 140 mg/mL and 290 mg/mL;
 - (b) a histidine buffer, an acetate buffer, or a succinate buffer;
 - (c) arginine and/or methionine or a salt solution thereof; and
 - (d) a poloxamer;
- wherein the formulation is at pH 5.0 to 7.0.

[0071] In certain other embodiments, the formulation comprises:

- (a) an interleukin 13 (IL-13) antibody present at a concentration of about 180 mg/mL;
 - (b) a histidine buffer at a concentration of about 10 mM, wherein the histidine buffer comprises L-histidine and L-histidine HCl monohydrate;
 - (c) an L-arginine salt solution at a concentration of about 120 mM;
 - (d) L-methionine at a concentration of about 10 mM; and
 - (e) poloxamer 188 at a concentration of about 0.5 mg/ml;
- wherein the formulation is at a pH of about 6.0.

In certain embodiments of the formulations, the IL-13 antibody comprises:

- (i) a variable heavy (VH) chain sequence comprising three heavy chain CDR sequences, CDR-H1, CDR-H2, and CDR-H3; and
- (ii) a variable light (VL) chain sequence comprising three light chain CDR sequences, CDR-L1, CDR-L2, and CDR-L3; wherein:
 - a. CDR-H1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 58-99 and 121;
 - b. CDR-H2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 100-111;
 - c. CDR-H3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 112-120 and 130-140,
 - d. CDR-L1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 141-144 and 149-152,
 - e. CDR-L2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 153-158 and the amino acid sequence LAS; and
 - f. CDR-L3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 165-172.

In certain embodiments of the formulations, the IL-13 antibody comprises:

- (i) a variable heavy (VH) chain sequence comprising three heavy chain CDR sequences, CDR-H1, CDR-H2, and CDR-H3; and
- (ii) a variable light (VL) chain sequence comprising three light chain CDR sequences, CDR-L1, CDR-L2, and CDR-L3; wherein:
 - a. CDR-H1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 58-99 and 121;
 - b. CDR-H2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 100-111;
 - c. CDR-H3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 112-120 and 130-140,
 - d. CDR-L1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 141-144 and 149-152,
 - e. CDR-L2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 153-158 and the amino acid sequence LAS; and
 - f. CDR-L3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 165-172.

In other embodiments of the formulation, the IL-13 antibody comprises:

- (i) a variable heavy (VH) chain sequence comprising three heavy chain CDR sequences, CDR-H1, CDR-H2, and CDR-H3; and
- (ii) a variable light (VL) chain sequence comprising three light chain CDR sequences, CDR-L1, CDR-L2, and CDR-L3; wherein:
 - a. CDR-H1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 58, SEQ ID NO: 68, and SEQ ID NO: 85;
 - b. CDR-H2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 100, SEQ ID NO: 104, and SEQ ID NO: 108;
 - c. CDR-H3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 112 and SEQ ID NO: 130,
 - d. CDR-L1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 141 and SEQ ID NO: 149,
 - e. CDR-L2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 153 and SEQ ID NO: 164; and
 - f. CDR-L3 comprises the sequence set forth in SEQ ID NO: 165.

In other embodiments of the formulation, the IL-13 antibody comprises:

- (i) a variable heavy (VH) chain sequence comprising three heavy chain CDR sequences, CDR-H1, CDR-H2, and CDR-H3; and
- (ii) a variable light (VL) chain sequence comprising three light chain CDR sequences, CDR-L1, CDR-L2, and CDR-L3; wherein:
 - a. CDR-H1 comprises the sequence set forth in SEQ ID NO: 58 or 67;
 - b. CDR-H2 comprises the sequence set forth in SEQ ID NO: 100 or 104;
 - c. CDR-H3 comprises the sequence set forth in SEQ ID NO: 112;
 - d. CDR-L1 comprises the sequence set forth in SEQ ID NO: 141 or 149;
 - e. CDR-L2 comprises the sequence set forth in SEQ ID NO: 153 or 596; and
 - f. CDR-L3 comprises the sequence set forth in SEQ ID NO: 165.

In embodiments, the IL-13 antibody comprises a means for extending the half-life of the IL-13 antibody. In embodiments, the means comprises at least one amino acid modification in the IL-13 antibody, as described further herein.

In embodiments, the formulation further comprises a sugar or sugar alcohol.

Brief Description of the Drawings

[0072] These and other features, aspects, and advantages of the present invention will become better understood with regard to the following description, and accompanying drawings, where:

[0073] **FIG. 1** is a graph depicting the viscosity in centipoise (cP) of a formulation of an interleukin 13 (IL-13) antibody (200 mg/mL, except where indicated), when stored at 20 °C (light grey) or 25 °C (dark gray). Abbreviations: His, histidine buffer (*i.e.*, combination L-histidine and L-histidine HCl buffer); Su, sucrose; Met, L-Methionine; R. HCl, L-Arginine-HCl (Arg-HCl); Pro, L-proline; Gly, glycine.

[0074] **FIG. 2** is a graph depicting the average gliding force in Newtons (N) (y-axis) at room temperature of a formulation with varied concentrations of an IL-13 antibody (x-axis) and including 150 mM Arg-HCl, 80 mM Arg-HCl and 3% w/v sucrose, or 120 mM Arg-HCl injected through a pre-filled syringe (PFS). All three formulations had 10 mM histidine buffer (*i.e.*, combination L-histidine and L-histidine HCl buffer), 10 mM L-methionine, 0.05% polysorbate 80, at a pH of 5.8.

[0075] FIG. 3A-3B show bar graphs of the levels of subvisible particles equal to or greater than 2µm (FIG. 3A) or 10 µm (FIG. 3B) in samples tested with different syringes and plungers.

[0076] FIG. 4A-4B show bar graphs of pH (FIG. 4A) and PS80 stability (FIG. 4B) in samples tested with different combinations of syringes (C and D) and plungers (A and B).

[0077] FIG. 5 shows bar graphs of SEC results for samples tested with different combinations of syringes (C and D) and plungers (A and B), wherein the data has been normalized to 100% at T=0.

[0078] FIG. 6 shows bar graphs of iCIEF results for samples tested with different combinations of syringes (C and D) and plungers (A and B), wherein the data has been normalized to 100% at T=0.

[0079] FIG. 7A-7B show bar graphs of CE-SDS-NR (FIG. 7A) and CE-SDS-R (FIG. 7B) results in samples tested with different combinations of syringes (C and D) and plungers (A and B).

[0080] FIG. 8 shows a bar graph of ELISA results for container closure compatibility for samples tested with different combinations of syringes (C and D) and plungers (A and B).

Detailed Description

Definitions

[0081] Unless otherwise defined, all terms of art, notations and other scientific terminology used herein are intended to have the meanings commonly understood by those of skill in the art. In some cases, terms with commonly understood meanings are defined herein for clarity and/or for ready reference, and the inclusion of such definitions herein should not necessarily be construed to represent a difference over what is generally understood in the art. The techniques and procedures described or referenced herein are generally well understood and commonly employed using conventional methodologies by those skilled in the art, such as, for example, the widely utilized molecular cloning methodologies described in Sambrook *et al.*, Molecular Cloning: A Laboratory Manual 4th ed. (2012) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY. As appropriate, procedures involving the use of commercially available kits and reagents are generally carried out in accordance with manufacturer-defined protocols and conditions unless otherwise noted.

[0082] As used herein, the singular form “a,” “an,” and “the” includes plural references unless indicated otherwise.

[0083] It is understood that aspects and embodiments of the invention described herein include “comprising,” “consisting,” and “consisting essentially of” aspects and embodiments.

[0084] For all compositions described herein, and all methods using a composition described herein, the compositions can either comprise the listed components or steps, or can “consist essentially of” the listed components or steps. When a composition is described as “consisting essentially of” the listed components, the composition contains the components listed, and may contain other components which do not substantially affect the condition being treated, but do not contain any other components which substantially affect the condition being treated other than those components expressly listed; or, if the composition does contain extra components other than those listed which substantially affect the condition being treated, the composition does not contain a sufficient concentration or amount of the extra components to substantially affect the condition being treated. When a method is described as “consisting essentially of” the listed steps, the method contains the steps listed, and may contain other steps that do not substantially affect the condition being treated, but the method does not contain any other steps which substantially affect the condition being treated other than those steps expressly listed. As a non-limiting specific example, when a composition is described as “consisting essentially of” a component, the composition may additionally contain any amount of pharmaceutically acceptable carriers, vehicles, or diluents and other such components which do not substantially affect the condition being treated.

[0085] An “effective amount” or “therapeutically effective amount” as used herein refers to an amount of therapeutic compound, such as an IL-13 antibody, administered to an individual, either as a single dose or as part of a series of doses, which is effective to produce or contribute to a desired therapeutic effect, either alone or in combination with another therapeutic modality. Examples of a desired therapeutic effect is enhancing an immune response, slowing or delaying tumor development; stabilization of disease; amelioration of one or more symptoms. An effective amount may be given in one or more dosages.

[0086] The term “treating” (and variations thereof such as “treat” or “treatment”) refers to clinical intervention in an attempt to alter the natural course of a disease or condition in a subject in need thereof. Treatment can be performed during the course of clinical pathology. Desirable effects of treatment include preventing recurrence of disease, alleviation of symptoms, diminishment of any direct or indirect pathological consequences of the disease,

preventing metastasis, decreasing the rate of disease progression, amelioration or palliation of the disease state, and remission or improved prognosis.

[0087] The term “sufficient amount” means an amount sufficient to produce a desired effect, *e.g.*, an amount sufficient to modulate an immune response in a subject.

[0088] As used herein, the terms “subject”, “patient”, and “individual” are used interchangeably herein. The term “subject”, “patient”, or “individual” means a mammalian subject. Exemplary subjects include humans, monkeys, dogs, cats, mice, rats, cows, horses, camels, goats, rabbits, and sheep. In certain embodiments, the subject is a human. In certain embodiments the subject has a disease or condition that can be treated with an antibody provided herein.

[0089] The term “pharmaceutical composition” refers to a preparation which is in such form as to permit the biological activity of an active ingredient contained therein to be effective in treating a subject, and which contains no additional components which are unacceptably toxic to the subject in the amounts provided in the pharmaceutical composition.

[0090] The terms “modulate” and “modulation” refer to reducing or inhibiting or, alternatively, activating or increasing, a recited variable.

[0091] The terms “increase” and “activate” refer to an increase of 10%, 20%, 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, 2-fold, 3-fold, 4-fold, 5-fold, 10-fold, 20-fold, 50-fold, 100-fold, or greater in a recited variable.

[0092] The terms “reduce” and “inhibit” refer to a decrease of 10%, 20%, 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 2-fold, 3-fold, 4-fold, 5-fold, 10-fold, 20-fold, 50-fold, 100-fold, or greater in a recited variable.

[0093] The term “about” indicates and encompasses an indicated value and a range above and below that value. In certain embodiments, the term “about” indicates the designated value $\pm 10\%$, $\pm 5\%$, or $\pm 1\%$. In certain embodiments, where applicable, the term “about” indicates the designated value(s) $\pm$ one standard deviation of that value(s).

[0094] For any of the structural and functional characteristics described herein, methods of determining these characteristics are known in the art.

[0095] The term “optionally” is meant, when used sequentially, to include from one to all of the enumerated combinations and contemplates all sub-combinations.

[0096] The term “amino acid” refers to the twenty common naturally occurring amino acids. Naturally occurring amino acids include alanine (Ala; A), arginine (Arg; R), asparagine (Asn; N), aspartic acid (Asp; D), cysteine (Cys; C); glutamic acid (Glu; E),

glutamine (Gln; Q), Glycine (Gly; G); histidine (His; H), isoleucine (Ile; I), leucine (Leu; L), lysine (Lys; K), methionine (Met; M), phenylalanine (Phe; F), proline (Pro; P), serine (Ser; S), threonine (Thr; T), tryptophan (Trp; W), tyrosine (Tyr; Y), and valine (Val; V). As used herein, an amino acid described herein may refer to its L-isomer form. For example, methionine may refer to L-methionine, proline may refer to L-proline, and arginine may refer to L-arginine.

[0097] The term “affinity” refers to the strength of the sum total of non-covalent interactions between a single binding site of a molecule (*e.g.*, an antibody) and its binding partner (*e.g.*, an antigen or epitope). Unless indicated otherwise, as used herein, “affinity” refers to intrinsic binding affinity, which reflects a 1:1 interaction between members of a binding pair (*e.g.*, antibody and antigen or epitope).

[0098] The term “ k_d ” (sec⁻¹), as used herein, refers to the dissociation rate constant of a particular antibody - antigen interaction. This value is also referred to as the koff value.

[0099] The term “ k_a ” (M⁻¹sec⁻¹), as used herein, refers to the association rate constant of a particular antibody -antigen interaction. This value is also referred to as the kon value.

[00100] The term “ K_D ” (M), as used herein, refers to the dissociation equilibrium constant of a particular antibody -antigen interaction. $K_D = k_d/k_a$. In certain embodiments, the affinity of an antibody is described in terms of the K_D for an interaction between such antibody and its antigen. For clarity, as known in the art, a smaller K_D value indicates a higher affinity interaction, while a larger K_D value indicates a lower affinity interaction.

[00101] The term “ K_A ” (M⁻¹), as used herein, refers to the association equilibrium constant of a particular antibody-antigen interaction. $K_A = k_a/k_d$.

[00102] The term “antibody” is used herein in its broadest sense and includes certain types of immunoglobulin molecules comprising one or more antigen-binding domains that specifically bind to an antigen or epitope. An antibody specifically includes intact antibodies (*e.g.*, intact immunoglobulins), antibody fragments, and multi-specific antibodies.

[00103] A “anti-IL-13 antibody,” “IL-13 antibody,” or “IL-13 specific antibody” is an antibody, as provided herein, which specifically binds to the antigen IL-13.

[00104] The term “epitope” means a portion of an antigen that specifically binds to an antibody.

[00105] The term “hypervariable region” or “HVR,” as used herein, refers to each of the regions of an antibody variable domain which are hypervariable in sequence and/or form structurally defined loops (“hypervariable loops”).

[00106] The term “antigen-binding domain” means the portion of an antibody that is capable of specifically binding to an antigen or epitope.

[00107] The term “chimeric antibody” refers to an antibody in which a portion of the heavy and/or light chain is derived from a particular source or species, while the remainder of the heavy and/or light chain is derived from a different source or species.

[00108] The term “human antibody” refers to an antibody which possesses an amino acid sequence corresponding to that of an antibody produced by a human or a human cell, or derived from a non-human source that utilizes a human antibody repertoire or human antibody-encoding sequences (*e.g.*, obtained from human sources or designed *de novo*). Human antibodies specifically exclude humanized antibodies.

[00109] The term “humanized antibody” refers to a protein having a sequence that differs from the sequence of an antibody derived from a non-human species by one or more amino acid substitutions, deletions, and/or additions, such that the humanized antibody is less likely to induce an immune response, and/or induces a less severe immune response, as compared to the non-human species antibody, when it is administered to a human subject.

[00110] The term “multispecific antibody” refers to an antibody that comprises two or more different antigen-binding domains that collectively specifically bind two or more different epitopes.

[00111] A “monospecific antibody” is an antibody that comprises one or more binding sites that specifically bind to a single epitope. An example of a monospecific antibody is a naturally occurring IgG molecule which, while divalent (*i.e.*, having two antigen-binding domains), recognizes the same epitope at each of the two antigen-binding domains. The binding specificity may be present in any suitable valency.

[00112] The term “monoclonal antibody” refers to an antibody from a population of substantially homogeneous antibodies. A population of substantially homogeneous antibodies comprises antibodies that are substantially similar and that bind the same epitope(s), except for variants that may normally arise during production of the monoclonal antibody. Such variants are generally present in only minor amounts. A monoclonal antibody is typically obtained by a process that includes the selection of a single antibody from a plurality of antibodies. For example, the selection process can be the selection of a unique clone from a plurality of clones, such as a pool of hybridoma clones, phage clones, yeast clones, bacterial clones, or other recombinant DNA clones. The selected antibody can be further altered, for

example, to improve affinity for the target (“affinity maturation”), to humanize the antibody, to improve its production in cell culture, and/or to reduce its immunogenicity in a subject.

[00113] The term “single-chain” refers to a molecule comprising amino acid monomers linearly linked by peptide bonds. In a particular such embodiment, the C-terminus of the Fab light chain is connected to the N-terminus of the Fab heavy chain in the single-chain Fab molecule. As described in more detail herein, an scFv has a variable domain of light chain (VL) connected from its C-terminus to the N-terminal end of a variable domain of heavy chain (VH) by a polypeptide chain. Alternately the scFv comprises of polypeptide chain where in the C-terminal end of the VH is connected to the N-terminal end of VL by a polypeptide chain.

[00114] The “Fab fragment” (also referred to as fragment antigen-binding) contains the constant domain (CL) of the light chain and the first constant domain (CH1) of the heavy chain along with the variable domains VL and VH on the light and heavy chains respectively. The variable domains comprise the complementarity determining loops (CDR, also referred to as hypervariable region) that are involved in antigen-binding. Fab’ fragments differ from Fab fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region.

[00115] “F(ab’)2” fragments contain two Fab’ fragments joined, near the hinge region, by disulfide bonds. F(ab’)2 fragments may be generated, for example, by recombinant methods or by pepsin digestion of an intact antibody. The F(ab’) fragments can be dissociated, for example, by treatment with β -mercaptoethanol.

[00116] “Fv” fragments comprise a non-covalently-linked dimer of one heavy chain variable domain and one light chain variable domain.

[00117] “Single-chain Fv” or “sFv” or “scFv” includes the VH and VL domains of an antibody, wherein these domains are present in a single polypeptide chain. In one embodiment, the Fv polypeptide further comprises a polypeptide linker between the VH and VL domains which enables the scFv to form the desired structure for antigen-binding. For a review of scFv see Pluckthun in *The Pharmacology of Monoclonal Antibodies*, vol. 113, Rosenberg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994). HER2 antibody scFv fragments are described in WO93/16185; U.S. Pat. No. 5,571,894; and U.S. Pat. No. 5,587,458.

[00118] “scFv-Fc” fragments comprise an scFv attached to an Fc domain. For example, an Fc domain may be attached to the C-terminal of the scFv. The Fc domain may follow the VH

or VL, depending on the orientation of the variable domains in the scFv (*i.e.*, VH -VL or VL - VH). Any suitable Fc domain known in the art or described herein may be used. In some cases, the Fc domain comprises an IgG4 Fc domain.

[00119] The term “single domain antibody” or “sdAb” refers to a molecule in which one variable domain of an antibody specifically binds to an antigen without the presence of the other variable domain. Single domain antibodies, and fragments thereof, are described in Arabi Ghahroudi *et al.*, *FEBS Letters*, 1998, 414:521-526 and Muyldermans *et al.*, *Trends in Biochem. Sci.*, 2001, 26:230-245, each of which is incorporated by reference in its entirety. Single domain antibodies are also known as sdAbs or nanobodies. Sdabs are fairly stable and easy to express as fusion partner with the Fc chain of an antibody (Harmsen MM, De Haard HJ (2007). “Properties, production, and applications of camelid single-domain antibody fragments”. *Appl. Microbiol Biotechnol.* 77(1): 13-22).

[00120] The terms “full length antibody,” “intact antibody,” and “whole antibody” are used herein interchangeably to refer to an antibody having a structure substantially similar to a naturally occurring antibody structure and having heavy chains that comprise an Fc region. For example, when used to refer to an IgG molecule, a “full length antibody” is an antibody that comprises two heavy chains and two light chains.

[00121] The term “antibody fragment” refers to an antibody that comprises a portion of an intact antibody, such as the antigen-binding or variable region of an intact antibody. Antibody fragments include, for example, Fv fragments, Fab fragments, F(ab')₂ fragments, Fab' fragments, scFv (sFv) fragments, and scFv-Fc fragments.

[00122] The term “Fc domain” or “Fc region” herein is used to define a C-terminal region of an immunoglobulin heavy chain that contains at least a portion of the constant region. The term includes native sequence Fc regions and variant Fc regions.

[00123] The term “purified” or “substantially purified” refers to a construct described herein, or variant thereof that may be substantially or essentially free of components that normally accompany or interact with the protein as found in its naturally occurring environment, *i.e.*, a native cell, or host cell in the case of recombinantly produced antibody that in certain embodiments, is substantially free of cellular material includes preparations of protein having less than about 30%, less than about 25%, less than about 20%, less than about 15%, less than about 10%, less than about 5%, less than about 4%, less than about 3%, less than about 2%, or less than about 1% (by dry weight or by relative concentration) of contaminating protein.

[00124] 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.*, using publicly available computer software such as BLAST, BLASTP, BLASTN, BLAST-2, ALIGN, MEGALIGN (DNASTAR), CLUSTALW, CLUSTAL OMEGA, or MUSCLE software or other algorithms available to persons of skill) or by visual inspection. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (ncbi.nlm.nih.gov). Those skilled in the art can determine appropriate parameters for aligning sequences, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. 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.

[00125] 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.

[00126] 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*).

[00127] Ranges recited herein are understood to be shorthand for all of the values within the range, inclusive of the recited endpoints. For example, a range of 1 to 50 is understood to include any number, combination of numbers, or sub-range from the group consisting of 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, 41, 42, 43, 44, 45, 46, 47, 48, 49, and 50.

[00128] 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.

[00129] The term “stable formulation” refers to a formulation in which the protein of interest (here an antibody or an antigen binding fragment thereof) essentially retains its physical, chemical and/or biological properties upon storage. In order to measure the protein stability in a formulation, various analytical methods are well within the knowledge of the skilled person (see some examples in the Example section). Stability is typically assessed at a selected temperature (for instance -70°C , -40°C , -20°C , $2-8^{\circ}\text{C}$, 25°C , 35°C , or more) for a selected time period (*e.g.*, 3 months, 6 months, 12 months, or more). As an antibody, once formulated, it may be stored frozen (-20°C to -70°C), under refrigerated conditions (typically $2-8^{\circ}\text{C}$), or at room temperature (typically $20-26^{\circ}\text{C}$) before being prepared for administration to a patient. It is important that the formulated antibody is stable over time at least at $2-25^{\circ}\text{C}$ or under frozen conditions (-20 to -70°C), as shown for example at $2-8^{\circ}\text{C}$, 25°C , -20°C , -40°C , and -70°C . Various values can be used to conclude about stability over a given time period (in comparison of the initial data), such as (and not limited to): 1) no more than 10% of alteration of the monomeric form of the antibody, 2) no more than 10% of increase in High Molecular Weight Species (HMW; also herein referred to as aggregates), 3) no more than 10% of increase in Low Molecular Weight species (LMW), 4) no more than $\pm 1-0.3$ unit variation of the pH, 5) changes in charge variation, 6) changes in potency, or 7) changes in particulates, the relevant changed ranges of which one of skill in the art could determine.

[00130] In all the embodiments of the invention, “formulation,” “pharmaceutical formulation,” and “pharmaceutical composition” can also be referred to as “stable formulation” without any differentiation.

[00131] As used herein, the term “vial” refers to a container that holds the drug product. In some embodiments, the vial may be a vial, a pen, an autoinjector, a cartridge or a syringe. In some embodiments, the vial may be a vial, *e.g.*, a glass vial or a pre-filled syringe or pre-filled autoinjector, *e.g.*, an autoinjector cartridge.

Anti-IL-13 Antibodies

[00132] In some embodiments, the present disclosure provides formulations comprising (a) an IL-13 antibody present at a concentration between, *e.g.*, about 140 mg/mL and about

290 mg/mL; (b) a histidine buffer (*e.g.*, combination L-histidine and L-histidine HCl buffer), an acetate buffer (*e.g.*, combination acetic acid and sodium acetate trihydrate), or a succinate buffer (*e.g.*, combination succinic acid and sodium succinate hexahydrate); (c) arginine and/or methionine (*e.g.*, L-arginine and/or L-methionine) or a salt solution thereof; and (d) a polysorbate or a poloxamer, wherein the formulation is at pH 5.0 to 7.0.

[00133] In some embodiments, the present disclosure further provides formulations comprising: (a) an IL-13 antibody present at a concentration of, *e.g.*, about 180 mg/mL; (b) a histidine buffer (*e.g.*, combination L-histidine and L-histidine HCl buffer) at a concentration of about 10 mM; (c) an L-arginine salt solution at a concentration of about 120 mM; (d) L-methionine at a concentration of about 10 mM; and (e) polysorbate 80 at a concentration of about 0.05% w/v, at pH of about 5.8.

[00134] In some embodiments, the present disclosure further provides formulations comprising: (a) an IL-13 antibody present at a concentration of, *e.g.*, about 180 mg/mL; (b) a histidine buffer (*e.g.*, combination L-histidine and L-histidine HCl buffer) at a concentration of about 10 mM; (c) an L-arginine salt solution at a concentration of about 80 mM; (d) L-methionine at a concentration of about 10 mM; and (e) polysorbate 80 at a concentration of about 0.05% w/v, at pH of about 5.8.

[00135] In some embodiments, the present disclosure further provides formulations comprising: (a) an IL-13 antibody present at a concentration of, *e.g.*, about 160-250 mg/mL (*e.g.*, 180 mg/mL or 200 mg/mL); (b) a histidine buffer (*e.g.*, combination L-histidine and L-histidine HCl buffer) at a concentration of about 10 mM; (c) an L-arginine salt solution at a concentration of about 120 mM; (d) L-methionine at a concentration of about 10 mM; and (e) polysorbate 80 at a concentration of about 0.05% w/v, at pH of about 5.5 to 7.0, *e.g.*, 5.8 or 6.0.

[00136] In some embodiments, the formulation comprises a sugar, for example, sucrose.

[00137] In some embodiments, the IL-13 antibody is a humanized, human, or chimeric antibody. In some embodiments, the IL-13 antibody is a humanized antibody.

Anti-IL-13 Antibody Structure

[00138] The present application provides antibodies and formulations comprising an IL-13 antibody.

[00139] The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. The “class” of an

antibody or immunoglobulin refers to the type of constant domain or constant region possessed by its heavy chain. There are five major classes of antibodies: IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into subclasses (isotypes), *e.g.*, IgG1, IgG2, IgG3, IgG4, IgA1, and IgA2. The heavy chain constant domains that correspond to the different classes of immunoglobulins are called α , δ , ϵ , γ , and μ , respectively.

[00140] An exemplary immunoglobulin (antibody) structural unit is composed of two pairs of polypeptide chains, each pair having one “light” (about 25 kD) and one “heavy” chain (about 50-70 kD). The N-terminal domain of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (VL) and variable heavy chain (VH) refer to these light and heavy chain domains respectively. The IgG1 heavy chain comprises of the VH, CH1, CH2, and CH3 domains respectively from the N- to C-terminus. The light chain comprises of the VL and CL domains from N- to C-terminus. The IgG1 heavy chain comprises a hinge between the CH1 and CH2 domains. In certain embodiments, the immunoglobulin constructs comprise at least one immunoglobulin domain from IgG, IgM, IgA, IgD, or IgE connected to a therapeutic polypeptide. In some embodiments, the immunoglobulin domain found in an antibody provided herein, is from or derived from an immunoglobulin based construct such as a diabody or a nanobody. In certain embodiments, the immunoglobulin constructs described herein comprise at least one immunoglobulin domain from a heavy chain antibody such as a camelid antibody. In certain embodiments, the immunoglobulin constructs provided herein comprise at least one immunoglobulin domain from a mammalian antibody such as a bovine antibody, a human antibody, a camelid antibody, a mouse antibody, or any chimeric antibody.

[00141] In some embodiments, the antibodies provided herein comprise a heavy chain. In one embodiment, the heavy chain is an IgA. In one embodiment, the heavy chain is an IgD. In one embodiment, the heavy chain is an IgE. In one embodiment, the heavy chain is an IgG. In one embodiment, the heavy chain is an IgM. In one embodiment, the heavy chain is an IgG1. In one embodiment, the heavy chain is an IgG2. In one embodiment, the heavy chain is an IgG3. In one embodiment, the heavy chain is an IgG4. In one embodiment, the heavy chain is an IgA1. In one embodiment, the heavy chain is an IgA2.

[00142] In some embodiments, an antibody is an IgG1 antibody. In some embodiments, an antibody is an IgG3 antibody. In some embodiments, an antibody is an IgG2 antibody. In some embodiments, an antibody is an IgG4 antibody.

[00143] Generally, native four-chain antibodies comprise six hypervariable regions (HVRs); three in the VH (H1, H2, and H3), and three in the VL (L1, L2, and L3). HVRs generally comprise amino acid residues from the hypervariable loops and/or from the complementarity determining regions (CDRs), the latter being of highest sequence variability and/or involved in antigen recognition. With the exception of CDR1 in VH, CDRs generally comprise the amino acid residues that form the hypervariable loops. HVRs are also referred to as CDRs, and these terms are used herein interchangeably in reference to portions of the variable region that form the antigen-binding regions. This particular region has been described by Kabat *et al.*, U.S. Dept. of Health and Human Services, Sequences of Proteins of Immunological Interest (1983) and by Chothia *et al.*, *J Mol Biol* 196:901-917 (1987), where the definitions include overlapping or subsets of amino acid residues when compared against each other. Nevertheless, application of either definition to refer to a CDR of an antibody or variants thereof is intended to be within the scope of the term as defined and used herein. The exact residue numbers which encompass a particular CDR will vary depending on the sequence and size of the CDR. Those skilled in the art can routinely determine which residues comprise a particular CDR given the variable region amino acid sequence of the antibody.

[00144] The amino acid sequence boundaries of a CDR can be determined by one of skill in the art using any of a number of known numbering schemes, including those described by Kabat *et al.*, supra (“Kabat” numbering scheme); Al-Lazikani *et al.*, 1997, *J. Mol. Biol.*, 273:927-948 (“Chothia” numbering scheme); MacCallum *et al.*, 1996, *J. Mol. Biol.* 262:732-745 (“Contact” numbering scheme); Lefranc *et al.*, *Dev. Comp. Immunol.*, 2003, 27:55-77 (“IMGT” numbering scheme); and Honegge and Plückthun, *J. Mol. Biol.*, 2001, 309:657-70 (“Aho” numbering scheme); each of which is incorporated by reference in its entirety.

[00145] **Table 1** provides the positions of CDR-L1, CDR-L2, CDR-L3, CDR-H1, CDR-H2, and CDR-H3 as identified by the Kabat and Chothia schemes. For CDR-H1, residue numbering is provided using both the Kabat and Chothia numbering schemes.

[00146] CDRs may be assigned, for example, using antibody numbering software, such as Abnum, available at www.bioinf.org.uk/abs/abnum/, and described in Abhinandan and Martin, *Immunology*, 2008, 45:3832-3839, incorporated by reference in its entirety.

Table 1. Residues in CDRs according to Kabat and Chothia numbering schemes

CDR	Kabat	Chothia
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L1	L24-L34	L24-L34
L2	L50-L56	L50-L56
L3	L89-L97	L89-L97
H1 (Kabat Numbering)	H31-H35B	H26-H32 or H34*
H1 (Chothia Numbering)	H31-H35	H26-H32
H2	H50-H65	H52-H56
H3	H95-H102	H95-H102

* The C-terminus of CDR-H1, when numbered using the Kabat numbering convention, varies between H32 and H34, depending on the length of the CDR.

[00147] The “EU numbering scheme” is generally used when referring to a residue in an antibody heavy chain constant region (*e.g.*, as reported in Kabat *et al.*, *supra*). Unless stated otherwise, the EU numbering scheme is used to refer to residues in antibody heavy chain constant regions described herein.

[00148] One example of an antigen-binding domain is an antigen-binding domain formed by a VH-VL dimer of an antibody. Another example of an antigen-binding domain is an antigen-binding domain formed by diversification of certain loops from the tenth fibronectin type III domain of an Adnectin. An antigen-binding domain can include CDRs 1, 2, and 3 from a heavy chain in that order; and CDRs 1, 2, and 3 from a light chain in that order.

[00149] Epitopes frequently consist of surface-accessible amino acid residues and/or sugar side chains and may have specific three-dimensional structural characteristics, as well as specific charge characteristics. Conformational and non-conformational epitopes are distinguished in that the binding to the former but not the latter may be lost in the presence of denaturing solvents. An epitope may comprise amino acid residues that are directly involved in the binding and other amino acid residues, which are not directly involved in the binding. The epitope to which an antibody binds can be determined using known techniques for epitope determination such as, for example, testing for antibody binding to IL-13 variants with different point-mutations or to chimeric IL-13 variants.

[00150] To screen for antibodies which bind to an epitope on a target antigen bound by an antibody of interest (*e.g.*, IL-13), a routine cross-blocking assay such as that described in Antibodies, A Laboratory Manual, Cold Spring Harbor Laboratory, Ed Harlow and David Lane (1988), can be performed. Alternatively, or additionally, epitope mapping can be performed by methods known in the art.

[00151] Chimeric antibodies are antibodies in which a portion of the heavy and/or light chain is derived from a particular source or species, while the remainder of the heavy and/or light chain is derived from a different source or species.

[00152] Human antibodies are antibodies which possess an amino acid sequence corresponding to that of an antibody produced by a human or a human cell, or derived from a non-human source that utilizes a human antibody repertoire or human antibody-encoding sequences (*e.g.*, obtained from human sources or designed *de novo*). Human antibodies specifically exclude humanized antibodies.

[00153] A humanized antibody has a sequence that differs from the sequence of an antibody derived from a non-human species by one or more amino acid substitutions, deletions, and/or additions, such that the humanized antibody is less likely to induce an immune response, and/or induces a less severe immune response, as compared to the non-human species antibody, when it is administered to a human subject. In one embodiment, certain amino acids in the framework and constant domains of the heavy and/or light chains of the non-human species antibody are mutated to produce the humanized antibody. In another embodiment, the constant domain(s) from a human antibody are fused to the variable domain(s) of a non-human species. In another embodiment, one or more amino acid residues in one or more CDR sequences of a non-human antibody are changed to reduce the likely immunogenicity of the non-human antibody when it is administered to a human subject, wherein the changed amino acid residues either are not critical for immunospecific binding of the antibody to its antigen, or the changes to the amino acid sequence that are made are conservative changes, such that the binding of the humanized antibody to the antigen is not significantly worse than the binding of the non-human antibody to the antigen. Examples of how to make humanized antibodies can be found in U.S. Pat. Nos. 6,054,297, 5,886,152 and 5,877,293. For further details, see Jones *et al.*, *Nature*, 1986, 321:522-525; Riechmann *et al.*, *Nature*, 1988, 332:323-329; and Presta, *Curr. Op. Struct. Biol.*, 1992, 2:593-596, each of which is incorporated by reference in its entirety.

[00154] The two or more different epitopes may be epitopes on the same antigen (*e.g.*, a single IL-13) or on different antigens (*e.g.*, different IL-13 molecules, or a IL-13 molecule and a non- IL-13 molecule). In some embodiments, a multi-specific antibody binds two different epitopes (*i.e.*, a “bispecific antibody”). In some embodiments, a multi-specific antibody binds three different epitopes (*i.e.*, a “trispecific antibody”).

[00155] Anti-IL-13 antibodies can include those described herein such as the clones set forth in the drawings and/or tables. In some embodiments, the antibody comprises an alternative scaffold. In some embodiments, the antibody consists of an alternative scaffold. In some embodiments, the antibody consists essentially of an alternative scaffold. In some embodiments, the antibody comprises an antibody fragment. In some embodiments, the antibody consists of an antibody fragment. In some embodiments, the antibody consists essentially of an antibody fragment.

[00156] In some embodiments the antibodies are monoclonal antibodies.

[00157] In some embodiments the antibodies are polyclonal antibodies.

[00158] In some embodiments the antibodies are produced by hybridomas. In other embodiments, the antibodies are produced by recombinant cells engineered to express the desired variable and constant domains.

[00159] In some embodiments the antibodies may be single chain antibodies or other antibody derivatives retaining the antigen specificity and the lower hinge region or a variant thereof.

[00160] In some embodiments the antibodies may be polyfunctional antibodies, recombinant antibodies, human antibodies, humanized antibodies, fragments or variants thereof. In particular embodiments, the antibody fragment or a derivative thereof is selected from a Fab fragment, a Fab'2 fragment, a CDR, and ScFv.

[00161] In some embodiments, the antibodies are capable of forming an immune complex. For example, an immune complex can be a tumor cell covered by antibodies.

Sequences of IL-13 Antibodies

VH Domains

[00162] In some embodiments, the present disclosure further provides formulations comprising: (a) an IL-13 antibody present at a concentration between 140 mg/mL and 290 mg/mL; (b) a histidine buffer (*e.g.*, combination L-histidine and L-histidine HCl buffer), an acetate buffer (*e.g.*, combination acetic acid and sodium acetate trihydrate), or a succinate buffer (*e.g.*, combination succinic acid and sodium succinate hexahydrate); (c) arginine and/or methionine (*e.g.*, L-arginine and/or L-methionine) or a salt solution thereof; and (d) a polysorbate or a poloxamer, at pH 5.0 to 7.0. In some embodiments, the IL-13 antibody comprises: (i) a variable heavy (VH) chain sequence comprising three heavy chain CDR sequences, CDR-H1, CDR-H2, and CDR-H3; and (ii) a variable light (VL) chain sequence

comprising three light chain CDR sequences, CDR-L1, CDR-L2, and CDR-L3; wherein: (a) CDR-H1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 58-99 and 121; (b) CDR-H2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 100-111; (c) CDR-H3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 112-120 and 130-140, (d) CDR-L1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 141-144 and 149-152, (e) CDR-L2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 153-158 and the amino acid sequence LAS; and (f) CDR-L3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 165-172.

[00163] In some embodiments, the present disclosure further provides formulations comprising: (a) an IL-13 antibody present at a concentration, *e.g.*, between 140 mg/mL and 290 mg/mL; (b) a histidine buffer (*e.g.*, combination L-histidine and L-histidine HCl buffer), an acetate buffer (*e.g.*, combination acetic acid and sodium acetate trihydrate), or a succinate buffer (*e.g.*, combination succinic acid and sodium succinate hexahydrate); (c) arginine and/or methionine (*e.g.*, L-arginine and/or L-methionine) or a salt solution thereof; and (d) a polysorbate or a poloxamer, at pH 5.0 to 7.0. In some embodiments, the IL-13 antibody comprises: (i) a variable heavy (VH) chain sequence comprising three heavy chain CDR sequences, CDR-H1, CDR-H2, and CDR-H3; and (ii) a variable light (VL) chain sequence comprising three light chain CDR sequences, CDR-L1, CDR-L2, and CDR-L3; wherein: (a) CDR-H1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 58, SEQ ID NO: 68, and SEQ ID NO: 85; (b) CDR-H2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 100, SEQ ID NO: 104, and SEQ ID NO: 108; (c) CDR-H3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 112 and SEQ ID NO: 130, (d) CDR-L1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 141 and SEQ ID NO: 149, (e) CDR-L2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 153 and SEQ ID NO: 164; and (f) CDR-L3 comprises the sequence set forth in SEQ ID NO: 165.

[00164] In some embodiments, an antibody provided herein comprises a VH sequence selected from SEQ ID NOs: 1-32.

[00165] In some embodiments, an antibody provided herein comprises a VH sequence having at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to an VH sequence provided in SEQ ID NOs: 1-32. In some embodiments, an antibody provided herein comprises a VH sequence provided in SEQ ID NOs: 1-32, with up

to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions. In some embodiments, the antibodies described in this paragraph are referred to herein as “variants.” In some embodiments, such variants are derived from a sequence provided herein, for example, by affinity maturation, site directed mutagenesis, random mutagenesis, or any other method known in the art or described herein. In some embodiments, such variants are not derived from a sequence provided herein and may, for example, be isolated *de novo* according to the methods provided herein for obtaining antibodies.

VL Domains

[00166] In some embodiments, an antibody provided herein comprises a VL sequence selected from SEQ ID NOs: 33-57.

[00167] In some embodiments, an antibody provided herein comprises a VL sequence having at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to an VL sequence provided in SEQ ID NOs: 33-57. In some embodiments, an antibody provided herein comprises a VL sequence provided in SEQ ID NOs: 33-57 with up to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions. In some embodiments, the antibodies described in this paragraph are referred to herein as “variants.” In some embodiments, such variants are derived from a sequence provided herein, for example, by affinity maturation, site directed mutagenesis, random mutagenesis, or any other method known in the art or described herein. In some embodiments, such variants are not derived from a sequence provided herein and may, for example, be isolated *de novo* according to the methods provided herein for obtaining antibodies.

VH-VL Combinations

[00168] In some embodiments, an antibody provided herein comprises a VH sequence selected from SEQ ID NOs: 1-32; and a VL sequence selected from SEQ ID NOs: 33-57, such as any of the VH-VL combinations set forth for Constructs 3-127 and 132-144 in **Table 2**, below.

[00169] In certain aspects, any of SEQ ID NOs: 1-32 can be combined with any of SEQ ID NOs: 33-57.

[00170] In certain embodiments, the antibody comprises a VH sequence selected from the sequences set forth in SEQ ID NOs: 1-32 and a VL sequence set forth in SEQ ID NO: 39.

[00171] In certain embodiments, the antibody comprises the VH sequence set forth in SEQ ID NO: 3 and the VL sequence set forth in SEQ ID NO: 39.

[00172] In certain embodiments, the antibody comprises a VH sequence selected from the sequences set forth in SEQ ID NOs: 1-32 and a VL sequence set forth in SEQ ID NO: 51.

[00173] In some embodiments, an antibody provided herein comprises a VH sequence having at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to an VH sequence provided in SEQ ID NOs: 1-32; and a VL sequence having at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to an VL sequence provided in SEQ ID NOs: 33-57. In some embodiments, an antibody provided herein comprises a VH sequence provided in SEQ ID NOs: 1-32, with up to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions; and a VL sequence provided in SEQ ID NOs: 33-57, with up to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions. In some embodiments, the antibodies described in this paragraph are referred to herein as “variants.” In some embodiments, such variants are derived from a sequence provided herein, for example, by affinity maturation, site directed mutagenesis, random mutagenesis, or any other method known in the art or described herein. In some embodiments, such variants are not derived from a sequence provided herein and may, for example, be isolated *de novo* according to the methods provided herein for obtaining antibodies.

[00174] In some embodiments, an antibody provided herein comprises a VH sequence and a VL sequence selected from combinations set forth for Constructs 3-127 and 132-144 in **Table 2**, below. In certain embodiments, the antibody comprises a VH sequence set forth in SEQ ID NO: 1 and a VL sequence set forth in SEQ ID NO: 33. In certain embodiments, the antibody comprises a VH sequence set forth in SEQ ID NO: 2 and a VL sequence set forth in SEQ ID NO: 33. In certain embodiments, the antibody comprises a VH sequence set forth in SEQ ID NO: 3 and a VL sequence set forth in SEQ ID NO: 35. In certain embodiments, the antibody comprises a VH sequence set forth in SEQ ID NO: 4 and a VL sequence set forth in SEQ ID NO: 35. In certain embodiments, the antibody comprises a VH sequence set forth in SEQ ID NO: 5 and a VL sequence set forth in SEQ ID NO: 35. In certain embodiments, the antibody comprises a VH sequence set forth in SEQ ID NO: 6 and a VL sequence set forth in SEQ ID NO: 35. In certain embodiments, the antibody comprises a VH sequence set forth in SEQ ID NO: 7 and a VL sequence set forth in SEQ ID NO: 35. In certain embodiments, the

[illegible]

[illegible]

certain embodiments, the antibody comprises a VH sequence set forth in SEQ ID NO: 22 and a VL sequence set forth in SEQ ID NO: 39. In certain embodiments, the antibody comprises a VH sequence set forth in SEQ ID NO: 23 and a VL sequence set forth in SEQ ID NO: 39. In certain embodiments, the antibody comprises a VH sequence set forth in SEQ ID NO: 24 and a VL sequence set forth in SEQ ID NO: 39. In certain embodiments, the antibody comprises a VH sequence set forth in SEQ ID NO: 25 and a VL sequence set forth in SEQ ID NO: 39. In certain embodiments, the antibody comprises a VH sequence set forth in SEQ ID NO: 26 and a VL sequence set forth in SEQ ID NO: 39. In certain embodiments, the antibody comprises a VH sequence set forth in SEQ ID NO: 27 and a VL sequence set forth in SEQ ID NO: 39. In certain embodiments, the antibody comprises a VH sequence set forth in SEQ ID NO: 28 and a VL sequence set forth in SEQ ID NO: 39. In certain embodiments, the antibody comprises a VH sequence set forth in SEQ ID NO: 28 and a VL sequence set forth in SEQ ID NO: 39. In certain embodiments, the antibody comprises a VH sequence set forth in SEQ ID NO: 29 and a VL sequence set forth in SEQ ID NO: 39. In certain embodiments, the antibody comprises a VH sequence set forth in SEQ ID NO: 30 and a VL sequence set forth in SEQ ID NO: 39. In certain embodiments, the antibody comprises a VH sequence set forth in SEQ ID NO: 31 and a VL sequence set forth in SEQ ID NO: 39. In certain embodiments, the antibody comprises a VH sequence set forth in SEQ ID NO: 32 and a VL sequence set forth in SEQ ID NO: 39. In certain embodiments, the antibody comprises a VH sequence set forth in SEQ ID NO: 8 and a VL sequence set forth in SEQ ID NO: 39. In certain embodiments, the antibody comprises a VH sequence set forth in SEQ ID NO: 8 and a VL sequence set forth in SEQ ID NO: 51. In certain embodiments, the antibody comprises a VH sequence set forth in SEQ ID NO: 3 and a VL sequence set forth in SEQ ID NO: 51.

[00175] In certain embodiments, the IL-13 antibody comprises a heavy chain variable domain comprising a framework region sequence selected from a sequence set forth in SEQ ID NOs: 198-229, 255-256, 258-259, 261-285, 311-315, 317-342, 368-369, 371-399, and 540-580. In certain embodiments, the IL-13 antibody comprises a heavy chain variable domain comprising 1, 2, 3, or 4 framework region sequences selected from a sequence set forth in SEQ ID NOs: 198-229, 255-256, 258-259, 261-285, 311-315, 317-342, 368-369, 371-399, and 540-580.

[00176] In certain embodiments, the IL-13 antibody comprises a light chain variable domain comprising a framework region sequence selected from a sequence set forth in SEQ ID NOs: 230-231, 233-235, 239, 241-254, 286, 288, 290-291, 293, 296-310, 343-345, 347,

400-424, and 581-609. In certain embodiments, the IL-13 antibody comprises a light chain variable domain comprising 1, 2, 3, or 4 framework region sequences selected from a sequence set forth in SEQ ID NOs: 230-231, 233-235, 239, 241-254, 286, 288, 290-291, 293, 296-310, 343-345, 347, 400-424, and 581-609.

[00177] In certain embodiments, the IL-13 antibody comprises a heavy chain variable domain comprising 1, 2, 3, or 4 framework region sequences selected from a sequence set forth in SEQ ID NOs: 198-229, 255-256, 258-259, 261-285, 311-315, 317-342, 368-369, 371-399, and 540-580, and comprises a light chain variable domain comprising 1, 2, 3, or 4 framework region sequences selected from a sequence set forth in SEQ ID NOs: 230-231, 233-235, 239, 241-254, 286, 288, 290-291, 293, 296-310, 343-345, 347, 400-424, and 581-609.

Table 2. Anti-interleukin (IL)-13 antibody VH-VL sequences

Construct ID	VH; VL; HC constant; and LC constant names, respectively*	VH sequence	VL sequence
1 (Lebrikizumab)	Lebrikizumab – HC; Lebrikizumab – LC; IgG4-SP; Human kappa LC	QVTLRESGPALVKPTQ TLTLTCTVSGFSLAYS VNWIRQPPGKALEWL AMIWGDGKIVYNSAL KSRLTISKDTSKNQVV LTMTNMDPVDATYY CAGDGYYPYAMDNW GQGS�TVSS (SEQ ID NO: 470)	DIVMTQSPDSLVS�GER ATINCRASKSVDSYGNSF MHWYQQKPGQPPLLIY LASNLESGVPDRFSGSGS GTDFTLTISSLQAEDVAV YYCQQNNEPRTFGGGT KVEIK (SEQ ID NO: 471)
2	Lebrikizumab – HC; Lebrikizumab – LC; hIgG1-LAGA YTE;	QVTLRESGPALVKPTQ TLTLTCTVSGFSLAYS VNWIRQPPGKALEWL AMIWGDGKIVYNSAL KSRLTISKDTSKNQVV LTMTNMDPVDATYY	DIVMTQSPDSLVS�GER ATINCRASKSVDSYGNSF MHWYQQKPGQPPLLIY LASNLESGVPDRFSGSGS GTDFTLTISSLQAEDVAV

	Human kappa LC	CAGDGYYPYAMDNW GQGS LVTVSS (SEQ ID NO: 470)	YYCQQNNEDPRTFGGGT KVEIK (SEQ ID NO: 471)
3	HC0; LC0; hIgG1-LAGA YTE; Human kappa LC	QVQLQESGPGLVAPSQ SLSITCTVSGFSLNAYS VNWVRQPPGKGLEWL GMIWGDGKIVYNSAL KSRLNISKDSSKSQVFL KMSSLQSDDTARYYC AGDGYYPYAMDNWG HGTSVTVSS (SEQ ID NO: 1)	NIVLTQSPASLAVSLGQR ATISCRASKSVDSYGNSF MHWYQQKPGQPPKLLIY LASNLESGVPARFSGSGS RTDFTLTIDPVEADDAAS YYCQQNNEDPRTFGGGT KLEIK (SEQ ID NO: 33)
4	HC0_M; LC0; hIgG1- LAGA YTE; Human kappa LC	QVQLQESGPGLVAPSQ SLSITCTVSGFSLNAYS VNWVRQPPGKGLEWL GMIWGDGKIVYNSAL KSRLTISKDSSKSQVFL KMSSLQSDDTARYYC AGDGYYPYAMDNWG HGTSVTVSS (SEQ ID NO: 2)	NIVLTQSPASLAVSLGQR ATISCRASKSVDSYGNSF MHWYQQKPGQPPKLLIY LASNLESGVPARFSGSGS RTDFTLTIDPVEADDAAS YYCQQNNEDPRTFGGGT KLEIK (SEQ ID NO: 33)
5	HC1; LC2; hIgG1-LAGA YTE; Human kappa LC	EVQLQESGPGLVKPSE TSLTCTVSGFSLNAYS VNWIRQPPGKGLEWL GMIWGDGKIVYNSAL KSRLTISKDSSKNQVSL KLSSVTAADTAVYYC AGDGYYPYAMDNWG QGTTVTVSS (SEQ ID NO: 3)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS RTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 35)
6	HC2; LC2; hIgG1-LAGA	EVQLVQSGAEVKKPG ASVKVSCKASGFSLNA YSVNWVRQAPGQGLE	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY

	YTE; Human kappa LC	WLGMIWGDGKIVYNS ALKSRLTITKDSSTSTV YMELSSLRSED TAVYY CAGDGYYPYAMD NW GQGTTVTVSS (SEQ ID NO: 4)	LASNLESGVPSRFSGSGS RTDFTLTISSLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 35)
7	HC3; LC2; hIgG1-LAGA YTE; Human kappa LC	EVQLVQSGAEVKKPGS SVKVSCKASGFSLNAY SVNWVRQAPGQGLEW LGMIWGDGKIVYNSA LKSRLTITKDSSTSTVY MELSSLRSED TAVYYC AGDGYYPYAMD NWG QGTTVTVSS (SEQ ID NO: 5)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS RTDFTLTISSLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 35)
8	HC4; LC2; hIgG1-LAGA YTE; Human kappa LC	EVQLVESGGGLVKPG GSLRLSCAASGFSLNA YSVNWVRQAPGKGLE WLGMIWGDGKIVYNS ALKSRLTISKDSSKNTV YLQMNSLKTEDTAVY YCAGDGYYPYAMD N WGQGTTVTVSS (SEQ ID NO: 6)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS RTDFTLTISSLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 35)
9	HC5; LC2; hIgG1-LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMD NW GQGTTVTVSS (SEQ ID NO: 7)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS RTDFTLTISSLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 35)

10	HC1; LC3; hIgG1-LAGA YTE; Human kappa LC	EVQLQESGPGGLVKPSE TSLTCTVSGFSLNAYS VNWIRQPPGKGLEWL GMIWGDGKIVYNSAL KSRLTISKDSSKNQVSL KLSSVTAADTAVYYC AGDGYYPYAMDNDWG QGTTVTVSS (SEQ ID NO: 3)	EIVLTQSPATLSVSPGERA TLSCRASKSVDSYGNSF MHWYQQKPGQAPRLLIY LASNLESGIPARFSGSGSR TEFTLTISSLQSEDAVYY CQQNNEDPRTFGGGTKV EIK (SEQ ID NO: 36)
11	HC2; LC3; hIgG1-LAGA YTE; Human kappa LC	EVQLVQSGAEVKKPG ASVKVSCASGFSLNA YSVNWVRQAPGQGLE WLGMIWGDGKIVYNS ALKSRLTITKDSSTSTV YMELSSLRSEDVAVYY CAGDGYYPYAMDNDW GQGTTVTVSS (SEQ ID NO: 4)	EIVLTQSPATLSVSPGERA TLSCRASKSVDSYGNSF MHWYQQKPGQAPRLLIY LASNLESGIPARFSGSGSR TEFTLTISSLQSEDAVYY CQQNNEDPRTFGGGTKV EIK (SEQ ID NO: 36)
12	HC3; LC3; hIgG1-LAGA YTE; Human kappa LC	EVQLVQSGAEVKKPGS SVKVSCASGFSLNAY SVNWVRQAPGQGLEW LGMIWGDGKIVYNSA LKSRLTITKDSSTSTVY MELSSLRSEDVAVYYC AGDGYYPYAMDNDWG QGTTVTVSS (SEQ ID NO: 5)	EIVLTQSPATLSVSPGERA TLSCRASKSVDSYGNSF MHWYQQKPGQAPRLLIY LASNLESGIPARFSGSGSR TEFTLTISSLQSEDAVYY CQQNNEDPRTFGGGTKV EIK (SEQ ID NO: 36)
13	HC4; LC3; hIgG1-LAGA YTE; Human kappa LC	EVQLVESGGGLVKPG GSLRLSCAASGFSLNA YSVNWVRQAPGKGLE WLGMIWGDGKIVYNS ALKSRLTISKDSSKNTV YLQMNSLKTEDTAVY	EIVLTQSPATLSVSPGERA TLSCRASKSVDSYGNSF MHWYQQKPGQAPRLLIY LASNLESGIPARFSGSGSR TEFTLTISSLQSEDAVYY

		YCAGDGYYPYAMD WGQTTVTVSS (SEQ ID NO: 6)	CQQNNEDPRTFGGGTKV EIK (SEQ ID NO: 36)
14	HC5; LC3; hIgG1-LAGA YTE; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMD WGQTTVTVSS (SEQ ID NO: 7)	EIVLTQSPATLSVSPGERA TLSCRASKSVDSYGNSF MHWYQQKPGQAPRLIY LASNLESGIPARFSGSGSR TEFTLTISSLQSEDAVYY CQQNNEDPRTFGGGTKV EIK (SEQ ID NO: 36)
15	HC1; LC6; hIgG1-LAGA YTE; Human kappa LC	EVQLQESGPGLVKPSE TLSTCTVSGFSLNAYS VNWIRQPPGKGLEWL GMIWGDGKIVYNSAL KSRLTISKDSSKNQVSL KLSSVTAADTAVYYC AGDGYYPYAMD WGQTTVTVSS (SEQ ID NO: 3)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISSLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
16	HC2; LC6; hIgG1-LAGA YTE; Human kappa LC	EVQLVQSGAEVKKPGS SVKVSCKASGFSLNAY SVNWVRQAPGQGLEW LGMIWGDGKIVYNSA LKSRLTITKDSSTSTVY MELSSLRSED TAVYYC AGDGYYPYAMD NWGQTTVTVSS (SEQ ID NO: 710)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISSLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
17	HC3; LC6; hIgG1-LAGA	EVQLVQSGAEVKKPGS SVKVSCKASGFSLNAY SVNWVRQAPGQGLEW	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY

	YTE; Human kappa LC	LGMIWGDGKIVYNSA LKSRLTITKDSSTSTVY MELSSLRSED TAVYYC AGDGYYPYAMDNDWG QGTTVTVSS (SEQ ID NO: 5)	LASNLESGVPSRFSGSGS GTDFTLTISSLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
18	HC4; LC6; hIgG1-LAGA YTE; Human kappa LC	EVQLVESGGGLVKPG GSLRLSCAASGFSNA YSVNWVRQAPGKGLE WLGMWGDGKIVYNS ALKSRLTISKDSSKNTV YLQMNSLKTEDTAVY YCAGDGYYPYAMDND WGQGTTVTVSS (SEQ ID NO: 6)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISSLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
19	HC5; LC6; hIgG1-LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFSNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNDW GQGTTVTVSS (SEQ ID NO: 7)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISSLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
20	HC1; LC7; hIgG1-LAGA YTE; Human kappa LC	EVQLQESGPGLVKPSE TSLTCTVSGFSLNAYS VNWIRQPPGKGLEWL GMIWGDGKIVYNSAL KSRLTISKDSSKNQVSL KLSSVTAADTAVYYC AGDGYYPYAMDNDWG QGTTVTVSS (SEQ ID NO: 3)	EIVLTQSPATLSVSPGERA TLSCRASKSVDSYGNSF MHWYQQKPGQAPRLIY LASNLESGIPARFSGSGSG TEFTLTISSLQSEDFAVYY CQQNNEDPRTFGGGTKV EIK (SEQ ID NO: 40)

21	HC2; LC7; hIgG1-LAGA YTE; Human kappa LC	EVQLVQSGAEVKKPGS SVKVSCKASGFSLNAY SVNWVRQAPGQGLEW LGMIWGDGKIVYNSA LKSRLTITKDSSTSTVY MELSSLRSEDFAVYYC AGDGYYPYAMDNDWG QGTTVTVSS (SEQ ID NO: 710)	EIVLTQSPATLSVSPGERA TLSCRASKSVDSYGNSF MHWYQQKPGQAPRLLIY LASNLESGIPARFSGSGSG TEFTLTISSLQSEDFAVYY CQQNNEDPRTFGGGTKV EIK (SEQ ID NO: 40)
22	HC3; LC7; hIgG1-LAGA YTE; Human kappa LC	EVQLVQSGAEVKKPGS SVKVSCKASGFSLNAY SVNWVRQAPGQGLEW LGMIWGDGKIVYNSA LKSRLTITKDSSTSTVY MELSSLRSEDFAVYYC AGDGYYPYAMDNDWG QGTTVTVSS (SEQ ID NO: 5)	EIVLTQSPATLSVSPGERA TLSCRASKSVDSYGNSF MHWYQQKPGQAPRLLIY LASNLESGIPARFSGSGSG TEFTLTISSLQSEDFAVYY CQQNNEDPRTFGGGTKV EIK (SEQ ID NO: 40)
23	HC4; LC7; hIgG1-LAGA YTE; Human kappa LC	EVQLVESGGGLVKPG GSLRLSCAASGFSLNA YSVNWVRQAPGKGLE WLGMIWGDGKIVYNS ALKSRLTISKDSSKNTV YLQMNSLKTEDTAVY YCAGDGYYPYAMDND WGQGTTVTVSS (SEQ ID NO: 6)	EIVLTQSPATLSVSPGERA TLSCRASKSVDSYGNSF MHWYQQKPGQAPRLLIY LASNLESGIPARFSGSGSG TEFTLTISSLQSEDFAVYY CQQNNEDPRTFGGGTKV EIK (SEQ ID NO: 40)
24	HC5; LC7; hIgG1-LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY	EIVLTQSPATLSVSPGERA TLSCRASKSVDSYGNSF MHWYQQKPGQAPRLLIY LASNLESGIPARFSGSGSG TEFTLTISSLQSEDFAVYY

		LQMNSLRAEDTAVYY CAGDGYYPYAMD NW GQGTTVTVSS (SEQ ID NO: 7)	CQQNNEDPRTFGGGTKV EIK (SEQ ID NO: 40)
25	HC6; LC9; hIgG1-LAGA YTE; Human kappa LC	EVQLQESGPGLVKPSE TSLTCTVSGGSLNAY SVNWVRQPPGKGLEW LGMIWGDGKIVYNSA LKSRLTISLDTSKSQVF LKMSLTAADTAVYY CARDGYYPYAMD NW GQGTTVTVSS (SEQ ID NO: 8)	DIVLTQSPASLAVSPGER ATISCRASKSVDSYGNSF MHWYQQKPGQPPKLLIY LASNLESGVPDRFSGSGS GTDFTLTISRVEADDAV YYCQQNNEDPRTFGGGT KLEIK (SEQ ID NO: 42)
26	HC7; LC10; hIgG1-LAGA YTE; Human kappa LC	QVQLQESGPGLVKPSE TSLTCTVSGGSLNAY SWNWVRQPPGKGLEW LGYYIGDGKTNYPAL KSRLTISLDTSKSQVFL KMSSLTAADTAVYYC ARDGYYYAMDVWG QGTTVTVSS (SEQ ID NO: 9)	DIVLTQSPASLAVSPGER ATISCRASQSVDSNGNNF LHWYQQKPGQPPKLLIY LASNRESGVPDRFSGSGS GTDFTLTISRVEADDAV YYCQQNNHTPRTFGGGT KLEIK (SEQ ID NO: 43)
90	HC5; LC6; hIgG1-LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMD NW GQGTTVTVSS (SEQ ID NO: 7)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
91	HC5; LC6_m1;	EVQLLES GGGLVQPGG SLRLSCAASGFSLNAY	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSR

	hIgG1-LAGA YTE; Human kappa LC	SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNDW GQGTTVTVSS (SEQ ID NO: 7)	MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISSLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 44)
92	HC5; LC6_m2; hIgG1-LAGA YTE; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNDW GQGTTVTVSS (SEQ ID NO: 7)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSS MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISSLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 45)
93	HC5; LC6_m3; hIgG1-LAGA YTE; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNDW GQGTTVTVSS (SEQ ID NO: 7)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSS MHWYQQKPGKAPKLLIR LASNLESGVPSRFSGSGS GTDFTLTISSLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 46)
94	HC5; LC6_m4; hIgG1-LAGA YTE; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNDW	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSS MHWYQQKPGKAPKLLIF LASNLESGVPSRFSGSGS GTDFTLTISSLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 47)

		GQGTTVTVSS (SEQ ID NO: 7)	
95	HC5; LC6_m5; hIgG1-LAGA YTE; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNW GQGTTVTVSS (SEQ ID NO: 7)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASHLESGVPSRFSGSGS GTDFTLTISSLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 48)
96	HC5; LC6_m6; hIgG1-LAGA YTE; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNW GQGTTVTVSS (SEQ ID NO: 7)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASDLESGVPSRFSGSGS GTDFTLTISSLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 49)
97	HC5; LC6_m7; hIgG1-LAGA YTE; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNW GQGTTVTVSS (SEQ ID NO: 7)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASQLESGVPSRFSGSGS GTDFTLTISSLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 50)
98	HC5; LC6_m8; hIgG1-LAGA	EVQLLESGGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASELESGVPSRFSGSGS

	YTE; Human kappa LC	LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNDW GQGTTVTVSS (SEQ ID NO: 7)	GTDFTLTISSLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 51)
99	HC5; LC6_m9; hIgG1-LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNDW GQGTTVTVSS (SEQ ID NO: 7)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISSLQPEDFATY YCQQNHEDPRTFGGGTK VEIK (SEQ ID NO: 52)
100	HC5; LC6_m10; hIgG1-LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNDW GQGTTVTVSS (SEQ ID NO: 7)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISSLQPEDFATY YCQQNYEDPRTFGGGTK VEIK (SEQ ID NO: 53)
101	HC5; LC6_m11; hIgG1-LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNDW GQGTTVTVSS (SEQ ID NO: 7)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISSLQPEDFATY YCQQNSEDPRTFGGGTK VEIK (SEQ ID NO: 54)

102	HC5; LC6_m12; hIgG1-LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNW GQGTTVTVSS (SEQ ID NO: 7)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNRDPRTFGGGTK VEIK (SEQ ID NO: 55)
103	HC5; LC6_m13; hIgG1-LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNW GQGTTVTVSS (SEQ ID NO: 7)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNDDPRTFGGGTK VEIK (SEQ ID NO: 56)
104	HC5; LC6_m14; hIgG1-LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNW GQGTTVTVSS (SEQ ID NO: 7)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNQDPRTFGGGTK VEIK (SEQ ID NO: 57)
105	HC5_m1; LC6; hIgG1- LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGYSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY

		CAGDGYYPYAMDNW GQGTTVTVSS (SEQ ID NO: 10)	YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
106	HC5_m2; LC6; hIgG1- LAGA YTE; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFSRLRAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNW GQGTTVTVSS (SEQ ID NO: 11)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
107	HC5_m3; LC6; hIgG1- LAGA YTE; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFSRLHAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNW GQGTTVTVSS (SEQ ID NO: 12)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
108	HC5_m4; LC6; hIgG1- LAGA YTE; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFSRLDAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNW GQGTTVTVSS (SEQ ID NO: 13)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
109	HC5_m5; LC6; hIgG1- LAGA YTE;	EVQLLESGGGLVQPGG SLRLSCAASGFSLYAY SVNWVRQAPGKGLEW	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY

	Human kappa LC	LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNDW GQGTTVTVSS (SEQ ID NO: 14)	LASNLESGVPSRFSGSGS GTDFTLTISSLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
110	HC5_m6; LC6; hIgG1- LAGA YTE; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFSLSAYS VNWVRQAPGKGLEWL GMIWGDGKIVYNSAL KSRLTISKDSSKNTVYL QMNSLRAEDTAVYYC AGDGYYPYAMDNDWG QGTTVTVSS (SEQ ID NO: 15)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISSLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
111	HC5_m7; LC6; hIgG1- LAGA YTE; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFSLNRY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNDW GQGTTVTVSS (SEQ ID NO: 16)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISSLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
112	HC5_m8; LC6; hIgG1- LAGA YTE; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFSLNKY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNDW GQGTTVTVSS (SEQ ID NO: 17)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISSLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)

113	HC5_m9; LC6; hIgG1- LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFSLNHY SVNWVRQAPGKGLEW LGMIWGDGKIVYN SA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMD NW GQGTTVTVSS (SEQ ID NO: 18)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
114	HC5_m10; LC6; hIgG1- LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFSLNQY SVNWVRQAPGKGLEW LGMIWGDGKIVYN SA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMD NW GQGTTVTVSS (SEQ ID NO: 19)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
115	HC5_m11; LC6; hIgG1- LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFSLNEYS VNWVRQAPGKGLEWL GMIWGDGKIVYNSAL KSRLTISKDSSKNTVYL QMNSLRAEDTAVYYC AGDGYYPYAMD NWG QGT TVTVSS (SEQ ID NO: 20)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
116	HC5_m12; LC6; hIgG1- LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFSLNSYS VNWVRQAPGKGLEWL GMIWGDGKIVYNSAL KSRLTISKDSSKNTVYL QMNSLRAEDTAVYYC	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY

		AGDGYYPYAMDNWG QGTTVTVSS (SEQ ID NO: 21)	YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
117	HC5_m13; LC6; hIgG1- LAGA YTE; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFSLNYY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNW QGTTVTVSS (SEQ ID NO: 22)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
118	HC5_m14; LC6; hIgG1- LAGA YTE; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFSLNAES VNWVRQAPGKGLEWL GMIWGDGKIVYNSAL KSRLTISKDSSKNTVYL QMNSLRAEDTAVYYC AGDGYYPYAMDNWG QGTTVTVSS (SEQ ID NO: 23)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
119	HC5_m15; LC6; hIgG1- LAGA YTE; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWSDGKIVYNSAL KSRLTISKDSSKNTVYL QMNSLRAEDTAVYYC AGDGYYPYAMDNWG QGTTVTVSS (SEQ ID NO: 24)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
120	HC5_m16; LC6; hIgG1- LAGA YTE;	EVQLLESGGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY

	Human kappa LC	LGMIWADGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNDW GQGTTVTVSS (SEQ ID NO: 25)	LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
121	HC5_m17; LC6; hIgG1- LAGA YTE; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGHGYYPYAMDNDW GQGTTVTVSS (SEQ ID NO: 26)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
122	HC5_m18; LC6; hIgG1- LAGA YTE; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDLYYPYAMDNDW GQGTTVTVSS (SEQ ID NO: 27)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
123	HC5_m19; LC6; hIgG1- LAGA YTE; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDKYYPYAMDNDW GQGTTVTVSS (SEQ ID NO: 28)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)

124	HC5_m20; LC6; hIgG1- LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYGYAMDNDW GQGTTVTVSS (SEQ ID NO: 29)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
125	HC5_m21; LC6; hIgG1- LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYAYAMDNDW GQGTTVTVSS (SEQ ID NO: 30)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
126	HC5_m22; LC6; hIgG1- LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYSYAMDNDW GQGTTVTVSS (SEQ ID NO: 31)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
127	HC5_m23; LC6; hIgG1- LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY

		CAGDGYTYAMD NW GQGT TVTVSS (SEQ ID NO: 32)	YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
128	Lebrikizumab – HC; Lebrikizumab – LC; hIgG4- YTE; Human kappa LC	QVTLRESGPALVKPTQ TLTLTCTVSGFSLAYS VNWIRQPPGKALEWL AMIWGDGKIVYNSAL KSRLTISKDTSKNQVV LTMTNMDPVDATYY CAGDGYTPYAMD NW GQGS LTVTVSS (SEQ ID NO: 470)	DIVMTQSPDSLVS SLGER ATINCRASKSVDSY GNSF MHWYQQKPGQP PKLLIY LASNLESGVPDR FSGSGS GTDFTLTISLQA EDVAV YYCQQNNEDPRT FGGGT KVEIK (SEQ ID NO: 471)
129	Lebrikizumab – HC; Lebrikizumab – LC; hIgG4- LS; Human kappa LC	QVTLRESGPALVKPTQ TLTLTCTVSGFSLAYS VNWIRQPPGKALEWL AMIWGDGKIVYNSAL KSRLTISKDTSKNQVV LTMTNMDPVDATYY CAGDGYTPYAMD NW GQGS LTVTVSS (SEQ ID NO: 470)	DIVMTQSPDSLVS SLGER ATINCRASKSVDSY GNSF MHWYQQKPGQP PKLLIY LASNLESGVPDR FSGSGS GTDFTLTISLQA EDVAV YYCQQNNEDPRT FGGGT KVEIK (SEQ ID NO: 471)
130	Lebrikizumab – HC; Lebrikizumab – LC; hIgG1- LALA-YTE; Human kappa LC	QVTLRESGPALVKPTQ TLTLTCTVSGFSLAYS VNWIRQPPGKALEWL AMIWGDGKIVYNSAL KSRLTISKDTSKNQVV LTMTNMDPVDATYY CAGDGYTPYAMD NW GQGS LTVTVSS (SEQ ID NO: 470)	DIVMTQSPDSLVS SLGER ATINCRASKSVDSY GNSF MHWYQQKPGQP PKLLIY LASNLESGVPDR FSGSGS GTDFTLTISLQA EDVAV YYCQQNNEDPRT FGGGT KVEIK (SEQ ID NO: 471)
131	Lebrikizumab – HC; Lebrikizumab	QVTLRESGPALVKPTQ TLTLTCTVSGFSLAYS VNWIRQPPGKALEWL	DIVMTQSPDSLVS SLGER ATINCRASKSVDSY GNSF MHWYQQKPGQP PKLLIY

	– LC; hIgG1-LALA-LS; Human kappa LC	AMIWGDGKIVYNSAL KSRLTISKDTSKNQVV LTMTNMDPVDATYY CAGDGYYPYAMDNDW GQGS LVTVSS (SEQ ID NO: 470)	LASNLESGVPDRFSGSGS GTDFTLTISSLQAEDVAV YYCQNNEDPRTFGGGT KVEIK (SEQ ID NO: 471)
132	HC5; LC6; hIgG1-LALA YTE; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNDW GQGTTVTVSS (SEQ ID NO: 7)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISSLQPEDFATY YCQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
133	HC1; LC6; hIgG1-LALA YTE; Human kappa LC	EVQLQESGPGLVKPSE TSLTCTVSGFSLNAYS VNWIRQPPGKGLEWL GMIWGDGKIVYNSAL KSRLTISKDSSKNQVSL KLSSVTAADTAVYYC AGDGYYPYAMDNDWG QGTTVTVSS (SEQ ID NO: 3)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISSLQPEDFATY YCQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
134	HC1; LC6; hIgG4-YTE; Human kappa LC	EVQLQESGPGLVKPSE TSLTCTVSGFSLNAYS VNWIRQPPGKGLEWL GMIWGDGKIVYNSAL KSRLTISKDSSKNQVSL KLSSVTAADTAVYYC AGDGYYPYAMDNDWG QGTTVTVSS (SEQ ID NO: 3)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISSLQPEDFATY YCQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)

135	HC1; LC6; hIgG4-LS; Human kappa LC	EVQLQESGPGLVKPSE TSLTCTVSGFSLNAYS VNWIRQPPGKGLEWL GMIWGDGKIVYNSAL KSRLTISKDSSKNQVSL KLSSVTAADTAVYYC AGDGYYPYAMDNDWG QGTTVTVSS (SEQ ID NO: 3)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
136	HC1; LC6; hIgG1-LALA LS; Human kappa LC	EVQLQESGPGLVKPSE TSLTCTVSGFSLNAYS VNWIRQPPGKGLEWL GMIWGDGKIVYNSAL KSRLTISKDSSKNQVSL KLSSVTAADTAVYYC AGDGYYPYAMDNDWG QGTTVTVSS (SEQ ID NO: 3)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
137	HC5; LC6_m8; hIgG1-LALA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNDW GQGTTVTVSS (SEQ ID NO: 7)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASELESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 51)
138	HC5; LC6_m8; hIgG4-YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASELESGVPSRFSGSGS GTDFTLTISLQPEDFATY

		CAGDGYYPYAMDNW GQGTTVTVSS (SEQ ID NO: 7)	YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 51)
139	HC5; LC6_m8; hIgG4-LS; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNW GQGTTVTVSS (SEQ ID NO: 7)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASELESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 51)
140	HC5; LC6_m8; hIgG1-LALA LS; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNW GQGTTVTVSS (SEQ ID NO: 7)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASELESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 51)
141	HC1; LC6_m8; hIgG1-LALA YTE; Human kappa LC	EVQLQESGPGLVKPSE TSLTCTVSGFSLNAYS VNWIRQPPGKGLEWL GMIWGDGKIVYNSAL KSRLTISKDSSKNQVSL KLSSVTAADTAVYYC AGDGYYPYAMDNWG QGTTVTVSS (SEQ ID NO: 3)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASELESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 51)
142	HC1; LC6_m8; hIgG4 YTE;	EVQLQESGPGLVKPSE TSLTCTVSGFSLNAYS VNWIRQPPGKGLEWL	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY

	Human kappa LC	GMIWGDGKIVYNSAL KSRLTISKDSSKNQVSL KLSSVTAADTAVYYC AGDGYYPYAMDNDWG QGTTVTVSS (SEQ ID NO: 3)	LASELESGVPSRFSGSGS GTDFTLTISSLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 51)
143	HC1; LC6_m8; hIgG4 LS; Human kappa LC	EVQLQESGPGLVKPSE TSLTCTVSGFSLNAYS VNWIRQPPGKGLEWL GMIWGDGKIVYNSAL KSRLTISKDSSKNQVSL KLSSVTAADTAVYYC AGDGYYPYAMDNDWG QGTTVTVSS (SEQ ID NO: 3)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASELESGVPSRFSGSGS GTDFTLTISSLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 51)
144	HC1; LC6_m8; hIgG1-LALA LS; Human kappa LC	EVQLQESGPGLVKPSE TSLTCTVSGFSLNAYS VNWIRQPPGKGLEWL GMIWGDGKIVYNSAL KSRLTISKDSSKNQVSL KLSSVTAADTAVYYC AGDGYYPYAMDNDWG QGTTVTVSS (SEQ ID NO: 3)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASELESGVPSRFSGSGS GTDFTLTISSLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 51)

*Names correspond with name in informal sequence listing

[00178] In some embodiments, a VH domain listed for any one of Constructs 3-127 and 132-144 in **Table 2** can be combined with a heavy chain constant (HC) domain provided herein. In certain embodiments, an IL-13 antibody comprises a VH domain selected from any one the VH domains of Constructs 3-127 and 132-144 in **Table 2** or a VH domain having at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity thereto, and a HC domain comprising a sequence selected from any one of SEQ ID NOs: 425-468, 484-539, and 610-709 or an HC domain having at least about 80%, 90%, 91%, 92%, 93%,

94%, 95%, 96%, 97%, 98% or 99% identity thereto. In some embodiments, a VH domain listed for any one of Constructs 3-127 and 132-144 in **Table 2** can be combined with a heavy chain constant (HC) domain provided herein. In certain embodiments, an IL-13 antibody comprises a VH domain selected from any one the VH domains of Constructs 3-127 and 132-144 in **Table 2** or a VH domain having at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity thereto, and a HC domain comprising a sequence selected from any one of SEQ ID NOs: 610, 615-641, and 654-709 or an HC domain having at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity thereto. Each and every combination of (1) VH/VL listed for Constructs 3-127 and 132-144 in **Table 2** and (2) HC domain is contemplated herein. In certain embodiments, the HC domain is an IgG1 HC domain.

[00179] In certain embodiments, the HC domain includes IgG4-SP, hIgG1-LALA-YTE, hIgG1-LAGA YTE, hIgG1-LALA-LS, IgG4-YTE HC, and IgG4-LS.

[00180] In some embodiments, such an IgG4-SP HC constant domain has the sequence:
ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ
SSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEFLG
GPSVFLFPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNAKTKPRE
EQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTL
LPDSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
RLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLSPG (SEQ ID NO: 427).

[00181] In some embodiments, such a hIgG1-LALA-YTE HC constant domain has the sequence:

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
QSSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP
EAAGGPSVFLFPPKPKDTLYITREPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAK
TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
SFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPG (SEQ ID NO: 439).

[00182] In some embodiments, such a hIgG1-LAGA YTE HC constant domain has the sequence:

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
QSSGLYSLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP
ELAGAPSVFLFPPKPKDTLYITREPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT

KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS
FFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG (SEQ ID NO: 440).

[00183] In some embodiments, such a hIgG1-LALA-LS HC constant domain has the sequence:

[00184] ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV
HTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT
CPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGV
EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVLHEALHSHYTQKSLSLSPG (SEQ ID
NO: 446).

[00185] In some embodiments, such an IgG4-YTE HC constant domain has the sequence:
ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ
SSGLYSLSSVTVPSSSLGTQTYTCNVDHKPSNTKVDKRVESKYGPPCPSCAPEFLG
GPSVFLFPPKPKDTLYITREPEVTCVVDVVSQEDPEVQFNWYVDGVEVHNAKTKPRE
EQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYT
LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
RLTVDKSRWQEGNVFCFSVMHEALHNHYTQKSLSLGLGK (SEQ ID NO: 457).

[00186] In some embodiments, such an IgG4-LS HC constant domain has the sequence:
ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ
SSGLYSLSSVTVPSSSLGTQTYTCNVDHKPSNTKVDKRVESKYGPPCPSCAPEFLG
GPSVFLFPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGVEVHNAKTKPRE
EQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYT
LPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
RLTVDKSRWQEGNVFCFSVLHEALHSHYTQKSLSLGLGK (SEQ ID NO: 460).

[00187] In some embodiments, such a hIgG1-LALA-YTE HC C-terminal lysine variant constant domain has the sequence:

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP
EAAGGPSVFLFPPKPKDTLYITREPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAK
TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG

SFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID NO: 624).

[00188] In some embodiments, such a hIgG1-LAGA YTE HC C-terminal lysine variant constant domain has the sequence:

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP
ELAGAPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGS
FFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID NO: 625).

[00189] In some embodiments, such a hIgG1-LALA-LS HC C-terminal lysine variant constant domain has the sequence:

[00190] ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV
HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT
CPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ
ID NO: 631).

[00191] In some embodiments, a VL domain listed for Constructs 3-127 and 132-144 in **Table 2** can be combined with a light chain constant (LC) domain provided herein. In some embodiments, the LC domain is a human kappa LC constant domain. In some embodiments, such a human kappa LC constant domain has the sequence:

RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVT
EQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID
NO: 469).

CDRs

[00192] In some embodiments, an antibody provided herein comprises one to three CDRs of a VH domain selected from SEQ ID NOs: 1-32, such as any of the CDRs listed in **Table 3**, **Table 4**, or **Table 5**, below. In some embodiments, an antibody provided herein comprises two to three CDRs of a VH domain selected from SEQ ID NOs: 1-32. In some embodiments, an antibody provided herein comprises three CDRs of a VH domain selected from SEQ ID NOs: 1-32. In some embodiments, the CDRs are Exemplary CDRs. In some embodiments,

the CDRs are Kabat CDRs. In some embodiments, the CDRs are Chothia CDRs. In some embodiments, the CDRs are IMGT CDRs. In some embodiments, the CDRs are AbM CDRs. In some embodiments, the CDRs are Contact CDRs.

[00193] In some embodiments, the CDRs are CDRs having at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identity with a CDR-H1, CDR-H2, or CDR-H3 of SEQ ID NOs: 58-140. In some embodiments, the CDR-H1 is a CDR-H1 of a VH domain selected from SEQ ID NOs: 1-32, with up to 1, 2, 3, 4, or 5 amino acid substitutions. In some embodiments, the CDR-H2 is a CDR-H2 of a VH domain of SEQ ID NO: 1-32, with up to 1, 2, 3, 4, 5, 6, 7, or 8 amino acid substitutions. In some embodiments, the CDR-H3 is a CDR-H3 of a VH domain selected from SEQ ID NOs: 1-32, with up to 1, 2, 3, 4, 5, 6, 7, or 8 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions. In some embodiments, the antibodies described in this paragraph are referred to herein as “variants.” In some embodiments, such variants are derived from a sequence provided herein, for example, by affinity maturation, site directed mutagenesis, random mutagenesis, or any other method known in the art or described herein. In some embodiments, such variants are not derived from a sequence provided herein and may, for example, be isolated de novo according to the methods provided herein for obtaining antibodies.

[00194] In some embodiments, an antibody provided herein comprises one to three CDRs of a VL domain of SEQ ID NOs: 33-57, such as any of the CDRs listed in **Table 6**, **Table 7**, or **Table 8**, below. In some embodiments, an antibody provided herein comprises two to three CDRs of a VL domain of SEQ ID NOs: 33-57. In some embodiments, an antibody provided herein comprises three CDRs of a VL domain of SEQ ID NOs: 33-57. In some embodiments, the CDRs are Exemplary CDRs. In some embodiments, the CDRs are Kabat CDRs. In some embodiments, the CDRs are Chothia CDRs. In some embodiments, the CDRs are IMGT CDRs. In some embodiments, the CDRs are AbM CDRs. In some embodiments, the CDRs are Contact CDRs.

[00195] In some embodiments, the CDRs are CDRs having at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identity with a CDR-L1, CDR-L2, or CDR-L3 of SEQ ID NOs: 141-188. In some embodiments, the CDR-L1 is a CDR-L1 of a VL domain of SEQ ID NOs: 33-57, with up to 1, 2, 3, 4, or 5 amino acid substitutions. In some embodiments, the CDR-L2 is a CDR-L2 of a VL domain of SEQ ID NOs: 33-57, with up to 1, 2, 3, 4, 5, 6, 7, or 8 amino acid substitutions. In some embodiments, the CDR-L3 is a CDR-

L3 of a VL domain of SEQ ID NOs: 33-57, with up to 1, 2, 3, 4, 5, 6, 7, or 8 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions. In some embodiments, the antibodies described in this paragraph are referred to herein as “variants.” In some embodiments, such variants are derived from a sequence provided herein, for example, by affinity maturation, site directed mutagenesis, random mutagenesis, or any other method known in the art or described herein. In some embodiments, such variants are not derived from a sequence provided herein and may, for example, be isolated de novo according to the methods provided herein for obtaining antibodies.

[00196] In some embodiments, an antibody provided herein comprises one to three CDRs of a VH domain selected from SEQ ID NOs: 1-32 and one to three CDRs of a VL domain of SEQ ID NOs: 33-57. In some embodiments, an antibody provided herein comprises two to three CDRs of a VH domain selected from SEQ ID NOs: 1-32 and two to three CDRs of a VL domain of SEQ ID NOs: 33-57. In some embodiments, an antibody provided herein comprises three CDRs of a VH domain selected from SEQ ID NOs: 1-32 and three CDRs of a VL domain of SEQ ID NOs: 33-57. In some embodiments, the CDRs are Exemplary CDRs. In some embodiments, the CDRs are Kabat CDRs. In some embodiments, the CDRs are Chothia CDRs. In some embodiments, the CDRs are IMGT CDRs. In some embodiments, the CDRs are AbM CDRs. In some embodiments, the CDRs are Contact CDRs.

[00197] In some embodiments, an antibody provided herein comprises a CDR-H3 selected of SEQ ID NOs: 112-120 and 130-40. In some embodiments, the CDR-H3 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-H3 of SEQ ID NOs: 112-120 or 130-40. In some embodiments, the CDR-H3 is a CDR-H3 selected of SEQ ID NOs: 112-120 and 130-40, with up to 1, 2, 3, 4, 5, 6, 7, or 8 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions. In some embodiments, the antibodies described in this paragraph are referred to herein as “variants.” In some embodiments, such variants are derived from a sequence provided herein, for example, by affinity maturation, site directed mutagenesis, random mutagenesis, or any other method known in the art or described herein. In some embodiments, such variants are not derived from a sequence provided herein and may, for example, be isolated de novo according to the methods provided herein for obtaining antibodies.

[00198] In some embodiments, an antibody provided herein comprises a CDR-H1 of SEQ ID NOs: 58-99 and 121. In some embodiments, the CDR-H1 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-H1 of SEQ ID NOs: 58-99 or 121. In some embodiments, the CDR-H1 is a CDR-H1 of SEQ ID NOs: 58-99 or 121, with up to 1, 2, 3, 4, 5, 6, 7, or 8 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions. In some embodiments, the antibodies described in this paragraph are referred to herein as “variants.” In some embodiments, such variants are derived from a sequence provided herein, for example, by affinity maturation, site directed mutagenesis, random mutagenesis, or any other method known in the art or described herein. In some embodiments, such variants are not derived from a sequence provided herein and may, for example, be isolated de novo according to the methods provided herein for obtaining antibodies.

[00199] In some embodiments, an antibody provided herein comprises a CDR-H2 of any one of SEQ ID NOs: 100-111. In some embodiments, the CDR-H2 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-H2 of any one of SEQ ID NOs: 100-111. In some embodiments, the CDR-H2 is a CDR-H2 of any one of SEQ ID NOs: 100-111, with up to 1, 2, 3, 4, 5, 6, 7, or 8 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions. In some embodiments, the antibodies described in this paragraph are referred to herein as “variants.” In some embodiments, such variants are derived from a sequence provided herein, for example, by affinity maturation, site directed mutagenesis, random mutagenesis, or any other method known in the art or described herein. In some embodiments, such variants are not derived from a sequence provided herein and may, for example, be isolated de novo according to the methods provided herein for obtaining antibodies.

[00200] In some embodiments, an antibody provided herein comprises a CDR-L3 selected from SEQ ID NOs: 165-172. In some embodiments, the CDR-L3 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-L3 of SEQ ID NOs: 165-172. In some embodiments, the CDR-L3 is a CDR-L3 of SEQ ID NOs: 165-172, with up to 1, 2, 3, 4, 5, 6, 7, or 8 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions. In some embodiments, the antibodies described in this paragraph are referred to herein as “variants.” In some embodiments, such variants are derived from a sequence provided herein, for example, by affinity maturation, site directed mutagenesis, random mutagenesis, or any other method

known in the art or described herein. In some embodiments, such variants are not derived from a sequence provided herein and may, for example, be isolated de novo according to the methods provided herein for obtaining antibodies.

[00201] In some embodiments, an antibody provided herein comprises a CDR-L2 selected from SEQ ID NOs: 153-158 and the amino acid sequence LAS. In some embodiments, the CDR-L2 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-L2 selected from SEQ ID NOs: 153-158 and the amino acid sequence LAS. In some embodiments, the CDR-L2 is a CDR-L2 selected from SEQ ID NOs: 153-158 and the amino acid sequence LAS, with up to 1, 2, 3, 4, 5, 6, 7, or 8 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions. In some embodiments, the antibodies described in this paragraph are referred to herein as “variants.” In some embodiments, such variants are derived from a sequence provided herein, for example, by affinity maturation, site directed mutagenesis, random mutagenesis, or any other method known in the art or described herein. In some embodiments, such variants are not derived from a sequence provided herein and may, for example, be isolated de novo according to the methods provided herein for obtaining antibodies.

[00202] In some embodiments, an antibody provided herein comprises a CDR-L1 selected from SEQ ID NOs: 141-144 and 149-152. In some embodiments, the CDR-L1 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-L1 selected from SEQ ID NOs: 141-144 and 149-152. In some embodiments, the CDR-L1 is a CDR-L1 selected from SEQ ID NOs: 141-144 and 149-152, with up to 1, 2, 3, 4, 5, 6, 7, or 8 amino acid substitutions. In some embodiments, the amino acid substitutions are conservative amino acid substitutions. In some embodiments, the antibodies described in this paragraph are referred to herein as “variants.” In some embodiments, such variants are derived from a sequence provided herein, for example, by affinity maturation, site directed mutagenesis, random mutagenesis, or any other method known in the art or described herein. In some embodiments, such variants are not derived from a sequence provided herein and may, for example, be isolated de novo according to the methods provided herein for obtaining antibodies.

[00203] In some embodiments, an antibody provided herein comprises a CDR-H3 selected from SEQ ID NOs: 112-120 and 130-140, a CDR-H2 of SEQ ID NOs: 100-111, a CDR-H1 selected from SEQ ID NOs: 58-99 and 121, a CDR-L3 selected from SEQ ID NOs: 165-172, a CDR-L2 selected from SEQ ID NOs: 153-158 and the amino acid sequence LAS, and a

CDR-L1 selected from SEQ ID NOs: 141-144 and 149-152. In some embodiments, the CDR-H3 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-H3 selected from SEQ ID NOs: 112-120 and 130-140, the CDR-H2 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-H2 of SEQ ID NOs: 100-111, the CDR-H1 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-H1 selected from SEQ ID NOs: 58-99 and 121, the CDR-L3 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-L3 selected from SEQ ID NOs: 165-172, the CDR-L2 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-L2 selected from SEQ ID NOs: 153-158 and the amino acid sequence LAS, and the CDR-L1 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-L1 selected from SEQ ID NOs: 141-144 and 149-152. In some embodiments, the CDR-H3 is a CDR-H3 selected from SEQ ID NOs: 112-120 and 130-140, with up to 1, 2, 3, 4, 5, 6, 7, or 8 amino acid substitutions; the CDR-H2 is a CDR-H2 of SEQ ID NOs: 100-111, with up to 1, 2, 3, 4, 5, 6, 7, or 8 amino acid substitutions; the CDR-H1 is a CDR-H1 selected from SEQ ID NOs: 58-99 and 121, with up to 1, 2, 3, 4, or 5 amino acid substitutions; the CDR-L3 is a CDR-L3 selected from SEQ ID NOs: 165-172, with up to 1, 2, 3, 4, or 5 amino acid substitutions; the CDR-L2 is a CDR-L2 selected from SEQ ID NOs: 153-158 and the amino acid sequence LAS, with up to 1, 2, 3, or 4 amino acid substitutions; and the CDR-L1 is a CDR-L1 selected from SEQ ID NOs: 141-144 and 149-152, with up to 1, 2, 3, 4, 5, or 6 amino acid substitutions.

[00204] In some embodiments, an antibody provided herein comprises a CDR-H3 of SEQ ID NOs: 112, 121, and 130, a CDR-H2 of SEQ ID NOs: 100, 104, and 108, a CDR-H1 of SEQ ID NOs: 58, 68, and 85, a CDR-L3 of SEQ ID NOs: 168, 173, and 181, a CDR-L2 of SEQ ID NOs: 153 and the amino acid sequence LAS, and a CDR-L1 of SEQ ID NOs: 141 and 149. In some embodiments, the CDR-H3 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-H3 of SEQ ID NOs: 112 or 130, the CDR-H2 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-H2 of SEQ ID NOs: 100, 104 or 108, the CDR-H1 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-H1 of SEQ ID NOs: 58, 68 or 85, the CDR-L3 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-L3 of SEQ ID NO: 168, the CDR-L2 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a

CDR-L2 of SEQ ID NOs: 153 or the amino acid sequence LAS, and the CDR-L1 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-L1 of SEQ ID NOs: 141 or 149. In some embodiments, the CDR-H3 is a CDR-H3 of SEQ ID NOs: 112 or 130, with up to 1, 2, 3, 4, 5, 6, 7, or 8 amino acid substitutions; the CDR-H2 is a CDR-H2 of SEQ ID NOs: 100, 104 or 108, with up to 1, 2, 3, 4, 5, 6, 7, or 8 amino acid substitutions; the CDR-H1 is a CDR-H1 of SEQ ID NOs: 58, 68 or 85, with up to 1, 2, 3, 4, or 5 amino acid substitutions; the CDR-L3 is a CDR-L3 of SEQ ID NO: 168 with up to 1, 2, 3, 4, or 5 amino acid substitutions; the CDR-L2 is a CDR-L2 of SEQ ID NOs: 153 or the amino acid sequence LAS, with up to 1, 2, 3, or 4 amino acid substitutions; and the CDR-L1 is a CDR-L1 of SEQ ID NOs: 141 or 149, with up to 1, 2, 3, 4, 5, or 6 amino acid substitutions.

[00205] In some embodiments, an antibody provided herein comprises a CDR-H3 of SEQ ID NOs: 112, 121 or 130, a CDR-H2 of SEQ ID NOs: 100, 104 or 108, a CDR-H1 of SEQ ID NOs: 58, 68, or 85, a CDR-L3 of SEQ ID NO: 165, a CDR-L2 of SEQ ID NOs: 153 or the amino acid sequence LAS, and a CDR-L1 of SEQ ID NOs: 141 or 149. In some embodiments, the CDR-H3 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-H3 of SEQ ID NOs: 112 or 130, the CDR-H2 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-H2 of SEQ ID NOs: 100, 104 or 108, the CDR-H1 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-H1 of SEQ ID NOs: 58, 68 or 85, the CDR-L3 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-L3 of SEQ ID NO: 165, the CDR-L2 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-L2 of SEQ ID NOs: 153 or the amino acid sequence LAS, and the CDR-L1 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-L1 of SEQ ID NOs: 141 or 149. In some embodiments, the CDR-H3 is a CDR-H3 of SEQ ID NOs: 112 or 130, with up to 1, 2, 3, 4, 5, 6, 7, or 8 amino acid substitutions; the CDR-H2 is a CDR-H2 of SEQ ID NOs: 100, 104 or 108, with up to 1, 2, 3, 4, 5, 6, 7, or 8 amino acid substitutions; the CDR-H1 is a CDR-H1 of SEQ ID NOs: 58, 68 or 85, with up to 1, 2, 3, 4, or 5 amino acid substitutions; the CDR-L3 is a CDR-L3 of SEQ ID NO: 165, with up to 1, 2, 3, 4, or 5 amino acid substitutions; the CDR-L2 is a CDR-L2 of SEQ ID NO: 153 or the amino acid sequence LAS, with up to 1, 2, 3, or 4 amino acid substitutions; and the CDR-L1 is a CDR-L1 of SEQ ID NOs: 141 or 149, with up to 1, 2, 3, 4, 5, or 6 amino acid substitutions.

[00206] In some embodiments, an antibody provided herein comprises a CDR-H3 of SEQ ID NOs: 112 or 130, a CDR-H2 of SEQ ID NOs: 100, 104, or 108, a CDR-H1 of SEQ ID NOs: 58, 68, or 85, a CDR-L3 of SEQ ID NO: 165, a CDR-L2 of SEQ ID NO: 158 or the amino acid sequence LAS, and a CDR-L1 of SEQ ID NOs: 141 or 149. In some embodiments, the CDR-H3 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-H3 of SEQ ID NOs: 112 or 130, the CDR-H2 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-H2 of SEQ ID NOs: 100, 104, or 108, the CDR-H1 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-H1 of SEQ ID NOs: 58, 68 or 85, the CDR-L3 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-L3 of SEQ ID NO: 165, the CDR-L2 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-L2 of SEQ ID NO: 158 or the amino acid sequence LAS, and the CDR-L1 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-L1 of SEQ ID NOs: 141 or 149. In some embodiments, the CDR-H3 is a CDR-H3 of SEQ ID NOs: 112 or 130, with up to 1, 2, 3, 4, 5, 6, 7, or 8 amino acid substitutions; the CDR-H2 is a CDR-H2 of SEQ ID NOs: 100, 104, or 108, with up to 1, 2, 3, 4, 5, 6, 7, or 8 amino acid substitutions; the CDR-H1 is a CDR-H1 of SEQ ID NOs: 58, 68, or 85, with up to 1, 2, 3, 4, or 5 amino acid substitutions; the CDR-L3 is a CDR-L3 of SEQ ID NO: 165, with up to 1, 2, 3, 4, or 5 amino acid substitutions; the CDR-L2 is a CDR-L2 of SEQ ID NO: 158 or the amino acid sequence LAS, with up to 1, 2, 3, or 4 amino acid substitutions; and the CDR-L1 is a CDR-L1 of SEQ ID NOs: 141 or 149, with up to 1, 2, 3, 4, 5, or 6 amino acid substitutions.

[00207] In some embodiments, an antibody provided herein comprises a CDR-H3 of SEQ ID NOs: 112, 121 or 130, a CDR-H2 of SEQ ID NOs: 100, 104 or 108, a CDR-H1 of SEQ ID NOs: 58, 67, or 84, a CDR-L3 of SEQ ID NO: 165, a CDR-L2 of SEQ ID NOs: 153 or the amino acid sequence LAS, and a CDR-L1 of SEQ ID NOs: 141 or 149. In some embodiments, the CDR-H3 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-H3 of SEQ ID NOs: 112 or 130, the CDR-H2 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-H2 of SEQ ID NOs: 100, 104 or 108, the CDR-H1 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-H1 of SEQ ID NOs: 58, 67 or 84, the CDR-L3 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-L3 of SEQ ID NO: 165, the CDR-L2 has at least about

80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-L2 of SEQ ID NOs: 153 or the amino acid sequence LAS, and the CDR-L1 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-L1 of SEQ ID NOs: 141 or 149. In some embodiments, the CDR-H3 is a CDR-H3 of SEQ ID NOs: 112 or 130, with up to 1, 2, 3, 4, 5, 6, 7, or 8 amino acid substitutions; the CDR-H2 is a CDR-H2 of SEQ ID NOs: 100, 104 or 108, with up to 1, 2, 3, 4, 5, 6, 7, or 8 amino acid substitutions; the CDR-H1 is a CDR-H1 of SEQ ID NOs: 58, 67 or 84, with up to 1, 2, 3, 4, or 5 amino acid substitutions; the CDR-L3 is a CDR-L3 of SEQ ID NO: 165, with up to 1, 2, 3, 4, or 5 amino acid substitutions; the CDR-L2 is a CDR-L2 of SEQ ID NO: 153 or the amino acid sequence LAS, with up to 1, 2, 3, or 4 amino acid substitutions; and the CDR-L1 is a CDR-L1 of SEQ ID NOs: 141 or 149, with up to 1, 2, 3, 4, 5, or 6 amino acid substitutions.

[00208] In some embodiments, an antibody provided herein comprises a CDR-H3 of SEQ ID NOs: 112 or 130, a CDR-H2 of SEQ ID NOs: 100, 104, or 108, a CDR-H1 of SEQ ID NOs: 58, 67, or 84, a CDR-L3 of SEQ ID NO: 165, a CDR-L2 of SEQ ID NO: 158 or the amino acid sequence LAS, and a CDR-L1 of SEQ ID NOs: 141 or 149. In some embodiments, the CDR-H3 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-H3 of SEQ ID NOs: 112 or 130, the CDR-H2 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-H2 of SEQ ID NOs: 100, 104, or 108, the CDR-H1 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-H1 of SEQ ID NOs: 58, 67 or 84, the CDR-L3 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-L3 of SEQ ID NO: 165, the CDR-L2 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-L2 of SEQ ID NO: 158 or the amino acid sequence LAS, and the CDR-L1 has at least about 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a CDR-L1 of SEQ ID NOs: 141 or 149. In some embodiments, the CDR-H3 is a CDR-H3 of SEQ ID NOs: 112 or 130, with up to 1, 2, 3, 4, 5, 6, 7, or 8 amino acid substitutions; the CDR-H2 is a CDR-H2 of SEQ ID NOs: 100, 104, or 108, with up to 1, 2, 3, 4, 5, 6, 7, or 8 amino acid substitutions; the CDR-H1 is a CDR-H1 of SEQ ID NOs: 58, 67, or 84, with up to 1, 2, 3, 4, or 5 amino acid substitutions; the CDR-L3 is a CDR-L3 of SEQ ID NO: 165, with up to 1, 2, 3, 4, or 5 amino acid substitutions; the CDR-L2 is a CDR-L2 of SEQ ID NO: 158 or the amino acid sequence LAS, with up to 1, 2, 3, or 4 amino acid substitutions; and the CDR-L1 is a CDR-L1 of SEQ ID NOs: 141 or 149, with up to 1, 2, 3, 4, 5, or 6 amino acid substitutions.

[00209] In some embodiments, the amino acid substitutions are conservative amino acid substitutions. In some embodiments, the antibodies described in this disclosure are referred to herein as “variants” or “clones”. In some embodiments, such variants or clones are derived from a sequence provided herein, for example, by affinity maturation, site directed mutagenesis, random mutagenesis, or any other method known in the art or described herein. In some embodiments, such variants or clones are not derived from a sequence provided herein and may, for example, be isolated *de novo* according to the methods provided herein for obtaining antibodies.

[00210] In certain aspects, the antibodies disclosed herein do not include antibodies disclosed in US Patent number 9,067,994.

Table 3. Anti-interleukin (IL)-13 antibody Heavy Chain Kabat CDRs

Construct ID	VH Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
1 (lebrikizu mab), 2, and 128- 131	Lebrikizumab - HC	QVTLR ESGPA LVKPT QTLTL TCTVS GFSLS	540	AYSVN	58	WIRQP PGKAL EWLA	255	MIWG DGKIV YNSAL KS	100	RLTISK DTSKN QVVLT MTNM DPVDT ATYYC AG	311	DGYYP YAMD N	112	WGQG SLVTV SS	368

Construct ID	VH Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
3	HC0	QVQLQ ESGPG LVAPS QSLST CTVSG FSLN	198	AYSVN	58	WVRQ PGKG LEWLG	256	MIWG DGKIV YNSAL KS	100	RLNIS KDSSK SQVFL KMSSL QSDDT ARYYC AG	312	DGYYP YAMD N	112	WGHG TSVTV SS	369
4	HC0_M	QVQLQ ESGPG LVAPS QSLST CTVSG FSLN	198	AYSVN	58	WVRQ PGKG LEWLG	256	MIWG DGKIV YNSAL KS	100	RLTISK DSSKS QVFLK MSSLQ SDDTA RYYCA G	313	DGYYP YAMD N	112	WGHG TSVTV SS	369
5, 10, 15, 20, 133- 136, and 141-144	HC1	EVQLQ ESGPG LVKPS ETLSL TCTVS GFSLN	200	AYSVN	58	WVRQ PGKGL EWLG	258	MIWG DGKIV YNSAL KS	100	RLTISK DSSKN QVSLK LSSVT AADTA VYYCA G	314	DGYYP YAMD N	112	WQQG TTVTV SS	371
6, 11, 16, and 21	HC2	EVQLV QSGAE VKKPG ASVKV SCKAS GFSLN	201	AYSVN	58	WVRQ APGQG LEWLG	259	MIWG DGKIV YNSAL KS	100	RLTITK DSSTS TVYME LSSLRS EDTAV YYCAG	315	DGYYP YAMD N	112	WQQG TTVTV SS	371

Construct ID	VH Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
7, 12, 17, and 22	HC3	EVQLV QSGAE VKKPG SSVKV SCKAS GFSLN	202	AYSVN	58	WVRQ APGQG LEWLG	259	MIWG DGKIV YNSAL KS	100	RLTIK DSSTS TVYME LSSLRS EDTAV YYCAG	315	DGYYP YAMD N	112	WGQG TTVTV SS	371
8, 13, 18, and 23	HC4	EVQLV ESGGG LVKPG GSLRL SCAAS GFSLN	203	AYSVN	58	WVRQ APGKG LEWLG	262	MIWG DGKIV YNSAL KS	100	RLTISK DSSKN TVYLQ MNSLK TEDTA VYYCA G	317	DGYYP YAMD N	112	WGQG TTVTV SS	371
9, 14, 19, 24, 90-104, 132, and 137-140	HC5	EVQLL ESGGG LVQPG GSLRL SCAAS GFSLN	204	AYSVN	58	WVRQ APGKG LEWLG	262	MIWG DGKIV YNSAL KS	100	RLTISK DSSKN TVYLQ MNSLR AEDTA VYYCA G	318	DGYYP YAMD N	112	WGQG TTVTV SS	371
25	HC6	EVQLQ ESGPG LVKPS ETLSL TCTVS GGSLN	205	AYSVN	58	WVRQ PPGKG LEWLG	256	MIWG DGKIV YNSAL KS	100	RLTISL DTSKS QVFLK MSSLT AADTA VYYCA R	319	DGYYP YAMD N	112	WGQG TTVTV SS	371

Construct ID	VH Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
26	HC7	QVQLQ ESGPG LVKPS ETLSL TCTVS GGSLN	206	AYSW N	541	WVRQ PGKG LEWLG	256	YIYGD GKTNY NPALK S	101	RLTISL DTSKS QVFLK MSSLT AADTA VYYCA R	319	DGYYP YYAM DV	113	WGQG TTVT SS	371
105	HC5_m1	EVQLL ESGGG LVQPG GSLRL SCAAS GYSLN	207	AYSVN	58	WVRQ APGKG LEWLG	262	MIWG DGKIV YNSAL KS	100	RLTISK DSSKN TVYLQ MNSLR AEDTA VYYCA G	318	DGYYP YAMD N	112	WGQG TTVT SS	371
106	HC5_m2	EVQLL ESGGG LVQPG GSLRL SCAAS GFSLR	208	AYSVN	58	WVRQ APGKG LEWLG	262	MIWG DGKIV YNSAL KS	100	RLTISK DSSKN TVYLQ MNSLR AEDTA VYYCA G	318	DGYYP YAMD N	112	WGQG TTVT SS	371
107	HC5_m3	EVQLL ESGGG LVQPG GSLRL SCAAS GFSLH	209	AYSVN	58	WVRQ APGKG LEWLG	262	MIWG DGKIV YNSAL KS	100	RLTISK DSSKN TVYLQ MNSLR AEDTA VYYCA G	318	DGYYP YAMD N	112	WGQG TTVT SS	371

Construct ID	VH Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
108	HC5_m4	EVQLL ESGGG LVQPG GSLRL SCAAS GFSLD	210	AYSVN	58	WVRQ APGKG LEWLG	262	MIWG DGKIV YNSAL KS	100	RLTISK DSSKN TVYLQ MNSLR AEDTA VYYCA G	318	DGYYP YAMD N	112	WGQG TTVTV SS	371
109	HC5_m5	EVQLL ESGGG LVQPG GSLRL SCAAS GFSLY	211	AYSVN	58	WVRQ APGKG LEWLG	262	MIWG DGKIV YNSAL KS	100	RLTISK DSSKN TVYLQ MNSLR AEDTA VYYCA G	318	DGYYP YAMD N	112	WGQG TTVTV SS	371
110	HC5_m6	EVQLL ESGGG LVQPG GSLRL SCAAS GFSLS	212	AYSVN	58	WVRQ APGKG LEWLG	262	MIWG DGKIV YNSAL KS	100	RLTISK DSSKN TVYLQ MNSLR AEDTA VYYCA G	318	DGYYP YAMD N	112	WGQG TTVTV SS	371
111	HC5_m7	EVQLL ESGGG LVQPG GSLRL SCAAS GFSLN	204	RYSVN	59	WVRQ APGKG LEWLG	262	MIWG DGKIV YNSAL KS	100	RLTISK DSSKN TVYLQ MNSLR AEDTA VYYCA G	318	DGYYP YAMD N	112	WGQG TTVTV SS	371

Construct ID	VH Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
112	HC5_m8	EVQLL ESGGG LVQPG GSLRL SCAAS GFSLN	204	KYSVN	60	WVRQ APGKG LEWLG	262	MIWG DGKIV YNSAL KS	100	RLTISK DSSKN TVYLQ MNSLR AEDTA VYYCA G	318	DGYYP YAMD N	112	WGQG TTVTV SS	371
113	HC5_m9	EVQLL ESGGG LVQPG GSLRL SCAAS GFSLN	204	HYSVN	61	WVRQ APGKG LEWLG	262	MIWG DGKIV YNSAL KS	100	RLTISK DSSKN TVYLQ MNSLR AEDTA VYYCA G	318	DGYYP YAMD N	112	WGQG TTVTV SS	371
114	HC5_m10	EVQLL ESGGG LVQPG GSLRL SCAAS GFSLN	204	QYSVN	62	WVRQ APGKG LEWLG	262	MIWG DGKIV YNSAL KS	100	RLTISK DSSKN TVYLQ MNSLR AEDTA VYYCA G	318	DGYYP YAMD N	112	WGQG TTVTV SS	371
115	HC5_m11	EVQLL ESGGG LVQPG GSLRL SCAAS GFSLN	204	EYSVN	63	WVRQ APGKG LEWLG	262	MIWG DGKIV YNSAL KS	100	RLTISK DSSKN TVYLQ MNSLR AEDTA VYYCA G	318	DGYYP YAMD N	112	WGQG TTVTV SS	371

Construct ID	VH Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
116	HC5_m12	EVQLL ESGGG LVQPG GSLRL SCAAS GFSLN	204	SYSVN	64	WVRQ APGKG LEWLG	262	MIWG DGKIV YNSAL KS	100	RLTISK DSSKN TVYLQ MNSLR AEDTA VYYCA G	318	DGYYP YAMD N	112	WGQG TTVTV SS	371
117	HC5_m13	EVQLL ESGGG LVQPG GSLRL SCAAS GFSLN	204	YYSVN	65	WVRQ APGKG LEWLG	262	MIWG DGKIV YNSAL KS	100	RLTISK DSSKN TVYLQ MNSLR AEDTA VYYCA G	318	DGYYP YAMD N	112	WGQG TTVTV SS	371
118	HC5_m14	EVQLL ESGGG LVQPG GSLRL SCAAS GFSLN	204	AESVN	66	WVRQ APGKG LEWLG	262	MIWG DGKIV YNSAL KS	100	RLTISK DSSKN TVYLQ MNSLR AEDTA VYYCA G	318	DGYYP YAMD N	112	WGQG TTVTV SS	371
119	HC5_m15	EVQLL ESGGG LVQPG GSLRL SCAAS GFSLN	204	AYSVN	58	WVRQ APGKG LEWLG	262	MIWSD GKIVY NSALK S	102	RLTISK DSSKN TVYLQ MNSLR AEDTA VYYCA G	318	DGYYP YAMD N	112	WGQG TTVTV SS	371

Construct ID	VH Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
120	HC5_m16	EVQLL ESGGG LVQPG GSLRL SCAAS GFSLN	204	AYSVN	58	WVRQ APGKG LEWLG	262	MIWA DGKIV YNSAL KS	103	RLTISK DSSKN TVYLQ MNSLR AEDTA VYYCA G	318	DGYYP YAMD N	112	WGQG TTVTV SS	371
121	HC5_m17	EVQLL ESGGG LVQPG GSLRL SCAAS GFSLN	204	AYSVN	58	WVRQ APGKG LEWLG	262	MIWG DGKIV YNSAL KS	100	RLTISK DSSKN TVYLQ MNSLR AEDTA VYYCA G	318	HGYYP YAMD N	114	WGQG TTVTV SS	371
122	HC5_m18	EVQLL ESGGG LVQPG GSLRL SCAAS GFSLN	204	AYSVN	58	WVRQ APGKG LEWLG	262	MIWG DGKIV YNSAL KS	100	RLTISK DSSKN TVYLQ MNSLR AEDTA VYYCA G	318	DLYYP YAMD N	115	WGQG TTVTV SS	371
123	HC5_m19	EVQLL ESGGG LVQPG GSLRL SCAAS GFSLN	204	AYSVN	58	WVRQ APGKG LEWLG	262	MIWG DGKIV YNSAL KS	100	RLTISK DSSKN TVYLQ MNSLR AEDTA VYYCA G	318	DKYYP YAMD N	116	WGQG TTVTV SS	371

Construct ID	VH Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
124	HC5_m20	EVQLL ESGGG LVQPG GSLRL SCAAS GFSLN	204	AYSVN	58	WVRQ APGKG LEWLG	262	MIWG DGKIV YNSAL KS	100	RLTISK DSSKN TVYLQ MNSLR AEDTA VYYCA G	318	DGYG GYAM DN	117	WGQG TTVT SS	371
125	HC5_m21	EVQLL ESGGG LVQPG GSLRL SCAAS GFSLN	204	AYSVN	58	WVRQ APGKG LEWLG	262	MIWG DGKIV YNSAL KS	100	RLTISK DSSKN TVYLQ MNSLR AEDTA VYYCA G	318	DGYG AYAM DN	118	WGQG TTVT SS	371
126	HC5_m22	EVQLL ESGGG LVQPG GSLRL SCAAS GFSLN	204	AYSVN	58	WVRQ APGKG LEWLG	262	MIWG DGKIV YNSAL KS	100	RLTISK DSSKN TVYLQ MNSLR AEDTA VYYCA G	318	DGYYS YAMD N	119	WGQG TTVT SS	371
127	HC5_m24	EVQLL ESGGG LVQPG GSLRL SCAAS GFSLN	204	AYSVN	58	WVRQ APGKG LEWLG	262	MIWG DGKIV YNSAL KS	100	RLTISK DSSKN TVYLQ MNSLR AEDTA VYYCA G	318	DGYYT YAMD N	120	WGQG TTVT SS	371

*Names correspond with name in informal sequence listing.

Table 4. Anti-interleukin (IL)-13 antibody Heavy Chain Chothia CDRs

Construct ID	VH Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
1 (lebrizumab), 2, and 128-131	Lebrizumab-HC	QVTLR ESGPA LVKPT QTLTL TCTVS	542	GFSL AY	67	SVNWI RQPPG KALE WLAMI	550	WGDG K	104	IVYNS ALKSR LTISKD TSKNQ VVLTM TNMDP VDTAT YYCAG	556	DGYYP YAMD N	112	WGQG SLVTV SS	368
3	HC0	QVQLQ ESGPG LVAPS QSLST CTVS	543	GFSLN AY	68	SVNW VRQPP GKGLE WLGMI	551	WGDG K	104	IVYNS ALKSR LNISK DSSKS QVFLK MSSLQ SDDTA RYYCA G	557	DGYYP YAMD N	112	WGHG TSVTV SS	369

Construct ID	VH Name*	FR1	SEQ ID NO: 543	CDR1	SEQ ID NO: 68	FR2	SEQ ID NO: 551	CDR2	SEQ ID NO: 104	FR3	SEQ ID NO: 558	CDR3	SEQ ID NO: 112	FR4	SEQ ID NO: 369
4	HC0_M	QVQLQ ESGPG LVAPS QSLTIT CTVS		GFSLN AY		SVNW VRQPP GKGLE WLGMI		WGDG K		IVYNS ALKSR LTISKD SSKSQ VFLKM SSLQS DDTAR YYCAG		DGYYP YAMD N		WGHG TSVTV SS	
5, 10, 15, 20, 133- 136, and 141-144	HC1	EVQLQ ESGPG LVKPS ETLSL TCTVS	544	GFSLN AY	68	SVNWI RQPPG KGLE WLGMI	552	WGDG K	104	IVYNS ALKSR LTISKD SSKNQ VSLKL SSVTA ADTAV YYCAG	559	DGYYP YAMD N	112	WGQG TTVTV SS	371
6, 11, 16, and 21	HC2	EVQLV QSGAE VKKPG ASVKV SCKAS	545	GFSLN AY	68	SVNW VRQAP GQGLE WLGMI	553	WGDG K	104	IVYNS ALKSR LTITK DSSTS TVYME LSSLRS EDTAV YYCAG	560	DGYYP YAMD N	112	WGQG TTVTV SS	371

Construct ID	VH Name*	FR1	SEQ ID NO: 546	CDR1	SEQ ID NO: 68	FR2	SEQ ID NO: 553	CDR2	SEQ ID NO: 104	FR3	SEQ ID NO: 560	CDR3	SEQ ID NO: 112	FR4	SEQ ID NO: 371
7, 12, 17, and 22	HC3	EVQLV QSGAE VKKPG SSVKV SCKAS		GFSLN AY		SVNW VRQAP GQGLE WLGMI		WGDG K		IVYNS ALKSR LTITK DSSTS TVYME LSSLRS EDTAV YYCAG		DGYYP YAMD N		WGQG TTVTV SS	371
8, 13, 18, and 23	HC4	EVQLV ESGGG LVKPG GSLRL SCAAS	547	GFSLN AY	68	SVNW VRQAP GQGLE WLGMI	554	WGDG K	104	IVYNS ALKSR LTISKD SSKNT VYLQ MNSLK TEDTA VYYCA G	561	DGYYP YAMD N	112	WGQG TTVTV SS	371
9, 14, 19, 24, 90-104, 132, and 137-140	HC5	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN AY	68	SVNW VRQAP GQGLE WLGMI	554	WGDG K	104	IVYNS ALKSR LTISKD SSKNT VYLQ MNSLR AEDTA VYYCA G	562	DGYYP YAMD N	112	WGQG TTVTV SS	371

Construct ID	VH Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
25	HC6	EVQLQ ESGPG LVKPS ETLSL TCTVS	544	GGSLN AY	69	SVNW VRQPP GKGLE WLGMI	551	WGDG K	104	IVYNS ALKSR LTISLD TSKSQ VFLKM SSLTA ADTAV YYCAR	563	DGYYP YAMD N	112	WGQG TTVT SS	371
26	HC7	QVQLQ ESGPG LVKPS ETLSL TCTVS	549	GGSLN AY	69	SVNW VRQPP GKGLE WLGMI	555	YGDG K	105	TNYNP ALKSR LTISLD TSKSQ VFLKM SSLTA ADTAV YYCAR	564	DGYYP YYAM DV	113	WGQG TTVT SS	371
105	HC5_m1	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GYSLN AY	71	SVNW VRQAP GKGLE WLGMI	554	WGDG K	104	IVYNS ALKSR LTISKD SSKNT VYLQ MNSLR AEDTA VYYCA G	562	DGYYP YAMD N	112	WGQG TTVT SS	371

Construct ID	VH Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
106	HC5_m2	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLR AY	72	SVNW VRQAP GKGLE WLGMI	554	WGDG K	104	IVYNS ALKSR LTISKD SSKNT VYLQ MNSLR AEDTA VYYCA G	562	DGYYP YAMD N	112	WGQG TTVTV SS	371
107	HC5_m3	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLR AY	73	SVNW VRQAP GKGLE WLGMI	554	WGDG K	104	IVYNS ALKSR LTISKD SSKNT VYLQ MNSLR AEDTA VYYCA G	562	DGYYP YAMD N	112	WGQG TTVTV SS	371
108	HC5_m4	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLD AY	74	SVNW VRQAP GKGLE WLGMI	554	WGDG K	104	IVYNS ALKSR LTISKD SSKNT VYLQ MNSLR AEDTA VYYCA G	562	DGYYP YAMD N	112	WGQG TTVTV SS	371

Construct ID	VH Name*	FR1	SEQ ID NO: 548	CDR1	SEQ ID NO: 75	FR2	SEQ ID NO: 554	CDR2	SEQ ID NO: 104	FR3	SEQ ID NO: 562	CDR3	SEQ ID NO: 112	FR4	SEQ ID NO: 371
109	HC5_m5	EVQLL ESGGG LVQPG GSLRL SCAAS		GFSLY AY		SVNW VRQAP GKGLE WLGMI		WGDG K		IVYNS ALKSR LTISKD SSKNT VYLQ MNSLR AEDTA VYYCA G		DGYYP YAMD N		WGQG TTVTV SS	
110	HC5_m6	EVQLL ESGGG LVQPG GSLRL SCAAS		GFSLS AY		SVNW VRQAP GKGLE WLGMI		WGDG K		IVYNS ALKSR LTISKD SSKNT VYLQ MNSLR AEDTA VYYCA G		DGYYP YAMD N		WGQG TTVTV SS	
111	HC5_m7	EVQLL ESGGG LVQPG GSLRL SCAAS		GFSLN RY		SVNW VRQAP GKGLE WLGMI		WGDG K		IVYNS ALKSR LTISKD SSKNT VYLQ MNSLR AEDTA VYYCA G		DGYYP YAMD N		WGQG TTVTV SS	

Construct ID	VH Name*	FR1	SEQ ID NO: 548	CDR1	SEQ ID NO: 77	FR2	SEQ ID NO: 554	CDR2	SEQ ID NO: 104	FR3	SEQ ID NO: 562	CDR3	SEQ ID NO: 112	FR4	SEQ ID NO: 371
112	HC5_m8	EVQLL ESGGG LVQPG GSLRL SCAAS		GFSLN KY		SVNW VRQAP GKGLE WLGMI		WGDG K		IVYNS ALKSR LTISKD SSKNT VYLQ MNSLR AEDTA VYYCA G		DGYYP YAMD N		WGQG TTVTV SS	
113	HC5_m9	EVQLL ESGGG LVQPG GSLRL SCAAS		GFSLN HY	78	SVNW VRQAP GKGLE WLGMI		WGDG K		IVYNS ALKSR LTISKD SSKNT VYLQ MNSLR AEDTA VYYCA G		DGYYP YAMD N		WGQG TTVTV SS	
114	HC5_m10	EVQLL ESGGG LVQPG GSLRL SCAAS		GFSLN QY	79	SVNW VRQAP GKGLE WLGMI		WGDG K		IVYNS ALKSR LTISKD SSKNT VYLQ MNSLR AEDTA VYYCA G		DGYYP YAMD N		WGQG TTVTV SS	

Construct ID	VH Name*	FR1	SEQ ID NO: 548	CDR1	SEQ ID NO: 80	FR2	SEQ ID NO: 554	CDR2	SEQ ID NO: 104	FR3	SEQ ID NO: 562	CDR3	SEQ ID NO: 112	FR4	SEQ ID NO: 371
115	HC5_m11	EVQLL ESGGG LVQPG GSLRL SCAAS		GFSLN EY		SVNW VRQAP GKGLE WLGMI		WGDG K		IVYNS ALKSR LTISKD SSKNT VYLQ MNSLR AEDTA VYYCA G		DGYYP YAMD N		WGQG TTVTV SS	
116	HC5_m12	EVQLL ESGGG LVQPG GSLRL SCAAS		GFSLN SY		SVNW VRQAP GKGLE WLGMI		WGDG K		IVYNS ALKSR LTISKD SSKNT VYLQ MNSLR AEDTA VYYCA G		DGYYP YAMD N		WGQG TTVTV SS	
117	HC5_m13	EVQLL ESGGG LVQPG GSLRL SCAAS		GFSLN YY		SVNW VRQAP GKGLE WLGMI		WGDG K		IVYNS ALKSR LTISKD SSKNT VYLQ MNSLR AEDTA VYYCA G		DGYYP YAMD N		WGQG TTVTV SS	

Construct ID	VH Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
118	HC5_m14	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN AE	83	SVNW VRQAP GKGLE WLGMI	554	WGDG K	104	IVYNS ALKSR LTISKD SSKNT VYLQ MNSLR AEDTA VYYCA G	562	DGYYP YAMD N	112	WGQG TTVTV SS	371
119	HC5_m15	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN AY	68	SVNW VRQAP GKGLE WLGMI	554	WSDG K	106	IVYNS ALKSR LTISKD SSKNT VYLQ MNSLR AEDTA VYYCA G	562	DGYYP YAMD N	112	WGQG TTVTV SS	371
120	HC5_m16	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN AY	68	SVNW VRQAP GKGLE WLGMI	554	WADG K	107	IVYNS ALKSR LTISKD SSKNT VYLQ MNSLR AEDTA VYYCA G	562	DGYYP YAMD N	112	WGQG TTVTV SS	371

Construct ID	VH Name*	FR1	SEQ ID NO: 548	CDR1	SEQ ID NO: 68	FR2	SEQ ID NO: 554	CDR2	SEQ ID NO: 104	FR3	SEQ ID NO: 562	CDR3	SEQ ID NO: 114	FR4	SEQ ID NO: 371
121	HC5_m17	EVQLL ESGGG LVQPG GSLRL SCAAS		GFSLN AY		SVNW VRQAP GKGLE WLGMI		WGDG K		IVYNS ALKSR LTISKD SSKNT VYLQ MNSLR AEDTA VYYCA G		HGYYP YAMD N		WGQG TTVTV SS	
122	HC5_m18	EVQLL ESGGG LVQPG GSLRL SCAAS		GFSLN AY		SVNW VRQAP GKGLE WLGMI		WGDG K		IVYNS ALKSR LTISKD SSKNT VYLQ MNSLR AEDTA VYYCA G		DLYYP YAMD N		WGQG TTVTV SS	
123	HC5_m19	EVQLL ESGGG LVQPG GSLRL SCAAS		GFSLN AY		SVNW VRQAP GKGLE WLGMI		WGDG K		IVYNS ALKSR LTISKD SSKNT VYLQ MNSLR AEDTA VYYCA G		DKYYP YAMD N		WGQG TTVTV SS	

Construct ID	VH Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
124	HC5_m20	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN AY	68	SVNW VRQAP GKGLE WLGMI	554	WGDG K	104	IVYNS ALKSR LTISKD SSKNT VYLQ MNSLR AEDTA VYYCA G	562	DGY Y GYAM DN	117	WGQG TTVTV SS	371
125	HC5_m21	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN AY	68	SVNW VRQAP GKGLE WLGMI	554	WGDG K	104	IVYNS ALKSR LTISKD SSKNT VYLQ MNSLR AEDTA VYYCA G	562	DGY Y AYAM DN	118	WGQG TTVTV SS	371
126	HC5_m22	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN AY	68	SVNW VRQAP GKGLE WLGMI	554	WGDG K	104	IVYNS ALKSR LTISKD SSKNT VYLQ MNSLR AEDTA VYYCA G	562	DGYYS YAMD N	119	WGQG TTVTV SS	371

Construct ID	VH Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
127	HC5_m24	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN AY	68	SVNW VRQAP GKGLE WLGMI	554	WGDG K	104	IVYNS ALKSR LTISKD SSKNT VYLQ MNSLR AEDTA VYYCA G	562	DGYYT YAMD N	120	WGQG TTVT SS	371

*Names correspond with name in informal sequence listing.

Table 5. Anti-interleukin (IL)-13 antibody Heavy Chain IMGT CDRs

Construct ID	VH Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
1 (lebrikizumab), 2, and 128-131	Lebrikizumab - HC	QVTLR ESGPA LVKPT QTLTL TCTVS	542	GFSLS AYS	84	VNWIR QPPGK ALEWL AM	566	IWGDG KI	108	VYNSA LKSRL TISKDT SKNQV VLMT NMDP VDTAT YYC	572	AGDG YYPYA MDN	130	WGQG SLVT SS	368

Construct ID	VH Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
3	HC0	QVQLQ ESGPG LVAPS QSLTIT CTVS	543	GFSLN AYS	85	VNWV RQPPG KGLE WLGGM	567	IWGDG KI	108	VYNSA LKSRL NISKD SSKSQ VFLKM SSLQS DDTAR YYC	573	AGDG YYPYA MDN	130	WGHG TSVTV SS	369
4	HC0_M	QVQLQ ESGPG LVAPS QSLTIT CTVS	543	GFSLN AYS	85	VNWV RQPPG KGLE WLGGM	567	IWGDG KI	108	VYNSA LKSRL TISKDS SKSQV FLKMS SLQSD DTARY YC	574	AGDG YYPYA MDN	130	WGHG TSVTV SS	369
5, 10, 15, 20, and 133-136	HC1	EVQLQ ESGPG LVKPS ETLSL TCTVS	544	GFSLN AYS	85	VNWIR QPPGK GLEWL GM	568	IWGDG KI	108	VYNSA LKSRL TISKDS SKNQV SLKLS SVTAA DTAVY YC	575	AGDG YYPYA MDN	130	WQGG TTVTV SS	371

Construct ID	VH Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
6, 11, 16, and 21	HC2	EVQLV QSGAE VKKPG ASVKV SCKAS	545	GFSLN AYS	85	VNWV RQAPG QGLE WLGMI	569	IWGDG KI	108	VYNSA LKSRL TITKDS STSTV YMELS SLRSE DTAVY YC	576	AGDG YYPYA MDN	130	WGQG TTVTV SS	371
7, 12, 17, and 22	HC3	EVQLV QSGAE VKKPG SSVKV SCKAS	546	GFSLN AYS	85	VNWV RQAPG QGLE WLGMI	569	IWGDG KI	108	VYNSA LKSRL TITKDS STSTV YMELS SLRSE DTAVY YC	576	AGDG YYPYA MDN	130	WGQG TTVTV SS	371
8, 13, 18, and 23	HC4	EVQLV ESGGG LVKPG GSLRL SCAAS	547	GFSLN AYS	85	VNWV RQAPG KGLE WLGMI	570	IWGDG KI	108	VYNSA LKSRL TISKDS SKNTV YLQM NSLKT EDTAV YYC	577	AGDG YYPYA MDN	130	WGQG TTVTV SS	371

Construct ID	VH Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
9, 14, 19, 24, 90-104, 132, and 137-140	HC5	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN AYS	85	VNWV RQAPG KGLE WLGGM	570	IWGDG KI	108	VNSA LKSRL TISKDS SKNTV YLQM NSLRA EDTAV YYC	578	AGDG YYPYA MDN	130	WGQG TTVTV SS	371
25	HC6	EVQLQ ESGPG LVKPS ETLSL TCTVS	544	GGSLN AYS	86	VNWV RQPPG KGLE WLGGM	567	IWGDG KI	108	VNSA LKSRL TISLDT SKSQV FLKMS SLTAA DTAVY YC	579	ARDGY YPYA MDN	131	WGQG TTVTV SS	371
26	HC7	QVQLQ ESGPG LVKPS ETLSL TCTVS	549	GGSLN AYS	86	WNWV RQPPG KGLE WLGY	571	IYGDG KT	109	NYNPA LKSRL TISLDT SKSQV FLKMS SLTAA DTAVY YC	580	ARDGY YYPYA MDV	132	WGQG TTVTV SS	371

Construct ID	VH Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
105	HC5_m1	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GYSLN AYS	87	VNWV RQAPG KGLE WLGGM	570	IWGDG KI	108	VYNSA LKSRL TISKDS SKNTV YLQM NSLRA EDTAV YYC	578	AGDG YYPYA MDN	130	WGQG TTVTV SS	371
106	HC5_m2	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLR AYS	88	VNWV RQAPG KGLE WLGGM	570	IWGDG KI	108	VYNSA LKSRL TISKDS SKNTV YLQM NSLRA EDTAV YYC	578	AGDG YYPYA MDN	130	WGQG TTVTV SS	371
107	HC5_m3	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLH AYS	89	VNWV RQAPG KGLE WLGGM	570	IWGDG KI	108	VYNSA LKSRL TISKDS SKNTV YLQM NSLRA EDTAV YYC	578	AGDG YYPYA MDN	130	WGQG TTVTV SS	371

Construct ID	VH Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
108	HC5_m4	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLD AYS	90	VNWV RQAPG KGLE WLGGM	570	IWGDG KI	108	VYNSA LKSRL TISKDS SKNTV YLQM NSLRA EDTAV YYC	578	AGDG YYPYA MDN	130	WGQG TTVTV SS	371
109	HC5_m5	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLY AYS	91	VNWV RQAPG KGLE WLGGM	570	IWGDG KI	108	VYNSA LKSRL TISKDS SKNTV YLQM NSLRA EDTAV YYC	578	AGDG YYPYA MDN	130	WGQG TTVTV SS	371
110	HC5_m6	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLS AYS	84	VNWV RQAPG KGLE WLGGM	570	IWGDG KI	108	VYNSA LKSRL TISKDS SKNTV YLQM NSLRA EDTAV YYC	578	AGDG YYPYA MDN	130	WGQG TTVTV SS	371

Construct ID	VH Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
111	HC5_m7	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN RYS	93	VNWV RQAPG KGLE WLGGM	570	IWGDG KI	108	VYNSA LKSRL TISKDS SKNTV YLQM NSLRA EDTAV YYC	578	AGDG YYPYA MDN	130	WGQG TTVTV SS	371
112	HC5_m8	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN KYS	94	VNWV RQAPG KGLE WLGGM	570	IWGDG KI	108	VYNSA LKSRL TISKDS SKNTV YLQM NSLRA EDTAV YYC	578	AGDG YYPYA MDN	130	WGQG TTVTV SS	371
113	HC5_m9	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN HYS	95	VNWV RQAPG KGLE WLGGM	570	IWGDG KI	108	VYNSA LKSRL TISKDS SKNTV YLQM NSLRA EDTAV YYC	578	AGDG YYPYA MDN	130	WGQG TTVTV SS	371

Construct ID	VH Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
114	HC5_m10	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN QYS	96	VNWV RQAPG KGLE WLGGM	570	IWGDG KI	108	VYNSA LKSRL TISKDS SKNTV YLQM NSLRA EDTAV YYC	578	AGDG YYPYA MDN	130	WGQG TTVTV SS	371
115	HC5_m11	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN EYS	97	VNWV RQAPG KGLE WLGGM	570	IWGDG KI	108	VYNSA LKSRL TISKDS SKNTV YLQM NSLRA EDTAV YYC	578	AGDG YYPYA MDN	130	WGQG TTVTV SS	371
116	HC5_m12	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN SYS	565	VNWV RQAPG KGLE WLGGM	570	IWGDG KI	108	VYNSA LKSRL TISKDS SKNTV YLQM NSLRA EDTAV YYC	578	AGDG YYPYA MDN	130	WGQG TTVTV SS	371

Construct ID	VH Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
117	HC5_m13	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN YYS	98	VNWV RQAPG KGLE WLGGM	570	IWGDG KI	108	VYNSA LKSRL TISKDS SKNTV YLQM NSLRA EDTAV YYC	578	AGDG YYPYA MDN	130	WGQG TTVTV SS	371
118	HC5_m14	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN AES	99	VNWV RQAPG KGLE WLGGM	570	IWGDG KI	108	VYNSA LKSRL TISKDS SKNTV YLQM NSLRA EDTAV YYC	578	AGDG YYPYA MDN	130	WGQG TTVTV SS	371
119	HC5_m15	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN AYS	85	VNWV RQAPG KGLE WLGGM	570	IWSDG KI	110	VYNSA LKSRL TISKDS SKNTV YLQM NSLRA EDTAV YYC	578	AGDG YYPYA MDN	130	WGQG TTVTV SS	371

Construct ID	VH Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
120	HC5_m16	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN AYS	85	VNWV RQAPG KGLE WLGGM	570	IWADG KI	111	VYNSA LKSRL TISKDS SKNTV YLQM NSLRA EDTAV YYC	578	AGDG YYPYA MDN	130	WGQG TTVTV SS	371
121	HC5_m17	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN AYS	85	VNWV RQAPG KGLE WLGGM	570	IWGDG KI	108	VYNSA LKSRL TISKDS SKNTV YLQM NSLRA EDTAV YYC	578	AGHG YYPYA MDN	133	WGQG TTVTV SS	371
122	HC5_m18	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN AYS	85	VNWV RQAPG KGLE WLGGM	570	IWGDG KI	108	VYNSA LKSRL TISKDS SKNTV YLQM NSLRA EDTAV YYC	578	AGDLY YPYA MDN	134	WGQG TTVTV SS	371

Construct ID	VH Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
123	HC5_m19	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN AYS	85	VNWV RQAPG KGLE WLGGM	570	IWGDG KI	108	VYNSA LKSRL TISKDS SKNTV YLQM NSLRA EDTAV YYC	578	AGDK YYPYA MDN	135	WGQG TTVT SS	371
124	HC5_m20	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN AYS	85	VNWV RQAPG KGLE WLGGM	570	IWGDG KI	108	VYNSA LKSRL TISKDS SKNTV YLQM NSLRA EDTAV YYC	578	AGDG YYGY AMDN	136	WGQG TTVT SS	371
125	HC5_m21	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN AYS	85	VNWV RQAPG KGLE WLGGM	570	IWGDG KI	108	VYNSA LKSRL TISKDS SKNTV YLQM NSLRA EDTAV YYC	578	AGDG YYAY AMDN	137	WGQG TTVT SS	371

Construct ID	VH Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
126	HC5_m22	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN AYS	85	VNWV RQAPG KGLE WLGGM	570	IWGDG KI	108	VYNSA LKSRL TISKDS SKNTV YLQM NSLRA EDTAV YYC	578	AGDG YYTYA MDN	138	WGQG TTVTV SS	371
127	HC5_m24	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN AYS	85	VNWV RQAPG KGLE WLGGM	570	IWGDG KI	108	VYNSA LKSRL TISKDS SKNTV YLQM NSLRA EDTAV YYC	578	AGDG YYTYA MDN	139	WGQG TTVTV SS	371

*Names correspond with name in informal sequence listing.

Table 6. Anti-interleukin (IL)-13 antibody Light Chain Kabat CDRs

Construct ID	VL Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
1 (lebrikizu mab), 2, and 128-131	Lebrikizumab - LC	DIVMT QSPDS LSVSL GERAT INC	581	RASKS VDSYG NSFMH	141	WYQQ KPGQP PKLLIY	286	LASNLS ES	153	GVPPDR FSGSG SGTDF TLTISS LQAED VAVY YC	343	QQNNE DPRT	165	FGGGT KVEIK	400
3 and 4	LC0	NIVLT QSPAS LAVSL GQRAT ISC	230	RASKS VDSYG NSFMH	141	WYQQ KPGQP PKLLIY	286	LASNLS ES	153	GVPPAR FSGSG SRTDF TLTIDP VEADD AASYC	344	QQNNE DPRT	165	FGGGT KLEIK	401
-	LC1	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSFMH	141	WYQQ KPGKA PKLLIY	288	LASNLS ES	153	GVPSR FSGSG SRTDF TLTISS LQPED FATY	712	QQNNE DPRT	165	FGGGT KVEIK	400
5-9	LC2	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSFMH	141	WYQQ KPGKA PKLLIY	288	LASNLS ES	153	GVPSR FSGSG SRTDF TLTISS LQPED FATY C	345	QQNNE DPRT	165	FGGGT KVEIK	400

Construct ID	VL Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
10-14	LC3	EIVLT QSPAT LSVSP GERAT LSC	233	RASKS VDSYG NSFMH	141	WYQQ KPGQA PRLIY	290	LASNL ES	153	GIPARF SGSGS RTEFT LTISSL QSEDF AVYYC	347	QQNNE DPRT	165	FGGGT KVEIK	400
-	LC4	DIVLT QSPLS LPVTP GEPASI SC	234	RASKS VDSYG NSFMH	141	WYLTQ KPGQS PQLLIY	291	LASNL ES	153	GVPDR FSGSG SRTDF TLKISR VEAED VGVY YC	348	QQNNE DPRT	165	FGGGT KVEIK	400
-	LC5	DIVLT QSPDS LAVSL GERAT INC	235	RASKS VDSYG NSFMH	141	WYQQ KPGQP PKLLIY	286	LASNL ES	153	GVPDR FSGSG SGTDF TLTISS LQAED VAVY YC	343	QQNNE DPRT	165	FGGGT KVEIK	400
15-19, 90, 105-127, and 132- 136	LC6	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSFMH	141	WYQQ KPGKA PKLLIY	288	LASNL ES	153	GVPSR FSGSG SGTDF TLTISS LQPED FATYY C	349	QQNNE DPRT	165	FGGGT KVEIK	400

Construct ID	VL Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
20-24	LC7	EIVLT QSPAT LSVSP GERAT LSC	233	RASKS VDSYG NSFMH	141	WYQQ KPGQA PRLIY	290	LASNL ES	153	GIPARF SGSGS GTEFT LTISSL QSEDF AVYYC	351	QQNNE DPRT	165	FGGGT KVEIK	400
-	LC8	DIVLT QSPLS LPVTP GEPASI SC	234	RASKS VDSYG NSFMH	141	WYVQ KPGQS PQLLIY	291	LASNL ES	153	GVPDR FSGSG SGTDF TLKISR VEAED VGVY YC	352	QQNNE DPRT	165	FGGGT KVEIK	400
25	LC9	DIVLT QSPAS LAVSP GERAT ISC	239	RASKS VDSYG NSFMH	141	WYQQ KPGQP PKLLIY	286	LASNL ES	153	GVPDR FSGSG SGTDF TLTISR VEADD VAVY YC	353	QQNNE DPRT	165	FGGGT KLEIK	401
26	LC10	DIVLT QSPAS LAVSP GERAT ISC	239	RASQS VDSNG NNFLH	142	WYQQ KPGQP PKLLIY	286	LASNR ES	158	GVPDR FSGSG SGTDF TLTISR VEADD VAVY YC	353	QQNN HTPRT	166	FGGGT KLEIK	401

Construct ID	VL Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
91	LC6_m1	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSRMH	143	WYQQ KPGKA PKLLIY	288	LASNL ES	153	GVPSR FSGSG SGTDF TLTISS LQPED FATYY C	349	QQNNE DPRT	165	FGGGT KVEIK	400
92	LC6_m2	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG SSMH	711	WYQQ KPGKA PKLLIY	288	LASNL ES	153	GVPSR FSGSG SGTDF TLTISS LQPED FATYY C	349	QQNNE DPRT	165	FGGGT KVEIK	400
93	LC6_m3	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSFMH	141	WYQQ KPGKA PKLLIR	300	LASNL ES	153	GVPSR FSGSG SGTDF TLTISS LQPED FATYY C	349	QQNNE DPRT	165	FGGGT KVEIK	400
94	LC6_m4	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSFMH	141	WYQQ KPGKA PKLLIF	301	LASNL ES	153	GVPSR FSGSG SGTDF TLTISS LQPED FATYY C	349	QQNNE DPRT	165	FGGGT KVEIK	400

Construct ID	VL Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
95	LC6_m5	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSFMH	141	WYQQ KPGKA PKLLIY	288	LASHL ES	154	GVPSR FSGSG SGTDF TLTISS LQPED FATYY C	349	QQNNE DPRT	165	FGGGT KVEIK	400
96	LC6_m6	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSFMH	141	WYQQ KPGKA PKLLIY	288	LASDL ES	155	GVPSR FSGSG SGTDF TLTISS LQPED FATYY C	349	QQNNE DPRT	165	FGGGT KVEIK	400
97	LC6_m7	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSFMH	141	WYQQ KPGKA PKLLIY	288	LASQL ES	156	GVPSR FSGSG SGTDF TLTISS LQPED FATYY C	349	QQNNE DPRT	165	FGGGT KVEIK	400
98 and 137-140	LC6_m8	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSFMH	141	WYQQ KPGKA PKLLIY	288	LASEL ES	157	GVPSR FSGSG SGTDF TLTISS LQPED FATYY C	349	QQNNE DPRT	165	FGGGT KVEIK	400

Construct ID	VL Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
99	LC6_m9	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSFMH	141	WYQQ KPGKA PKLLIY	288	LASNL ES	153	GVPSR FSGSG SGTDF TLTISS LQPED FATYY C	349	QQNHE DPRT	167	FGGGT KVEIK	400
100	LC6_m10	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSFMH	141	WYQQ KPGKA PKLLIY	288	LASNL ES	153	GVPSR FSGSG SGTDF TLTISS LQPED FATYY C	349	QQNHE DPRT	168	FGGGT KVEIK	400
101	LC6_m11	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSFMH	141	WYQQ KPGKA PKLLIY	288	LASNL ES	153	GVPSR FSGSG SGTDF TLTISS LQPED FATYY C	349	QQNSE DPRT	169	FGGGT KVEIK	400
102	LC6_m12	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSFMH	141	WYQQ KPGKA PKLLIY	288	LASNL ES	153	GVPSR FSGSG SGTDF TLTISS LQPED FATYY C	349	QQNNR DPRT	170	FGGGT KVEIK	400

Construct ID	VL Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
103	LC6_m13	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSFMH	141	WYQQ KPGKA PKLLIY	288	LASN L	153	GVPSR FSGSG SGTDF TLTISS LQPED FATYY C	349	QQNN DDPRT	171	FGGGT KVEIK	400
104	LC6_m14	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSFMH	141	WYQQ KPGKA PKLLIY	288	LASN L	153	GVPSR FSGSG SGTDF TLTISS LQPED FATYY C	349	QQNN QDPRT	172	FGGGT KVEIK	400

*Names correspond with name in informal sequence listing.

Table 7. Anti-interleukin (IL)-13 antibody Light Chain Chothia CDRs

Construct ID	VL Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
1 (lebrikizumab), 2, and 128-131	Lebrikizumab - LC	DIVMT QSPDS LSVSL GERAT INC	581	RASKS VDSYG NSFMH	141	WYQQ KPGQP PKLLIY	286	LASN L	153	GVPSR FSGSG SGTDF TLTISS LQAED VAVY YC	343	QQNNE DPRT	165	FGGGT KVEIK	400

Construct ID	VL Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
3 and 4	LC0	NIVLT QSPAS LAVSL GQRAT ISC	230	RASKS VDSYG NSFMH	141	WYQQ KPGQP PKLLIY	286	LASNL ES	153	GVPAR FSGSG SRTDF TLTIDP VEADD AASYC	344	QQNNE DPRT	165	FGGGT KLEIK	401
-	LC1	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSFMH	141	WYQQ KPGKA PKLLIY	288	LASNL ES	153	GVPSR FSGSG SRTDF TLTISS LQPED FATY C	345	QQNNE DPRT	165	FGGGT KVEIK	400
5-9	LC2	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSFMH	141	WYQQ KPGKA PKLLIY	288	LASNL ES	153	GVPSR FSGSG SRTDF TLTISS LQPED FATY C	345	QQNNE DPRT	165	FGGGT KVEIK	400
10-14	LC3	EIVLT QSPAT LSVSP GERAT LSC	233	RASKS VDSYG NSFMH	141	WYQQ KPGQA PRLIY	290	LASNL ES	153	GIPARF SGSGS RTEFT LTISSL QSEDF AVYYC	347	QQNNE DPRT	165	FGGGT KVEIK	400

Construct ID	VL Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
-	LC4	DIVLT QSPLS LPVTP GEPASI SC	234	RASKS VDSYG NSFMH	141	WYQQ KPGQS PQLLIY	291	LASN L ES	153	GVPDR FSGSG SRTDF TLKISR VEAED VG VY YC	348	QQNNE DPRT	165	FGGGT KVEIK	400
-	LC5	DIVLT QSPDS LAVSL GERAT INC	235	RASKS VDSYG NSFMH	141	WYQQ KPGQP PKLLIY	286	LASN L ES	153	GVPDR FSGSG SGTDF TLTISS LQAED VAVY YC	713	QQNNE DPRT	165	FGGGT KVEIK	400
15-19, 90, 105-127, and 132- 136	LC6	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSFMH	141	WYQQ KPGKA PKLLIY	288	LASN L ES	153	GVPDR FSGSG SGTDF TLTISS LQPED FATY YC	349	QQNNE DPRT	165	FGGGT KVEIK	400
20-24	LC7	EIVLT QSPAT LSVSP GERAT LSC	233	RASKS VDSYG NSFMH	141	WYQQ KPGQA PRLIY	290	LASN L ES	153	GIPARF SGSGS GTEFT LTISSL QSEDF AVYYC	351	QQNNE DPRT	165	FGGGT KVEIK	400

Construct ID	VL Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
-	LC8	DIVLT QSPS LPVTP GEPASI SC	234	RASKS VDSYG NSFMH	141	WYLQ KPGQS PQLLIY	291	LASNL ES	153	GVPDR FSGSG SGTDF TLKISR VEAED VGVIY YC	352	QQNNE DPRT	165	FGGGT KVEIK	400
25	LC9	DIVLT QSPAS LAVSP GERAT ISC	239	RASKS VDSYG NSFMH	141	WYQQ KPGQP PKLLIY	286	LASNL ES	153	GVPDR FSGSG SGTDF TLTISR VEADD VAVY YC	353	QQNNE DPRT	165	FGGGT KLEIK	401
26	LC10	DIVLT QSPAS LAVSP GERAT ISC	239	RASQS VDSNG NNFLH	142	WYQQ KPGQP PKLLIY	286	LASNLR ES	158	GVPDR FSGSG SGTDF TLTISR VEADD VAVY YC	353	QQNN HTPRT	166	FGGGT KLEIK	401
91	LC6_m1	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSRMH	143	WYQQ KPGKA PKLLIY	288	LASNLR ES	153	GVPDR FSGSG SGTDF TLTISS LQPED FATYY C	349	QQNNE DPRT	165	FGGGT KVEIK	400

Construct ID	VL Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
92	LC6_m2	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSSMH	144	WYQQ KPGKA PKLLIY	288	LASNL ES	153	GVPSR FSGSG SGTDF TLTISS LQPED FATYY C	349	QQNNE DPRT	165	FGGGT KVEIK	400
93	LC6_m3	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSFMH	141	WYQQ KPGKA PKLLIR	300	LASNL ES	153	GVPSR FSGSG SGTDF TLTISS LQPED FATYY C	349	QQNNE DPRT	165	FGGGT KVEIK	400
94	LC6_m4	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSFMH	141	WYQQ KPGKA PKLLIF	301	LASNL ES	153	GVPSR FSGSG SGTDF TLTISS LQPED FATYY C	349	QQNNE DPRT	165	FGGGT KVEIK	400
95	LC6_m5	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSFMH	141	WYQQ KPGKA PKLLIY	288	LASHL ES	154	GVPSR FSGSG SGTDF TLTISS LQPED FATYY C	349	QQNNE DPRT	165	FGGGT KVEIK	400

Construct ID	VL Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
96	LC6_m6	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSFMH	141	WYQQ KPGKA PKLLIY	288	LASDL ES	155	GVPSR FSGSG SGTDF TLTISS LQPED FATYY C	349	QQNNE DPRT	165	FGGGT KVEIK	400
97	LC6_m7	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSFMH	141	WYQQ KPGKA PKLLIY	288	LASQL ES	156	GVPSR FSGSG SGTDF TLTISS LQPED FATYY C	349	QQNNE DPRT	165	FGGGT KVEIK	400
98 and 137-144	LC6_m8	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSFMH	141	WYQQ KPGKA PKLLIY	288	LASEL ES	157	GVPSR FSGSG SGTDF TLTISS LQPED FATYY C	349	QQNNE DPRT	165	FGGGT KVEIK	400
99	LC6_m9	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSFMH	141	WYQQ KPGKA PKLLIY	288	LASNL ES	153	GVPSR FSGSG SGTDF TLTISS LQPED FATYY C	349	QQNNE DPRT	167	FGGGT KVEIK	400

Construct ID	VL Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
100	LC6_m10	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSFMH	141	WYQQ KPGKA PKLLIY	288	LASNL ES	153	GVPSR FSGSG SGTDF TLTISS LQPED FATYY C	349	QQNYE DPRT	168	FGGGT KVEIK	400
101	LC6_m11	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSFMH	141	WYQQ KPGKA PKLLIY	288	LASNL ES	153	GVPSR FSGSG SGTDF TLTISS LQPED FATYY C	349	QQNSE DPRT	169	FGGGT KVEIK	400
102	LC6_m12	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSFMH	141	WYQQ KPGKA PKLLIY	288	LASNL ES	153	GVPSR FSGSG SGTDF TLTISS LQPED FATYY C	349	QQNR DPRT	170	FGGGT KVEIK	400
103	LC6_m13	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSFMH	141	WYQQ KPGKA PKLLIY	288	LASNL ES	153	GVPSR FSGSG SGTDF TLTISS LQPED FATYY C	349	QQNN DDPRT	171	FGGGT KVEIK	400

Construct ID	VL Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
104	LC6_m14	DIQLT QSPSSL SASVG DRVTI TC	231	RASKS VDSYG NSFMH	141	WYQQ KPGKA PKLLIY	288	LASN L ES	153	GVPSR FSGSG SGTDF TLTISS LQPED FATYY C	349	QQNN QDPRT	172	FGGGT KVEIK	400

*Names correspond with name in informal sequence listing.

Table 8. Anti-interleukin (IL)-13 antibody Light Chain IMGT CDRs

Construct ID	VL Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
1 (lebrikizu mab), 2, and 128-131	Lebrikizum ab - LC	DIVMT QSPDS LSVSL GERAT INCRA S	582	KSVDS YGNSF	149	MHWY QQKPG QPPKL LIY	589	LAS	NLESG VPDRF SGSGS GTDFT LTISSL QAEDV AVYYC	596	QQNNE DPRT	165	FGGGT KVEIK	400
3 and 4	LC0	NIVLT QSPAS LAVSL GQRAT ISCRAS	583	KSVDS YGNSF	149	MHWY QQKPG QPPKL LIY	589	LAS	NLESG VPARF SGSGS RTDFT LTIDPV EADDA ASYVC	597	QQNNE DPRT	165	FGGGT KLEIK	401

Construct ID	VL Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
-	LC1	DIQLT QSPSSL SASVG DRVTI TCRAS	584	KSVDS YGNSF	149	MHWY QQKPG KAPKL LIY	590	LAS	NLESG VPSRF SGSGS RTDFT LTISSL QPEDF ATYYC	598	QQNNE DPRT	165	FGGGT KVEIK	400
5-9	LC2	DIQLT QSPSSL SASVG DRVTI TCRAS	584	KSVDS YGNSF	149	MHWY QQKPG KAPKL LIY	590	LAS	NLESG VPSRF SGSGS RTDFT LTISSL QPEDF ATYYC	598	QQNNE DPRT	165	FGGGT KVEIK	400
10-14	LC3	EIVLT QSPAT LSVSP GERAT LSCRA S	585	KSVDS YGNSF	149	MHWY QQKPG QAPRL LIY	591	LAS	NLESGI PARFS GSGSR TEFTL TISSLQ SEDA VYYC	599	QQNNE DPRT	165	FGGGT KVEIK	400
-	LC4	DIVLT QSPLS LPVTP GEPASI SCRAS	586	KSVDS YGNSF	149	MHWY LQKPG QSPQL LIY	592	LAS	NLESG VPDRF SGSGS RTDFT LKISR VEAED VGVY YC	600	QQNNE DPRT	165	FGGGT KVEIK	400

Construct ID	VL Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
-	LC5	DIVLT QSPDS LAVSL GERAT INCRA S	587	KSVDS YGNSF	149	MHWY QQKPG QPPKL LIY	589	LAS	NLESG VPDRF SGSGS GTDFT LTISSL QAEDV AVYYC	596	QQNNE DPRT	165	FGGGT KVEIK	400
15-19, 90, 105-127, and 132- 136	LC6	DIQLT QSPSSL SASVG DRVTI TCRAS	584	KSVDS YGNSF	149	MHWY QQKPG KAPKL LIY	590	LAS	NLESG VPSRF SGSGS GTDFT LTISSL QPEDF ATYYC	601	QQNNE DPRT	165	FGGGT KVEIK	400
20-24	LC7	EIVLT QSPAT LSVSP GERAT LSCRA S	585	KSVDS YGNSF	149	MHWY QQKPG QAPRL LIY	591	LAS	NLESGI PARFS SGSGG TEFTL TISSLQ SEDA VYYC	602	QQNNE DPRT	165	FGGGT KVEIK	400
-	LC8	DIVLT QSPLS LPVTP GEPASI SCRAS	586	KSVDS YGNSF	149	MHWY LQKPG QSPQL LIY	592	LAS	NLESG VPDRF SGSGS GTDFT LKISR VEAED VGVY YC	603	QQNNE DPRT	165	FGGGT KVEIK	400

Construct ID	VL Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
25	LC9	DIVLT QSPAS LAVSP GERAT ISCRAS	588	KSVDS YGNFS	149	MHWY QQKPG QPPKL LIY	589	LAS	NLESG VPDRF SGSGS GTDFT LTISR EADDV AVYYC	604	QQNNE DPRT	165	FGGGT KLEIK	401
26	LC10	DIVLT QSPAS LAVSP GERAT ISCRAS	588	QSVDS NGNFS	150	LHWY QQKPG QPPKL LIY	593	LAS	NRESG VPDRF SGSGS GTDFT LTISR EADDV AVYYC	605	QQNN HTPRT	166	FGGGT KLEIK	401
91	LC6_m1	DIQLT QSPSSL SASVG DRVTI TCRAS	584	KSVDS YGNFS	151	MHWY QQKPG KAPKL LIY	590	LAS	NLESG VPSRF SGSGS GTDFT LTISSL QPEDF ATYYC	601	QQNNE DPRT	165	FGGGT KVEIK	400
92	LC6_m2	DIQLT QSPSSL SASVG DRVTI TCRAS	584	KSVDS YGNSS	152	MHWY QQKPG KAPKL LIY	590	LAS	NLESG VPSRF SGSGS GTDFT LTISSL QPEDF ATYYC	601	QQNNE DPRT	165	FGGGT KVEIK	400

Construct ID	VL Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
93	LC6_m3	DIQLT QSPSSL SASVG DRVTI TCRAS	584	KSVDS YGNSF	149	MHWY QQKPG KAPKL LIR	594	LAS	NLESG VPSRF SGSGS GTDFT LTISSL QPEDF ATYYC	601	QQNNE DPRT	165	FGGGT KVEIK	400
94	LC6_m4	DIQLT QSPSSL SASVG DRVTI TCRAS	584	KSVDS YGNSF	149	MHWY QQKPG KAPKL LIF	595	LAS	NLESG VPSRF SGSGS GTDFT LTISSL QPEDF ATYYC	601	QQNNE DPRT	165	FGGGT KVEIK	400
95	LC6_m5	DIQLT QSPSSL SASVG DRVTI TCRAS	584	KSVDS YGNSF	149	MHWY QQKPG KAPKL LIY	590	LAS	HLESG VPSRF SGSGS GTDFT LTISSL QPEDF ATYYC	606	QQNNE DPRT	165	FGGGT KVEIK	400
96	LC6_m6	DIQLT QSPSSL SASVG DRVTI TCRAS	584	KSVDS YGNSF	149	MHWY QQKPG KAPKL LIY	590	LAS	DLESG VPSRF SGSGS GTDFT LTISSL QPEDF ATYYC	607	QQNNE DPRT	165	FGGGT KVEIK	400

Construct ID	VL Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
97	LC6_m7	DIQLT QSPSSL SASVG DRVTI TCRAS	584	KSVDS YGNSF	149	MHWY QQKPG KAPKL LIY	590	LAS	QLESG VPSRF SGSGS GTDFT LTISSL QPEDF ATYYC	608	QQNNE DPRT	165	FGGGT KVEIK	400
98 and 137-144	LC6_m8	DIQLT QSPSSL SASVG DRVTI TCRAS	584	KSVDS YGNSF	149	MHWY QQKPG KAPKL LIY	590	LAS	ELESG VPSRF SGSGS GTDFT LTISSL QPEDF ATYYC	609	QQNNE DPRT	165	FGGGT KVEIK	400
99	LC6_m9	DIQLT QSPSSL SASVG DRVTI TCRAS	584	KSVDS YGNSF	149	MHWY QQKPG KAPKL LIY	590	LAS	NLESG VPSRF SGSGS GTDFT LTISSL QPEDF ATYYC	601	QQNHE DPRT	167	FGGGT KVEIK	400
100	LC6_m10	DIQLT QSPSSL SASVG DRVTI TCRAS	584	KSVDS YGNSF	149	MHWY QQKPG KAPKL LIY	590	LAS	NLESG VPSRF SGSGS GTDFT LTISSL QPEDF ATYYC	601	QQNNE DPRT	168	FGGGT KVEIK	400

Construct ID	VL Name*	FR1	SEQ ID NO:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
101	LC6_m11	DIQLT QSPSSL SASVG DRVTI TCRAS	584	KSVDS YGNSF	149	MHWY QQKPG KAPKL LIY	590	LAS	NLESG VPSRF SGSGS GTDFT LTISSL QPEDF ATYYC	601	QQNSE DPRT	169	FGGGT KVEIK	400
102	LC6_m12	DIQLT QSPSSL SASVG DRVTI TCRAS	584	KSVDS YGNSF	149	MHWY QQKPG KAPKL LIY	590	LAS	NLESG VPSRF SGSGS GTDFT LTISSL QPEDF ATYYC	601	QQNNR DPRT	170	FGGGT KVEIK	400
103	LC6_m13	DIQLT QSPSSL SASVG DRVTI TCRAS	584	KSVDS YGNSF	149	MHWY QQKPG KAPKL LIY	590	LAS	NLESG VPSRF SGSGS GTDFT LTISSL QPEDF ATYYC	601	QQNN DDPRT	171	FGGGT KVEIK	400
104	LC6_m14	DIQLT QSPSSL SASVG DRVTI TCRAS	584	KSVDS YGNSF	149	MHWY QQKPG KAPKL LIY	590	LAS	NLESG VPSRF SGSGS GTDFT LTISSL QPEDF ATYYC	601	QQNN QDPRT	172	FGGGT KVEIK	400

*Names correspond with name in informal sequence listing.

[00211] In some embodiments, IL-13 antibody does not comprise: (a) CDR-H1 set forth in SEQ ID NO: 58; CDR-H2 set forth in SEQ ID NO: 100; CDR-H3 set forth in SEQ ID NO: 112; CDR-L1 set forth in SEQ ID NO: 141; CDR-L2 set forth in SEQ ID NO: 153; and CDR-L3 set forth in SEQ ID NO: 165; or (b) CDR-H1 set forth in SEQ ID NO: 67; CDR-H2 set forth in SEQ ID NO: 104; CDR-H3 set forth in SEQ ID NO: 112; CDR-L1 set forth in SEQ ID NO: 141; CDR-L2 set forth in SEQ ID NO: 153; and CDR-L3 set forth in SEQ ID NO: 165; or (c) CDR-H1 set forth in SEQ ID NO: 84; CDR-H2 set forth in SEQ ID NO: 108; CDR-H3 set forth in SEQ ID NO: 130; CDR-L1 set forth in SEQ ID NO: 149; CDR-L2 set forth in the amino acid sequence LAS; and CDR-L3 set forth in SEQ ID NO: 165.

[00212] In some embodiments, IL-13 antibody does not comprise any combination of: (a) a CDR-H1 set forth in any of SEQ ID NOs: 58, 67, or 84; (b) a CDR-H2 set forth in any of SEQ ID NOs: 100, 104, or 108; (c) a CDR-H3 set forth in any of SEQ ID NOs: 112 or 130; (d) a CDR-L1 set forth in any of SEQ ID NOs: 141 or 149; (e) a CDR-L2 set forth in any of SEQ ID NOs: 153 or 154; and (f) a CDR-L3 set forth in SEQ ID NO: 165.

Fc Region

[00213] The structures of the Fc regions of various immunoglobulins, and the glycosylation sites contained therein, are known in the art. See Schroeder and Cavacini, *J. Allergy Clin. Immunol.*, 2010, 125:S41-52, incorporated by reference in its entirety. The Fc region may be a naturally occurring Fc region, or an Fc region modified as described in the art or elsewhere in this disclosure.

[00214] Unless otherwise specified herein, numbering of amino acid residues in the Fc region or constant region is according to the EU numbering system, also called the EU index, as described in Kabat et al, *Sequences of Proteins of Immunological Interest*, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD, 1991. An “Fc polypeptide” of a dimeric Fc as used herein refers to one of the two polypeptides forming the dimeric Fc domain, *i.e.*, a polypeptide comprising C-terminal constant regions of an immunoglobulin heavy chain, capable of stable self-association. For example, an Fc polypeptide of a dimeric IgG Fc comprises an IgG CH2 and an IgG CH3 constant domain sequence. An Fc can be of the class IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into subclasses (isotypes), *e.g.*, IgG₁, IgG₂, IgG₃, IgG₄, IgA₁, and IgA₂.

[00215] The terms “Fc receptor” and “FcR” are used to describe a receptor that binds to the Fc region of an antibody. For example, an FcR can be a native sequence human FcR. Generally, an FcR is one which binds an IgG antibody (a gamma receptor) and includes receptors of the FcγRI, FcγRII, and FcγRIII subclasses, including allelic variants and alternatively spliced forms of these receptors. FcγRII receptors include FcγRIIA (an “activating receptor”) and FcγRIIB (an “inhibiting receptor”), which have similar amino acid sequences that differ primarily in the cytoplasmic domains thereof. Immunoglobulins of other isotypes can also be bound by certain FcRs (see, *e.g.*, Janeway *et al.*, *Immuno Biology: the immune system in health and disease*, (Elsevier Science Ltd., NY) (4th ed., 1999)). Activating receptor FcγRIIA contains an immunoreceptor tyrosine-based activation motif (ITAM) in its cytoplasmic domain. Inhibiting receptor FcγRIIB contains an immunoreceptor tyrosine-based inhibition motif (ITIM) in its cytoplasmic domain (reviewed in Daëron, *Annu. Rev. Immunol.* 15:203-234 (1997)). FcRs are reviewed in Ravetch and Kinet, *Annu. Rev. Immunol.* 9:457-92 (1991); Capel *et al.*, *Immunomethods* 4:25-34 (1994); and de Haas *et al.*, *J. Lab. Clin. Med.* 126:330-41 (1995). Other FcRs, including those to be identified in the future, are encompassed by the term “FcR” herein. The term also includes the neonatal receptor, FcRn, which is responsible for the transfer of maternal IgGs to the fetus (Guyer *et al.*, *J. Immunol.* 117:587 (1976); and Kim *et al.*, *J. Immunol.* 24:249 (1994)).

[00216] Modifications in the CH2 domain can affect the binding of FcRs to the Fc. A number of amino acid modifications in the Fc region are known in the art for selectively altering the affinity of the Fc for different Fcγ receptors. In some aspects, the Fc comprises one or more modifications to promote selective binding of Fc-gamma receptors.

[00217] Exemplary mutations that alter the binding of FcRs to the Fc are listed below:

[00218] S298A/E333A/K334A, S298A/E333A/K334A/K326A (Lu Y, Vernes JM, Chiang N, *et al. J Immunol Methods.* 2011 Feb 28;365(1-2):132-41);

[00219] F243L/R292P/Y300L/V305I/P396L, F243L/R292P/Y300L/L235V/P396L (Stavenhagen JB, Gorlatov S, Tuailon N, *et al. Cancer Res.* 2007 Sep 15;67(18):8882-90; Nordstrom JL, Gorlatov S, Zhang W, *et al. Breast Cancer Res.* 2011 Nov 30;13(6):R123);

[00220] F243L (Stewart R, Thom G, Levens M, *et al. Protein Eng Des Sel.* 2011 Sep;24(9):671-8.), S298A/E333A/K334A (Shields RL, Namenuk AK, Hong K, *et al. J Biol Chem.* 2001 Mar 2;276(9):6591-604);

[00221] S239D/I332E/A330L, S239D/I332E (Lazar GA, Dang W, Karki S, *et al. Proc Natl Acad Sci U S A.* 2006 Mar 14;103(11):4005-10);

[00222] S239D/S267E, S267E/L328F (Chu SY, Vostiar I, Karki S, *et al. Mol Immunol.* 2008 Sep;45(15):3926-33);

[00223] S239D/D265S/S298A/I332E, S239E/S298A/K326A/A327H, G237F/S298A/A330L/I332E, S239D/I332E/S298A, S239D/K326E/A330L/I332E/S298A, G236A/S239D/D270L/I332E, S239E/S267E/H268D, L234F/S267E/N325L, G237F/V266L/S267D and other mutations listed in WO2011/120134 and WO2011/120135, herein incorporated by reference. *Therapeutic Antibody Engineering* (by William R. Strohl and Lila M. Strohl, Woodhead Publishing series in Biomedicine No 11, ISBN 1 907568 37 9, Oct 2012) lists mutations on page 283.

[00224] In certain embodiments an antibody described herein includes modifications designed to improve its ability to mediate effector function. Such modifications are known in the art and include afucosylation, or engineering of the affinity of the Fc towards an activating receptor, mainly FCGR3a for ADCC, and towards C1q for CDC. The following **Table 9** summarizes various designs reported in the literature for effector function engineering.

[00225] Methods of producing antibodies with little or no fucose on the Fc glycosylation site (Asn 297 EU numbering) without altering the amino acid sequence are well known in the art. The GlymaX® technology (ProBioGen AG) is based on the introduction of a gene for an enzyme which deflects the cellular pathway of fucose biosynthesis into cells used for antibody production. This prevents the addition of the sugar “fucose” to the N-linked antibody carbohydrate part by antibody-producing cells. (von Horsten *et al.* (2010) *Glycobiology*. 2010 Dec; 20 (12):1607-18. Another approach to obtaining antibodies with lowered levels of fucosylation can be found in U.S. Patent No. 8,409,572, which teaches selecting cell lines for antibody production for their ability to yield lower levels of fucosylation on antibodies can be fully afucosylated (meaning they contain no detectable fucose) or they can be partially afucosylated, meaning that the isolated antibody contains less than 95%, less than 85%, less than 75%, less than 65%, less than 55%, less than 45%, less than 35%, less than 25%, less than 15% or less than 5% of the amount of fucose normally detected for a similar antibody produced by a mammalian expression system.

[00226] Thus, in one embodiment, an antibody described herein can include a dimeric Fc that comprises one or more amino acid modifications as noted in **Table 9** that confer improved

effector function. In another embodiment, the antibody can be afucosylated to improve effector function.

Table 9. CH2 domains and effector function engineering

Reference	Mutations	Effect
Lu, 2011, Ferrara 2011, Mizushima 2011	Afucosylated	Increased ADCC
Lu, 2011	S298A/E333A/K334A	Increased ADCC
Lu, 2011	S298A/E333A/K334A/K326A	Increased ADCC
Stavenshagen, 2007	F243L/R292P/Y300L/V305I/P396L	Increased ADCC
Nordstrom, 2011	F243L/R292P/Y300L/L235V/P396L	Increased ADCC
Stewart, 2011	F243L	Increased ADCC
Shields, 2001	S298A/E333A/K334A	Increased ADCC
Lazar, 2006	S239D/I332E/A330L	Increased ADCC
Lazar, 2006	S239D/I332E	Increased ADCC
Bowles, 2006	AME-D, not specified mutations	Increased ADCC
Heider, 2011	37.1, mutations not disclosed	Increased ADCC
Moore, 2010	S267E/H268F/S324T	Increased CDC

[00227] Fc modifications designed to reduce FcγR and/or complement binding and/or effector function are known in the art. Recent publications describe strategies that have been used to engineer antibodies with reduced or silenced effector activity (see Strohl, WR (2009), *Curr Opin Biotech* 20:685-691, and Strohl, WR and Strohl LM, “Antibody Fc engineering for optimal antibody performance” In *Therapeutic Antibody Engineering*, Cambridge: Woodhead Publishing (2012), pp 225-249). These strategies include reduction of effector function through modification of glycosylation, use of IgG2/IgG4 scaffolds, or the introduction of mutations in the hinge or CH2 regions of the Fc. For example, U.S. Patent Publication No. 2011/0212087 (Strohl), International Patent Publication No. WO 2006/105338 (Xencor), U.S. Patent Publication No. 2012/0225058 (Xencor), U.S. Patent Publication No. 2012/0251531 (Genentech), and Strop et al

((2012) *J. Mol. Biol.* 420: 204-219) describe specific modifications to reduce FcγR or complement binding to the Fc.

[00228] Specific, non-limiting examples of known amino acid modifications designed to reduce FcγR or complement binding to the Fc include those identified in the following **Table 10**:

Table 10. Modifications to reduce FcγR or complement binding to the Fc

Company	Modifications
GSK	N297A
Ortho Biotech	L234A/L235A
Protein Design labs	IgG2 V234A/G237A
Wellcome Labs	IgG4 L235A/G237A/E318A
GSK	IgG4 S228P/L236E
Alexion	IgG2/IgG4combo
Merck	IgG2 H268Q/V309L/A330S/A331S
Bristol-Myers	C220S/C226S/C229S/P238S
Seattle Genetics	C226S/C229S/E3233P/L235V/L235A
Amgen	E.coli production, non glyco
Medimmune	L234F/L235E/P331S
Trubion	Hinge mutant, possibly C226S/P230S

[00229] Methods of producing antibodies with little or no fucose on the Fc glycosylation site (Asn 297 EU numbering) without altering the amino acid sequence are well known in the art. The GlymaxX® technology (ProBioGen AG) is based on the introduction of a gene for an enzyme which deflects the cellular pathway of fucose biosynthesis into cells used for antibody

production. This prevents the addition of the sugar “fucose” to the N-linked antibody carbohydrate part by antibody-producing cells. (von Horsten *et al.* (2010) *Glycobiology*. 2010 Dec; 20 (12):1607-18.) Examples of cell lines capable of producing defucosylated antibody include CHO-DG44 with stable overexpression of the bacterial oxidoreductase GDP-6-deoxy-D-lyxo-4-hexylose reductase (RMD) (*see* Henning von Horsten *et al.*, *Glycobiol* 2010, 20:1607-1618) or Lec13 CHO cells, which are deficient in protein fucosylation (*see* Ripka *et al.*, *Arch. Biochem. Biophys.*, 1986, 249:533-545; U.S. Pat. Pub. No. 2003/0157108; WO 2004/056312; each of which is incorporated by reference in its entirety), and knockout cell lines, such as alpha-1,6-fucosyltransferase gene or FUT8 knockout CHO cells (*see* Yamane-Ohnuki *et al.*, *Biotech. Bioeng.*, 2004, 87: 614-622; Kanda *et al.*, *Biotechnol. Bioeng.*, 2006, 94:680-688; and WO 2003/085107; each of which is incorporated by reference in its entirety). Another approach to obtaining antibodies with lowered levels of fucosylation can be found in U.S. Patent No. 8,409,572, which teaches selecting cell lines for antibody production for their ability to yield lower levels of fucosylation on antibodies.

[00230] Examples of cell lines capable of producing defucosylated antibody include CHO-DG44 with stable overexpression of the bacterial oxidoreductase GDP-6-deoxy-D-lyxo-4-hexylose reductase (RMD) (*see* Henning von Horsten *et al.*, *Glycobiol* 2010, 20:1607-1618) or Lec13 CHO cells, which are deficient in protein fucosylation (*see* Ripka *et al.*, *Arch. Biochem. Biophys.*, 1986, 249:533-545; U.S. Pat. Pub. No. 2003/0157108; WO 2004/056312; each of which is incorporated by reference in its entirety), and knockout cell lines, such as alpha-1,6-fucosyltransferase gene or FUT8 knockout CHO cells (*see* Yamane-Ohnuki *et al.*, *Biotech. Bioeng.*, 2004, 87: 614-622; Kanda *et al.*, *Biotechnol. Bioeng.*, 2006, 94:680-688; and WO 2003/085107; each of which is incorporated by reference in its entirety).

[00231] Antibodies can be fully afucosylated (meaning they contain no detectable fucose) or they can be partially afucosylated, meaning that the antibody contains less than 95%, less than 85%, less than 75%, less than 65%, less than 55%, less than 45%, less than 35%, less than 25%, less than 15% or less than 5% of the amount of fucose normally detected for a similar antibody produced by a mammalian expression system.

[00232] In some aspects, an antibody provided herein comprises an IgG1 domain with reduced fucose content at position Asn 297 compared to a naturally occurring IgG1 domain. Such Fc domains are known to have improved ADCC. *See* Shields *et al.*, *J. Biol. Chem.*, 2002,

277:26733-26740, incorporated by reference in its entirety. In some aspects, such antibodies do not comprise any fucose at position Asn 297. The amount of fucose may be determined using any suitable method, for example as described in WO 2008/077546, incorporated by reference in its entirety.

[00233] In certain embodiments, an antibody provided herein comprises an Fc region with one or more amino acid substitutions which improve ADCC, such as a substitution at one or more of positions 298, 333, and 334 of the Fc region. In certain embodiments, an antibody provided herein comprises an Fc region with one or more amino acid substitutions at positions 239, 332, and 330, as described in Lazar *et al.*, *Proc. Natl. Acad. Sci. USA*, 2006,103:4005-4010, incorporated by reference in its entirety.

[00234] Other illustrative glycosylation variants which may be incorporated into the antibodies provided herein are described, for example, in U.S. Pat. Pub. Nos. 2003/0157108, 2004/0093621, 2003/0157108, 2003/0115614, 2002/0164328, 2004/0093621, 2004/0132140, 2004/0110704, 2004/0110282, 2004/0109865; International Pat. Pub. Nos. 2000/61739, 2001/29246, 2003/085119, 2003/084570, 2005/035586, 2005/035778; 2005/053742, 2002/031140; Okazaki *et al.*, *J. Mol. Biol.*, 2004, 336:1239-1249; and Yamane-Ohnuki *et al.*, *Biotech. Bioeng.*, 2004, 87: 614-622; each of which is incorporated by reference in its entirety.

[00235] In certain embodiments, an antibody provided herein comprises an Fc region with at least one galactose residue in the oligosaccharide attached to the Fc region. Such antibody variants may have improved CDC function. Examples of such antibody variants are described, for example, in WO 1997/30087; WO 1998/58964; and WO 1999/22764; each of which is incorporated by reference in its entirety.

[00236] In certain embodiments, an antibody provided herein comprises one or more alterations that improves or diminishes C1q binding and/or CDC. See U.S. Pat. No. 6,194,551; WO 99/51642; and Idusogie *et al.*, *J. Immunol.*, 2000, 164:4178-4184; each of which is incorporated by reference in its entirety.

[00237] In certain embodiments, an antibody provided herein comprises a heavy chain comprising a constant heavy chain (HC) region comprising an amino acid sequence set forth in SEQ ID NO: 439 or SEQ ID NO: 624.

[00238] In certain embodiments, an antibody provided herein comprises a constant light chain (LC) region comprising an amino acid sequence set forth in SEQ ID NO: 469.

[00239] In certain embodiments, an antibody provided herein comprises (1) a constant heavy chain (HC) region comprising an amino acid sequence set forth in SEQ ID NO: 439 or SEQ ID NO: 624 or a HC region comprising sequence comprising an amino acid sequence having at least 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 439 or SEQ ID NO: 624 (2) a constant light chain (LC) region comprising an amino acid sequence set forth in SEQ ID NO: 469, or a LC region comprising sequence comprising an amino acid sequence having at least 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 469 (3) a VH comprising an amino acid sequence set forth in SEQ ID NO: 3 or a VH having at least 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 3 and (4) a VL comprising an amino acid sequence set forth in SEQ ID NO: 39 or a VL comprising an amino acid sequence at least 95% 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 39.

[00240] In certain embodiments, the isolated antibody comprises a heavy chain constant (HC) region comprising an amino acid sequence set forth in SEQ ID NO: 439 or 624 and a light chain constant (LC) region comprising an amino acid sequence set forth in SEQ ID NO: 469, wherein the antibody further comprises a VH comprising an amino acid sequence having at least 95%, 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 3 and a VL comprising an amino acid sequence at least 95% 96%, 97%, 98%, 99% or 100% sequence identity to SEQ ID NO: 39, wherein the VH comprises a HCDR1 comprising SEQ ID NO: 58, SEQ ID NO: 68, or SEQ ID NO: 85; a HCDR2 comprising SEQ ID NO: 100, SEQ ID NO: 104, or SEQ ID NO: 108; and a HCDR3 comprising SEQ ID NO: 112 or SEQ ID NO: 130; and the VL comprises a LCDR1 comprising SEQ ID NO: 141 or SEQ ID NO: 149; a LCDR2 comprising SEQ ID NO: 153 or SEQ ID NO: 164, and a LCDR3 comprising SEQ ID NO: 165.

[00241] In certain embodiments, the isolated antibody comprises a HCDR1 comprising SEQ ID NO: 58, a HCDR2 comprising SEQ ID NO: 100, a HCDR3 comprising SEQ ID NO: 112, a LCDR1 comprising SEQ ID NO: 141, a LCDR2 comprising SEQ ID NO: 153, and a LCDR3 comprising SEQ ID NO: 165. In certain embodiments, the isolated antibody comprises a VH comprising an amino acid sequence set forth in SEQ ID NO:3. In certain embodiments, the isolated antibody comprises a VL comprising an amino acid sequence set forth in SEQ ID NO:39. In certain embodiments, the isolated antibody comprises a VH comprising an amino acid sequence set forth in SEQ ID NO:3 and a VL comprising an amino acid sequence set forth in SEQ ID NO:39. In certain embodiments, the isolated antibody comprises a heavy chain

constant (HC) region comprising an amino acid sequence set forth in SEQ ID NO: 439. In certain embodiments, the isolated antibody comprises a heavy chain constant (HC) region comprising an amino acid sequence set forth in SEQ ID NO: 624. In certain embodiments, the isolated antibody comprises a constant light chain (LC) region comprising an amino acid sequence set forth in SEQ ID NO: 469. In certain embodiments, the isolated antibody comprises a heavy chain constant (HC) region comprising an amino acid sequence set forth in SEQ ID NO: 439 or 624 and a constant light chain (LC) region comprising an amino acid sequence set forth in SEQ ID NO: 469.

[00242] In certain embodiments, the isolated antibody comprises the HCDR1, HCDR2, HCDR3, LCDR1, LCDR2 and LCDR3 of Construct 133. In certain embodiments, the isolated antibody comprises the VH of Construct 133. In certain embodiments, the isolated antibody comprises the VL of Construct 133. In certain embodiments, the isolated antibody comprises the VH and VL of Construct 133. In certain embodiments, the isolated antibody comprises the heavy chain constant (HC) region of Construct 133. In certain embodiments, the isolated antibody comprises the constant light chain (LC) region of Construct 133. In certain embodiments, the isolated antibody comprises the heavy chain constant (HC) region and constant light chain (LC) region of Construct 133.

[00243] In certain embodiments, the isolated antibody comprises Construct 133, *i.e.*, comprising a HCDR1 comprising SEQ ID NO: 58, a HCDR2 comprising SEQ ID NO: 100, a HCDR3 comprising SEQ ID NO: 112, a LCDR1 comprising SEQ ID NO: 141, a LCDR2 comprising SEQ ID NO: 153, a LCDR3 comprising SEQ ID NO: 165, a VH comprising SEQ ID NO: 3, a VL comprising SEQ ID NO: 39, a heavy chain constant (HC) region comprising an amino acid sequence set forth in SEQ ID NO: 439 or 624 and a constant light chain (LC) region comprising an amino acid sequence set forth in SEQ ID NO: 469.

[00244] In certain embodiments, the Fc region comprises one or more amino acid substitutions, wherein the one or more substitutions result in increased antibody half-life, increased ADCC activity, increased ADCP activity, or increased CDC activity compared with the Fc without the one or more substitutions. In certain embodiments, the one or more amino acid substitutions results in increased antibody half-life at pH 6.0 compared to an antibody comprising a wild-type Fc region.

[00245] In certain embodiments, the one or more amino acid substitutions is selected from the group consisting of S228P (SP); M252Y, S254T, T256E, T256D, T250Q, H285D, T307A, T307Q, T307R, T307W, L309D, Q411H, Q311V, A378V, E380A, M428L, N434A, N434S, N297A, D265A, L234A, L235A, and N434W. In certain embodiments, the one or more amino acid substitutions comprises a plurality of amino acid substitutions selected from the group consisting of M428L/N434S (LS); M252Y/S254T/T256E (YTE); T250Q/M428L; T307A/E380A/N434A; T256D/T307Q (DQ); T256D/T307W (DW); M252Y/T256D (YD); T307Q/Q311V/A378V (QVV); T256D/H285D/T307R/Q311V/A378V (DDRVV); L309D/Q311H/N434S (DHS); S228P/L235E (SPLE); L234A/L235A (LA), M428L/N434A L234A/G237A (LALA), L234A/L235A/G237A, L234A/L235A/P329G, N297A, D265A/YTE, LALA/YTE, LAGA/YTE, LALAGA/YTE, LALAPG/YTE, N297A/LS; D265A/LS; LALA/LS; LALAGA/LS; LALAPG/LS; N297A/DHS; D265A/DHS; LALA/DHS; LAGA/DHS; LALAGA/DHS; LALAPG/DHS; SP/YTE; SPLE/YTE; SP/LS; SPLE/LS, SP/DHS; SPLE/DHS; N297A/LA; D265A/LA, LALA/LA, LAGA/LA, LALAGA/LA, LALAPG/LA, N297A/N434A; D265A/N434A; LALA/N434A, LAGA/N434A, LALAGA/N434A, LALAPG/N434A, N297A/N434W, D265A/N434W, LALA/N434W, LAGA/N434W, LALAGA/N434W, LALAPG/N434W, N297A/DQ, D265A/DQ, LALA/DQ, LAGA/DQ, LALAGA/DQ, LALAPG/DQ, N297A/DW, D265A/DW, LALA/DW, LAGA/DW, LALAGA/DW, LALAPG/DW N297A/YD, D265A/YD, LALA/YD, LAGA/YD, LALAGA/YD, LALAPG/YD, T307Q/Q311V/A378V (QVV), N297A/QVV, D265A/QVV, LALA/QVV, LAGA/QVV, LALAGA/QVV, LALAPG/QVV, DDRVV, N297A/DDRVV, D265A/DDRVV, LALA/DDRVV, LAGA/DDRVV, LALAGA/DDRVV, and LALAPG/DDRVV.

[00246] In certain embodiments, the antibodies described herein comprise an Fc region with YTE mutations at positions 253, 255, and 257. In certain embodiments, the antibodies described herein comprise an Fc region with LALA mutations at positions 235 and 236, respectively. In certain embodiments, the antibodies described herein comprise an Fc region with YTE mutations at positions 253, 255 and 257 and with LALA mutations at positions 235 and 236. In certain embodiments, the antibodies described herein comprise the heavy and light chain variable regions (VH and VL) as set forth in SEQ ID NOs: 3 and 39, respectively, and an Fc region comprising YTE mutations at positions 253, 255 and 257, respectively and with LALA mutations at positions 235 and 236, respectively.

[00247] In certain embodiments, the antibodies described herein comprise a human IgG1 Fc with LALA mutations. In certain embodiments, the antibodies described herein comprise a human IgG1 Fc with YTE mutations. In certain embodiments, the antibodies described herein comprise a human IgG1 Fc with LALA and YTE mutations. In certain embodiments, when direct numbering is used these “YTE” and “LALA” mutations can be located at different amino acid position numbers. For example, in one embodiment, the human Fc region comprises a human IgG1 Fc with LALA mutations at L235A/L236A and/or YTE mutations at M253Y/S255T/T257E.

[00248] In certain embodiments, the Fc region binds an Fcγ Receptor selected from the group consisting of: FcγRI, FcγRIIa, FcγRIIb, FcγRIIc, FcγRIIIa, and FcγRIIIb. In certain embodiments, the Fc region binds an Fcγ Receptor with higher affinity at pH 6.0 compared to an antibody comprising a wild-type Fc region.

Modifications

YTE Modifications

[00249] In certain embodiments, the fragment crystallizable region (Fc region) of the IL-13 antibody described herein carries a triple substitution M252Y/S254T/T256E (YTE) designed to increase the half-life of the IgG. In certain embodiments, the Fc region of the anti-IL-13 antibody described herein carries a triple substitution M253Y/S255T/T257E (YTE) designed to increase the half-life of the IgG. YTE substitutions increase the binding of the modified IgG to the human neonatal Fc receptor (FcRn). FcRn-bound IgG is recycled via lysosomal salvage, resulting in the IgG returning to the circulation. Thus, the YTE substitutions confer greater FcRn-IgG binding, prolonging the IgG serum half-life compared to an unmodified IgG.

LALA Modification

[00250] In certain embodiments, the IL-13 antibodies described herein additionally carries Fc region amino acid modifications L234A/L235A or L235A/L236A in the IgG1 heavy chain, commonly called LALA mutations. These changes can impair Fc receptor binding to IgG and prevent undesired effector cell activation.

Binding

[00251] In certain embodiments, an IL-13 antibody described herein is a high-affinity IgG1 humanized monoclonal antibody (mAb) that binds IL-13. In certain embodiments, the IL-13 antibody described herein contains YTE and LALA modifications and is built on an IgG1 backbone.

[00252] Without wishing to be bound by theory, the binding of the IL-13 antibodies described herein to IL-13 prevent the formation of the IL-13R α 1/IL-4R α active receptor heterodimer and subsequent IL-13-mediated signaling. The direct consequences of IL-13 signaling in atopic dermatitis (AD) pathology include dermal thickening, increased CD4⁺ T cell infiltration, and dermal barrier disruption. Consequently, preventing receptor heterodimer formation is believed to decrease the clinical severity of AD.

[00253] The affinity of a molecule X for its partner Y can be represented by the dissociation equilibrium constant (K_D). The kinetic components that contribute to the dissociation equilibrium constant are described in more detail below. Affinity can be measured by common methods known in the art, including those described herein, such as surface plasmon resonance (SPR) technology (*e.g.*, BIACORE®) or biolayer interferometry (*e.g.*, FORTEBIO®).

[00254] With regard to the binding of an antibody to a target molecule, the terms “bind,” “specific binding,” “specifically binds to,” “specific for,” “selectively binds,” and “selective for” a particular antigen (*e.g.*, a polypeptide target) or an epitope on a particular antigen mean binding that is measurably different from a non-specific or non-selective interaction (*e.g.*, with a non-target molecule). Specific binding can be measured, for example, by measuring binding to a target molecule (*i.e.*, IL-13) and comparing it to binding to a non-target molecule. Specific binding can also be determined by competition with a control molecule that mimics the epitope recognized on the target molecule. In that case, specific binding is indicated if the binding of the antibody to the target molecule is competitively inhibited by the control molecule. In certain embodiments, the affinity of an IL-13 antibody for a non-target molecule is less than about 50% of the affinity for IL-13. In certain embodiments, the affinity of an IL-13 antibody for a non-target molecule is less than about 40% of the affinity for IL-13. In certain embodiments, the affinity of an IL-13 antibody for a non-target molecule is less than about 30% of the affinity for IL-13. In certain embodiments, the affinity of an IL-13 antibody for a non-target molecule is less than about 20% of the affinity for IL-13. In certain embodiments, the affinity of an IL-13

antibody for a non-target molecule is less than about 10% of the affinity for IL-13. In certain embodiments, the affinity of an IL-13 antibody for a non-target molecule is less than about 1% of the affinity for IL-13. In certain embodiments, the affinity of an IL-13 antibody for a non-target molecule is less than about 0.1% of the affinity for IL-13.

[00255] When used herein in the context of two or more antibodies, the term “competes with” or “cross-competes with” indicates that the two or more antibodies compete for binding to an antigen (*e.g.*, IL-13). In one exemplary assay, IL-13 is coated on a surface and contacted with a first IL-13 antibody, after which a second IL-13 antibody is added. In another exemplary assay, a first IL-13 antibody is coated on a surface and contacted with IL-13, and then a second IL-13 antibody is added. If the presence of the first IL-13 antibody reduces binding of the second IL-13 antibody, in either assay, then the antibodies compete with each other. The term “competes with” also includes combinations of antibodies where one antibody reduces binding of another antibody, but where no competition is observed when the antibodies are added in the reverse order. However, in certain embodiments, the first and second antibodies inhibit binding of each other, regardless of the order in which they are added. In certain embodiments, one antibody reduces binding of another antibody to its antigen by at least 25%, at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% as measured in a competitive binding assay. A skilled artisan can select the concentrations of the antibodies used in the competition assays based on the affinities of the antibodies for IL-13 and the valency of the antibodies. The assays described in this definition are illustrative, and a skilled artisan can utilize any suitable assay to determine if antibodies compete with each other. Suitable assays are described, for example, in Cox *et al.*, “Immunoassay Methods,” in Assay Guidance Manual [Internet], Updated December 24, 2014 (ncbi.nlm.nih.gov/books/NBK92434/; accessed September 29, 2015); Silman *et al.*, Cytometry, 2001, 44:30-37; and Finco *et al.*, *J. Pharm. Biomed. Anal.*, 2011, 54:351-358; each of which is incorporated by reference in its entirety.

[00256] A test antibody competes with a reference antibody if an excess of a test antibody (*e.g.*, at least 2x, 5x, 10x, 20x, or 100x) inhibits or blocks binding of the reference antibody by, *e.g.*, at least 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, or 99% as measured in a competitive binding assay. Antibodies identified by competition assay (competing antibody) include antibodies binding to the same epitope as the reference antibody and antibodies binding to an adjacent epitope sufficiently proximal to the epitope bound by the reference antibody for steric

hindrance to occur. For example, a second, competing antibody can be identified that competes for binding to IL-13 with a first antibody described herein. In certain instances, the second antibody can block or inhibit binding of the first antibody by, *e.g.*, at least 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, or 99% as measured in a competitive binding assay. In certain instances, the second antibody can displace the first antibody by greater than 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, or 99%.

[00257] In certain embodiments, the antibody binds an IL-13 sequence set forth in SEQ ID NOs: 472-475.

[00258] In certain embodiments, the antibody binds to an IL-13 sequence set forth in SEQ ID NOs: 472-475 with a K_D of less than or equal to about 1, 2, 3, 4, 5, 6, 7, 8, 9×10^{-9} M, as measured by surface plasmon resonance (SPR). In certain embodiments, the antibody binds to an IL-13 sequence set forth in SEQ ID NOs: 472-475 with a K_D of less than or equal to about 1×10^{-10} M, as measured by surface plasmon resonance (SPR). In certain embodiments, the antibody binds to human IL-13 with a K_D of less than or equal to about 1×10^{-9} M, as measured by surface plasmon resonance (SPR).

[00259] In certain embodiments, an antibody provided herein binds IL-13 with a K_D of less than or equal to about 0.01, 0.02, 0.03, 0.04, 0.05, 0.06, 0.07, 0.08, 0.09, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 1.95, 2, 2.5, 3, 3.5, 4, 4.5, 5, 6, 7, 8, 9, or 10×10^{-8} M, as measured by ELISA or any other suitable method known in the art. In certain embodiments, an antibody provided herein binds IL-13 with a K_D of less than or equal to about 0.01, 0.02, 0.03, 0.04, 0.05, 0.06, 0.07, 0.08, 0.09, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, 1.9, 1.95, 2, 2.5, 3, 3.5, 4, 4.5, 5, 6, 7, 8, 9, or 10×10^{-9} M, as measured by ELISA or any other suitable method known in the art.

[00260] In certain embodiments, the K_D of an antibody provided herein for the binding of IL-13 is between about 0.001-0.01, 0.01-0.1, 0.01-0.05, 0.05-0.1, 0.1-0.5, 0.5-1, 0.25-0.75, 0.25-0.5, 0.5-0.75, 0.75-1, 0.75-2, 1.1-1.2, 1.2-1.3, 1.3-1.4, 1.4-1.5, 1.5-1.6, 1.6-1.7, 1.7-1.8, 1.8-1.9, 1.9-2, 1-2, 1-5, 2-7, 3-8, 3-5, 4-6, 5-7, 6-8, 7-9, 7-10, or $5-10 \times 10^{-8}$ M, as measured by ELISA or any other suitable method known in the art. In certain embodiments, an antibody provided herein binds IL-13 with a K_D of less than or equal to about 1×10^{-8} M, or less than or equal to above 1×10^{-9} M as measured by ELISA or any other suitable method known in the art.

[00261] In certain embodiments, an antibody provided herein binds IL-13 with a K_D of less than or equal to about 10, 9, 8, 7, 6, 5, 4.5, 4, 3.5, 3, 2.5, 2, 1.98, 1.95, 1.9, 1.85, 1.8, 1.75, 1.7, 1.65, 1.6, 1.55, 1.50, 1.45, 1.4, 1.3, 1.2, 1.1, 1, 0.9, 0.85, 0.8, 0.75, 0.7, 0.65, 0.6, 0.55, 0.5, 0.45, 0.4, 0.35, 0.3, 0.25, 0.2, 0.15, 0.1, 0.05, 0.01, 0.005, 0.001, 0.0005, or 0.0001×10^{-8} M, or less, as measured by ELISA or any other suitable method known in the art. In certain embodiments, an antibody provided herein binds IL-13 with a K_D between 5-3, 4-2, 3-1, 1.9-1.8, 1.8-1.7, 1.7-1.6, 1.6-1.5, 1.5-1.4, 1.4-1.3, 1.3-1.2, 1.2-1.1, 1.1-1, 1-0.9, 0.9-0.8, 0.8-0.7, 0.7-0.6, 0.6-0.5, 0.5-0.4, 0.4-0.3, 0.3-0.2, 0.2-0.1, 0.1-0.01, 0.01-0.001, or $0.001-0.0001 \times 10^{-8}$ M as measured by ELISA or any other suitable method known in the art.

Pharmaceutical Formulations and Methods of Manufacture Thereof

[00262] In some embodiments, the present disclosure provides pharmaceutical formulations that comprise a therapeutically effective amount of an IL-13 antibody disclosed herein. The pharmaceutical formulation comprises one or more excipients and/or surfactants and is maintained at a certain pH. Non-limiting examples of an “excipient,” as used herein, include any non-therapeutic agent added to the formulation to provide a desired physical or chemical property, for example, pH, osmolality, viscosity, clarity, color, isotonicity, odor, sterility, stability, rate of dissolution or release, adsorption, or penetration.

[00263] Methods of manufacturing pharmaceutical formulations of the disclosure are also contemplated. The method can include adjusting the matrix of an intermediate preparation of the disclosure (*e.g.*, changing the buffer composition and/or the concentration of a purified preparation of an IL-13 antibody), such as by Ultrafiltration and Diafiltration (UFDF), to increase a concentration of an IL-13 antibody.

[00264] In certain aspects, described herein is a method of manufacturing an intermediate preparation of an interleukin 13 (IL-13) antibody comprising: (a) obtaining a purified preparation of the IL-13 antibody; and (b) adjusting the matrix of the purified preparation of step (a), wherein adjusting the matrix of comprises performing Ultrafiltration and Diafiltration (UFDF) with the diafiltration buffer of the above described aspect or any one of the embodiments thereof, thereby obtaining the intermediate preparation of the IL-13 antibody. In some embodiments, the intermediate preparation (*e.g.*, a UFDF intermediate preparation) can be used to prepare a final preparation through the addition of excipients and/or dilution.

[00265] In certain embodiments, the intermediate preparation of the IL-13 antibody has a higher concentration of the IL-13 antibody relative to the purified preparation.

[00266] In certain embodiments, the method of manufacturing further comprises: (c) formulating the intermediate preparation to obtain a formulation of the IL-13 antibody. In certain embodiments, the formulation of the IL-13 antibody comprises a formulation described herein.

[00267] In some embodiments, described herein is a diafiltration buffer comprising: (a) a histidine buffer; and (b) arginine or a salt solution thereof, at pH of from 5.4 to 7.0, e.g., from 5.5-6.5. In some embodiments, the pH is from about 5.7 to about 6.5. In some embodiments, the pH is about 5.8 or about 6.0.

[00268] In some embodiments, the histidine buffer comprises a histidine and a histidine salt. In some embodiments, the histidine is L-histidine. In some embodiments, the histidine salt is L-histidine HCl monohydrate. Histidine buffer can be present in an amount of about 15-20 mM, for example, at about 18 mM.

[00269] In some embodiments, the diafiltration buffer comprises arginine, and wherein the arginine is L-arginine. In some embodiments, the diafiltration buffer comprises an L-arginine salt solution. In some embodiments, the L-arginine salt solution comprises HCl monohydrate. In some embodiments, the L-arginine salt solution is at a concentration between 40 mM and 200 mM. In some embodiments, the L-arginine salt solution is at a concentration of about 50 mM. In some embodiments, the L-arginine salt solution is at a concentration of about 100 mM. In some embodiments, the L-arginine salt solution is at a concentration of about 120 mM. In some embodiments, the L-arginine salt solution is at a concentration of about 170 mM.

[00270] Additional methods for the manufacture of pharmaceutical formulations of the disclosure are known in the art.

Excipients, Surfactants, and pH

[00271] Excipients may be selected for their suitability for intravenous or subcutaneous administration, providing the necessary stabilizing, buffering capacity, viscosity, and tonicity. The formulation can improve the stability of the IL-13 antibody and can provide a sterile solution suitable for subcutaneous or intravenous administration. In some embodiments the excipients and/or surfactants contained in the formulation are pharmacopoeial grade excipients. In some embodiments, the excipients in the formulation comprise a histidine buffer (also referred

to as a His buffer) (*e.g.*, a combination L-histidine and L-histidine HCl buffer, also referred to as L-His and L-His HCl), an acetate buffer, or a succinate buffer; arginine (Arg) and/or methionine (Met) (*e.g.*, L-arginine (L-Arg) and/or L-methionine (L-Met)) or a salt solution thereof; and a polysorbate or a poloxamer. In some embodiments, the formulation further comprises a sugar or sugar alcohol.

[00272] The one or more excipients in the pharmaceutical formulation of the present invention can comprise a buffering agent. The term “buffering agent,” as used herein, refers to one or more components that when added to an aqueous solution is able to protect the solution against variations in pH when adding acid or alkali, or upon dilution with a solvent. In addition to histidine buffers, acetate buffers, and succinate buffers, in certain embodiments, phosphate buffers, glycinate buffers, carbonate buffers, citrate buffers and the like can be used. In some embodiments, sodium, potassium or ammonium ions can serve as counterion.

[00273] In certain embodiments, the buffer or buffer system, such as a histidine buffer (*e.g.*, a combination L-histidine and L-histidine HCl buffer), acetate buffer, or succinate buffer, comprises at least one buffer that has a buffering range that overlaps fully or in part with the range of between 5.5 and 7.0 (*e.g.*, between 5.6 and 6.5, and 5.7 and 6.2). In some embodiments, the pH is between 5.6 and 6.5. In some embodiments, the pH is between 5.8 and 6.0.

[00274] In some embodiments, the buffer has a pH of about 5.5. In some embodiments, the buffer has a pH of about 5.6. In some embodiments, the buffer has a pH of about 5.7. In some embodiments, the buffer has a pH of about 5.8. In some embodiments, the buffer has a pH of about 5.9. In some embodiments, the buffer has a pH of about 6.0. In some embodiments, the buffer has a pH of about 6.1. In some embodiments, the buffer has a pH of about 6.2. In some embodiments, the buffer has a pH of about 6.3. In some embodiments, the buffer has a pH of about 6.4. In some embodiments, the buffer has a pH of about 6.5. In some embodiments, the buffer has a pH of about 5.9-6.3. In some embodiments, the buffer has a pH of about 6.0. Under the rules of scientific rounding, a pH greater than or equal to 5.45 and smaller than or equal to 5.55 is rounded as 5.5.

[00275] In some embodiments, the histidine buffer (*e.g.*, a combination L-histidine and L-histidine HCl buffer), acetate buffer, or succinate buffer is at a concentration between 5 mM and 20 mM (*e.g.*, between 6 mM and 19 mM, 7 mM and 18 mM, 8 mM and 17 mM, 9 mM and 16 mM, and 10 mM and 15 mM). In some embodiments, the histidine buffer, acetate buffer, or

succinate buffer is at a concentration between 6 mM and 19 mM. In some embodiments, the histidine buffer, acetate buffer, or succinate buffer is at a concentration between 7 mM and 18 mM. In some embodiments, the histidine buffer, acetate buffer, or succinate buffer is at a concentration between 8 mM and 17 mM. In some embodiments, the histidine buffer, acetate buffer, or succinate buffer is at a concentration between 9 mM and 16 mM. In some embodiments, the histidine buffer, acetate buffer, or succinate buffer is at a concentration between 10 mM and 15 mM.

[00276] In some embodiments, the histidine buffer (*e.g.*, a combination L-histidine and L-histidine HCl buffer), acetate buffer, or succinate buffer is at a concentration of about 1 mM. In some embodiments, the histidine buffer, acetate buffer, or succinate buffer is at a concentration of about 2 mM. In some embodiments, the histidine buffer, acetate buffer, or succinate buffer is at a concentration of about 3 mM. In some embodiments, the histidine buffer, acetate buffer, or succinate buffer is at a concentration of about 4 mM. In some embodiments, the histidine buffer, acetate buffer, or succinate buffer is at a concentration of about 5 mM. In some embodiments, the histidine buffer, acetate buffer, or succinate buffer is at a concentration of about 6 mM. In some embodiments, the histidine buffer, acetate buffer, or succinate buffer is at a concentration of about 7 mM. In some embodiments, the histidine buffer, acetate buffer, or succinate buffer is at a concentration of about 8 mM. In some embodiments, the histidine buffer, acetate buffer, or succinate buffer is at a concentration of about 9 mM. In some embodiments, the histidine buffer, acetate buffer, or succinate buffer is at a concentration of about 10 mM. In some embodiments, the histidine buffer, acetate buffer, or succinate buffer is at a concentration of about 11 mM. In some embodiments, the histidine buffer, acetate buffer, or succinate buffer is at a concentration of about 12 mM. In some embodiments, the histidine buffer, acetate buffer, or succinate buffer is at a concentration of about 13 mM. In some embodiments, the histidine buffer, acetate buffer, or succinate buffer is at a concentration of about 14 mM. In some embodiments, the histidine buffer, acetate buffer, or succinate buffer is at a concentration of about 15 mM. In some embodiments, the histidine buffer, acetate buffer, or succinate buffer is at a concentration of about 16 mM. In some embodiments, the histidine buffer, acetate buffer, or succinate buffer is at a concentration of about 17 mM. In some embodiments, the histidine buffer, acetate buffer, or succinate buffer is at a concentration of about 18 mM. In some embodiments, the histidine buffer, acetate buffer, or succinate buffer is at a concentration of about 19 mM. In some

embodiments, the histidine buffer, acetate buffer, or succinate buffer is at a concentration of about 20 mM.

[00277] In some embodiments the formulation comprises a histidine buffer (*e.g.*, a combination L-histidine and L-histidine HCl buffer), acetate buffer, or succinate buffer. In some embodiments the formulation comprises a histidine buffer. In some embodiments, the histidine buffer comprises L-histidine and L-histidine HCl. In some embodiments the formulation comprises an acetate buffer. In some embodiments, the formulation comprises a succinate buffer.

[00278] In some embodiments, a histidine buffer (*e.g.*, L-histidine and L-histidine HCl monohydrate) acts as a buffering agent. In some embodiments, the histidine buffer comprises a histidine and a histidine salt. In some embodiments, the histidine is L-histidine. In some embodiments, the histidine salt is L-histidine HCl monohydrate.

[00279] In some embodiments, the formulation comprises methionine. In some embodiments, the methionine is L-methionine.

[00280] In some embodiments, the methionine (*e.g.*, L-methionine) is at a concentration between 1 mM and 20 mM (*e.g.*, between 2 mM and 19 mM, 3 mM and 18 mM, 4 mM and 17 mM, 5 mM and 16 mM, and 5 mM and 15 mM). In some embodiments, the L-methionine is at a concentration between 1 mM and 19 mM. In some embodiments, the L-methionine is at a concentration between 2 mM and 18 mM. In some embodiments, the L-methionine is at a concentration between 3 mM and 17 mM. In some embodiments, the L-methionine is at a concentration between 4 mM and 16 mM. In some embodiments, the L-methionine is at a concentration between 5 mM and 15 mM.

[00281] In some embodiments, the methionine (*e.g.*, L-methionine) is at a concentration of about 1 mM. In some embodiments, the L-methionine is at a concentration of about 2 mM. In some embodiments, the L-methionine is at a concentration of about 3 mM. In some embodiments, the L-methionine is at a concentration of about 4 mM. In some embodiments, the L-methionine is at a concentration of about 5 mM. In some embodiments, the L-methionine is at a concentration of about 6 mM. In some embodiments, the L-methionine is at a concentration of about 7 mM. In some embodiments, the L-methionine is at a concentration of about 8 mM. In some embodiments, the L-methionine is at a concentration of about 9 mM. In some embodiments, the L-methionine is at a concentration of about 10 mM. In some embodiments, the L-methionine is at a concentration of about 11 mM. In some embodiments, the L-methionine is

at a concentration of about 12 mM. In some embodiments, the L-methionine is at a concentration of about 13 mM. In some embodiments, the L-methionine is at a concentration of about 14 mM. In some embodiments, the L-methionine is at a concentration of about 15 mM. In some embodiments, the L-methionine is at a concentration of about 16 mM. In some embodiments, the L-methionine is at a concentration of about 17 mM. In some embodiments, the L-methionine is at a concentration of about 18 mM. In some embodiments, the L-methionine is at a concentration of about 19 mM. In some embodiments, the L-methionine is at a concentration of about 20 mM.

[00282] In some embodiments, the formulation comprises arginine. In some embodiments, the arginine is L-arginine. In some embodiments, the formulation comprises an L-arginine salt solution. In some embodiments, the L-arginine or L-arginine salt solution acts as a viscosity modulator. In some embodiments, the L-arginine salt solution salt solution comprises HCl monohydrate.

[00283] In some embodiments, the arginine (*e.g.*, L-arginine) salt solution is at a concentration between 40 mM and 250 mM (*e.g.*, between 50 mM and 200 mM, 60 mM and 150 mM, 70 mM and 125 mM, 80 mM and 100 mM, and about 90 mM). For example, in some embodiments, the arginine (*e.g.*, L-arginine) salt solution is at a concentration between 70 mM and 130 mM.

[00284] In some embodiments, the L-arginine salt solution is at a concentration of about 40 mM. In some embodiments, the L-arginine salt solution is at a concentration of about 50 mM. In some embodiments, the L-arginine salt solution is at a concentration of about 60 mM. In some embodiments, the L-arginine salt solution is at a concentration of about 70 mM. In some embodiments, the L-arginine salt solution is at a concentration of about 80 mM. In some embodiments, the L-arginine salt solution is at a concentration of about 90 mM. In some embodiments, the L-arginine salt solution is at a concentration of about 100 mM. In some embodiments, the L-arginine salt solution is at a concentration of about 120 mM. In some embodiments, the L-arginine salt solution is at a concentration of about 125 mM. In some embodiments, the L-arginine salt solution is at a concentration of about 150 mM. In some embodiments, the L-arginine salt solution is at a concentration of about 170 mM. In some embodiments, the L-arginine salt solution is at a concentration of about 200 mM. In some embodiments, the L-arginine salt solution is at a concentration of about 250 mM.

[00285] The one or more excipients in the pharmaceutical formulation disclosed herein further comprises a surfactant. The term “surfactant,” as used herein, refers to a surface active molecule containing both a hydrophobic portion (*e.g.*, alkyl chain) and a hydrophilic portion (*e.g.*, carboxyl and carboxylate groups). Surfactants are useful in pharmaceutical formulations for reducing aggregation of a therapeutic protein. Surfactants suitable for use in the pharmaceutical formulations are generally non-ionic surfactants and include, but are not limited to, polysorbates (*e.g.*, polysorbates 20 or 80); poloxamers (*e.g.*, poloxamer 188); sorbitan esters and derivatives; Triton; sodium laurel sulfate; sodium octyl glycoside; lauryl-, myristyl-, linoleyl-, or stearyl-sulfobetadine; lauryl-, myristyl-, linoleyl- or stearyl-sarcosine; linoleyl-, myristyl-, or cetyl-betaine; lauramidopropyl-cocamidopropyl-, linoleamidopropyl-, myristamidopropyl-, palmidopropyl-, or isostearamidopropylbetaine (*e.g.*, lauroamidopropyl); myristamidopropyl-, palmidopropyl-, or isostearamidopropyl-dimethylamine; sodium methyl cocoyl-, or disodium methyl oleyl-taurate; and the MONAQUATTM series (Mona Industries, Inc., Paterson, N.J.), polyethylene glycol, polypropyl glycol, and copolymers of ethylene and propylene glycol (*e.g.*, Pluronic, PF68, etc.). In certain embodiments, the surfactant is a polysorbate. In certain embodiments, the surfactant is polysorbate 80. In certain embodiments, the surfactant is a poloxamer. In certain embodiments, the surfactant is poloxamer 188.

[00286] In some embodiments, a polysorbate or poloxamer acts as a stabilizer. In some embodiments, the polysorbate or poloxamer is at a concentration between 0.005% w/v and 0.15% w/v or between 0.01% w/v and 0.15% w/v (*e.g.*, between 0.02% and 0.14%, 0.03% and 0.13%, 0.04% and 0.12%, 0.05% and 0.11%, or about 0.1%). In some embodiments, the polysorbate or poloxamer is at a concentration between 0.02% and 0.14%. In some embodiments, the polysorbate or poloxamer is at a concentration between 0.03% and 0.13%. In some embodiments, the polysorbate or poloxamer is at a concentration between 0.04% and 0.12%. In some embodiments, the polysorbate or poloxamer is at a concentration between 0.05% and 0.11%. In some embodiments, the polysorbate or poloxamer is at a concentration between 0.005% w/v and 0.10% w/v, or between 0.005% w/v and 0.05% w/v or between 0.05% w/v and 0.10 w/v, or at about 0.05% w/v or at 0.05% w/v.

[00287] In some embodiments, the polysorbate or poloxamer is at a concentration of about 0.005% w/v. In some embodiments, the polysorbate or poloxamer is at a concentration of about 0.01% w/v. In some embodiments, the polysorbate or poloxamer is at a concentration of about

0.02% w/v. In some embodiments, the polysorbate or poloxamer is at a concentration of about 0.03% w/v. In some embodiments, the polysorbate or poloxamer is at a concentration of about 0.04% w/v. In some embodiments, the polysorbate or poloxamer is at a concentration of about 0.05% w/v. In some embodiments, the polysorbate or poloxamer is at a concentration of about 0.06% w/v. In some embodiments, the polysorbate or poloxamer is at a concentration of about 0.07% w/v. In some embodiments, the polysorbate or poloxamer is at a concentration of about 0.08% w/v. In some embodiments, the polysorbate or poloxamer is at a concentration of about 0.09% w/v. In some embodiments, the polysorbate or poloxamer is at a concentration of about 0.1% w/v. In some embodiments, the polysorbate or poloxamer is at a concentration of about 0.11% w/v. In some embodiments, the polysorbate or poloxamer is at a concentration of about 0.12% w/v. In some embodiments, the polysorbate or poloxamer is at a concentration of about 0.13% w/v. In some embodiments, the polysorbate or poloxamer is at a concentration of about 0.14% w/v. In some embodiments, the polysorbate or poloxamer is at a concentration of about 0.15% w/v.

[00288] In some embodiments, the polysorbate is polysorbate 20, polysorbate 40, polysorbate 60, or polysorbate 80. In some embodiments, the polysorbate is polysorbate 20. In some embodiments, the polysorbate is polysorbate 40. In some embodiments, the polysorbate is polysorbate 60. In some embodiments, the polysorbate is polysorbate 80.

[00289] In some embodiments, the poloxamer is poloxamer 188, also referred to herein as P188. In some embodiments, P188 is included in the formulation at a concentration in a range of, for example 0.1-2.0 mg/ml, 0.25-1.5 mg/ml or 0.5-1.0 mg/ml, or at a concentration of 0.25 mg/ml, 0.5 mg/ml, 0.75 mg/ml or 1.0 mg/ml. In some embodiments, the formulation comprises P188 at a concentration of 0.5 mg/ml.

[00290] The one or more excipients in the pharmaceutical formulation of the present invention can further comprise a metal ion chelator. Metal ion chelators, also known as chelating agents, bind metal ions to form water soluble complexes and thus can be used to remove metal ions from a formulation. In embodiments, the metal ion chelator is ethylenediaminetetraacetic acid (EDTA), or a salt thereof (*e.g.*, disodium EDTA, sodium calcium edetate, tetrasodium EDTA). In embodiments, the metal ion chelator is EDTA disodium salt (EDTA-2Na). In embodiments, the metal ion chelator is EDTA-2Na, which is included in the formulation at a concentration in a range of, for example, 0.001-1 mM or 0.01-1mM or 0.001-0.5 mM or 0.01-0.5 mM or at a

concentration of 0.01 mM, 0.02 mM, 0.03 mM, 0.04 mM, 0.05 mM, 0.06 mM, 0.07 mM, 0.08 mM, 0.09 mM, 0.1 mM, 0.2 mM, 0.3 mM, 0.4 mM, 0.5 mM, 0.6 mM, 0.7 mM, 0.8 mM, 0.9 mM or 1 mM. In embodiments, the formulation comprises EDTA (e.g., EDTA-2Na) at a concentration of 0.05 mM.

[00291] Other metal ion chelators are known in the art, non-limiting examples of which include ethylenediamine (1,2-diaminoethane), diethylenetriaminepentaacetic acid (DTPA), ethylene glycol-bis(beta-aminoethyl ether)-N,N,N',N'-tetraacetic acid (EGTA), succimer (dimercaptanol), dimercaprol (BAL), nitrilotriacetic acid (NTA), iminodisuccinic acid (IDS), polyaspartic acid, S,S-ethylenediamine-N,N'-disuccinic acid (EDDS), methylglycinediacetic acid (MGDA), L-Glutamic acid N,N-diacetic acid, tetrasodium salt (GLDA), metachelate and citric acid.

[00292] The one or more excipients in the pharmaceutical formulation of the present invention can further comprise a sugar or sugar alcohol. Sugars and sugar alcohols are useful in pharmaceutical formulations as a thermal stabilizer. In certain embodiments, the pharmaceutical formulation comprises a sugar, for example, a monosaccharide (glucose, xylose, or erythritol), a disaccharide (e.g., sucrose, trehalose, maltose, or galactose), or an oligosaccharide (e.g., stachyose). In specific embodiments, the pharmaceutical formulation comprises sucrose. In certain embodiments, the pharmaceutical composition comprises a sugar alcohol, for example, a sugar alcohol derived from a monosaccharide (e.g., mannitol, sorbitol, or xylitol), a sugar alcohol derived from a disaccharide (e.g., lactitol or maltitol), or a sugar alcohol derived from an oligosaccharide. In specific embodiments, the pharmaceutical formulation comprises sucrose.

[00293] In some embodiments, a sugar or sugar alcohol (e.g., sucrose) acts as a stabilizer. In some embodiments, the sugar or sugar alcohol is at a concentration between 1% w/v and 5% w/v (e.g., between 2% w/v and 4% w/v, or about 3% w/v). In some embodiments, the sugar or sugar alcohol is at a concentration between 2% w/v and 4% w/v.

[00294] In some embodiments, the sugar or sugar alcohol is at a concentration of about 1% w/v. In some embodiments, the sugar or sugar alcohol is at a concentration of about 2% w/v. In some embodiments, the sugar or sugar alcohol is at a concentration of about 3% w/v. In some embodiments, the sugar or sugar alcohol is at a concentration of about 4% w/v. In some embodiments, the sugar or sugar alcohol is at a concentration of about 5% w/v.

[00295] In some embodiments, the sugar or sugar alcohol is a disaccharide. In some embodiments, the disaccharide is sucrose.

[00296] In some embodiments, the formulation is adjusted to final volume in water for injection (WFI).

[00297] In certain embodiments, the drug product is diluted in an aqueous carrier suitable for the route of administration, *e.g.*, intravenous administration. Exemplary carriers include sterile water for injection (SWFI), bacteriostatic water for injection (BWFI), a pH buffered solution (*e.g.*, phosphate-buffered saline), sterile saline solution, Ringer's solution, or dextrose solution. In one embodiment, when the pharmaceutical formulation is prepared for intravenous administration, the pharmaceutical formulation can be diluted in a 5% dextrose solution (D5W).

Exemplary Formulations

[00298] In some embodiments, the pharmaceutical formulation of the present invention comprises: (a) an IL-13 antibody present at a concentration between 140 mg/mL and 290 mg/mL; (b) a histidine buffer (*e.g.*, combination L-histidine and L-histidine HCl buffer), an acetate buffer (*e.g.*, combination acetic acid and sodium acetate trihydrate), or a succinate buffer (*e.g.*, combination succinic acid and sodium succinate hexahydrate); (c) arginine and/or methionine (*e.g.*, L-arginine and/or L-methionine) or a salt solution thereof; and (d) a polysorbate or a poloxamer, at pH 5.0 to 7.0.

[00299] In some embodiments, the pharmaceutical formulation of the present invention comprises: (a) IL-13 antibody present at a concentration between 140 mg/mL and 290 mg/mL; (b) a histidine buffer (*e.g.*, combination L-histidine and L-histidine HCl buffer), an acetate buffer (*e.g.*, combination acetic acid and sodium acetate trihydrate), or a succinate buffer (*e.g.*, combination succinic acid and sodium succinate hexahydrate); (c) arginine and/or methionine (*e.g.*, L-arginine and/or L-methionine) or a salt solution thereof; and (d) a polysorbate or a poloxamer, at pH 5.0 to 7.0. In some embodiments, the IL-13 antibody comprises: (i) a variable heavy (VH) chain sequence comprising three heavy chain CDR sequences, CDR-H1, CDR-H2, and CDR-H3; and (ii) a variable light (VL) chain sequence comprising three light chain CDR sequences, CDR-L1, CDR-L2, and CDR-L3; wherein: (a) CDR-H1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 58-99 and 121; (b) CDR-H2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 100-111;

(c) CDR-H3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 112-120 and 130-140, (d) CDR-L1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 141-144 and 149-152, (e) CDR-L2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 153-158 and the amino acid sequence LAS; and (f) CDR-L3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 165-172.

[00300] In some embodiments, the pharmaceutical formulation of the present invention comprises: (a) an IL-13 antibody at a concentration, *e.g.*, between 140 mg/mL and 290 mg/mL; (b) a histidine buffer (*e.g.*, a combination L-histidine and L-histidine HCl buffer), an acetate buffer, or a succinate buffer; (c) arginine and/or methionine (*e.g.*, L-arginine and/or L-methionine) or a salt solution thereof; and (d) a polysorbate or a poloxamer, at pH 5.0 to 7.0. In some embodiments, the IL-13 antibody comprises: (i) a variable heavy (VH) chain sequence comprising three heavy chain CDR sequences, CDR-H1, CDR-H2, and CDR-H3; and (ii) a variable light (VL) chain sequence comprising three light chain CDR sequences, CDR-L1, CDR-L2, and CDR-L3; wherein: (a) CDR-H1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 58, SEQ ID NO: 68, and SEQ ID NO: 85; (b) CDR-H2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 100, SEQ ID NO: 104, and SEQ ID NO: 108; (c) CDR-H3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 112 and SEQ ID NO: 130, (d) CDR-L1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 141 and SEQ ID NO: 149, (e) CDR-L2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 153 and SEQ ID NO: 164; and (f) CDR-L3 comprises the sequence set forth in SEQ ID NO: 165.

[00301] In some embodiments, the pharmaceutical formulation of the present invention comprises: (a) an IL-13 present at a concentration of, *e.g.*, about 180 mg/mL; (b) a histidine buffer (*e.g.*, a combination L-histidine and L-histidine HCl buffer) at a concentration of about 10 mM; (c) an L-arginine salt solution at a concentration of about 120 mM; (d) L-methionine at a concentration of about 10 mM; and (e) polysorbate 80 at a concentration of about 0.05% w/v, at pH of about 5.8.

[00302] In some embodiments, the pharmaceutical formulation of the present invention comprises: (a) IL-13 antibody present at a concentration of, *e.g.*, about 180 mg/mL; (b) a

histidine buffer (*e.g.*, a combination L-histidine and L-histidine HCl buffer) at a concentration of about 10 mM; (c) an L-arginine salt solution at a concentration of about 80 mM; (d) L-methionine at a concentration of about 10 mM; and (e) polysorbate 80 at a concentration of about 0.05% w/v, at pH of about 5.8.

[00303] In some embodiments, the pharmaceutical formulation of the present invention comprises: (a) IL-13 antibody present at a concentration of, *e.g.*, about 200 mg/mL; (b) a histidine buffer (*e.g.*, a combination L-histidine and L-histidine HCl buffer) at a concentration of about 10 mM; (c) an L-arginine salt solution at a concentration of about 120 mM; (d) L-methionine at a concentration of about 10 mM; and (e) polysorbate 80 at a concentration of about 0.05% w/v, at pH of about 5.8.

[00304] In some embodiments, the pharmaceutical formulation of the present invention comprises: (a) an IL-13 antibody present at a concentration of, *e.g.*, about 180 mg/mL (*e.g.*, at 180 mg/ml); (b) a histidine buffer (*e.g.*, a combination L-histidine and L-histidine HCl buffer) at a concentration of about 10 mM (*e.g.*, at 10 mM); (c) an L-arginine salt solution at a concentration of about 120 mM (*e.g.*, at 120 mM); (d) L-methionine at a concentration of about 10 mM (*e.g.*, at 10 mM); (e) polysorbate 80 at a concentration of about 0.05% w/v (*e.g.*, at 0.05% w/v); and (f) EDTA or a salt thereof (*e.g.*, EDTA-2Na) at a concentration of about 0.05 mM (*e.g.*, at 0.05 mM), at pH of about 5.8-6.0 (*e.g.*, at pH 5.8 or pH 6.0).

[00305] In some embodiments, the pharmaceutical formulation of the present invention comprises: (a) an IL-13 antibody present at a concentration of, *e.g.*, about 180 mg/mL (*e.g.*, at 180 mg/ml); (b) a histidine buffer (*e.g.*, a combination L-histidine and L-histidine HCl buffer) at a concentration of about 10 mM (*e.g.*, at 10 mM); (c) an L-arginine salt solution at a concentration of about 120 mM (*e.g.*, at 120 mM); (d) L-methionine at a concentration of about 10 mM (*e.g.*, at 10 mM); (e) poloxamer 188 at a concentration of about 0.5 mg/ml (*e.g.*, at 0.5 mg/ml), at pH of about 5.8-6.0 (*e.g.*, at pH 5.8 or pH 6.0).

[00306] In some embodiments, the formulation comprises a sugar, for example, sucrose at a concentration between about 2% w/v and 8% w/v, such as a concentration of about 3% w/v or about 5% w/v.

Stability of the Anti-IL-13 Antibody

[00307] The pharmaceutical formulations of the present invention exhibit high levels of stability. A pharmaceutical formulation is stable when the IL-13 antibody within the formulation retains an acceptable degree of physical property, chemical structure, and/or biological function after storage under defined conditions.

[00308] Exemplary methods to determine stability of the IL-13 antibody in the pharmaceutical formulation are described in the **Examples** of the present disclosure. Additionally, stability of the protein can be assessed by measuring the binding affinity of the IL-13 antibody to its targets or the biological activity of the IL-13 antibody in certain *in vitro* assays.

[00309] The pharmaceutical formulation can be prepared and stored as a liquid formulation. In certain embodiments, the pharmaceutical formulation is a liquid formulation for storage frozen (-20 to -70° C), under refrigerated conditions (typically 2-8° C), or at room temperature (typically 20-26° C) before preparation for administration. In certain embodiments, the pharmaceutical formulation is a liquid formulation for storage at a suitable temperature and protected from light.

[00310] Stability studies have found an antibody concentration for solution of 180 mg/mL or 200 mg/mL for injection to be compatible with its excipients and primary packaging materials. Antibody 180 mg/mL or 200 mg/mL concentrate for injection is suitable for subcutaneous administration with disposable syringes, without dilution or with dilution in a carrier buffer. Materials found to be compatible with an antibody herein comprise injection syringes composed of polypropylene or polycarbonate, and needles for injection composed of stainless steel. Compatibility of antibody concentrate for solution for injection has been demonstrated with pre-filled syringes for an antibody concentration of from 160 mg/mL and 250 mg/mL.

Dosage Forms

[00311] Prior to pharmaceutical use, the pharmaceutical formulation can be diluted in an aqueous carrier if suitable for the route of administration. In some embodiments, a IL-13 antibody is fully formulated for subcutaneous administration (*i.e.*, no diluents are added), and thus is identical in composition to the formulation described herein. Alternatively, if suitable for the route of administration, *e.g.*, for intravenous administration, the IL-13 antibody may be further diluted in an appropriate carrier prior to pharmaceutical use.

[00312] For intravenous administration, suitable carriers include sterile water for injection (SWFI), bacteriostatic water for injection (BWFI), a pH buffered solution (*e.g.*, phosphate-buffered saline), sterile saline solution, Ringer's solution, or dextrose solution. For example, when the pharmaceutical formulation is prepared for intravenous administration, the pharmaceutical formulation may comprises a dextrose solution, such as a 5% dextrose solution (D5W). In certain embodiments, the diluted pharmaceutical formulation is isotonic and suitable for administration by intravenous infusion, *e.g.*, D5W. In certain embodiments, the formulation is diluted in about 50 mL D5W, 100 mL D5W, 150 mL D5W, 200 mL D5W, 250 mL D5W, 300 mL D5W, 350 mL D5W, 400 mL D5W, 450 mL D5W, 500 mL D5W, or 1 L D5W.

[00313] The pharmaceutical formulation comprises the IL-13 antibody at a concentration suitable for storage. In certain embodiments, the pharmaceutical formulation comprises the IL-13 antibody at a concentration between 160 mg/mL and 250 mg/mL (*e.g.*, between 170 mg/mL and 210 mg/mL, 180 mg/mL and 200 mg/mL, or about 190 mg/mL). In some embodiments, the IL-13 antibody is at a concentration between 170 mg/mL and 210 mg/mL. In some embodiments, the IL-13 antibody is at a concentration between 180 mg/mL and 200 mg/mL.

[00314] In some embodiments, the IL-13 antibody is at a concentration of about 160 mg/mL. In some embodiments, the IL-13 antibody is at a concentration of about 170 mg/mL. In some embodiments, the IL-13 antibody is at a concentration of about 180 mg/mL. In some embodiments, the IL-13 antibody is at a concentration of about 190 mg/mL. In some embodiments, the IL-13 antibody is at a concentration of about 200 mg/mL. In some embodiments, the IL-13 antibody is at a concentration of about 210 mg/mL. In some embodiments, the IL-13 antibody is at a concentration of about 220 mg/mL. In some embodiments, the IL-13 antibody is at a concentration of about 230 mg/mL. In some embodiments, the IL-13 antibody is at a concentration of about 240 mg/mL. In some embodiments, the IL-13 antibody is at a concentration of about 250 mg/mL.

[00315] In some embodiments, the IL-13 antibody is at a concentration of 160 mg/mL. In some embodiments, the IL-13 antibody is at a concentration of 170 mg/mL. In some embodiments, the IL-13 antibody is at a concentration of 180 mg/mL. In some embodiments, the IL-13 antibody is at a concentration of 190 mg/mL. In some embodiments, the IL-13 antibody is at a concentration of 200 mg/mL. In some embodiments, the IL-13 antibody is at a concentration of 210 mg/mL. In some embodiments, the IL-13 antibody is at a concentration of 220 mg/mL. In

some embodiments, the IL-13 antibody is at a concentration of 230 mg/mL. In some embodiments, the IL-13 antibody is at a concentration of 240 mg/mL. In some embodiments, the IL-13 antibody is at a concentration of 250 mg/mL.

[00316] Formulations described herein may be included in *e.g.*, a vial, bag, bottle or on-body device. In some embodiments, the vial is a syringe. In some embodiments, the vial is a glass syringe. In some embodiments, the syringe is a prefilled syringe. In some embodiments, the prefilled syringe is a prefilled glass syringe. Additionally, formulations herein may be included in and administered by pens, autoinjectors, including autoinjector syringes and cartridges, and on-body devices. In some embodiments, when an on-body device is used for administration, up to 5 mL of the formulation may be present in the device.

[00317] In some embodiments, an extractable volume of the vial (*e.g.*, prefilled syringe) is between 1.0 mL and 10.0 mL, *e.g.*, between 1.0 mL and 3.0 mL or between 3.0 mL and 10.0 mL. In some embodiments, the extractable volume of the vial is about 1.0, 2.0 mL, 3.0 mL, 4.0 mL, 5.0 mL, 6.0 mL, 7.0 mL, 8.0 mL, 9.0 mL or 10.0 mL. As used herein, the “extractable volume” of the vial is the amount that can be withdrawn from the receptacle. The fill volume is greater than the extractable volume to ensure that the extractable volume can be obtained.

[00318] In certain embodiments, the pharmaceutical formulation is packaged in a vial (*e.g.*, a pen or syringe). In certain embodiments, the vial comprises an overfill to allow for complete removal of the intended dose. In certain embodiments, the vial comprises an overfill of 5 to 35%, 10 to 30%, 15 to 25%, or 10 to 20%. In a particular embodiment, the vial comprises an overfill of about 20%.

[00319] In certain embodiments, the formulation may be a liquid formulation. In certain embodiments, the amount of IL-13 antibody in the container is suitable for administration as a single dose. In certain embodiments, the amount of IL-13 antibody in the container is suitable for administration in multiple doses. In certain embodiments, the pharmaceutical formulation comprises the IL-13 antibody in an amount of 0.1 to 200 mg. In certain embodiments, the pharmaceutical formulation comprises the IL-13 antibody in an amount of 1 to 200 mg, 10 to 200 mg, 20 to 200 mg, 50 to 200 mg, 100 to 200 mg, 200 to 500 mg, 500 to 2000 mg, 1000 to 2000 mg, 0.1 to 1000 mg, 1 to 1000 mg, 10 to 1000 mg, 20 to 1000 mg, 50 to 1000 mg, 100 to 1000 mg, 200 to 1000 mg, 500 to 1000 mg, 0.1 to 500 mg, 1 to 500 mg, 10 to 500 mg, 20 to 500 mg, 50 to 500 mg, 100 to 500 mg, 200 to 500 mg, 0.1 to 200 mg, 1 to 200 mg, 10 to 200 mg, 20

to 200 mg, 50 to 200 mg, 100 to 200 mg, 0.1 to 100 mg, 1 to 100 mg, 10 to 100 mg, 20 to 100 mg, 50 to 100 mg, 0.1 to 50 mg, 1 to 50 mg, 10 to 50 mg, 20 to 50 mg, 0.1 to 20 mg, 1 to 20 mg, 10 to 20 mg, 0.1 to 10 mg, 1 to 10 mg, or 0.1 to 1 mg. In certain embodiments, the pharmaceutical formulation comprises the IL-13 antibody in an amount of about 0.1 mg, about 0.5 mg, about 1 mg, about 1.5 mg, about 2 mg, about 2.5 mg, about 5 mg, about 10 mg, about 20 mg, about 30 mg, about 40 mg, about 50 mg, about 60 mg, about 70 mg, about 80 mg, about 90 mg, about 100 mg, about 150 mg, about 200 mg, about 250 mg, about 300 mg, about 400 mg, about 450 mg, about 500 mg, about 600 mg, about 700 mg, about 800 mg, about 900 mg, about 1000 mg, about 1500 mg, or about 2000 mg.

Methods of Use

[00320] The present application provides compositions comprising a formulation or vial described herein for use in the treatment of an inflammatory disorder or disease. In some embodiments, the present application also provides compositions comprising a formulation or vial (*e.g.*, pre-filled syringe) described herein for use in methods of treating inflammatory, allergic, and immunologic diseases, such as atopic dermatitis, in a patient in need thereof. In certain embodiments, the patient has been diagnosed with moderate-to-severe atopic dermatitis. In certain embodiments, the patient has had moderate-to-severe atopic dermatitis for at least one year. In certain embodiments, the patient is a pediatric patient.

[00321] In certain embodiments, the patient has one or more of: (a) an Eczema Area and Severity Index Score (EASI) of ≥ 10 (*e.g.*, an EASI of ≥ 16 or an EASI ≥ 10 and < 16), (b) an Investigator Global Assessment (IGA) score of ≥ 3 and (c) a body surface area (BSA) of $\geq 10\%$. In certain embodiments, the patient has an Eczema Area and Severity Index Score (EASI) of ≥ 10 . In certain embodiments, the patient has an Eczema Area and Severity Index Score (EASI) of ≥ 16 . In certain embodiments, the patient has an Eczema Area and Severity Index Score (EASI) of ≥ 10 and less than 16. In certain embodiments, the patient has an Investigator Global Assessment (IGA) score of ≥ 3 . In certain embodiments, the patient has a body surface area (BSA) of $\geq 10\%$.

[00322] The “Investigator Global Assessment” or “IGA” is an assessment measure used globally to rate the severity of the patient’s AD (Simpson E, *et al. J Am Acad Dermatol.* 2020;83(3):839-846). It is based on a 5-point scale ranging from 0 (clear) to 4 (severe) and a

score is selected using descriptors that best describe the overall appearance of the lesions at a given time point. It is not necessary that all characteristics under Morphological Description be present. The IGA can be conducted prior to conducting the EASI and BSA assessments.

[00323] The “Eczema Area and Severity Index” or “EASE is a measure used in clinical settings to assess the severity and extent of AD (Hanifin *et al.*, *Exp Dermatol.* 2001; 10: 11-18). EASI is a composite index with scores ranging from 0 to 72, with the higher values indicating more severe and or extensive disease. The severity of erythema, induration/papulation, excoriation, and lichenification can be assessed by a clinician or other medical professional on a scale of 0 (absent) to 3 (severe) for each of the 4 body areas: head and neck, trunk, upper limbs, and lower limbs, with half points allowed. In addition, the extent of AD involvement in each of the 4 body areas can be assessed as a percentage by body surface area of head, trunk, upper limbs, and lower limbs, and converted to a score of 0 to 6. A total score (0 – 72) is assigned based on the sum of total scores for each of the four body region scores.

[00324] The “Scoring of Atopic Dermatitis” or “SCORAD” is a validated clinical tool for assessing the extent and intensity of AD developed by the European Task Force on Atopic Dermatitis (Consensus report of the European Task Force on Atopic Dermatitis. *Dermatology.* 1993; 186(1):23-31). There are 3 components to the assessment: (i) the extent of AD is assessed as a percentage of each defined body area and reported as the sum of all areas, with a score ranging from 0 to 100 (assigned as “A” in the overall SCORAD calculation); (ii) the severity of 6 symptoms of AD: redness, swelling, oozing/crusting, excoriation, skin thickening/lichenification, dryness. Each item is graded as follows: none (0), mild (1), moderate (2), or severe (3) (for a maximum of 18 total points, assigned as “B” in the overall SCORAD calculation); (iii) subjective assessment of itch and of sleeplessness is recorded for each symptom using a visual analogue scale (VAS), where 0 is no itch (or sleeplessness) and 10 is the worst imaginable itch (or sleeplessness), with a maximum possible score of 20 (assigned as “C” in the overall SCORAD calculation). The SCORAD Index formula is: $A/5 + 7B/2 + C$. The maximal score of the SCORAD Index is 103.

[00325] Pruritus Numerical Rating Scale (NRS) is an 11 -point scale used by patients (and if applicable, with help of parents/ caregiver if required) to rate their worst itch severity over the past 24 hours with 0 indicating “No itch” and 10 indicating “Worst itch imaginable” (Phan NQ, *et al. Acta Derm Venereol* 2012; 92: 502-507). Assessments are recorded by the patient daily

using an electronic diary. The baseline pruritus NRS is determined based on the average of daily Pruritus NRS during the 7 days immediately preceding baseline. A minimum of 4 daily scores out of the 7 days immediately preceding baseline is required for this calculation.

[00326] Sleep loss scale rates patient's sleep loss due to pruritus on a 5-point Likert scale (with scores ranging from 0 [not at all], 1 [a little], 2 [moderately], 3 [quite a bit], to 4 [unable to sleep at all]). Assessments will be recorded daily by the patient using an electronic diary.

[00327] The Patient-Oriented Eczema Measure (POEM) is a 7-item, validated, questionnaire completed by the patient (and if applicable, with help of parents/ caregiver if required) to assess disease symptoms over the last week (Centre of Evidence Based Dermatology. POEM – Patient Oriented Eczema Measure. Available at

www.nottingham.ac.uk/research/groups/cebd/resources/poem.aspx). Patients are asked to respond to 7 questions on skin dryness, itching, flaking, cracking, sleep loss, bleeding, and weeping. All 7 answers carry equal weight with a total possible score from 0 to 28 (answers scored as: No days=0; 1- 2 days = 1; 3-4 days = 2; 5-6 days = 3; everyday = 4). A high score is Indicative of a poor quality of life. POEM responses are captured weekly using an electronic diary.

[00328] The Dermatology Life Quality Index (DLQI) is a 10-item, validated questionnaire completed by the patient or caregiver, used to assess the impact of skin disease on the quality of life of the patient (Finlay, A. Y. and Khan, G. K. 1994. *Clinical and Experimental Dermatology* 1993 Sep 23; 19:210-216). The 10 questions cover the following topics: symptoms, embarrassment, shopping and home care, clothes, social and leisure, sport, work or study, close relationships, sex, and treatment, over the previous week. Each question is scored from 0 to 3 ("not at all," "a little," "a lot," and "very much"), giving a total score ranging from 0 to 30. A high score is indicative of a poor quality of life.

[00329] In certain embodiments, methods described herein comprise determining one or more of the following characteristics of the patient at baseline and during and after the induction period: Eczema Area and Severity Index (EASI), Investigator Global Assessment (IGA), Body Surface Area (BSA), Pruritus Numerical Rating Scale (NRS), Sleep loss scale, SCORing Atopic Dermatitis (SCORAD), Patient Oriented Eczema Measure (POEM), Dermatology Life Quality Index (DLQI). In certain embodiments, methods described herein comprise determining the following characteristic of the patient at baseline and during and after the induction period:

Eczema Area and Severity Index (EASI). In certain embodiments, methods described herein comprise determining the following characteristic of the patient at baseline and during and after the induction period: Investigator Global Assessment (IGA). In certain embodiments, methods described herein comprise determining the following characteristic of the patient at baseline and during and after the induction period: Body Surface Area (BSA). In certain embodiments, methods described herein comprise determining the following characteristic of the patient at baseline and during and after the induction period: Pruritus Numerical Rating Scale (NRS). In certain embodiments, methods described herein comprise determining the following characteristic of the patient at baseline and during and after the induction period: Sleep loss scale, SCORing Atopic Dermatitis (SCORAD). In certain embodiments, methods described herein comprise determining the following characteristic of the patient at baseline and during and after the induction period: Patient Oriented Eczema Measure (POEM). In certain embodiments, methods described herein comprise determining the following characteristic of the patient at baseline and during and after the induction period: Dermatology Life Quality Index (DLQI).

[00330] In certain embodiments, a patient described herein is determined to have one or more of the following characteristics of the patient at baseline and during and after the induction period: Eczema Area and Severity Index (EASI), Investigator Global Assessment (IGA), Body Surface Area (BSA), Pruritus Numerical Rating Scale (NRS), Sleep loss scale, SCORing Atopic Dermatitis (SCORAD), Patient Oriented Eczema Measure (POEM), Dermatology Life Quality Index (DLQI). In certain embodiments, a patient herein is determined to have a characteristic Eczema Area and Severity Index (EASI) at baseline and during and after the induction period. In certain embodiments, a patient herein is determined to have a characteristic Investigator Global Assessment (IGA) at baseline and during and after the induction period. In certain embodiments, a patient herein is determined to have a characteristic Body Surface Area (BSA) at baseline and during and after the induction period. In certain embodiments, a patient herein is determined to have a characteristic Pruritus Numerical Rating Scale (NRS) at baseline and during and after the induction period. In certain embodiments, a patient herein is determined to have a characteristic Sleep loss scale, SCORing Atopic Dermatitis (SCORAD) at baseline and during and after the induction period. In certain embodiments, a patient herein is determined to have a characteristic Patient Oriented Eczema Measure (POEM) at baseline and during and after the induction period.

In certain embodiments, a patient herein is determined to have a characteristic Dermatology Life Quality Index (DLQI) at baseline and during and after the induction period.

[00331] In an aspect, the present application provides methods of contacting IL-13 with an IL-13 antibody, such as a human, humanized, or chimeric antibody, which results in inhibition of IL-13 binding to an IL-13 receptor expressed on a cell.

[00332] In an aspect, the present application provides compositions comprising a formulation or vial described herein for use in the treatment of an inflammatory disorder or disease selected from the group consisting of asthma, idiopathic pulmonary fibrosis, alopecia areata, chronic sinusitis with nasal polyps, Chronic Rhinosinusitis without Nasal Polyps (CRSsNP), eosinophilic esophagitis (EoE), an Eosinophilic gastrointestinal disorder or disease (ENID) selected from the group consisting of Eosinophilic Gastritis (EoG), Eosinophilic Enteritis (EoN), Eosinophilic Colitis (EoC), and Eosinophilic Gastroenteritis (EGE), Churg-Strauss syndrome/Eosinophilic granulomatosis with polyangiitis (EGPA), Prurigo Nodularis (PN), of Chronic Spontaneous Urticaria (CSU), Chronic Pruritis of Unknown Origin (CPUO), Bullous Pemphigoid (BP), Cold Inducible Urticaria (ColdU), Allergic Fungal Rhinosinusitis (AFRS), Allergic Bronchopulmonary Aspergillosis (ABPA), and Chronic Obstructive Pulmonary Disease (COPD).

[00333] In an aspect, the present application provides methods for treating an inflammatory disorder or disease in a mammalian subject in need thereof, the method comprising administering to the mammalian subject a therapeutically effective amount of the formulation described herein.

[00334] In some embodiments, the inflammatory disorder or disease is atopic dermatitis.

[00335] In some embodiments, the inflammatory disorder or disease is selected from the group consisting of asthma, idiopathic pulmonary fibrosis, alopecia areata, chronic sinusitis with nasal polyps, Chronic Rhinosinusitis without Nasal Polyps (CRSsNP), eosinophilic esophagitis (EoE), an Eosinophilic gastrointestinal disorder or disease (ENID) selected from the group consisting of Eosinophilic Gastritis (EoG), Eosinophilic Enteritis (EoN), Eosinophilic Colitis (EoC), and Eosinophilic Gastroenteritis (EGE), Churg-Strauss syndrome/Eosinophilic granulomatosis with polyangiitis (EGPA), Prurigo Nodularis (PN), of Chronic Spontaneous Urticaria (CSU), Chronic Pruritis of Unknown Origin (CPUO), Bullous Pemphigoid (BP), Cold Inducible Urticaria (ColdU), Allergic Fungal Rhinosinusitis (AFRS), Allergic

Bronchopulmonary Aspergillosis (ABPA), and Chronic Obstructive Pulmonary Disease (COPD).

[00336] In some embodiments, the inflammatory disorder or disease is asthma. In some embodiments, the inflammatory disorder or disease is idiopathic pulmonary fibrosis. In some embodiments, the inflammatory disorder or disease is alopecia areata. In some embodiments, the inflammatory disorder or disease is chronic sinusitis with nasal polyps. In some embodiments, the inflammatory disorder or disease is Chronic Rhinosinusitis without Nasal Polyps (CRSsNP). In some embodiments, the inflammatory disorder or disease is eosinophilic esophagitis (EoE). In some embodiments, the inflammatory disorder or disease is an Eosinophilic gastrointestinal disorder or disease (ENID) selected from the group consisting of Eosinophilic Gastritis (EoG). In some embodiments, the inflammatory disorder or disease is Eosinophilic Enteritis (EoN). In some embodiments, the inflammatory disorder or disease is Eosinophilic Colitis (EoC). In some embodiments, the inflammatory disorder or disease is and Eosinophilic Gastroenteritis (EGE). In some embodiments, the inflammatory disorder or disease is Churg-Strauss syndrome/Eosinophilic granulomatosis with polyangiitis (EGPA). In some embodiments, the inflammatory disorder or disease is Prurigo Nodularis (PN). In some embodiments, the inflammatory disorder or disease is of Chronic Spontaneous Urticaria (CSU). In some embodiments, the inflammatory disorder or disease is Chronic Pruritis of Unknown Origin (CPUO). In some embodiments, the inflammatory disorder or disease is Bullous Pemphigoid (BP). In some embodiments, the inflammatory disorder or disease is Cold Inducible Urticaria (ColdU). In some embodiments, the inflammatory disorder or disease is Allergic Fungal Rhinosinusitis (AFRS). In some embodiments, the inflammatory disorder or disease is Allergic Bronchopulmonary Aspergillosis (ABPA). In some embodiments, the inflammatory disorder or disease is Chronic Obstructive Pulmonary Disease (COPD).

[00337] In an aspect, the present application provides methods for treating a pathology associated with elevated levels of IL-13 in a mammalian subject in need thereof, the method comprising administering to the mammalian subject a therapeutically effective amount of the formulation described herein.

[00338] In an aspect, the present application provides methods of reducing biological activity of IL-13 in a mammalian subject in need thereof, the method comprising administering to the mammalian subject a therapeutically effective amount of the formulation described herein.

[00339] In an aspect, the present application provides methods of inhibiting the TH2 type allergic response in a mammalian subject in need thereof, the method comprising administering to the mammalian subject a therapeutically effective amount of the formulation described herein.

[00340] In an aspect, the present application provides methods of reducing levels of Thymus and Activation Regulated Chemokine (TARC)/CCL17 in a mammalian subject in need thereof, the method comprising administering to the mammalian subject a therapeutically effective amount of the formulation described herein.

[00341] In an aspect, the present application provides methods of preventing an inflammatory disorder or disease in a mammalian subject in need thereof, the method comprising administering to the mammalian subject a therapeutically effective amount of the formulation described herein.

[00342] In some embodiments, the formulation is administered subcutaneously or intravenously.

EXAMPLES

[00343] The disclosure now being generally described, will be more readily understood by reference to the following examples, which are included merely for purposes of illustration of certain aspects and embodiments of the present disclosure, and are not intended to limit the scope of the disclosure in any way.

Example 1: Formulation of an Anti-Interleukin 13 Antibody: pH and Buffer Studies

[00344] This Example describes formulation studies of an interleukin 13 (IL-13) antibody, Construct 133. In formulating the antibody, twelve pH/buffers were investigated under stress conditions (40 °C for up to 4 weeks) to select pH and buffer system that stabilize the antibody.

[00345] A panel of analytical methods were used to characterize the pH and buffer studies, including appearance, pH, protein concentration, size exclusion-ultra performance liquid chromatography (SE-UPLC), imaged capillary isoelectric focusing (iCIEF), chip method of sodium dodecyl sulfate-polyacrylamide capillary electrophoresis (non-reduced and reduced, Caliper-SDS-NR & R, respectively), and differential scanning calorimetry (DSC), described below.

[00346] The pH studies evaluated pH from about 4.5 to about 7.5, such as pH 5.5, 6.0, and 6.5. It was determined that the range of 5.5 to 6.5 was suitable for a formulation described

herein, and a pH of 5.8 was selected due to its favorable results in SE-UPLC experiments. Buffers tested included a histidine buffer (*i.e.*, combination L-histidine and L-histidine HCl buffer), an acetate buffer, a succinate buffer, and a phosphate buffer (PB). The histidine, acetate, and succinate buffers stabilized the antibody well.

Materials and Methods

Appearance

[00347] The appearance of samples, including color, clarity, and visible particles, was examined against black and white background using YB-2 lightbox. Light intensity of lightbox was set as 2000~3750 lx.

Protein Concentration (A280)

[00348] Protein concentration was measured using a UV/visual light absorbance spectrometer (Lunatic, Unchained Labs or SoloVPE). According to the Lambert-Beer law, the concentration of a protein solution was calculated based on its absorbance at a given wavelength, the cuvette cell path length, and extinction coefficient value. The absorbance at 280 nm relied on the absorption properties of the aromatic amino acid residues in a respective protein. After loading a 2 μ L sample volume, the spectrometer was used to measure the absorbance in two cuvettes in parallel, and the concentration value was calculated. The SoloVPE system was dependent on the variable pathlength Spectroscopy Technology. Slope $m = A/L$ was obtained by measuring the absorbance at multiple different path lengths (>5 data points). Through the curve of path length and absorbance, the slope m was calculated. As $C = m/\epsilon$, with ϵ and m known, the concentration was calculated. The extinction coefficient used in this evaluation was $1.45 \text{ (mg/mL)}^{-1}\text{-cm}^{-1}$.

pH

[00349] The pH of samples was measured using a pH meter with a glass electrode at 25 °C. The pH meter was calibrated with three different standards (pH 4.01, 7.00, and 9.21) prior to usage. The slope of calibration was between 95.0% to 105.0%. Each sample was measured twice, and an average result was reported.

SE-UPLC

[00350] SE-UPLC was used as a purity analysis method to separate proteins based on their sizes. Size exclusion chromatography was performed on an Agilent UPLC system with a size

exclusion chromatography (SEC) column (Waters Acquity BEH 150×4.6 mm, 1.7 μ m). The sampler temperature was set to 5 ± 3 °C and the column oven temperature was set as 25 ± 3 °C. The mobile phase was 50 mM PB, 300 mM NaCl, pH 6.8 ± 0.1 ; and the flow rate was set as 0.4 mL/min. 10 μ g of each sample was injected. Detection wavelength was set at 280 nm and the run time was 8 min. Data was analyzed by Agilent CDS Software.

iCIEF

[00351] iCIEF was used to monitor the distribution of charged variants. The isoelectric point (pI), which is an intrinsic property of a given protein, is the pH at which the protein molecule did not carry net electrical charge. Under an external electric field, the charge variants moved along a continuous pH gradient formed by carrier ampholytes and stopped where the pH equaled its pI.

[00352] Antibody samples were mixed with master mixture to generate loading mixture, which contained 4.0 μ L Pharmalyte 3-10, 35 μ L 1% MC, 0.5 μ L pI marker 4.65, 0.5 μ L pI marker 9.22, 37.5 μ L 8 M urea solution, and 2.5 μ L ultrapure water at a final protein concentration of 1.0 mg/mL. The loading mixture was loaded into a Maurice iCIEF cartridge and analyzed with Maurice Capillary Isoelectric Focusing Analyzer with whole-column detection camera. After the analysis, the raw data were processed with Empower 3.

Caliper-SDS-NR & R

[00353] Non-reduced Caliper Sodium Dodecyl Sulfate (SDS, Caliper-SDS-NR) was performed based on a PerkinElmer Caliper automated electrophoresis that allowed protein separation by size. In the non-reduced microchip capillary electrophoresis (CE) SDS (CE-SDS) analysis, samples were diluted to 1 mg/mL with pure water. 2 μ L of diluted samples were mixed with 7 μ L of the sample denaturing solution (the mixture of sample buffer, 10% SDS solution, and 100 mM N-Ethylmaleimide (NEM), with the volume ratio of 100:10:4). The well-mixed samples were incubated at 70 °C for 10 min. 35 μ L of water was added to each sample, vortexed for 10 seconds, and centrifuged at 14000 rpm for 1 min. 42 μ L of the prepared samples were transferred to a 96-well plate, centrifuged at 4000 rpm for 15 min, placed onto a Labchip GXII's plate holder, separated, and detected in the HT Protein Express LabChip filled with destain-gel, gel-dye, and lower marker. Results were analyzed with LabChip GX Reviewer software.

[00354] Reduced Caliper SDS (Caliper-SDS-R) was performed based on a PerkinElmer Caliper automated electrophoresis that allowed protein separation by size after reduction of

sample. In the reduced microchip CE-SDS analysis, samples were diluted to 1 mg/mL with pure water. 2 μ L of diluted samples were mixed with 7 μ L of the sample denaturing solution (the mixture of sample buffer, 10% SDS solution, and 1 M dithiothreitol as a reduction agent, with the volume ratio of 100:10:4). The well-mixed samples were incubated at 70 °C for 10 min. 35 μ L of water was added to each sample, vortexed for 10 seconds, and centrifuged at 14000 rpm for 1 min. 42 μ L of the prepared samples were transferred to a 96-well plate, centrifuged at 4000 rpm for 15 min, placed onto a Labchip GXII's plate holder, separated, and detected in the HT Protein Express LabChip filled with destain-gel, gel-dye, and lower marker. Results were analyzed with LabChip GX Reviewer software.

DSC

[00355] The DSC thermos-analytical technique was used to characterize the thermal stability of protein samples and assess conformational differences between them. Measurements were performed on MicroCal™ VP Capillary DSC for thermal transition midpoint (T_m) and onset of unfolding (T_{onset}) testing. Samples were diluted to 1 mg/mL with the reference buffer. 400 μ L of respective reference buffers were added into the odd-numbered wells of a 96-well plate, and 400 μ L of samples were added into the even-numbered wells of the same plate. Experimental parameters were set such that the scan temperature ramped from 10 °C to 95 °C at a scan rate of 200 °C/hour. Data analysis was performed in MicroCal VP Capillary DSC automated data analysis software.

Results

[00356] A total of 12 pH/buffer systems covering the pH range from 4.5 to 7.5 were designed, including 20 mM acetate buffer (pH 4.5, pH 5.0, and pH 5.5), 20 mM succinate buffer (pH 5.0, pH 5.5, and pH 6.0), 20 mM histidine buffer (pH 5.5, pH 6.0, and pH 6.5; histidine buffers refers throughout Examples to a combination of L-histidine and L-histidine HCl), and 20 mM phosphate buffer (PB) (pH 6.5, pH 7.0, and pH 7.5). The antibody was buffer-exchanged into 12 buffers, then concentrated to target protein concentration (150 mg/mL), respectively. Each of the 12 solutions was filtered with a 0.22 μ m polyvinylidene fluoride (PVDF) filter and filled into 2 mL glass vials (1 mL per vial), then stoppered, capped, and labeled. Each of the twelve samples was tested for appearance, protein concentration, SE-UPLC, iCIEF, Caliper-SDS-NR & R, DSC,

and pH at Day 0. Additionally, at Day 0, after testing, the twelve samples were stored at 40 °C for up to 4 weeks. At Week 2 and Week 4, the samples were further tested for appearance, protein concentration, SE-UPLC, iCIEF, and Caliper-SDS-NR & R.

[00357] *Appearance:* all samples remained slightly yellow, slightly opalescent, liquid, and free of visible particles after incubation at 40 °C for 4 weeks. The sample opalescent strength varied across formulations with different buffer type, with opalescent strength greatest in the PB group, followed in-order by, succinate, histidine, and acetate. With an increase of pH, the opalescent intensity increased gradually in succinate and PB buffer groups.

[00358] *pH and protein concentration:* the pH and protein concentration of the formulations were assessed over 4 weeks. The pH was observed near the target value at T0, and protein concentration (approximately 150.0 mg/mL) of all candidates remained relatively consistent after 4 weeks of incubation at 40 °C compared to those at T0, indicating that these parameters were stable under the tested thermal stress condition.

[00359] *SE-UPLC:* All candidates showed a decline in the main peak % (2.4% to 16.8%) after 4 weeks of incubation at 40 °C. This change was the most pronounced in the acetate buffer at pH 4.5 (B1) and PB buffer at pH 7.5 (B12), while the acetate buffer at pH 5.5 (B3) and histidine buffer at pH 5.5, 6.0, and 6.5 (B7, B8, and B9, respectively) showed the smallest changes in main peak purity and high molecular weight species (HMW). Taken together, the results of the SE-UPLC experiments demonstrated that the antibody was the least stable in the acetate buffer at pH 4.5 (B1) and PB buffer at pH 7.5 (B12), and most stable in the acetate buffer at pH 5.5 (B3) and histidine buffer at pH 5.5, 6.0, and 6.5 (B7, B8, and B9, respectively).

[00360] *Caliper-SDS-NR & R:* For Caliper-SDS-NR, the purity of all samples decreased with the increase of incubation time at 40 °C for up to 4 weeks (up to 22.0%). Acetate at pH 4.5 (B1), PB at pH 7.0 and 7.5 (B11 and B12, respectively) showed a faster and greater decline (> 8% by 4 weeks) than the samples in the other pH/buffer systems. Samples in the succinate and histidine buffer systems, particularly succinate at pH 6.0 (B6) and histidine at pH 5.5, 6.0, and 6.5 (B7, B8 and B9, respectively) performed relatively better. For Caliper-SDS-R, less changes were seen in all the samples (up to 10.8%) compared with Caliper-SDS-NR results, indicating that the fragmentation of the protein may, without being bound by theory, be primarily caused by inter-chain disulfide bonds breakage during incubation at 40 °C. There was a decline in the purity after 4 weeks of incubation at 40 °C in the samples formulated in acetate at pH 4.5 (B1), succinate at

pH 5.0 (B4), and PB at pH 7.0 and 7.5 (B11, and B12, respectively). Aside from the change in these four samples, no substantial difference in purity was observed among the other samples. Taken together, the results of the Caliper-SDS-NR & R experiments demonstrated that the succinate buffer at pH 6.0 (B) and histidine buffer at pH 5.5, 6.0, and 6.5 (B7, B8, and B9, respectively) performed relatively better in improving the stability of the antibody protein compared with other buffers.

[00361] *iCIEF*: The measured pI value of all samples was 8.0. A decline in the main peak % (more than 26.2% for acetate at pH 4.5 and 5.0 (B1 and B2, respectively), succinate at pH 5.0 and 5.5 (B4 and B5, respectively), and PB buffer) was seen in all buffers after incubation at 40 °C for 4 weeks. Taken together, the results of the *iCIEF* studies demonstrated that the histidine buffer system performed better than the succinate and acetate buffer systems, followed by the PB buffer. Specifically, histidine at pH 5.5, 6.0, and 6.5 (B7, B8, and B9, respectively) showed the best performance, followed by succinate at pH 6.0 (B6) and acetate at pH 5.5 (B3). Further, the data from the *iCIEF* study indicated that the antibody protein was most stable in buffer systems with pH from 6.5 to 5.5 (except for PB buffer at pH 6.5 (B10) and succinate buffer at pH 5.5 (B5)), among which, the histidine at pH 5.5, 6.0, and 6.5 (B7, B8, and B9, respectively) buffer performed the best.

[00362] *DSC*: the T_{Onset} (°C) and T_m values (T_{m1} , T_{m2} , and T_{m3} at °C) increased with the increase of pH for the same buffer (except for histidine buffer at pH 6.5 (B9)). Additionally, T_{Onset} values were higher than 55.0 °C in all formulations except acetate buffer at pH 4.5 (B1) and succinate buffer at pH 5.0 (B4), indicating good conformational thermal stability overall.

[00363] In summary, the pH/buffer studies investigated twelve pH/buffer types under stress conditions (40 °C for up to 4 weeks), and the results showed that stability of the antibody was dependent upon both the pH and buffer. Taken together, the studies herein demonstrated relatively poor protein stability in acetate at pH 4.5 and 5.0 (B1 and B2, respectively), succinate at pH 5.0 and 5.5 (B4 and B5, respectively) and all PB buffer systems (pH 6.5-7.5, B10-B12, respectively). Good protein stability was observed in acetate at pH 5.5 (B3), succinate at pH 5.5 (B6), and histidine buffer systems overall (pH 5.5-6.5, B7-B9, respectively). Given these results, it was identified that a histidine buffer, an acetate buffer, or a succinate buffer can be used to formulate an IL-13 antibody. Among the twelve total formulations tested, histidine at pH 5.5,

6.0, and 6.5 (B7, B8, and B9, respectively) showed the best performance, followed by acetate at pH 5.5 (B3) and succinate at pH 6.0 (B6).

[00364] A formulation including an IL-13 antibody and a histidine buffer at pH 6.0 (B8) was further investigated for optimal excipient and surfactant strength (see **Example 2**).

Example 2: Formulation of an Anti-IL-13 Antibody: Excipients and Surfactant Strength Studies

[00365] This Example describes formulation studies of an IL-13 antibody. In formulating the antibody, different types of excipients (*e.g.*, sucrose, α/α -trehalose dihydrate, and L-arginine hydrochloride (Arg-HCl), L-methionine, etc.), as well as various concentration of a polysorbate (*e.g.*, polysorbate 80 (PS80) at 0.02% w/v, 0.04% w/v, and 0.06% w/v) and a poloxamer (*e.g.*, poloxamer 188 (P188) at 0.05% w/v, 0.08% w/v, and 0.10% w/v) were evaluated under stress conditions (40 °C for up to 4 weeks, agitation at 300 rpm for up to 3 days, and freeze and thaw for up to 5 cycles) to select suitable excipients and surfactant strengths to improve protein stability. A panel of analytical methods were used to characterize the excipients and surfactant strengths, including appearance, pH, protein concentration, SE-UPLC, Caliper-SDS-NR & R, and iCIEF (the Methods of which are described in **Example 1**), as well as osmolality, viscosity, and amount of sub-visible particles by micro-flow imaging (MFI), described below.

[00366] Among the different excipients tested, L-methionine was selected for further testing based upon the Caliper-SDS-NR & R data showing well-preserved purity as well as the SE-UPLC data that demonstrated that it helped maintain high molecular weight species (HMW). Additionally, the excipient L-arginine was selected for further testing based upon data that demonstrated that it improved (decreased) viscosity.

Materials and Methods

Excipients

[00367] Excipients used in the Examples are outlined in **Table 11**.

Table 11: Excipients

Name	Vendor	Cat. No.
Acetic acid, glacial	J. T. Baker	9526-03

Name	Vendor	Cat. No.
Sodium acetate, trihydrate	Avantor	3461-01
Succinic acid	Merck	1.00681.5000
Sodium succinate hexahydrate	Pfanstiehl	D-161
L-histidine	Pfanstiehl	H-116
L-histidine monohydrochloride	Merck	1.04354.9010
Sodium dihydrogen phosphate dihydrate	Merck	1.06345.5000
Di-sodium hydrogen phosphate dihydrate	Merck	1.06576.5000
Polysorbate 80 (PS80)	Croda	SR40925
L-arginine hydrochloride (Arg-HCl)	Merck	1.01544.5000
α,α -Trehalose dihydrate	Pfanstiehl	T-104-4
Sucrose	Pfanstiehl	S-124-1-MC
Sorbitol	Merck	1.11597.2500
Poloxamer 188 (P188)	Merck	1.37112.1000
L-Methionine	Evonik	95811601A2
Ethylene dinitrilo tetraacetic acid disodium salt dihydrate	Merck	1.37004.1000
L-Lysine Hydrochloride	Merck	1.05700
Glycine	Merck	1.00590
L-Proline	Merck	1.07430

Appearance, Protein Concentration (A280), pH, SE-UPLC, iCIEF, and Caliper-SDS-NR & R
[00368] See **Example 1**.

Osmolality

[00369] Osmolality was measured using an Advanced 2020 Multi-Sample Osmometer. Before and after the tests, the testing accuracy of the osmometer was confirmed with a Clinitrol 290 mOsm/kg reference solution. The sample volume for testing was 20 μ L, and only one test was performed for each sample.

Viscosity

[00370] A viscosity test was used to characterize the fluid properties of liquid sample. Measurements were performed by a VROC® initium one plus viscometer (Rheosense). When the sample fluid flowed through the VROC® chip with controlled flow rates, the pressure drop

of the fluid was detected by the sensors and the viscosity at a certain shear rate was determined using the Hagen-Poiseuille Principle. 35 μ L of samples were loaded on A05 chip and the set chip temperature was $25 \pm 0.1^\circ\text{C}$. The viscosity of the sample was measured at 3 different shear rates, and the testing at each shear rate was repeated 3 times. The mean value was reported as the final viscosity.

MFI

[00371] Sub-visible particles were monitored by a Micro Flow Imaging (MFI) system. 1.5 mL of each sample was transferred into the MFI 96-well plate for analysis. The results were analyzed by the vendor's MVSS software. The sub-visible particle amount in the equivalent circular diameter over 2 μm , 5 μm , 10 μm , and 25 μm was reported.

Stress Conditions

[00372] For freeze and thaw (FT), samples were completely frozen at -70°C and thawed at room temperature (RT). For thermal stress, samples were stored at 40°C for up to 4 weeks. For agitation stress, samples were agitated at 300 rpm at 25°C , for up to 3 days.

Study Design

[00373] The study design is outlined in **Table 12**.

Table 12: Study Design

Attributes	Condition	Sampling points and assay		
		T0	Week 2	Week 4
Thermal	40 °C	X, Y, Z, and S	X and Y (“40 °C-2 W”)	X, Y, and S (“40 °C-4 W”)
Agitation (A)	300 rpm, 25 °C		1 day (‘A-1 D’)	3 days (‘A-3 D’)
			X	X, Y, and S
Freeze and thaw (FT)	-70 °C to RT		3 cycles (“FT-3 CYS”)	5 cycles (“FT-5 CYS”)
			X	X, Y, and S

X = Appearance, protein concentration, and SE-UPLC

Y = Caliper-SDS-NR & R, and iCIEF

Z= Osmolality, pH, and viscosity

S= MFI

Results

[00374] An IL-13 antibody described herein was in 20 mM histidine buffer at pH 6.0. Stock solutions of 40% (w/w) sucrose, 22.5% (w/w) sorbitol, 44% (w/w) α/α -trehalose dihydrate, 700 mM Arg-HCl, 100 mM L-methionine (Met), 5 mM ethylene dinitrilo tetraacetic acid disodium salt dihydrate (EDTA-2Na), 5% (w/w) PS80, and 5% (w/w) P188 were prepared. The required amounts of antibody, excipient stock solutions, and surfactant stock solutions were calculated, weighed, and well-mixed based on the formulation recipes listed in **Table 13**. The proportion of excipients was adjusted based on the requirements for an isotonic solution.

[00375] Each of the formulation solutions were filtered with a 0.22 μ m PVDF filter and filled into 2 mL glass vials (1 mL per vial), then stoppered, capped, and labeled.

Table 13: Formulation Candidates with Various Excipients and Surfactants

Formulation No. (notable ingredients)	Protein concentration, buffer, pH	Excipients and surfactants	Comments
E1 (Sucrose, 0.02% PS80)	150 mg/mL, 20 mM histidine, pH 6.0	6% sucrose, 0.02% PS80	Groups to evaluate the effect of different excipients, including different Saccharides, salts, and amino acid
E2 (Sucrose, Methionine, 0.02% PS80)		6% sucrose, 10 mM Methionine, 0.02% PS80	
E1 (Sucrose, EDTA-2Na, 0.02% PS80)		6% sucrose, 0.05 mM EDTA-2Na, 0.02% PS80	
E4 (Sucrose, Arginine hydrochloride, 0.02% PS80)		4% sucrose, 50 mM Arg-HCl, 0.02% PS80	
E5 (Arginine hydrochloride, 0.02% PS80)		135 mM Arg-HCl, 0.02% PS80	
E6 (Trehalose, 0.02% PS80)		6.5% α/α -trehalose dihydrate, 0.02% PS80	

Formulation No. (notable ingredients)	Protein concentration, buffer, pH	Excipients and surfactants	Comments
E7 (Sorbitol, 0.02% PS80)		3.5% Sorbitol, 0.02% PS80	
E8 (Sucrose, 0.04% PS80)		6% sucrose, 0.04% PS80	
E9 (Sucrose, 0.06% PS80)		6% sucrose, 0.06% PS80	Groups to evaluate the effect of different surfactant types and strength
E10 (Sucrose, 0.1% P188)		6% sucrose, 0.1% P188	
E11 (Sucrose, 0.08% P188)		6% sucrose, 0.08% P188	
E12 (Sucrose, 0.05% P188)		6% sucrose, 0.05% P188	

All % in **Table 13** mean % (w/v).

[00376] *Appearance:* All formulations remained slightly yellow, slightly opalescent, liquid, and free of visible particles. Formulations E4 (4% sucrose, 50 mM Arg-HCl, 0.02% PS80) and E5 (135 mM Arg-HCl, 0.02% PS80), both of which contain Arg-HCl, showed relatively stronger opalescence than other formulations. However, no substantial changes of opalescence were observed in E4 and E5 with the increase of incubation time for up to 4 weeks at 40 °C.

[00377] *Osmolality, viscosity, and pH:* As shown in **Table 14**, the pH of all the tested formulations was reported at their target value at T0. The osmolality, which is not a stability-indicative parameter, of all samples was approximately 285 mOsm/kg to 320 mOsm/kg, which demonstrated suitability for subcutaneous administration. The viscosity of all samples was between 5.9 mPa-s to 9.3 mPa-s, where the addition of Arg-HCl (E4 and E5) reduced the viscosity compared to those of other formulations.

Table 14: Osmolality, pH, and Viscosity Results

Formulation No.	Osmolality (mOsm/kg)	pH	Viscosity (mPa-s)
	T0	T0	T0

E1 (Sucrose, 0.02% PS80)	302	6.0	8.4
E2 (Sucrose, Methionine, 0.02% PS80)	295	6.0	8.2
E3 (Sucrose, EDTA-2Na, 0.02% PS80)	298	6.0	8.5
E4 (Sucrose, Arginine hydrochloride, 0.02% PS80)	320	6.0	7.3
E5 (Arginine hydrochloride, 0.02% PS80)	309	6.0	5.9
E6 (Trehalose, 0.02% PS80)	285	6.0	8.8
E7 (Sorbitol, 0.02% PS80)	293	6.0	7.6
E8 (Sucrose, 0.04% PS80)	296	6.0	8.0
E9 (Sucrose, 0.06% PS80)	302	6.0	8.3
E10 (Sucrose, 0.1% P188)	300	6.0	8.5
E11 (Sucrose, 0.08% P188)	308	6.0	9.3
E12 (Sucrose, 0.05% P188)	312	6.0	9.2

[00378] *Protein concentration:* The protein concentration (approximately 150.0 mg/mL) remained relatively stable during the study.

[00379] *Sub-visible particle (MFI):* Compared with T0, no substantial changes were observed in the amount of sub-visible particles ($\geq 2 \mu\text{m}$, $\geq 10 \mu\text{m}$, or $\geq 25 \mu\text{m}$) after FT for 5 cycles, agitation for 3 days, or 40 °C incubation for 4 weeks in all tested formulations. By comparing samples within the same buffer system but different excipients (E1-E7), no differences of the amount of sub-visible particles were observed. Additionally, there were no obvious differences in the amount of the sub-visible particles in E1 (0.02% PS80), E8 (0.04% PS80), E9 (0.06% PS80), E10 (0.10% P188), E11 (0.08% P188), and E12 (0.05% P188).

[00380] *SE-UPLC:* The data summary from the SE-UPLC testing for excipients and surfactants strength study is provided in **Table 15**. After freeze and thaw for 5 cycles or agitation for 3 days, the main peak % of all the test formulations remained at approximately 99.0% indicating consistent antibody freeze and thaw stability and agitation stability under the studied parameter in all studied formulations.

[00381] After incubation at 40 °C for 4 weeks, the main peak % in all formulations declined by up to 2.9% compared to T0, although the differences were small. E8 and E9 (Sucrose, 0.04% and 0.06% PS80) showed slightly lower main peak levels. In addition, E2 (Sucrose, Methionine,

0.02% PS80) showed the smallest changes in main peak purity and HMW species, indicating that L-methionine helped control HMW formation.

Table 15: SE-UPLC Results

Formulation No.	Stress	SE-UPLC (Main peak % (Δ Main peak %, where applicable) / HMW % (Δ HMW %) / LMW%)
E1 (Succinate, 0.02% PS80)	T0	99.1 / 0.9 / 0.0
	FT-3 CYS	99.2 / 0.8 / 0.0
	FT-5 CYS	99.2 / 0.8 / 0.0
	A-1 D	99.1 / 0.9 / 0.0
	A-3 D	99.0 / 0.9 / 0.0
	40 °C-2 W	97.9 ($\downarrow$ 1.2) / 1.8 ($\uparrow$ 0.9) / 0.3
	40 °C-4 W	97.1 ($\downarrow$ 2.0) / 2.3 ($\uparrow$ 1.4) / 0.6
E2 (Succinate, Methionine)	T0	99.2 / 0.8 / 0.0
	FT-3 CYS	99.3 / 0.7 / 0.0
	FT-5 CYS	99.3 / 0.7 / 0.0
	A-1 D	99.1 / 0.8 / 0.0
	A-3 D	99.1 / 0.9 / 0.0
	40 °C-2 W	98.3 ($\downarrow$ 0.9) / 1.4 ($\uparrow$ 0.6) / 0.3
	40 °C-4 W	97.8 ($\downarrow$ 1.4) / 1.7 ($\uparrow$ 0.9) / 0.6
E3 (Succinate, EDTA-2Na, 0.02% PS80)	T0	99.1 / 0.8 / 0.0
	FT-3 CYS	99.3 / 0.7 / 0.0
	FT-5 CYS	99.3 / 0.7 / 0.0
	A-1 D	99.1 / 0.9 / 0.0
	A-3 D	99.1 / 0.9 / 0.0
	40 °C-2 W	98.1 ($\downarrow$ 1.0) / 1.6 ($\uparrow$ 0.8) / 0.3
	40 °C-4 W	97.3 ($\downarrow$ 1.8) / 2.1 ($\uparrow$ 1.3) / 0.6
E4 (Succinate, Arginine hydrochloride, 0.02% PS80)	T0	99.2 / 0.8 / 0.0
	FT-3 CYS	99.3 / 0.7 / 0.0

Formulation No.	Stress	SE-UPLC (Main peak % (Δ Main peak %, where applicable) / HMW % (Δ HMW %) / LMW%)
	FT-5 CYS	99.3 / 0.7 / 0.0
	A-1 D	99.2 / 0.8 / 0.0
	A-3 D	99.2 / 0.8 / 0.0
	40 °C-2 W	98.1 ($\downarrow$ 1.1) / 1.6 ($\uparrow$ 0.8) / 0.3
	40 °C-4 W	97.5 ($\downarrow$ 1.7) / 1.9 ($\uparrow$ 1.2) / 0.6
E5 (Arginine hydrochloride, 0.02% PS80)	T0	99.2 / 0.7 / 0.0
	FT-3 CYS	99.3 / 0.7 / 0.0
	FT-5 CYS	99.3 / 0.7 / 0.0
	A-1 D	99.2 / 0.7 / 0.0
	A-3 D	99.2 / 0.8 / 0.0
	40 °C-2 W	98.1 ($\downarrow$ 1.1) / 1.6 ($\uparrow$ 0.9) / 0.3
	40 °C-4 W	97.4 ($\downarrow$ 1.8) / 2.0 ($\uparrow$ 1.3) / 0.6
E6 (Tre, 0.02% PS80)	T0	99.1 / 0.8 / 0.0
	FT-3 CYS	99.3 / 0.7 / 0.0
	FT-5 CYS	99.3 / 0.7 / 0.0
	A-1 D	99.1 / 0.9 / 0.0
	A-3 D	99.0 / 0.9 / 0.0
	40 °C-2 W	97.9 ($\downarrow$ 1.2) / 1.8 ($\uparrow$ 1.0) / 0.
	40 °C-4 W	97.2 ($\downarrow$ 1.9) / 2.2 ($\uparrow$ 1.4) / 0.6
E7 (Sor, 0.02% PS80)	T0	99.1 / 0.8 / 0.0
	FT-3 CYS	99.3 / 0.7 / 0.0
	FT-5 CYS	99.2 / 0.8 / 0.0
	A-1 D	99.1 / 0.9 / 0.0
	A-3 D	99.0 / 0.9 / 0.0
	40 °C-2 W	97.9 ($\downarrow$ 1.2) / 1.9 ($\uparrow$ 1.1) / 0.3
	40 °C-4 W	97.2 ($\downarrow$ 1.9) / 2.2 ($\uparrow$ 1.4) / 0.6

Formulation No.	Stress	SE-UPLC (Main peak % (Δ Main peak %, where applicable) / HMW % (Δ HMW %) / LMW %)
E8 (Succinate, 0.04% PS80)	T0	99.1 / 0.8 / 0.0
	FT-3 CYS	99.2 / 0.8 / 0.0
	FT-5 CYS	99.2 / 0.8 / 0.0
	A-1 D	99.1 / 0.9 / 0.0
	A-3 D	99.0 / 0.9 / 0.0
	40 °C-2 W	97.5 ($\downarrow$ 1.6) / 2.2 ($\uparrow$ 1.4) / 0.3
	40 °C-4 W	96.4 ($\downarrow$ 2.7) / 3.0 ($\uparrow$ 2.2) / 0.7
E9 (Succinate, 0.06% PS80)	T0	99.1 / 0.8 / 0.0
	FT-3 CYS	99.3 / 0.7 / 0.0
	FT-5 CYS	99.2 / 0.8 / 0.0
	A-1 D	99.1 / 0.9 / 0.0
	A-3 D	99.0 / 0.9 / 0.0
	40 °C-2 W	97.4 ($\downarrow$ 1.7) / 2.3 ($\uparrow$ 1.5) / 0.3
	40 °C-4 W	96.2 ($\downarrow$ 2.9) / 3.1 ($\uparrow$ 2.3) / 0.7
E10 (Succinate, 0.1% P188)	T0	99.2 / 0.8 / 0.0
	FT-3 CYS	99.3 / 0.7 / 0.0
	FT-5 CYS	99.3 / 0.7 / 0.0
	A-1 D	99.1 / 0.9 / 0.0
	A-3 D	99.0 / 0.9 / 0.0
	40 °C-2 W	98.1 ($\downarrow$ 1.1) / 1.6 ($\uparrow$ 0.8) / 0.3
	40 °C-4 W	97.4 ($\downarrow$ 1.8) / 2.0 ($\uparrow$ 1.2) / 0.6
E11 (Succinate, 0.08% P188)	T0	99.1 / 0.8 / 0.0
	FT-3 CYS	99.2 / 0.8 / 0.0
	FT-5 CYS	99.2 / 0.8 / 0.0
	A-1 D	99.1 / 0.9 / 0.0
	A-3 D	98.8 / 1.2 / 0.0

Formulation No.	Stress	SE-UPLC (Main peak % (Δ Main peak %, where applicable) / HMW % (Δ HMW %) / LMW %)
E12 (Succinate, 0.05% P188)	40 °C-2 W	98.1 ($\downarrow$ 1.0) / 1.6 ($\uparrow$ 0.8) / 0.3
	40 °C-4 W	97.4 ($\downarrow$ 1.7) / 2.0 ($\uparrow$ 1.2) / 0.6
	T0	99.1 / 0.9 / 0.0
	FT-3 CYS	99.3 / 0.7 / 0.0
	FT-5 CYS	99.2 / 0.8 / 0.0
	A-1 D	99.1 / 0.9 / 0.0
	A-3 D	99.0 / 0.9 / 0.0
	40 °C-2 W	98.1 ($\downarrow$ 1.0) / 1.6 ($\uparrow$ 0.7) / 0.3
	40 °C-4 W	97.4 ($\downarrow$ 1.7) / 2.0 ($\uparrow$ 1.1) / 0.6

Abbreviations: HMW, high molecular weight; LMW, low molecular weight; FT, freeze and thaw; CYS, cycles; D, day (s); W, weeks.

[00382] *Caliper-SDS-NR & R*: The data summary from the Caliper-SDS-NR & R testing for excipients and surfactants strength study is provided in **Table A**.

Table A: Caliper-SDS-NR & R Results

Formulation No.	Stress	Caliper-SDS-NR (Purity % (Δ Purity %))	Caliper-SDS-R (Purity) %
E1 (Succinate, 0.02% PS80)	T0	97.1	99.6
	FT-5 CYS	97.1	98.6
	A-3 D	96.4	99.8
	40°C-2 W	95.4	99.8
	40°C-4 W	94.2 ($\downarrow$ 2.9)	97.3
E2 (Succinate, Methionine, 0.02% PS80)	T0	97.0	99.7
	FT-5 CYS	97.1	98.1
	A-3 D	96.7	99.5
	40°C-2 W	95.9	99.8

Formulation No.	Stress	Caliper-SDS-NR (Purity % (Δ Purity %))	Caliper-SDS-R (Purity) %
	40°C-4 W	95.0 ($\downarrow$ 2.0)	97.8
E3 (Succinate, EDTA·2Na, 0.02% PS80)	T0	97.2	99.7
	FT-5 CYS	96.9	98.1
	A-3 D	96.6	99.7
	40°C-2 W	95.8	99.7
	40°C-4 W	94.1 ($\downarrow$ 3.1)	97.7
E4 (Succinate, Arg-HCl, 0.02% PS80)	T0	97.2	99.6
	FT-5 CYS	96.9	97.9
	A-3 D	96.7	99.3
	40°C-2 W	95.4	99.7
	40°C-4 W	93.9 ($\downarrow$ 3.3)	97.8
E5 (Arg-HCl, 0.02% PS80)	T0	97.2	99.3
	FT-5 CYS	97.2	98.2
	A-3 D	97.0	99.8
	40°C-2 W	95.6	99.7
	40°C-4 W	93.9 ($\downarrow$ 3.3)	98.1
E6 (Trehalose, 0.02% PS80)	T0	97.1	99.6
	FT-5 CYS	97.0	98.1
	A-3 D	97.0	99.6
	40°C-2 W	95.4	99.7
	40°C-4 W	93.9 ($\downarrow$ 3.2)	98.0
E7 (Sorbitol, 0.02% PS80)	T0	97.0	99.7
	FT-5 CYS	97.1	98.1
	A-3 D	96.9	99.8
	40°C-2 W	95.7	99.7
	40°C-4 W	93.7 ($\downarrow$ 3.3)	97.7
E8 (Succinate, 0.04% PS80)	T0	97.1	99.5
	FT-5 CYS	97.0	97.9
	A-3 D	97.0	99.8

Formulation No.	Stress	Caliper-SDS-NR (Purity % (Δ Purity %))	Caliper-SDS-R (Purity) %
	40°C-2 W	95.0 ($\downarrow$ 2.1)	99.7
	40°C-4 W	93.0 ($\downarrow$ 4.1)	97.1
E9 (Succinate, 0.06% PS80)	T0	97.0	99.4
	FT-5 CYS	97.0	98.0
	A-3 D	97.0	99.8
	40°C-2 W	95.1	99.7
	40°C-4 W	93.3 ($\downarrow$ 3.7)	97.2
E10 (Succinate, 0.1% P188)	T0	96.8	99.6
	FT-5 CYS	97.1	98.1
	A-3 D	97.2	99.7
	40°C-2 W	95.2	99.6
	40°C-4 W	94.2 ($\downarrow$ 2.6)	97.4
E11 (Succinate, 0.08% P188)	T0	96.9	99.7
	FT-5 CYS	97.0	98.3
	A-3 D	97.1	99.8
	40°C-2 W	96.0	99.6
	40°C-4 W	94.2 ($\downarrow$ 2.7)	97.9
E12 (Succinate, 0.05% P188)	T0	96.8	99.6
	FT-5 CYS	97.2	97.9
	A-3 D	97.3	99.8
	40°C-2 W	95.8	99.6
	40°C-4 W	94.2 ($\downarrow$ 2.6)	97.3

Abbreviations: HMW, high molecular weight; LMW, low molecular weight; FT, freeze and thaw; CYS, cycles; D, day(s); W, weeks.

[00383] After freeze and thaw for 5 cycles or agitation for 3 days, both Caliper-SDS-NR & R testing data indicated that purity remained stable. After incubation at 40 °C for 4 weeks, the purity for all formulations remained stable in the Caliper-SDS-R testing. Slight 2.6% to 4.1% declines of Caliper-SDS-NR purity were observed in all formulations except E2 (Sucrose, Methionine, 0.02% PS80), which showed the lowest change of 2.0% decline in the main peak.

Together, this data indicated that under thermal condition (40 °C incubation for 4 weeks) slight declines in Caliper-SDS-NR purity and Caliper-SDS-R were observed in all formulations.

[00384] *iCIEF*: The measured pI value of all samples was 8.3. After freeze and thaw for 5 cycles or agitation for 3 days, no substantial changes of main peak % were observed in all samples. After incubation at 40 °C for 4 weeks, 19.5% to 24.4% iCIEF main peak % declines were observed in all formulations compared to T0, where E4 and E5 (both containing Arg-HCl) showed the lowest changes of main peak % (< 20%). Overall, all samples degraded similarly.

[00385] The results of the studies undertaken to select one or more excipients and identify optimal surfactant strength to maximize the antibody protein stability are summarized qualitatively in **Table 16**. By comparing formulations with different excipients (E1-E7), E2 (Sucrose, Methionine), E4 (Sucrose, Arg-HCl), and E5 (Arg-HCl) showed relatively better performance compared to other formulations. E1 (Sucrose), E3 (Sucrose, EDTA-2Na), E6 (Trehalose dihydrate), and E7 (Sorbitol) showed acceptable performance. By comparing formulations with different surfactant types and strength, E1, E8, E9 (0.02%, 0.04% and 0.06% PS80, respectively), E10, E11, and E12 (0.10%, 0.08% and 0.05% P188, respectively) showed comparable and good performance.

Table 16: Stability Performance Comparison of Formulations

Formulation No. (Notable Ingredients)	Performance					
	Appearance	SE-UPLC	iCIEF	Caliper-SDS-NR	Caliper-SDS-R	Sub-visible particles
E1 (Sucrose, 0.02% PS80)	Good	Good	Medium	Medium	Good	Good
E2 (Sucrose, Methionine, 0.02% PS80)	Good	Good	Medium	Good	Good	Good
E3 (Sucrose, EDTA-2Na, 0.02% PS80)	Good	Good	Medium	Medium	Good	Good
E4 (Sucrose, Arginine hydrochloride, 0.02% PS80)	Good	Good	Good	Medium	Good	Good
E5 (Arginine hydrochloride, 0.02% PS80)	Good	Good	Good	Medium	Good	Good
E6 (Trehalose, 0.02% PS80)	Good	Good	Medium	Medium	Good	Good
E7 (Sorbitol, 0.02% PS80)	Good	Good	Medium	Medium	Good	Good
E8 (Sucrose, 0.04% PS80)	Good	Good	Medium	Medium	Good	Good
E9 (Sucrose, 0.06% PS80)	Good	Good	Medium	Medium	Good	Good
E10 (Sucrose, 0.1% P188)	Good	Good	Medium	Medium	Good	Good
E11 (Sucrose, 0.08% P188)	Good	Good	Medium	Medium	Good	Good
E12 (Sucrose, 0.05% P188)	Good	Good	Medium	Medium	Good	Good

Appearance: good performance, FP throughout the study.
SE-UPLC: good performance, decrease of main peak % no more than 3.0%.
iCIEF:

medium performance, decrease of main peak % > 20%;
good performance, decrease of main peak % no more than 20.0%.
Caliper-SDS-NR:
medium performance, decrease of purity > 2.0%;
good performance, no substantial changes.
Caliper-SDS-R:
good performance, no substantial changes.
MFI:
good performance, no substantial changes.

[00386] Methionine and sucrose were selected as the leading excipients and the three excipients Arg-HCl, glycine, and proline underwent further testing (See **Example 3**). Also, considering the large volume, antibody freeze-thaw stability, and antibody long-term storage stability, 0.04% PS80 was selected for further studies. Therefore, variations of a formulation including 20 mM histidine buffer, 10 mM Methionine, and 0.04% (w/v) PS80 at pH 6.0 were further tested with or without sucrose and Arg-HCl (or other excipients *e.g.*, glycine and proline), as described in **Example 3**.

Example 3: Formulation of an Anti-IL-13 Antibody: Viscosity and Osmolality Studies

10 [00387] This Example describes formulation studies of an IL-13 antibody. In formulating the antibody, a key parameter was viscosity. Different excipients (*e.g.*, Arg-HCl, glycine, and proline) were evaluated for their ability to improve formulation viscosity, while maximizing protein stability. A panel of analytical methods were used to characterize the viscosity excipient studies, including appearance, MFI, protein concentration, SE-UPLC, pH, osmolality, and viscosity (the Methods of which are described in **Example 1** and **Example 2**). As described throughout **Examples 1-2**, the formulations selected for this stage of testing included a pH of about 5.8 due to its favorable results in SE-UPLC experiments (see **Example 1**), a histidine buffer (or comparable acetate or succinate buffer, respectively) and L-methionine, which was demonstrated to help control HMW formation and antibody purity (see **Example 2**). In the experiments herein, the excipient L-arginine was identified as useful for reducing viscosity.

Methods

[00388] In brief, the IL-13 antibody was in a histidine buffer system at pH 6.0 with protein concentration at 257 mg/mL. Stock solutions of 50% (w/w) sucrose, 1400 mM Arg.HCl, 200 mM L-Methionine, 2400 mM Glycine, 2400 mM L-Proline and 5% (w/w) PS80 were prepared. The required amounts of antibody, excipient stock solutions and surfactant stock solutions were calculated, weighed and well-mixed based on the formulation recipes listed in **Table 17**. Each of the formulation solutions were filtered with a 0.22 µm PVDF filter and filled into 2 mL (2R) glass vials (2.4 mL per vial), then stoppered, capped and labeled immediately. All samples filtration and aliquoting were carried out with aseptic procedures in a biosafety cabinet.

Analytical tests including appearance (visual inspection), pH, protein concentration, osmolality, viscosity, SE-UPLC and sub-visible particles were performed in this study.

Results

- 5 [00389] Formulation candidates with various excipients, outlined in **Table 17**, were tested.

Table 17: Formulations with Various Excipients Tested

Formulation No.	pH/buffer and surfactant	Target Antibody Concentration (mg/mL)	Excipients		
F1	10 mM Histidine buffer, pH 6.0 with 0.04% PS80	150	175 mM Sucrose	/	10 mM Methionine
F2		175	160 mM Sucrose	/	10 mM Methionine
F3		200	160 mM Sucrose	/	10 mM Methionine
F15		200	/	135 mM Arg-HCl	/
F4		200	50 mM Sucrose	90 mM Arg-HCl	/
F9		200	50 mM Sucrose	90 mM Arg-HCl	10 mM Methionine
F5		200	125 mM Sucrose	50 mM Arg-HCl	/
F10		200	125 mM Sucrose	50 mM Arg-HCl	10 mM Methionine
F14		200	/	240 mM Glycine	/
F6		200	50 mM Sucrose	150 mM Glycine	/
F11		200	50 mM Sucrose	150 mM Glycine	10 mM Methionine
F7		200	100 mM Sucrose	90 mM Glycine	/
F12		200	100 mM Sucrose	90 mM Glycine	10 mM Methionine
F8		200	/	240 mM Proline	/
F13		200	/	240 mM Proline	10 mM Methionine

Table 18: Sub-Visible Particles, Protein Concentration, SEC-ULPC Data, pH, Osmolality, and Viscosity Results

No.	Excipients			MFI (Counts/mL)			Protein Conc. (mg/mL)	SEC-ULPC		pH	Osmo. (mOsmol/ kg)	Viscosity (mPa·s)	
				≥2 µm	≥10 µm	≥25 µm		HMW %	Monomer %			20 °C	25 °C
F1	175 mM Sucrose	/	10 mM Methionine	218	14	0	143.7	1.2	98.8	5.9	296	10.7	8.9
F2	160 mM Sucrose	/	10 mM Methionine	878	9	0	165.9	1.2	98.8	6.0	283	17.6	14.1
F3	160 mM Sucrose	/	10 mM Methionine	225	14	2	195.4	1.2	98.8	6.0	307	33.7	26.6
F4	50 mM Sucrose	90 mM Arg-HCl	/	2171	9	0	196.3	1.1	98.9	6.0	328	24.0	19.4
F5	125 mM Sucrose	50 mM Arg-HCl	/	115	9	2	201.9	1.2	98.8	6.0	335	26.0	20.9
F6	50 mM Sucrose	150 mM Glycine	/	17	4	0	208.8	1.2	98.8	6.1	343	38.1	30.0
F7	100 mM Sucrose	90 mM Glycine	/	22	2	0	203.6	1.2	98.8	6.0	336	37.6	30.2
F8	/	240 mM Proline	/	59	0	0	201.7	1.2	98.8	6.0	351	30.4	23.7
F9	50 mM Sucrose	90 mM Arg-HCl	10 mM Methionine	76	5	0	209.9	1.1	98.9	6.0	340	24.9	19.4
F10	125 mM Sucrose	50 mM Arg-HCl	10 mM Methionine	230	20	5	201.7	1.2	98.8	6.0	382	28.9	23.5
F11	50 mM Sucrose	150 mM Glycine	10 mM Methionine	86	10	0	208.3	1.1	98.9	6.0	71	38.6	31.0
F12	100 mM Sucrose	90 mM Glycine	10 mM Methionine	7	2	0	201.6	1.2	98.8	6.0	381	40.7	32.6
F13	/	240 mM Proline	10 mM Methionine	59	5	0	196.1	1.2	98.8	6.0	388	28.0	22.5
F14	/	240 mM Glycine	/	102	10	4	201.6	1.2	98.8	6.1	356	32.0	27.8
F15	/	135 mM Arg-HCl	/	58	9	2	198.6	1.1	98.9	6.0	323	21.7	17.7

[00390] All formulations remained slightly yellow, slightly opalescent, liquid, and free of visible particles. Formulations F4, F5, F9, F10 and F15 (containing Arg.HCl) showed slightly stronger turbidity than other formulations, and the opalescence of all formulations was in the range from 3 NTU to 18 NTU. The sub-visible particles, protein concentration, SEC-ULPC data, pH, osmolality, and viscosity data of the above-described 15 formulations is shown in **Table 18**, and the viscosity data is further depicted in **FIG. 1**. The data in **Table 18** and **FIG. 1** show that inclusion of the excipient Arg-HCl reduced viscosity compared to corresponding glycine and proline groups.

[00391] Arg-HCl was selected as a viscosity modulator, and further experiments were conducted to identify a suitable Arg-HCl concentration to enable a high protein concentration, yet reduce viscosity.

[00392] To assess Arg-HCl and antibody protein concentrations that minimize viscosity and achieve osmolality in an acceptable range, further analytical testing was conducted. Analytical testing included measurement of protein concentration, pH, osmolality, and viscosity at 20 °C and 25 °C. The results are shown in **Table 19** and **Table 20**, with **Table 19** outlining the formulations used in the experiments of **Table 20**.

[00393] It was observed that both Arg-HCl concentration and product concentration impacted viscosity. Protein concentration was the main contributor to viscosity in the range of Arg-HCl tested. The 190 mM Arg formulations had a osmolality higher than desired for a subcutaneous formulation. The feasibility of manufacturing both a 200 mg/mL formulation and a 180 mg/mL formulation was demonstrated. Based upon the results of these studies, three formulations were identified for further testing:

Formulation A: 10 mM His buffer, 10 mM Met, 150 mM Arg-HCl, 0.05% PS80, pH 5.8;

Formulation B: 10 mM His buffer, 10 mM Met, 80 mM Arg-HCl, 3%(w/v) sucrose, 0.05% PS80, pH 5.8; and

Formulation C: 10 mM His buffer, 10 mM Met, 120 mM Arg-HCl, 0.05% PS80, pH 5.8.

[00394] Additional osmolality and viscosity experiments of the three formulations are shown in **Table 21**, which were used to characterize the formulations over a range of antibody protein concentration.

[00395] No major stability issues were observed for the selected formulations, and the results demonstrated that there was no impact to product quality as assayed by the analytical testing

panel. pH and protein concentration were close to the target, and the osmolality ranged from approximately 280 mOsm/kg to 390 mOsm/kg.

[00396] Taken together, based on the experiments described in this Example, Arg-HCl was selected for inclusion in the final formulation as a viscosity modifier and L-Methionine was included in the formulation based on experiments described in **Example 2**, particularly the finding that L-methionine helped control HMW formation and antibody purity. Additionally, sucrose may be advantageous as a cryoprotectant, however it increased viscosity and osmolality. Based upon this, the inclusion of sucrose was further tested with a reduced concentration of L-arginine to compensate for the impact to osmolality in long term storage and stability studies described in **Example 6** and **Example 7**.

Table 19: Formulations Tested in Further Viscosity Studies

Target concentration (mg/mL)	Final formulation
220	10 mM His, 190 mM Arg, 10 mM Met, 0.05% PS80, pH 5.8
210	
200	
190	
180	
170	
220	10 mM His, 120 mM Arg, 10 mM Met, 0.05% PS80, pH 5.8
210	
200	
190	
180	
170	

Table 20: Further Viscosity Study Results

[Arg-HCl]	Target conc. (mg/mL)	Measured protein conc. (mg/mL)	pH	Osmolality (mOsmol/kg)	Viscosity (mPa•S, 20°C)	Viscosity (mPa•S, 25°C)
Arg-HCl 190 mM	220	235.1	5.8	491	31.4	25.2
	210	NT	5.9	482	25.1	20.4
	200	212.8	5.8	477	20.3	16.6
	190	NT	5.8	466	16.6	13.5
	180	NT	5.8	462	13.7	11.2
	170	174.0	5.8	455	10.9	9.1
Arg-HCl 120 mM	220	231.4	5.8	353	33.0	26.2
	210	NT	5.8	341	26.3	21.1

[Arg-HCl]	Target conc. (mg/mL)	Measured protein conc. (mg/mL)	pH	Osmolality (mOsmol/kg)	Viscosity (mPa•S, 20°C)	Viscosity (mPa•S, 25°C)
	200	213.9	5.8	328	20.9	16.8
	190	NT	5.8	331	17.7	14.4
	180	NT	5.8	317	14.1	11.5
	170	175.0	5.8	309	11.3	9.3

Abbreviation: NT, not tested.

Table 21: Three Formulations and Osmolality and Viscosity Study Results Thereof

Formulation	Protein target conc. (mg/mL)	Measured protein conc. (mg/mL)	Osmolality (mOsmol/Kg)	Viscosity (mPa•s)	
				20 °C	25 °C
<i>Formulation A:</i> 10 mM His buffer, 10 mM Met, 150 mM Arg-HCl, 0.05% PS80, pH 5.8	170	180.1	365	11.6	9.6
	180	189.3	368	14.4	11.9
	190	204.2	376	17.8	14.6
	200	214.8	393	22.2	27.6
	210	224.6	423	28.3	22.7
	220	233.4	413	34.9	28.1
<i>Formulation B:</i> 10 mM His buffer, 10 mM Met, 80 mM Arg-HCl, 3%(w/v) sucrose, 0.05% PS80, pH 5.8	170	177.9	360	13.1	10.9
	180	190.0	361	16.5	13.5
	190	201.1	363	20.9	16.9
	200	212.5	392	25.5	20.4
	210	220.7	398	34.9	27.7
	220	235.9	421	42.0	33.3
<i>Formulation C:</i> 10 mM His buffer, 10 mM Met, 120 mM Arg-HCl, 0.05% PS80, pH 5.8	170	181.7	304	11.1	9.2
	180	191.8	317	13.9	11.5
	190	200.9	325	16.8	13.8
	200	209.7	332	21.6	17.6
	210	224.5	332	27.2	22.0
	220	241.6	350	34.6	27.7
<i>Formulation D:</i> 10 mM His buffer, 10 mM Met, 120 mM Arg-HCl, 0.05% PS80, pH 5.8	NA	NA	238	1.1	1.0
<i>Formulation E:</i> 10 mM His buffer, 10 mM Met, 80 mM Arg-HCl, 3%(w/v) sucrose, 0.05% PS80, pH 5.8	NA	NA	262	1.2	1.0

Abbreviation: NA, not applicable, as no protein present.

Example 4: Formulation of an Anti-IL-13 Antibody: UFDF Studies

[00397] Because ultrafiltration/diafiltration (UFDF) enables material to be prepared as a concentrated solution in a buffer of choice, ensuring that a formulation was compatible with a UFDF step was desirable, particularly as this step often presents challenges when the protein solution has a high viscosity. High viscosity can present challenges for the UFDF step due to increased back-pressure in the system as the protein gets more concentrated. As the pressure builds, the processing time gets longer and exposes the product to more shear stress. In these experiments, different diafiltration (DF) buffers were evaluated to see what impact Arg-HCl had on viscosity and manufacturing feasibility. Diafiltration was performed using a Millipore, PES Type D Screen, 30 kDa membrane, as well as the DF buffers listed in **Table 22**, below. An overconcentrated (OC) pool was analyzed, and the pH, osmolality, viscosity, and protein percent yield data was determined, as shown in **Table 22**.

[00398] In conclusion, it was observed that the addition of Arg-HCl to the DF buffer reduced the viscosity of the UFDF pool. The protein concentration also impacted the viscosity, and the increase in pH and reduction in the histidine concentration from the Donnan effect was reduced as the Arg-HCl concentration was increased in the DF buffer.

[00399] To identify how to prepare the formulation by UFDF to identify suitable formulations, the DF buffer was evaluated for its impact on pH from the Donnan effect during UFDF (3 runs at different pH). Further, the excipient concentrations following UFDF due to the Donnan effect were evaluated. The experiment consisted of: Run 1: 904.4 g/m², Run 2: 965.8 g/m², and Run 3: 971.9 g/m² using a Millipore, PES Type D Screen, 30 kDa membrane with 2 × 0.11 m² for Run 1 and 3 × 88 cm² for Runs 2 and 3. The DF buffers tested were 15 mM His-HCl, 120 mM Arg-HCl with a pH of 5.7, 5.5, and 5.9 for Runs 1-3, respectively. The results are provided in **Table 23**.

[00400] In comparison to the load sample, all overconcentrated pool (OC) samples showed a minimal (less than 0.3%) SEC-UPLC purity loss, and the yields with chase sample consistently exceed 95%. This ensured the maintenance of sample quality and yield throughout the process. The excipient concentrations shifted due to the Donnan effect, while the pH shift remained minimal (less than 0.1), consistent with the experiments described in **Table 22**. The viscosity of

the OC pool was previously reduced by the addition of Arg-HCl. These runs were pooled for subsequent experiments described and to demonstrate the manufacturing feasibility for this step.

Table 22: UFDF Buffers Tested and Results

DF Buffer	Sample	OC Pool Protein Conc. mg/mL	pH (Impact from the Donnan effect)	[His] (mM) *	[Arg] (Mm)*	[Cl-] (mM)*	Osmolality (mOsmol/kg)	Viscosity (20°C)(cP)	Viscosity (25°C)(cP)	Yield (%)
18 mM Histidine buffer, pH 5.7	OC-1	257.0	6.09 (↑0.4)	6.1	NA	28.2	90	289.9	199.7	71.8
18 mM Histidine buffer, 50 mM Arg-HCl, pH 5.7	OC-2	267.9	5.84 (↑0.2)	12.5	34.0	74.9	169	132.6	99.9	92.4
18 mM Histidine buffer, 100 mM Arg-HCl, pH 5.7	OC-3	259.5	5.80 (↑0.1)	13.6	77.1	120.4	279	85.0	66.0	89.4

Abbreviations: OC, overconcentrated pool; cP, centipoise.
* determined via High-performance liquid chromatography; method not provided.

Table 23: Results of UFDF Runs with Three Different DF Buffer pHs

Run	Step	Conc. (g/L)	Sample pH	SEC-UPLC (%) (Main/HMW/LMW)	Histidine Conc. (mM)	Arginine Conc. (mM)	Yield (%)	Osmolality (mOsmol/Kg)	Viscosity at 20 °C (cP)	Viscosity at 25 °C (cP)
1	Load	70.209	DF buffer: 5.68	99.4/0.6/ND	DF buffer: 15.285	DF Buffer: 121.939	NA	NA	NA	NA
	OC-1	259.3	5.67	99.3/0.7/ND	11.131	88.290	97.3	322	90.9	70.2
	Chasing	48.756	NT	NT	NT	NT	3.2	NT	NT	NT
2	Load	70.209	DF buffer: 5.49	99.4/0.6/ND	DF buffer: 15.543	DF Buffer: 123.678	NA	NA	NA	NA
	OC-2	260.6	5.55	99.3/0.7/ND	10.449	82.533	95.1	299	104.9	78.8

3	Chasing	35.614	NT	NT	NT	NT	4.7	NT	NT	NT
	Load	70.209	DF buffer: 5.92	99.4/0.6/ND	DF buffer: 15.266	DF Buffer: 123.831	NA	NA	NA	NA
	OC-3	264.8	5.93	99.2/0.8/ND	11.050	88.003	91.0	322	102.4	79.3
	Chasing	49.192	NT	NT	NT	NT	6.9	NT	NT	NT

OC: overconcentrated pool, HMW: high molecular weight, LMW: low molecular weight, ND: not detected; cP: centipoise.

Example 5: Formulation of an Anti-IL-13 Antibody: Injectability Study

[00401] This Example describes injectability studies to evaluate whether the forces required for injection would be acceptable for the formulation, as described and developed in **Examples 1-4**, of an IL-13 antibody. As described throughout **Examples 1-3**, the formulations selected for this stage of testing included a pH of about 5.8 due to its favorable results in SE-UPLC experiments (see **Example 1**), a histidine buffer (or comparable acetate or succinate buffer, respectively), L-methionine, which was demonstrated to help control HMW formation and antibody purity (see **Example 2**), and the excipient Arg-HCl, based on its ability to reduce viscosity (see **Example 3**).

Materials and Methods

[00402] The break-loose force and glide force method quantitatively measured the forces required to complete a prefilled syringe (PFS) injection (*i.e.*, expel the content of the PFS). Break-loose force was defined as the force required to cause a change (from a rested position) in the plunger stopper position. Glide force (maximum glide force) was defined as the maximum force measured on the glide force profile during the course of expelling the contents of a PFS. The test was conducted with an Instron materials testing machine-34TM-5 equipped with a 2000N load cell. The load cell was selected based on the sample property (the maximum force is within the 70% of the load cell range). The crosshead moved at a 140 mm/min speed to apply compressive force to the PFS plunger rod. The measured compression force was recorded at 60 Hz as the content of the PFS being extruded (expelled). The measurement stopped when the force reached end of test criteria where the plunger stopper hits the end of syringe barrel. Data are reported numerically in 2 decimal places (N).

[00403] The required amounts of material, excipient stock solutions, and surfactant stock solution were calculated, weighed, and well-mixed to prepare formulations with the target protein concentration at 220 mg/mL according to the formulation recipes listed in **Table 24**. Then, a stepwise gravimetric dilution on protein concentration from 220 mg/mL to 170 mg/mL in 10 mg/mL increments was performed with the respective formulation buffers. Each of the formulation solution were filtered with a 0.22 µm PES filter. All sample filtration and aliquoting was carried out with aseptic procedures in a bio-safety cabinet.

Results

[00404] The study was conducted in triplicate. Pre-filled syringes with plunger stoppers and standard syringes were evaluated. The formulations tested in the injectability studies are outlined in **Table 24**. It was observed that the increase of Arg-HCl concentration from 120 mM to 150 mM led to an increasing osmolality, but no substantial difference in viscosity were observed between these two formulations. The formulation with 3% sucrose had a higher viscosity than the other two formulations, and with the protein concentration increase, the osmolality and viscosity showed a substantial increase.

[00405] Based upon the force data, provided in **Table 25** and **FIG. 2**, it was observed that as the protein concentration increased, the Max/Average gliding force increased, and it was determined that a pre-filled syringe was suitable for administration of a formulation described herein. For the standard syringe with the 25 gauge needle, clogging of the needle was observed for many of the samples. The clogging may have been due to differences between the two formats in syringe barrel cross-sectional area, needle wall thickness, silicone distribution, and/or needle length.

Table 24: Formulations Tested in Injectability Study

Protein conc. (mg/mL)	Formulation
170, 180, 190, 200, 210, and 220	10 mM His buffer, 10 mM Met, 150 mM Arg-HCl, 0.05% PS80, pH 5.8
	10 mM His buffer, 10 mM Met, 80 mM Arg-HCl, 3.8%(w/v) sucrose, 0.05% PS80, pH 5.8
	10 mM His buffer, 10 mM Met, 120 mM Arg-HCl, 0.05% PS80, pH 5.8
Control	10 mM His buffer, 10 mM Met, 120 mM Arg-HCl, 0.05% PS80, pH 5.8
	10 mM His buffer, 10 mM Met, 80 mM Arg-HCl, 3.8%(w/v) sucrose, 0.05% PS80, pH 5.8

Table 25: Injectability Study Results

Formulation	Protein conc. (mg/mL)	Test Speed (mm/min)	Viscosity (mPa·S, 20 °C)	PFS		
				Average Gliding Force (N)	Average Max Gliding Force (N)	Average Breaking Loose Force (N)
10 mM His buffer, 10 mM Met, 150 mM	170	140	11.6	10.00	10.74	5.22
	180	140	14.4	11.80	12.78	4.78
	190	140	17.8	13.76	14.90	4.66

Arg-HCl, 0.05% PS80, pH 5.8	200	140	22.2	15.90	17.36	4.84
	210	140	28.3	18.74	20.79	4.50
	220	140	34.9	23.29	25.39	4.63
10 mM His buffer, 10 mM Met, 80 mM Arg- HCl, 3%(w/v) sucrose 0.05% PS80, pH 5.8	170	140	13.1	10.79	11.98	4.97
	180	140	16.5	12.36	13.44	4.47
	190	140	20.9	14.92	16.13	4.38
	200	140	25.5	17.85	19.51	5.21
	210	140	34.9	21.15	23.15	4.39
	220	140	42.0	25.77	28.42	4.72
10 mM His buffer, 10 mM Met, 120 mM Arg-HCl, 0.05% PS80, pH 5.8	170	140	11.1	9.92	10.71	5.48
	180	140	13.9	11.96	13.04	5.09
	190	140	16.8	13.60	15.15	4.28
	200	140	21.6	16.15	17.80	4.91
	210	140	27.2	19.69	21.60	4.95
	220	140	34.6	22.58	24.94	4.74
10 mM His buffer, 10 mM Met, 120 mM Arg-HCl, 0.05% PS80, pH 5.8	-	140	1.1	3.12	3.59	4.56
10 mM His buffer, 10 mM Met, 80 mM Arg- HCl, 3%(w/v) sucrose 0.05% PS80, pH 5.8	-	140	1.2	3.03	3.54	4.66

Example 6: Formulation of an Anti-IL-13 Antibody: Long-Term Storage Study

[00406] This Example describes long term stability studies, under different conditions, of the IL-13 antibody formulation described and developed in **Examples 1-5**.

5

Materials and Methods

[00407] A panel of analytical methods were used to evaluate long-term storage conditions, the Methods of which are described in **Example 1** and **Example 2** and in the *Potency* section, below. In brief, formulated antibody was used to fill either a 2R glass vial and stopper (*e.g.*,

10 Schott cat no 1626151 and West cat no 1970-0173) to represent a drug product configuration or a Sartorius Celsius FFT bag to represent a drug substance configuration. The vial configuration was tested at 5 °C (the intended storage temperature), 25 °C, or 40 °C, as well as for photostability under dark versus light conditions. The higher temperatures and photostability conditions were intended to evaluate more stressful conditions to provide an early indication of

15 potential degradation pathways that may occur during long term storage at the intended storage

temperature and/or manufacturing procedures. The bag configuration was tested at -70 °C and for freeze thaw cycles to evaluate stability during long term storage and/or manufacturing procedures.

Potency

- 5 **[00408]** The binding assay used was an enzyme-linked immunosorbent assay (ELISA). IL-13 is an immunoregulatory cytokine, which regulates the function of human B cells and monocytes. In this assay, IL-13 was immobilized onto a 96-well plate. WBP2546 was added and bound to the captured human IL-13. The bound WBP2546 was detected by anti-human IgG (F(ab')₂ specific)-peroxidase secondary antibody. 3,3',5,5' tetramethylbenzidine (TMB) substrate solution
- 10 was loaded into the wells subsequently. A blue color developed in proportion to the amount of bound secondary antibody. Blue color development was stopped by adding stop solution and the color changed to yellow. The measured absorbance at 450 nm was subtracted from absorbance at 650 nm, producing a signal that was proportional to the concentration of the analyte in the well.
- 15 **[00409]** Dose response curves were plotted according to a 4-parameter logistic (Auto-Estimate) regression model using the Softmax Pro Software for samples, as well as control and reference standards. Relative binding potency of the sample was calculated using the EC50 of reference to samples on the same plate derived from 4-parameter logistic fit.

Results

- 20 **[00410]** Formulated antibody was used to fill either a 2R glass vial to represent a drug product configuration or a Sartorius Celsius FFT bag to represent a drug substance configuration. The vial configuration was tested at 5 °C (the intended storage temperature), 25 °C, or 40 °C as well as for photostability under dark versus light conditions, The higher temperatures and photostability conditions were intended to evaluate more stressful conditions to provide an early
- 25 indication of potential degradation pathways that may occur during long term storage at the intended storage temperature and/or manufacturing procedures. The bag configuration was tested at -70 °C and for freeze thaw cycles to evaluate stability during long term storage and/or manufacturing procedures.
- 30 **[00411]** Using a fill volume of 2.7 mL per vial or bag, three formulations (F1, F2, and F3), outlined in **Table 26**, were tested under the various conditions. As described throughout

Examples 1-4, the formulations selected this stage of testing included a pH of about 5.8 due to its favorable results in SE-UPLC experiments (see **Example 1**), a histidine buffer (or comparable acetate or succinate buffer, respectively), L-methionine, which was demonstrated to help control HMW formation and antibody purity (see **Example 2**), and the excipient Arg-HCl, based on its ability to reduce viscosity (see **Example 3**).

Table 26: Formulations Tested for Long-Term Storage and Stability

No.	Protein conc. (mg/mL)	pH	Buffer and surfactant	Excipient 1	Excipient 2	Excipient 3
F1	200	5.8	10 mM His, 0.05% (w/v) PS80	120 mM Arg-HCl	10 mM Methionine	/
F2	180	5.8	10 mM His, 0.05% (w/v) PS80	120 mM Arg-HCl	10 mM Methionine	/
F3	180	5.8	10 mM His, 0.05% (w/v) PS80	80 mM Arg-HCl	10 mM Methionine	3% (w/v) sucrose

[00412] pH, appearance, sub-visible particles (MFI), protein concentration, SE-UPLC, iCIEF, and CE-SDS, were evaluated for the vial configuration using the Materials and Methods described throughout **Examples 1-2** after 1 month of storage at 5 °C, 25 °C, or 40 °C, photostability under dark and light conditions. Storage at -70 °C and free/thaw stability was evaluated for the bag configuration.

[00413] The T0 antibody, histidine, and L-arginine concentrations, osmolality, and viscosity data are presented in **Table 27**.

Table 27: Concentrations, Osmolality, and Viscosity Results

No.	Measured protein concentration at T=0 (mg/mL)	Osmolality (mOsmol/Kg)	Viscosity (mPa·s)		Measured Histidine concentration (mM)	Measured Arginine concentration (mM)
			20 °C	25 °C		
F1	199.1	323	21.6	17.6	10.283	122.479
F2	181.5	315	14.7	11.8	9.926	121.435
F3	183.5	342	14.9	12.7	10.244	75.760

[00414] As shown in **Table 28**, no substantial changes in F1, F2, and F3, were observed after storage at 5 °C for 1 month for any of the tested attributes.

[00415] After incubation at 25 °C for 1 month, small (0.5% - 0.6%) SEC monomer decreases were observed for F1, F2, and F3 groups, with no substantial differences between F1, F2 and F3.

5 After incubation at 25 °C for 1 month, decreases (about 50%) in PS80 concentration were observed in F1, F2, and F3, compared to T0. The formulation buffer control (F4; not shown) had even lower levels of PS80 after 2 weeks at 25 °C and 40 °C (< 0.010%), indicating that the degradation was slowed in the presence of antibody (**Table 28**). These results suggested that the PS80 may have undergone oxidative degradation which is a known degradation pathway that
10 may be accelerated at higher temperatures and/or light exposure.

[00416] After incubation at 40 °C for 1 month, for F1, F2 and F3, the color deepened slightly compared to the T0 samples, and substantial decreases were observed in SEC, CE-NR and iCIEF results demonstrating these methods as stability indicating. No substantial differences were observed between F1, F2, and F3 in all test results. After incubation at 40 °C for 1 month,
15 decreases (about 50%) in in PS80 concentration were observed in which F1, F2, and F3, compared with T0 (**Table 28**).

[00417] After 1000 lux light exposure at 25 °C for 14 days, substantial decreases in purity as assessed by SEC, CE-NR, and iCIEF were observed for F1, F2, and F3 (**Table 29**). In the CE-NR assay, without being bound by theory, the decreased purity may be caused by aggregates
20 instead of fragments. No substantial decreases were observed for dark control samples stored at 25°C for 7 days and 14 days (two weeks). No substantial difference between F1, F2, and F3 were observed after 1000 lux light exposure for 7 days (1 week) and 14 days (2 weeks). For F2, stored at -70 °C for 1 month (1M), a substantial increase in $\geq 2 \mu\text{m}$ was observed in sub-visible particles results (**Table 30**). For F1, F2, and F3, stored at -70 °C for 1 month, no substantial
25 changes were observed in SEC/Caliper/iCIEF/PS80 test results (**Table 30**).

[00418] For F3, after 5 freeze/thaw (F/T) cycles (F/T-5 Cycles), substantial increases ($\geq 2 \mu\text{m}$) were observed in sub-visible particles results (**Table 31**). For F1, F2, and F3, after 5 freeze/thaw cycles, no substantial changes were observed in SEC/Caliper/iCIEF/PS80 test results **Table 31**).

Table 28: pH, Appearance, MFI, SEC, CD-SDS-R & NR, iCIEF, PS80 Concentration, and Potency Results

Temp.	Form.	Condition	pH	Appearance	Sub-visible particles (MFI, AR < 0.85, counts/mL)			SEC purity			CE-SDS-R	CE-SDS-NR	iCIEF			PS80 (%)	Potency (%)
					≥ μm	2	10	25	Mono. %	HMW %	LMW %	Purity %	Basic peaks %	Acidic peaks %	Main peak %		
5C	F1	T0	5.8	SY, SOL, FP	204	9	2	99.3	0.7	ND	98.5	97.6	3.9	20.8	75.4	0.041	105
		5C-2W	5.8	SY, SOL, FP	127	2	0	99.3	0.7	ND	98.0	97.6	3.7	20.6	75.7	0.037	NT
		5C-1M	5.8	SY, SOL, FP	56	4	0	99.2	0.8	ND	98.1	97.5	4.0	18.8	77.2	0.042	79
	F2	T0	5.8	SY, SOL, FP	95	9	0	99.4	0.6	ND	98.1	97.6	3.8	19.9	76.3	0.043	100
		5C-2W	5.8	SY, SOL, FP	130	5	2	99.3	0.7	ND	97.9	97.5	3.6	20.3	76.0	0.042	NT
		5C-1MW	5.8	SY, SOL, FP	84	0	0	99.3	0.7	ND	98.2	97.6	4.2	19.3	76.4	0.043	95
	F3	T0	5.8	SY, SOL,	145	17	4	99.3	0.7	ND	98.4	97.6	3.3	20.5	76.1	0.041	99

[illegible]

[illegible]

		FP																		
40C- 2W	5.8	SOL, FP	56	2	0	98.3	1.3	0.4	97.2	96.0	6.6	29.0	64.4	0.018	NT					
40C- 1W	5.8	SOL, FP	115	4	0	97.3	2.0	0.7	96.7	94.4	8.9	41.2	49.9	0.020	90					

Abbreviations: W, Weeks; M, Months; SY, Slightly yellow; SOL, Slightly opalescent liquid; C, Colorless; CL, Clear liquid; FP, Free of visible particles. HMW, High molecular weight; LMW, Low molecular weight; Mono., monomer; NT, not tested.

Table 29: Photostability (pH, Appearance, MFI, SEC, CD-SDS-R & NR, and iCIEF) Results

Formulation	Condition	pH	Appearance	Sub-visible particles (MFL, AR < 0.85, counts/mL)			SEC purity			CE-SDS-R	CE-SDS-NR	iCIEF			
				≥ μm			Mono. %	HMW %	LMW %			Purity %	Basic peaks %	Acidic peaks %	Main peak %
					2	10									
F1	T0	5.8	SY, SOL, FP	204	9	2	99.3	0.7	ND	98.5	97.6	3.9	20.8	75.4	
	Dark1W	5.8	SY, SOL, FP	349	4	0	99.1	0.7	0.2	97.8	97.3	3.8	20.6	75.6	
	Dark2W	5.8	SY, SOL, FP	122	4	2	99.0	0.8	0.2	98.0	97.4	4.3	21.3	74.4	
	Light1W	5.8	SY, SOL, FP	522	15	0	98.5 (-0.8)	1.4 (+0.7)	0.1	98.0	96.7	4.0	21.5	74.5	
	Light2W	5.8	SY, SOL, FP	200	9	0	97.8 (-1.5)	2.0 (+1.3)	0.2	97.9	96.5 (-1.1)	4.3	24.1	71.5 (-3.9)	

F2	T0	5.8	SY, SOL, FP	95	9	0	99.4	0.6	ND	98.1	97.6	3.8	19.9	76.3
	Dark1W	5.8	SY, SOL, FP	84	0	0	99.1	0.7	0.1	98.0	97.6	4.2	21.4	74.5
	Dark2W	5.8	SY, SOL, FP	104	2	2	99.0	0.8	0.2	97.8	97.5	4.3	21.8	74.0
	Light1W	5.7	SY, SOL, FP	59	0	0	98.5 (-0.9)	1.3 (+0.7)	0.2	97.8	97.0	4.2	22.3	73.5
	Light2W	5.8	SY, SOL, FP	30	0	0	97.9 (-1.5)	1.9 (+1.3)	0.2	97.7	96.5 (-1.1)	4.3	23.3	72.4 (-3.9)
F3	T0	5.8	SY, SOL, FP	145	17	4	99.3	0.7	ND	98.4	97.6	3.3	20.5	76.1
	Dark1W	5.8	SY, SOL, FP	61	4	0	99.1	0.8	0.1	97.9	97.5	4.3	21.3	74.4
	Dark2W	5.8	SY, SOL, FP	53	0	0	99.0	0.8	0.2	97.9	97.4	4.1	21.6	74.3
	Light1W	5.7	SY, SOL, FP	136	7	0	98.5 (-0.8)	1.4 (+0.7)	0.1	97.8	97.1	3.9	22.3	73.7
	Light2W	5.8	SY, SOL, FP	158	2	0	97.8 (-1.5)	2.0 (+1.3)	0.2	98.0	96.5 (-1.1)	4.4	23.5	72.1 (-4.0)

Abbreviations: W, Week(s); SY, Slightly yellow; SOL, Slightly opalescent liquid; C, Colorless; CL, Clear liquid; FP, Free of visible particles. HMW, High molecular weight; LMW, Low molecular weight; Mono., monomer.

Table 30: -70 °C Results

Form. No.	Sampling Points	pH	Appearance	Sub-visible particles (MFI, Counts/mL)				SEC-UPLC			CE-SDS-R	CE-SDS-NR	iCIEF			PS80 (%)	Potency (%)
				≥ μm			Mono. %	HMW %	LMW %	Purity %		Basic peaks %	Acidic peaks %	Main peak %			
				2	10	25											
F1	T0	5.8	SY, SOL, FP	204	9	2	99.3	0.7	ND		98.5	97.6	3.9	20.8	75.4	0.041	105
	-70C-1M	5.8	SY, SOL, FP	711	87	17	99.2	0.8	ND		98.4	97.5	3.9	19.2	76.9	0.044	94
F2	T0	5.8	SY, SOL, FP	95	9	0	99.4	0.6	ND		98.1	97.6	3.8	19.9	76.3	0.043	100
	-70C-1M	5.8	SY, SOL, FP	1219	127	12	99.3	0.7	ND		98.1	97.6	3.9	19.2	77.0	0.044	96
F3	T0	5.8	SY, SOL, FP	145	17	4	99.3	0.7	ND		98.4	97.6	3.3	20.5	76.1	0.041	99
	-70C-1M	5.8	SY, SOL, FP	869	94	12	99.3	0.7	ND		98.3	97.6	3.9	19.7	76.5	0.043	93

Abbreviations: M, Month(s); SY, Slightly yellow; SOL, Slightly opalescent liquid; C, Colorless; CL, Clear liquid; FP, Free of visible particles. HMW, High molecular weight; LMW, Low molecular weight; Mono., monomer.

5 Table 31: Freeze/Thaw Bag Results

Formulation	Sampling Points	pH	Appearance	Sub-visible particles (MFI, counts/mL)			SEC purity			CE-SDS-R	CE-SDS-NR	iCIEF			
				μm ≥			Mono. %	HMW %	LMW %			Purity %	Basic peaks %	Acidic peaks %	Main peak %
					2	10									
F1	T0	5.8	SY, SOL, FP	204	9	2	99.3	0.7	ND	98.5	97.6	3.9	20.8	75.4	

	F/T-1 Cycle	5.8	SY, SOL, FP	738	66	5	99.2	0.8	ND	98.0	97.5	3.6	19.2	77.2
	F/T-5 Cycles	5.8	SY, SOL, FP	615	74	7	99.3	0.7	ND	98.0	97.6	4.1	19.2	76.8
F2	T0	5.8	SY, SOL, FP	95	9	0	99.4	0.6	ND	98.1	97.6	3.8	19.9	76.3
	F/T-1 Cycle	5.8	SY, SOL, FP	507	73	9	99.3	0.7	ND	98.1	97.5	3.8	19.8	76.4
	F/T-5 Cycles	5.8	SY, SOL, FP	656	33	4	99.3	0.7	ND	98.2	97.6	4.5	19.6	75.9
F3	T0	5.8	SY, SOL, FP	145	17	4	99.3	0.7	ND	98.4	97.6	3.3	20.5	76.1
	F/T-1 Cycle	5.8	SY, SOL, FP	723	89	10	99.2	0.8	ND	98.3	97.5	4.3	19.9	75.8
	F/T-5 Cycles	5.8	SY, SOL, FP	1430	97	10	99.3	0.7	ND	98.3	97.6	4.1	20.0	76.0

Abbreviations: F/T, freeze/thaw; SY, Slightly yellow; SOL, Slightly opalescent liquid; FP, Free of visible particles. HMW, High molecular weight; LMW, Low molecular weight; Mono., monomer.

Example 7: 12-Month Stability Study of Three Formulations

In this example, three formulations were tested for stability under various conditions over a 12-month period. The tested formulations are shown in **Table 32**, referred to as F1, F2 and F3, with the control formulation referred to as F4. The anti-IL-13 antibody (protein) used in this example was Construct 133.

Table 32: Formulations Tested

Formulation No.	Protein Conc. (mg/mL)	pH	Buffer and Surfactant	Excipient 1	Excipient 2	Excipient 3
F1	200	5.8	10 mM L-His/L-His-HCl, 0.05% (w/v) PS80	120 mM L-Arg-HCl	10 mM L-Met	/
F2	180	5.8	10 mM L-His/L-His-HCl, 0.05% (w/v) PS80	120 mM L-Arg-HCl	10 mM L-Met	/
F3	180	5.8	10 mM L-His/L-His-HCl, 0.05% (w/v), PS80	80 mM L-Arg-HCl	10 mM L-Met	3% (w/v) sucrose
F4	Control	10 mM L-His/L-His-HCl buffer, 0.05% (w/v) PS80, 120 mM L-Arg-HCl, 10 mM L-Met, pH 5.8				

Samples were prepared to a fill-volume of 2.7 ml/vial or 4 ml/bag. The study plan for the various conditions tested, and the sampling schedule, are shown in **Table 33**.

Table 33: Stability Study Plan

Formulation No.	Conditions	T0	Sampling points							
			1 W	2 W	1 M	3 M	6 M	9 M	12 M	Retain 1#
										Retain 2#

F1-F3	2-8 °C	X, Y, Z, W	/	X, W	X, Z,W	X	X, Z, W	X , W	X, Z, W	X, Z, W	X, Z, W
	25 °C		/	X, W	X, Z, W	X	/	/	/	/	/
	40 °C		X, W	X, W	X, Z, W	/	/	/	/	/	/
	-70 °C (Bag)		/	/	X, Z, W	X	X, Z, W	/	X, Z, W	X, Z, W	X, Z,W
	F/T (-70°C to RT, Bag)		1 Cycle				5 Cycles				
	Photostability (1000 lux, 25°C)		X				X				
			Dark control				Light exposure				
			7 days		14 days		7 days		14 days		
			X, Z, W		X, Z, W		X, Z, W		X, Z, W		
F4	Conditions	T0'	1 W	2 W	1 M	3 M	6 M	12 M	Retain 1#	Retain 2#	
	2-8 °C	X', Y'	/	X'	X'	X'	X'	X'	X'	X'	
	25 °C		/	X'	X'	X'	/	/	/	/	
	40 °C		X'	X'	X'	/	/	/	/	/	
	-70 °C (Bag)		/	/	X'	/	X'	X'	X'	X'	

X=pH, Appearance (Visual inspection), Sub-visible particles (MFI), Protein concentration, SE-UPLC, iCIEF, CE-SDS

Z= Potency

W= PS80

X'= pH, Appearance, Sub-visible particles (MFI), PS80

Y'= Viscosity, Osmolarity

The quality aspects set forth in **Table 33** were tested as described in previous examples.

The results for the stability data at 5°C, 25°C, 40°C and -70°C storage conditions are shown in **Table 34**, **Table 35**, **Table 36** and **Table 37**, respectively. The results of the freeze-

thaw study are shown in **Table 38**. The results of the photostability study are shown in **Table 39**.

Analysis of SE-UPLC is presented as monomer peak normalized to T0 and high molecular weight species (HMW) are presented as a fold-change over T0. Values for low molecular weight (LMW) species for all tested samples at all conditions < 1.0%. Analysis of iCIEF is presented as main peak (MP) normalized to T0 and acidic peaks (AP) and basic peaks (BP) are presented as a fold-change over T0. Abbreviations used in the tables are as follows: SY: Slightly yellow; SOL: Slightly opalescent liquid; FP: Free of visible particles; C: Clear; CL: Clear liquid.

Table 34: Formulation Stability Data at 5°C Storage Conditions

F#	Sampling pts	pH	Appearance	MFI, (AR<0.85, Counts/mL)			SE-UPLC		CE-SDS-R	CE-SDS-NR	iCIEF			PS80 (%)	Potency (%)
				≥ 2 μm	≥ 10 μm	≥ 25 μm	Normalized Monomer %	Fold-change in HMW			Fold-change in Basic peaks	Fold-change in Acidic peaks	Normalized Main peak %		
F1	T0	5.8	SY, SO, FP	204	9	2	100.0	1.0	98.5	97.6	1.0	1.0	100.0	0.041	105
	5C-2W	5.8	SY, SO, FP	127	2	0	100.0	1.0	98.0	97.6	0.9	1.0	100.4	0.037	/
	5C-1M	5.8	SY, SO, FP	56	4	0	99.9	1.1	98.1	97.5	1.0	0.9	102.4	0.042	79
	5C-3M	5.7	SY, SO, FP	518	58	4	99.7	1.3	98.6	97.4	1.1	0.9	101.6	0.041	/
	5C-6M	5.8	SY, SO, FP	584	33	2	99.6	1.3	98.5	97.5	1.2	1.0	99.7	0.029(10.012)	101
	5C-9M	5.7	SY, SO, FP	253	37	2	99.6	1.4	98.4	97.3	1.2	1.0	98.1	0.024(10.017)	/
F2	T0	5.8	SY, SO, FP	95	9	0	100.0	1.0	98.1	97.6	1.0	1.0	100.0	0.043	100
	5C-2W	5.8	SY, SO, FP	130	5	2	99.9	1.2	97.9	97.5	0.9	1.0	99.6	0.042	/
	5C-1M	5.8	SY, SO, FP	84	0	0	99.9	1.2	98.2	97.6	1.1	1.0	100.1	0.043	95
	5C-3M	5.7	SY, SO, FP	472	22	2	99.7	1.5	98.6	97.4	1.1	1.0	99.6	0.043	/
	5C-6M	5.7	SY, SO, FP	661	20	2	99.5	1.3	98.4	97.6	1.1	1.0	98.7	0.028(10.015)	91

	5C-9M	5.8	SY, SO, FP	225	12	4	99.5	1.7	98.3	97.4	1.2	1.1	97.0	0.021(10.022)	/
F3	T0	5.8	SY, SO, FP	145	17	4	100.0	1.0	98.4	97.6	1.0	1.0	100.0	0.041	99
	5C-2W	5.8	SY, SO, FP	249	2	0	100.0	1.0	98.1	97.5	1.0	1.0	100.8	0.043	/
	5C-1M	5.8	SY, SO, FP	71	4	2	99.9	1.1	98.2	97.6	1.2	1.0	100.4	0.043	106
	5C-3M	5.7	SY, SO, FP	313	12	0	99.7	1.3	98.6	97.4	1.4	1.0	99.6	0.039	/
	5C-6M	5.8	SY, SO, FP	389	7	0	99.6	1.3	98.3	97.6	1.3	1.0	98.6	0.029(10.012)	94
	5C-9M	5.7	SY, SO, FP	220	10	0	99.6	1.4	98.3	97.4	1.4	1.1	97.1	0.023(10.018)	/

Table 35: Formulation Stability Data at 25°C Storage Conditions

FB No.	Sampling pts	pH	Appearance	Sub-visible particles (MFL, AR<0.85, Counts/mL)			SEC purity		Fold-change in HMW	Purity %	CE-SDS-R	CE-SDS-NR	iCIEF			PS80 (%)	Potency (%)
				≥ 2 μm	≥ 10 μm	≥ 25 μm	Normalized Monomer %						Fold-change in Basic peaks	Fold-change in Acidic peaks	Normalized Main peak %		
F01	T0	5.8	SY, SOL, FP	204	9	2	100.0	1.0		98.5		97.6	1.0	1.0	100.0	0.041	105
	25C-2W	5.8	SY, SOL, FP	110	5	2	99.7	1.1		97.9		97.4	1.1	1.0	98.5	0.033	/
	25C-1M	5.8	SY, SOL, FP	158	10	0	99.5	1.4		98.0		96.7	1.3	1.0	98.0	0.020(10.021)	91

	25C-3M	5.7	SY, SOL, FP	374	33	4	99.1	2.0		97.9	96.3 (1.3)	1.6	1.2	91.5	0.018(0.023)	/
F02	T0	5.8	SY, SOL, FP	95	9	0	100.0	1.0		98.1	97.6	1.0	1.0	100.0	0.043	100
	25C-2W	5.8	SY, SOL, FP	102	0	0	99.7	1.3		98.1	97.5	1.1	1.1	97.4	0.035	/
	25C-1M	5.8	SY, SOL, FP	68	0	0	99.4	1.7		97.8	97.2	1.2	1.1	97.2	0.019(0.024)	103
	25C-3M	5.7	SY, SOL, FP	760	38	9	99.0	2.2		97.8	96.3 (1.3)	1.7	1.2	90.4	0.018(0.025)	/
F03	T0	5.8	SY, SOL, FP	145	17	4	100.0	1.0		98.4	97.6	1.0	1.0	100.0	0.041	99
	25C-2W	5.8	SY, SOL, FP	92	4	0	99.7	1.1		98.1	97.4	1.2	1.0	98.2	0.033	/
	25C-1M	5.8	SY, SOL, FP	199	10	0	99.5	1.4		97.9	97.2	1.5	1.1	95.3	0.021(0.020)	87
	25C-3M	5.7	SY, SOL, FP	361	14	0	99.1	1.9		98.0	96.4 (1.2)	1.8	1.2	90.5	0.018(0.023)	/
F04	T0	5.8	C, CL, FP	20	2	0	/	/		/	/	/	/	/	0.037	/
	25C-2W	5.9	C, CL, FP	73	2	0	/	/		/	/	/	/	/	<0.010	/
	25C-1M	5.8	C, CL, FP	15	0	0	/	/		/	/	/	/	/	<0.010	/
	25C-3M	5.8	C, CL, FP	79	0	0	/	/		/	/	/	/	/	<0.010 (0.0036)	/

Table 36: Formulation Stability Data at 40°C Storage Conditions

FB No.	Sampling points	pH	Appearance	MFI (AR<0.85, Counts/mL)			SEC purity		CE-SDS-R Purity %	CE-SDS-NR Purity %	iCIEF			PS80 (%)	Potency (%)
				≥ 2 μm	≥ 10 μm	≥ 25 μm	Normalized Monomer %	Fold-change in HMW			Fold-change in Basic peaks	Fold-change in Acidic peaks	Normalized Main peak %		
F01	T0	5.8	SY, SO, FP	204	9	2	100.0	1.0	98.5	97.6	1.0	1.0	100.0	0.041	105
	40C-1W	5.7	SY, SO, FP	354	5	2	99.3	1.7	97.4 (11.1)	97.0	1.5	1.2	92.3	0.026 (10.0 15)	/
	40C-2W	5.8	SY, SO, FP	104	0	0	98.8	2.1	97.0 (11.5)	96.0 (1.6)	1.7	1.4	85.7	0.020 (10.0 21)	/
	40C-1M	5.8	SY, SO, FP	32	5	0	97.8	3.3	96.6 (11.9)	94.0 (1.6)	2.2	2.0	67.1	0.022 (10.0 19)	103
F02	T0	5.8	SY, SO, FP	95	9	0	100.0	1.0	98.1	97.6	1.0	1.0	100.0	0.043	100
	40C-1W	5.7	SY, SO, FP	63	4	0	99.2	1.8	97.3	96.9	1.3	1.2	93.1	0.027 (10.0 16)	/
	40C-2W	5.8	SY, SO, FP	46	0	0	98.7	2.3	97.2	95.9 (1.7)	1.7	1.5	84.3	0.020 (10.0 23)	/
	40C-1M	5.8	SY, SO, FP	125	10	2	97.7	3.7	96.9 (11.2)	94.3 (1.3)	2.4	2.1	65.5	0.020 (10.0 23)	82
F03	T0	5.8	SY, SO, FP	145	17	4	100.0	1.0	98.4	97.6	1.0	1.0	100.0	0.041	99
	40C-1W	5.8	SY, SO, FP	302	22	7	99.4	1.6	97.3 (11.1)	96.9	1.7	1.2	91.3	0.028 (10.0 13)	/
	40C-2W	5.8	SY, SO, FP	56	2	0	99.0	1.9	97.2 (11.2)	96.0 (1.6)	2.0	1.4	84.6	0.018 (10.0 23)	/
	40C-1M	5.8	SY, SO, FP	115	4	0	98.0	2.9	96.7 (11.7)	94.4 (1.3)	2.7	2.0	65.6	0.020 (10.0 21)	90

F04	T0	5.8	C, CL, FP	20	2	0	/	/	/	/	/	0.037	/
	40C-1W	5.8	C, CL, FP	14	0	0	/	/	/	/	/	<0.010	/
	40C-2W	5.8	C, CL, FP	128	4	0	/	/	/	/	/	<0.010	/
	40C-1M	5.8	C, CL, FP	25	2	0	/	/	/	/	/	<0.010	/

Table 37: Formulation Stability Data at -70°C Storage Conditions

FB No.	Sampling points	pH	Appearance	Sub-visible particles (MFI, AR<0.85, Counts/mL)			SEC purity		CE-SDS-R	CE-SDS-NR	iCIEF			PS80 (%)	Potency (%)
				≥ 2 μm	≥ 10 μm	≥ 25 μm	Normalized Monomer%	Fold-change in HMW			Purity %	Fold-change in Basic peaks	Fold-change in Acidic peaks		
F01	T0	5.8	SY, SO, FP	204	9	2	100.0	1.0	98.5	97.6	1.0	1.0	100.0	0.041	105
	-70C-1M	5.8	SY, SO, FP	711	87	17	100.0	1.1	98.4	97.5	1.0	0.9	102.0	0.044	94
	-70C-3M	5.7	SY, SO, FP	1239	114	22	100.0	1.1	98.5	97.4	1.0	0.9	102.0	0.048	/
	-70C-6M	5.7	SY, SO, FP	667	55	10	100.0	1.0	98.5	97.7	1.1	1.0	100.0	0.039	93
F02	T0	5.8	SY, SO, FP	95	9	0	100.0	1.0	98.1	97.6	1.0	1.0	100.0	0.043	100
	-70C-1M	5.8	SY, SO, FP	1219	127	12	99.9	1.2	98.1	97.6	1.0	1.0	100.9	0.044	96
	-70C-3M	5.7	SY, SO, FP	942	182	22	99.8	1.3	98.4	97.5	1.1	1.0	100.1	0.048	/
	-70C-6M	5.8	SY, SO, FP	3147	322	27	99.9	1.2	98.5	97.7	1.1	1.0	99.3	0.039	93

F03	T0	5.8	SY, SO, FP	145	17	4	100.0	1.0	98.4	97.6	1.0	1.0	100.0	0.041	99
	-70C-1M	5.8	SY, SO, FP	869	94	12	100.0	1.0	98.3	97.6	1.2	1.0	100.5	0.043	93
	-70C-3M	5.7	SY, SO, FP	2005	251	22	99.9	1.1	98.5	97.5	1.3	0.9	100.7	0.048	/
	-70C-6M	5.8	SY, SO, FP	3679	292	37	100.0	1.0	98.5	97.8	1.3	1.0	99.5	0.040	88
F04	T0	5.8	C, CL, FP	20	2	0	/	/	/	/	/	/	/	0.037	/
	-70C-1M	5.8	C, CL, FP	1655	79	17	/	/	/	/	/	/	/	0.038	/
	-70C-6M	5.8	C, CL, FP	71	0	0	/	/	/	/	/	/	/	0.035	/

Table 38: Summary of Formulation Stability Data Upon Freeze-Thaw Cycle

FB No.	Sampling points	pH	Appearance	Sub-visible particles (MPL AR<0.85, Counts/mL)			SEC purity		CE-SDS-R	CE-SDS-NR	iCIEF		
				≥ 2 μm	≥ 10 μm	≥ 25 μm	Normalized Monomer%	Fold-change in HMW			Fold-change in Basic peaks	Fold-change in Acidic peaks	Normalized Main peak %
F01	T0	5.8	SY, SO, FP	204	9	2	100.0	1.0	98.5	97.6	1.0	1.0	100.0
	F/T-1 Cycle	5.8	SY, SO, FP	738	66	5	99.9	1.1	98.0	97.5	0.9	0.9	102.4
	F/T-5 Cycles	5.8	SY, SO, FP	615	74	7	100.0	1.0	98.0	97.6	1.1	0.9	101.9
F02	T0	5.8	SY, SO, FP	95	9	0	100.0	1.0	98.1	97.6	1.0	1.0	100.0

F03	F/T-1 Cycle	5.8	SY, SO, FP	507	73	9	99.9	1.2	98.1	97.5	1.0	1.0	100.1
	F/T-5 Cycles	5.8	SY, SO, FP	656	33	4	99.9	1.2	98.2	97.6	1.2	1.0	99.5
	T0	5.8	SY, SO, FP	145	17	4	100.0	1.0	98.4	97.6	1.0	1.0	100.0
	F/T-1 Cycle	5.8	SY, SO, FP	723	89	10	99.9	1.1	98.3	97.5	1.3	1.0	99.6
	F/T-5 Cycles	5.8	SY, SO, FP	1430	97	10	100.0	1.0	98.3	97.6	1.2	1.0	99.9

Table 39: Summary of Photostability Data

FB No.	Sampling points	pH	Appearance	Sub-visible particles (AR<0.85, Counts/mL)			SEC purity		CE- SDS-R	CE- SDS-NR	iCIEF			PS80 (%)	Potency (%)
				≥ 2 μm	≥ 10 μm	≥ 25 μm	Normalized Monomer%	Fold-change in HMW			Fold-change in Basic peaks	Fold-change in Acidic peaks	Normalized Main peak %		
F01	T0	5.8	SY, SO, FP	204	9	2	100.0	1.0	98.5	97.6	1.0	1.0	100.0	0.041	105
	Dark-7D	5.8	SY, SO, FP	349	4	0	99.8	1.0	97.8	97.3	1.0	1.0	100.3	0.040	99
	Dark-14D	5.8	SY, SO, FP	122	4	2	99.7	1.1	98.0	97.4	1.1	1.0	98.7	0.034	92

	Light-7D	5.8	SY, SO, FP	522	15	0	99.2		2.0	98.0	96.7	1.0	1.0	98.8	0.040	104
	Light-14D	5.8	SY, SO, FP	200	9	0	98.5		2.9	97.9	96.5 (↓1.1)	1.1	1.2	94.8	0.037	96
	T0	5.8	SY, SO, FP	95	9	0	100.0		1.0	98.1	97.6	1.0	1.0	100.0	0.043	100
	Dark-7D	5.8	SY, SO, FP	84	0	0	99.7		1.2	98.0	97.6	1.1	1.1	97.6	0.040	111
	Dark-14D	5.8	SY, SO, FP	104	2	2	99.6		1.3	97.8	97.5	1.1	1.1	97.0	0.035	109
	Light-7D	5.7	SY, SO, FP	59	0	0	99.1		2.2	97.8	97.0	1.1	1.1	96.3	0.040	97
	Light-14D	5.8	SY, SO, FP	30	0	0	98.5		3.2	97.7	96.5 (↓1.1)	1.1	1.2	94.9	0.034	106
	T0	5.8	SY, SO, FP	145	17	4	100.0		1.0	98.4	97.6	1.0	1.0	100.0	0.041	99
	Dark-7D	5.8	SY, SO, FP	61	4	0	99.8		1.1	97.9	97.5	1.3	1.0	97.8	0.040	107
	Dark-14D	5.8	SY, SO, FP	53	0	0	99.7		1.1	97.9	97.4	1.2	1.1	97.6	0.035	104
	Light-7D	5.7	SY, SO, FP	136	7	0	99.2		2.0	97.8	97.1	1.2	1.1	96.8	0.039	95
F02																
F03																

	Light-14D	5.8	SY, SO, FP	158	2	0	98.5	2.9	98.0	96.5 (↓1.1)	1.3	1.1	94.7	0.035	108
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Regarding storage at 5° C, there were no substantial changes in formulations F1 through F3 observed after storage at 5° C for 9 months in all tested quality aspects except PS80 exhibited a 0.017-0.022% decrease over that time.

Regarding storage at 25° C, after incubation for 3 months, SEC monomer slight decreases were observed, 1.2%-1.3% CE-SDS-NR purity decreases were observed and slight iCIEF main peak decreases were observed for the F1, F2 and F3 formulations. There were no substantial differences observed between F1, F2 and F3.

Regarding PS80 concentrations over time, after incubation at 25°C for one month there were substantial decreases in PS80 concentration observed in formulations F1 through F3 as compared to time zero (T0). For formulation F4, after incubation at 25°C for two weeks, the PS80 concentration was less than 0.010%.

Regarding storage at 40° C, after incubation for one month, the color of formulations F1 through F3 deepened slightly compared as compared to the time zero (T0) samples. In addition, substantial decreases in monomer, purity and main peak were observed in formulations F1 through F3 via SEC, CE-NR and iCIEF results, respectively. No substantial differences between formulations F1 through F3 were observed in any of the test results.

Regarding PS80 concentrations over time, after incubation at 40°C for one month there were substantial decreases in PS80 concentration observed in formulations F1 through F3 as compared to time zero (T0). For formulation F4, after incubation at 40°C for one week the PS80 concentration was less than 0.010%.

Regarding storage at -70° C, for formulations F1 through F4, after storage at -70°C for six months, there were substantial increases in sub-visible particles observed. These samples were filled in bags, whereby the samples stuck to the inlet of the bag and as a result may have impacted the sub-visible particle testing.

For formulations F1 through F3, no substantial changes were observed in monomer, purity and main peak via SEC, CE-NR and iCIEF, respectively, after storage at -70°C for six months. In addition, no substantial PS80 concentration changes were observed in formulations F1 through F3 after storage at -70°C for 6 months.

Regarding the freeze/thaw studies, F3 exhibited substantial increases ($\geq 2 \mu\text{m}$) in sub-visible particle testing results after five freeze/thaw cycles. For all three formulations tested, after five freeze/thaw cycles there were no substantial changes observed in monomer, purity or

main peak (tested via SEC/CE-NR and iCIEF, respectively) and there were also no substantial changes observed in PS80 concentration.

Regarding the photostability study, there were no substantial differences between formulations F1 through F3 observed after 1000 lux light exposure for 7 days and 14 days. However, after 1000 lux light exposure for 14 days, substantial decreases in monomer, purity and main peak were observed for all three formulations via SEC, CE-NR and iCIEF, respectively.

There were no substantial changes observed in dark control samples stored at 25°C for 7 days and 14 days.

F1, F2, and F3 were designed so that osmolality was approximately 300 mOsm/kg, which is a range that is suitable for injectable parenteral formulations. The osmolality and viscosity results were consistent with previous data for these formulations. For formulations F1 through F3 the histidine, arginine and chloride concentrations were close to the target values.

Example 8: Investigation of PS80 Degradation

In the stability studies described in Example 7, degradation of PS80 was observed in certain samples under certain conditions. Accordingly, studies were performed to identify the mechanism(s) of PS80 degradation.

In one study, formulation buffers were formulated with different lots of raw materials and a metal ion chelator (EDTA-2Na) was added to certain formulations, along with increasing the concentration of PS80 in certain formulations. The formulations tested in the study are shown in Table 40.

Table 40: Formulations Tested in Metal Ion Chelator Study

Formula No.	Formulation
F01	10 mM L-His/LHis-HCl, 120 mM L-Arg-HCl, 10 mM L-Met, 0.1 %(w/v) PS80, pH 5.8
F02	10 mM L-His/L-His-HCl, 120 mM L-Arg-HCl, 10 mM L-Met, 0.1 %(w/v) PS80, pH 5.8

F03	10 mM L-His/L-His-HCl, 120 mM L-Arg-HCl, 10 mM L-Met, 0.3 mM EDTA-2Na, 0.1 %(w/v) PS80, pH 5.8
F04	10 mM L-His/His-H, 120 mM L-Arg-HCl, 10 mM L-Met, 0.05%(w/v) PS80, pH 5.8
F05	10 mM L-His/L-His-HCl, 120 mM L-Arg-HCl, 10 mM L-Met, 0.3 mM EDTA-2Na, 0.05%(w/v) PS80, pH 5.8

Inductively coupled plasma mass spectrometry (ICP-MS) was used to determine the levels of iron (Fe), cobalt (Co), nickel (Ni), copper (Cu) and zinc (Zn) in the formulations. The concentration of PS80 was also measured in the formulations at T0 and after storage at 25°C for defined periods of time (1 week, 2 weeks, 1 month).

The results of the metal ion chelator study are summarized in **Table 41**.

Table 41: Metal Ion Chelator Study Results

<u>Analysis Result Summary</u>	<u>Fe</u> ($\mu\text{g/L}$,=ppb)	<u>Co</u> ($\mu\text{g/L}$)	<u>Ni</u> ($\mu\text{g/L}$)	<u>Cu</u> ($\mu\text{g/L}$)	<u>Zn</u> ($\mu\text{g/L}$)	<u>Comment</u> <u>(PS80 conc.)</u>
LOQ	10.000	2.000	10.000	2.000	10.000	NA
F01 (formulation buffer from 2 weeks study)	< 10.000 (3.71)	< 2.000 (0.00)	< 10.000 (0.16)	< 2.000 (1.42)	33.417	T0: 0.100% # 25C-1W: 0.100% # 25C-2W: 0.100% #
F1 (200 mg/mL, from study 2)	89.721	10.481	< 10.000 (2.59)	5.391	23.963	T0: 0.041% 25C-2W: 0.033% 25C-1M: 0.020%
F2 (180 mg/mL, from study 2)	100.053	11.134	< 10.000 (2.78)	5.663	61.439	T0: 0.043% 25C-2W: 0.035% 25C-1M: 0.019%
F3 (180 mg/mL, from study 2)	93.435	11.093	< 10.000 (2.72)	6.892	29.436	T0: 0.041% 25C-2W: 0.033%

						25C-1M: 0.021%
F4 (formulation buffer, from study 2)	15.660	< 2.000 (0.02)	< 10.000 (0.22)	< 2.000 (0.91)	17.728	T0: 0.037% 25C-2W: <0.010 25C-1M: <0.010
OC material (259.5mg/mL, from study 2)	146.230	17.144	< 10.000 (4.53)	8.445	17.964	NA
ENG DP	90.500	14.012	< 10.000 (6.71)	11.647	< 10.000 (3.75)	T0 (-70C): 0.032% 25C-6M: 0.012%

#: the PS80 concentration of F01 was measured by direct test, and for other samples, PS80 concentrations were tested with precipitation.

Additional investigational studies were performed to evaluate the impact on PS80 degradation of clone material, formulation buffers, water, PS80 lots and the material of construction of vials (glass vs. polymer). Representative results are shown in **Table 42**.

Table 42: Results of PS80 Degradation Study

Run	Water	PS Lot	Container	EDTA (0.05 mM)	PS80 (%)	Sample	T0 (same sequence as 2W)	40C-2W	T0 (same sequence as 4W)	40C-4W
1	WFI	2	polymer vials	w	0.04	DS-1 200 g/L	0.038	0.0369	0.037	0.036
2	WFI	2	polymer vials	w	1		0.93	0.89	0.81	0.83
3	WFI	2	polymer vials	w/o	0.04		0.032	0.032	0.030	0.027
4	WFI	2	polymer vials	w/o	1		0.93	0.7	0.83	0.55
5	WFI	2	polymer vials	w	0.04	DS-2 200 g/L	0.03	0.028	0.027	0.025
6	WFI	2	polymer vials	w	1		0.88	0.86	0.86	0.79
7	WFI	2	polymer vials	w/o	0.04		0.036	0.037	0.035	0.030
8	WFI	2	polymer vials	w/o	1		0.86	0.83	0.84	0.75
9	WFI	2	Glass vials	w	0.04	DS-2 200 g/L	0.036	0.034	0.032	0.028
10	WFI	2	Glass vials	w	1		0.86	0.83	0.79	0.73
11	WFI	2	Glass vials	w/o	0.04		0.033	0.03	0.033	0.025
12	WFI	2	Glass vials	w/o	1		0.86	0.69	0.87	0.53
13	WFI	2	polymer vials	w	0.04	Formulation buffer	0.031	0.03	0.029	0.029
14	WFI	2	polymer vials	w/o	0.04		0.03	0.029	0.031	0.030
15	WFI	1A	polymer vials	w/o	0.04		0.031	0.03	0.029	0.029
16	WFI	1B	polymer vials	w/o	0.04		0.033	0.032	0.030	0.031
17	WFI	1C	polymer vials	w/o	0.04		0.031	0.031	0.029	0.029
18	HPW	1A	Glass vials	w	0.04		0.029	0.031	0.029	0.029
19	HPW	1A	Glass vials	w/o	0.04		0.033	0.033	0.031	0.032
20	WFI	2	Glass vials	w/o	0.04		0.033	0.031	0.030	0.030
21	HPW	2	polymer vials	w/o	0.04		0.03	0.03	0.028	0.028
22	WFI	1A	Glass vials	w/o	0.04		0.031	0.024	0.028	0.029
23	HPW	2	Glass vials	w/o	0.04		0.032	0.032	0.031	0.032
24	HPW	1A	polymer vials	w/o	0.04		0.032	0.031	0.030	0.030

Regarding the results shown in **Table 42**, samples with added EDTA showed no significant degradation, while some samples with 1% PS80 added but without EDTA were observed to possibly undergo degradation. The protein-free formulation buffer did not undergo significant degradation under any conditions.

Overall, the results of the PS80 degradation studies determined that PS80 degradation was mediated by oxidation (major) and hydrolysis (minor). From a formulation perspective, PS80 degradation can be addressed by, for example, inclusion of a metal ion chelator in the formulation or by use of an alternate surfactant, as described further in Example 9.

Example 9: Formulations to Counteract PS80 Degradation

To evaluate formulations to counteract PS80 degradation, a panel of formulations was prepared that included either PS80 or P188 as surfactant. Additionally, a metal ion chelator was included in some formulations and omitted from others. The formulations were tested for various quality parameters, as described in previous examples.

Table 43 shows results for surfactant stability (%) over time at the indicated temperatures. **Table 44** and **Table 45** show the SE-UPLC results over time at 25°C and 5°C, respectively. **Table 46** and **Table 47** show the iCIEF results over time at 25°C and 5°C, respectively. Analysis of SE-UPLC is presented as monomer peak normalized to T0 and high molecular weight species (HMW) are presented as a fold-change over T0. Values for low molecular weight (LMW) species for all tested samples at all conditions < 1.0%. Analysis of iCIEF is presented as main peak (MP) normalized to T0 and acidic peaks (AP) and basic peaks (BP) are presented as a fold-change over T0. **Table 48** and **Table 49** show the CD-SDS-NR and CD-SDS-R results, respectively, over time at the indicated temperatures. **Table 50** shows the PS80-CAD results.

In Tables 43, 48 and 49, values in parentheses denote a significant change and indicate the associated change in the value.

Table 43: Surfactant Stability of PS80 and P188 Formulations

No.	Formulation		PS80/P188 %						
	Buffer	Excipients & surfactants (w/v)	T0	40°C-2 W (10.021)	40°C-4 W (10.026)	25°C-2 W	25°C-4 W (10.019)	5°C-2 W	5°C-4 W
F1	10 mM L-His/His-H , pH 5.8	120mM L-Arg-HCl, 10 mM L-Met, 0.05% PS80	0.048	0.027 (10.021)	0.022 (10.026)	0.042	0.029 (10.019)	0.046	0.048
F2		80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.05% PS80	0.046	0.023 (10.023)	0.021 (10.025)	0.041	0.026 (10.020)	0.045	0.044
F3		120mM L-Arg-HCl, 10 mM L-Met, 0.01 mM EDTA·2Na, 0.05% PS80	0.047	0.049	0.038	0.048	0.046	0.047	0.044
F4		80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.01 mM EDTA·2Na, 0.05% PS80	0.046	0.047	0.042	0.049	0.043	0.046	0.045
F5		120mM L-Arg-HCl, 10 mM L-Met, 0.05 mM EDTA·2Na, 0.05% PS80	0.047	0.047	0.042	0.047	0.043	0.051	0.044
F6		80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.05 mM EDTA·2Na, 0.05% PS80	0.047	0.048	0.041	0.049	0.042	0.049	0.044
F7		120mM L-Arg-HCl, 10 mM L-Met, 0.3 mM EDTA·2Na, 0.05% PS80	0.046	0.048	0.041	0.049	0.043	0.050	0.044
F8		80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.3 mM EDTA·2Na, 0.05% PS80	0.048	0.047	0.040	0.049	0.044	0.048	0.044
F9		120mM L-Arg-HCl, 10 mM L-Met, 1.0 mg/mL P 188	0.12	0.11	0.12	0.11	0.12	0.11	0.12
F10		80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 1.0 mg/mL P188	0.11	0.11	0.11	0.12	0.12	0.11	0.12
F11		120mM L-Arg-HCl, 10 mM L-Met, 0.5 mg/mL P188	0.058	0.057	0.06	0.058	0.06	0.058	0.06

F12	80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.5 mg/mL P188	0.056	0.054	0.06	0.053	0.06	0.053	0.06
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Table 44: SE-UPLC Data for PS80 and P188 Formulations at 25°C

No.	Excipients & surfactants (w/v)	SE-UPLC (Δ monomer%)							
		T0		25°C-2W		25°C-4W		Fold-change in HMW	Fold-change in HMW
		Normalized Monomer%	Fold-change in HMW	Normalized Monomer %	Fold-change in HMW	Normalized Monomer %	Fold-change in HMW		
F1	120mM L-Arg-HCl, 10 mM L-Met, 0.05% PS80	100.0	1.0	99.8	1.3	99.7	1.4		
F2	80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.05% PS80	100.0	1.0	99.8	1.3	99.7	1.4		
F3	120mM L-Arg-HCl, 10 mM L-Met, 0.01 mM EDTA-2Na, 0.05% PS80	100.0	1.0	99.7	1.3	99.7	1.3		
F4	80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.01 mM EDTA-2Na, 0.05% PS80	100.0	1.0	99.8	1.3	99.7	1.4		
F5	120mM L-Arg-HCl, 10 mM L-Met, 0.05 mM EDTA-2Na, 0.05% PS80	100.0	1.0	99.7	1.3	99.6	1.4		
F6	80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.05 mM EDTA-2Na, 0.05% PS80	100.0	1.0	99.8	1.3	99.7	1.4		
F7	120mM L-Arg-HCl, 10 mM L-Met, 0.3 mM EDTA-2Na, 0.05% PS80	100.0	1.0	99.7	1.3	99.6	1.3		

F8	80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.3 mM EDTA-2Na, 0.05% PS80	100.0	1.0	99.8	1.3	99.7	1.4
F9	120mM L-Arg-HCl, 10 mM L-Met, 1.0 mg/mL P188	100.0	1.0	99.7	1.3	99.6	1.4
F10	80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 1.0 mg/mL P188	100.0	1.0	99.7	1.3	99.6	1.4
F11	120mM L-Arg-HCl, 10 mM L-Met, 0.5 mg/mL P188	100.0	1.0	99.9	1.3	99.8	1.3
F12	80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.5 mg/mL P188	100.0	1.0	99.7	1.3	99.6	1.4

Table 45: SE-UPLC Data for PS80 and P188 Formulations at 5°C

No.	Excipients & surfactants (w/v)	SE-UPLC (Δ monomer %)							
		T0		5°C-2W		5°C-4W			
		Normalized Monomer %	Fold-change in HMW	Normalized Monomer %	Fold-change in HMW	Normalized Monomer %	Fold-change in HMW	Normalized Monomer %	Fold-change in HMW
F1	120mM L-Arg-HCl, 10 mM L-Met, 0.05% PS80	100.0	1.0	100.0	1.1	100.0	1.1	100.0	1.1
F2	80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.05% PS80	100.0	1.0	100.0	1.1	100.0	1.1	100.0	1.1
F3	120mM L-Arg-HCl, 10 mM L-Met, 0.01 mM EDTA-2Na, 0.05% PS80	100.0	1.0	99.9	1.1	99.9	1.1	99.9	1.1
F4	80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.01	100.0	1.0	100.0	1.1	100.0	1.1	100.0	1.1

	mM EDTA·2Na, 0.05% PS80							
F5	120mM L-Arg-HCl, 10 mM L-Met, 0.05 mM EDTA·2Na, 0.05% PS80	100.0	1.0	99.8	1.1	99.9	1.1	1.1
F6	80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.05 mM EDTA·2Na, 0.05% PS80	100.0	1.0	100.0	1.1	100.0	1.1	1.1
F7	120mM L-Arg-HCl, 10 mM L-Met, 0.3 mM EDTA·2Na, 0.05% PS80	100.0	1.0	99.9	1.0	99.9	1.1	1.1
F8	80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.3 mM EDTA·2Na, 0.05% PS80	100.0	1.0	100.0	1.1	100.0	1.1	1.1
F9	120mM L-Arg-HCl, 10 mM L-Met, 1.0 mg/mL P188	100.0	1.0	99.9	1.1	99.9	1.1	1.1
F10	80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 1.0 mg/mL P188	100.0	1.0	99.9	1.1	99.9	1.1	1.1
F11	120mM L-Arg-HCl, 10 mM L-Met, 0.5 mg/mL P188	100.0	1.0	100.0	1.0	100.0	1.0	1.0
F12	80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.5 mg/mL P188	100.0	1.0	99.9	1.1	99.9	1.1	1.1

Table 46: iCIEF Data for PS80 and P188 Formulations at 25°C

No.	Excipients & surfactants (w/v)	iCIEF, (Δmain peak %)		
		T0	25°C-2W	25°C-4W

		Fold- change in Acidic peaks	Normalized Main peaks %	Fold- change in Basic peaks	Fold- change in Acidic peaks	Normalized Main peaks %	Fold- change in Basic peaks	Fold- change in Acidic peaks	Normalized Main peaks %	Fold- change in Basic peaks
F1	120mM L-Arg-HCl, 10 mM L-Met, 0.05% PS80	1.0	100.0	1.0	1.0	98.0	1.2	1.1	95.6	1.4
F2	80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.05% PS80	1.0	100.0	1.0	1.0	97.6	1.3	1.1	96.1	1.3
F3	120mM L-Arg-HCl, 10 mM L-Met, 0.01 mM EDTA-2Na, 0.05% PS80	1.0	100.0	1.0	1.0	98.8	1.2	1.1	96.3	1.3
F4	80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.01 mM EDTA-2Na, 0.05% PS80	1.0	100.0	1.0	1.0	98.0	1.1	1.1	97.1	1.2
F5	120mM L-Arg-HCl, 10 mM L-Met, 0.05 mM EDTA-2Na, 0.05% PS80	1.0	100.0	1.0	1.0	97.4	1.4	1.1	96.0	1.5
F6	80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.05 mM EDTA-2Na, 0.05% PS80	1.0	100.0	1.0	1.1	97.8	1.2	1.1	96.0	1.4
F7	120mM L-Arg-HCl, 10 mM L-Met, 0.3 mM EDTA-2Na, 0.05% PS80	1.0	100.0	1.0	1.0	98.7	1.1	1.1	95.0	1.3
F8	80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.3 mM EDTA-2Na, 0.05% PS80	1.0	100.0	1.0	1.0	97.5	1.2	1.1	95.7	1.3
F9	120mM L-Arg-HCl, 10 mM L-Met, 1.0 mg/mL P 188	1.0	100.0	1.0	1.1	97.5	1.2	1.1	95.7	1.4
F10	80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 1.0 mg/mL P188	1.0	100.0	1.0	1.1	97.3	1.2	1.2	93.4	1.5
F11	120mM L-Arg-HCl, 10 mM L-Met, 0.5 mg/mL P188	1.0	100.0	1.0	1.1	97.9	1.1	1.1	95.6	1.2
F12	80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.5 mg/mL P188	1.0	100.0	1.0	1.0	99.3	1.0	1.1	97.4	1.2

Table 47: iCIEF Data for PS80 and P188 Formulations at 5°C

No.		iCIEF, (Δmain peak %)									
		T0				5°C-2W				5°C-4W	
		Fold- change in Acidic peaks	Normalized Main peaks %	Fold- change in Basic peaks	Fold- change in Acidic peaks	Normalized Main peaks %	Fold- change in Basic peaks	Fold- change in Acidic peaks	Normalized Main peaks %	Fold- change in Basic peaks	Fold- change in Acidic peaks
F1	Excipients & surfactants (w/v) 120mM L-Arg-HCl, 10 mM L-Met, 0.05% PS80	1.0	100.0	1.0	1.0	100.1	1.1	1.0	98.7	1.2	1.2
F2	80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.05% PS80	1.0	100.0	1.0	1.0	100.3	1.1	1.0	99.0	1.2	1.2
F3	120mM L-Arg-HCl, 10 mM L-Met, 0.01 mM EDTA·2Na, 0.05% PS80	1.0	100.0	1.0	1.0	100.8	1.0	1.0	99.1	1.1	1.1
F4	80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.01 mM EDTA·2Na, 0.05% PS80	1.0	100.0	1.0	1.0	100.1	1.0	1.0	98.7	1.1	1.1
F5	120mM L-Arg-HCl, 10 mM L-Met, 0.05 mM EDTA·2Na, 0.05% PS80	1.0	100.0	1.0	1.0	99.2	1.3	1.0	97.9	1.4	1.4
F6	80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.05 mM EDTA·2Na, 0.05% PS80	1.0	100.0	1.0	1.0	99.0	1.2	1.1	97.9	1.2	1.2
F7	120mM L-Arg-HCl, 10 mM L-Met, 0.3 mM EDTA·2Na, 0.05% PS80	1.0	100.0	1.0	1.0	100.4	1.0	1.0	99.2	1.1	1.1
F8	80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.3 mM EDTA·2Na, 0.05% PS80	1.0	100.0	1.0	1.0	100.1	1.1	1.0	98.7	1.1	1.1
F9	120mM L-Arg-HCl, 10 mM L-Met, 1.0 mg/mL P 188	1.0	100.0	1.0	1.0	98.4	1.2	1.1	97.5	1.2	1.2
F10	80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 1.0 mg/mL P188	1.0	100.0	1.0	1.0	99.0	1.1	1.1	97.8	1.2	1.2
F11	120mM L-Arg-HCl, 10 mM L-Met, 0.5 mg/mL P188	1.0	100.0	1.0	1.0	99.5	1.0	1.0	98.8	1.1	1.1

F12	80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.5 mg/mL P188		1.0	100.0	1.0	1.0	100.8	0.9	1.0	100.1	1.0
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No.	Formulation		CE-NR (APurity%)								
			T0	40°C-2 W	40°C-4 W	25°C-2 W	25°C-4W	5°C-2 W	5°C-4 W		
F1	10 mM L-His-HCl, 10 mM L-Met, 3% sucrose, 0.5 mg/mL P188, pH 5.8	120mM L-Arg-HCl, 10 mM L-Met, 0.05% PS80	97.6	96.2 (↓1.4)	94.2 (↓3.4)	97.4	97.3	97.6	97.5		
F2		80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.05% PS80	97.6	96.1 (↓1.5)	94.5 (↓3.1)	97.3	97.2	97.6	97.5		
F3		120mM L-Arg-HCl, 10 mM L-Met, 0.01 mM EDTA-2Na, 0.05% PS80	97.6	96.1 (↓1.5)	94.2 (↓3.4)	97.4	97.2	97.6	97.6		
F4		80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.01 mM EDTA-2Na, 0.05% PS80	97.5	96.0 (↓1.5)	94.3 (↓3.2)	97.3	97.2	97.5	97.6		
F5		120mM L-Arg-HCl, 10 mM L-Met, 0.05 mM EDTA-2Na, 0.05% PS80	97.6	96.2 (↓1.4)	94.2 (↓3.4)	97.3	97.2	97.5	97.6		
F6		80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.05 mM EDTA-2Na, 0.05% PS80	97.5	96.4 (↓1.1)	94.3 (↓3.2)	97.4	97.2	97.5	97.6		
F7		120mM L-Arg-HCl, 10 mM L-Met, 0.3 mM EDTA-2Na, 0.05% PS80	97.6	96.3 (↓1.3)	94.2 (↓3.4)	97.3	97.2	97.4	97.6		
F8		80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.3 mM EDTA-2Na, 0.05% PS80	97.6	96.3 (↓1.3)	94.3 (↓3.3)	97.4	97.3	97.5	97.6		
F9		120mM L-Arg-HCl, 10 mM L-Met, 1.0 mg/mL P 188	97.5	96.4 (↓1.1)	94.4 (↓3.1)	97.2	97.3	97.5	97.6		
F10		80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 1.0 mg/mL P188	97.6	96.3 (↓1.3)	94.4 (↓3.2)	97.3	97.2	97.6	97.6		
F11		120mM L-Arg-HCl, 10 mM L-Met, 0.5 mg/mL P188	97.6	96.2 (↓1.4)	94.3 (↓3.3)	97.4	97.3	97.5	97.6		

F12	80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.5 mg/mL P188										97.6	96.3(↓1.3)	94.5 (↓3.1)	97.4	97.2	97.5	97.6
Table 49: CE-SDS-R Data for PS80 and P188 Formulations at 5°C and 25°C																	
No.		Formulation		CE-R (ΔPurity %)													
		Buffer	Excipients & surfactants (w/v)	T0	40°C-2 W	40°C-4 W	25°C-2 W	25°C-4W	5°C-2 W	5°C-4 W							
F1			120mM L-Arg-HCl, 10 mM L-Met, 0.05% PS80	98.4	97.0 (↓1.4)	96.6 (↓1.8)	98.2	98.3	98.3	98.6	98.3	98.6					
F2			80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.05% PS80	98.4	97.3(↓1.1)	96.7 (↓1.7)	98.2	98.3	98.3	98.6	98.3	98.6					
F3			120mM L-Arg-HCl, 10 mM L-Met, 0.01 mM EDTA·2Na, 0.05% PS80	98.3	97.3(↓1.0)	96.9 (↓1.4)	98.0	98.3	98.2	98.6	98.2	98.6					
F4			80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.01 mM EDTA·2Na, 0.05% PS80	98.4	97.3(↓1.1)	96.7 (↓1.7)	98.4	98.3	98.1	98.6	98.1	98.6					
F5			120mM L-Arg-HCl, 10 mM L-Met, 0.05 mM EDTA·2Na, 0.05% PS80	98.4	97.4(↓1.0)	96.8 (↓1.6)	98.3	98.2	98.2	98.6	98.2	98.6					
F6			80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.05 mM EDTA·2Na, 0.05% PS80	98.3	97.3(↓1.0)	96.8 (↓1.5)	98.2	98.2	98.3	98.6	98.3	98.6					
F7			120mM L-Arg-HCl, 10 mM L-Met, 0.3 mM EDTA·2Na, 0.05% PS80	98.4	97.3(↓1.1)	96.7 (↓1.7)	98.2	98.1	98.3	98.5	98.3	98.5					
F8			80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.3 mM EDTA·2Na, 0.05% PS80	98.2	97.2(↓1.0)	96.6 (↓1.6)	98.1	98.1	98.3	98.5	98.3	98.5					
F9			120mM L-Arg-HCl, 10 mM L-Met, 1.0 mg/mL P 188	98.3	97.4(↓0.9)	96.5 (↓1.8)	98.1	98.2	98.2	98.5	98.2	98.5					
F10			80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 1.0 mg/mL P188	98.4	97.2(↓1.2)	96.7 (↓1.7)	98.2	98.2	98.0	98.5	98.0	98.5					

F11		120mM L-Arg-HCl, 10 mM L-Met, 0.5 mg/mL P188	98.1	97.2(↓0.9)	96.6 (↓1.5)	98.2	98.1	98.1	98.4
F12		80mM L-Arg-HCl, 10 mM L-Met, 3% sucrose, 0.5 mg/mL P188	98.2	97.4(↓0.8)	96.9 (↓1.3)	98.0	98.1	98.2	98.4

Table 50: PS80-CAD Results

No.	Buffer & Surfactant	Arg·HCl	Sucrose	EDTA·2Na	T0	5C-4W	25C-4W	40C-4W	
F01	200 mg/mL APG771, 10 mM L-His/His-H, 0.05% (w/v) PS80, 10 mM L-Met, pH5.8	120 mM	/	/	0.043	0.040	0.027	0.023	
F02		80 mM	3% (w/v)	/	0.042	0.041	0.024	0.022	
F03		120 mM	/	0.01 mM	0.049	0.049	0.046	0.043	
F04		80 mM	3% (w/v)	0.01 mM	0.047	0.047	0.044	0.046	
F05		120 mM	/	0.05 mM	0.047	0.048	0.044	0.042	
F06		80 mM	3% (w/v)	0.05 mM	0.046	0.046	0.043	0.042	
F07		120 mM	/	0.3 mM	0.047	0.047	0.045	0.040	
F08		80 mM	3% (w/v)	0.3 mM	0.047	0.047	/	0.041	

Regarding the surfactant stability data in **Table 43**, for F1-F8, PS80 content decrease was observed after 40 °C -4W and 25 °C -4W. In F01/F02 (no EDTA.2Na), adding EDTA.2Na (F3-F8) improved the PS80 stability. For F9-F12, no P188 content changes were observed after incubation at 40 °C, 25 °C and 5°C for 4 weeks.

Regarding the SE-UPLC data in **Table 44** and **Table 45**, no substantial changes of SEC monomer % were observed after 4 weeks incubation at either 25°C or 5°C for all formulations. No substantial differences were observed among all formulations.

Regarding the iCIEF data in **Table 46**, a slight decrease in main peak% was observed after 4 weeks incubation at 25°C compared with T0, whereas no substantial change of main peak% were observed after 4 weeks incubation at 5°C for all formulations compared with T0 (**Table 47**). No substantial differences were observed among all formulations.

Regarding the CE-SDS-NR data in **Table 48**, no substantial change of CE-NR purity was observed after 4W incubation at 5 °C or 25°C compared with T0. 3.1-3.4% CE-NR purity was observed in all formulations after 4W incubation at 40°C. Regarding the CE-SDS-NR data in **Table 49**, no substantial change of CE-R purity was observed after 4W incubation at 5 °C or 25°C compared with T0. 1.3-1.8% CE-R purity was observed in all formulations after 4W incubation at 40°C. No substantial differences were observed among all formulations.

Overall, the studies demonstrated that addition of a metal ion chelator (EDTA) to the formulations mitigated PS80 degradation and formulations that used P188 instead of PS80 exhibited no degradation over time at various temperatures.

Example 10: Determination of Minimum Effective Amount of PS80 to Protect Against Mechanical Shear Stress

This example describes a study to establish a minimum PS80 concentration that can protect the formulation against mechanical stress induced by agitation (e.g., during shipping). Formulations having PS80 concentrations of 0, 0.0005, 0.003, 0.005, 0.01, 0.03, 0.05 % (w/v) were evaluated for their resistance against agitation at 300 rpm for 3 days. Tested formulations are shown in **Table 51**.

Table 51: Formulations with Varying PS80 Concentrations

No.	Protein conc.	pH/buffer	Excipients	Surfactant
F8	180mg/mL	10 mM L-His/L-His-HCl, 6.0	120 mM L-Arg-HCl, 10 mM L-Met, 0.05 EDTA·2Na	0.05% PS80
F9				0.03% PS80
F10				0.01% PS80
F11				0.005% PS80
F12				0.003% PS80
F13				0.0005%PS80
F14				/

The study plan is summarized in **Table 52**. The formulations were tested for various quality parameters, as described in previous examples.

Table 52: Study Plan

Conditions	T0	Sampling points	
Agitation (300 rpm, 25°C)	X,Y	1 day	3 days
		X	X
X= Appearance (Visual inspection), Sub-visible particles (MFI), SE-UPLC, iCIEF, CE-SDS Y= pH, protein concentration, PS80			

The results for sub-visible particles (MFI), SE-UPLC, iCIEF and CE-SDS are shown in **Table 53**, **Table 54**, **Table 55** and **Table 56**, respectively.

Table 53: Sub-Visible Particle (MFD) Results

No.	Formulation	Surfactant (w/v)	T0				A-1D				A-3D			
			≥ 2 μm	≥ 10 μm	≥ 25 μm	≥ 2 μm	≥ 10 μm	≥ 25 μm	≥ 2 μm	≥ 10 μm	≥ 2 μm	≥ 10 μm	≥ 25 μm	≥ 2 μm
F8	180 mg/mL, 10 mM L-His/L-His-HCl, pH6.0 120 mM L-Arg-HCl, 10 mM L-Met, 0.05 mM EDTA·2Na	0.05% PS80	64	12	2	349	7	0	392	33	2			
F9		0.03% PS80	66	0	0	1434	81	2	1096	112	7			
F10		0.01% PS80	50	0	0	1193	33	5	413	37	4			
F11		0.005% PS80	77	9	0	2025	118	2	1388	146	9			
F12		0.003% PS80	32	2	0	824	63	2	746	125	2			
F13		0.0005%PS80	115	27	7	140688	47882	958	289134	98675	9997			
F14		/	187134	73968	1452	200421	80746	2324	153166	48142	4543			

Table 54: SE-UPLC Results

No.	Formulation	Surfactant (w/v)	T0			A-1D			A-3D	
			Normalized Monomer %	Fold-change in HMW	Normalized Monomer %	Normalized Monomer %	Fold-change in HMW	Normalized Monomer %	Normalized Monomer %	Fold-change in HMW

F8	180 mg/mL, 10 mM L- His/L-His- HCl, pH6.0 120 mM L- Arg-HCl, 10 mM L- Met, 0.05 mM EDTA.2Na	0.05% PS80	100.0	1.0	100.0	1.0	99.9		1.1
F9		0.03% PS80	100.0	1.0	100.0	1.0	100.0		1.0
F10		0.01% PS80	100.0	1.0	99.9	1.1	99.9		1.1
F11		0.005% PS80	100.0	1.0	99.9	1.1	99.9		1.1
F12		0.003% PS80	100.0	1.0	99.8	1.2	99.8		1.2
F13		0.0005%PS80	100.0	1.0	100.0	1.0	100.0		1.0
F14		/	100.0	1.0	100.0	1.0	100.0		1.0

Table 55: iCIEF Results

No.	Formulation	Surfactant (w/v)	T0			A-1D			A-3D		
			Normalized Main peaks %	Fold- change in Acidic peaks	Fold- change in Basic peaks	Normalized Main peaks %	Fold- change in Acidic peaks	Fold- change in Basic peaks	Normalized Main peaks %	Fold- change in Acidic peaks	Fold- change in Basic peaks
F8	180 mg/mL, 10 mM L- His/L-His- HCl, pH6.0 120 mM L- Arg-HCl, 10 mM L- Met,	0.05% PS80	100.0	1.0	1.0	99.7	1.0	1.0	98.5	1.0	1.0
F9		0.03% PS80	100.0	1.0	1.0	98.3	1.0	1.0	99.9	1.0	1.0
F10		0.01% PS80	100.0	1.0	1.0	98.8	1.0	1.0	98.3	1.0	1.0

F11	0.05 mM EDTA·2Na	0.005% PS80	100.0	1.0	1.0	100.0	1.0	1.0	98.2	1.0	1.0
F12		0.003% PS80	100.0	1.0	1.0	100.0	1.0	1.0	98.7	1.0	1.1
F13		0.0005% PS80	100.0	1.0	1.0	98.1	1.0	1.1	98.5	1.0	1.1
F14		/	100.0	1.0	1.0	100.0	1.0	1.0	101.0	1.0	1.0

Table 56: CE-R/NR Results

No.	Formulation	Surfactant (w/v)	T0		A-1D		A-3D	
			NR	R	NR	R	NR	R
F8	180 mg/mL, 10 mM L-His/L-His-HCl, pH6.0 120 mM L-Arg-HCl, 10 mM L-Met, 0.05 mM EDTA·2Na	0.05% PS80	96.8	97.2	96.6	96.7	96.7	97.0
F9		0.03% PS80	96.7	97.2	96.6	96.9	96.7	97.0
F10		0.01% PS80	96.7	97.3	96.6	96.9	96.7	97.0
F11		0.005% PS80	96.8	97.1	96.6	97.0	96.6	97.2
F12		0.003% PS80	96.6	97.2	96.7	97.3	96.7	97.0
F13		0.0005% PS80	96.7	97.3	96.7	97.2	96.7	97.1

F14		/		96.6	96.8	96.7	97.3	96.7	97.1
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Regarding the sub-visible particle data in **Table 53**, except for F07/F13/F14, no substantial changes of sub-visible particles were observed after 3 days of agitation. Analysis of SE-UPLC is presented as monomer peak normalized to T0 and high molecular weight species (HMW) are presented as a fold-change over T0. Values for low molecular weight (LMW) species for all tested samples at all conditions < 1.0%. Analysis of iCIEF is presented as main peak (MP) normalized to T0 and acidic peaks (AP) and basic peaks (BP) are presented as a fold-change over T0. Regarding the SE-UPLC data in **Table 54**, no substantial changes in SEC monomer % were observed after 3 days of agitation. Regarding the iCIEF data in **Table 55**, no substantial changes in the iCIEF main peak % were observed after 3 days of agitation.

Regarding the CE-SDS-R/NR data in **Table 56**, no substantial changes in CE-R or NR purity % were observed after 3 days of agitation.

Overall, no substantial changes were observed in all the tested quality items after 3 days of agitation except the visible particles and sub-visible particles in F13/F14. A PS80 concentration higher than 0.0005% was shown to efficiently protect against particle formation from agitation in the formulation. Samples with PS80 > 0.003% showed good resistance against mechanical stress induced by agitation.

Example 11: Compatibility Studies with Glass Pre-Filled Syringes and Rubber Plunger Stoppers

The IL-13 antibody formulation was evaluated for compatibility with additional pre-filled syringe (PFS) components: the syringes and plunger stoppers. Compatibility with two different syringe types from two different manufacturers (C and D) and two different plunger stoppers from two different manufacturers (A and B) were evaluated.

The results for subvisible particles over time and at increasing temperatures are shown in **FIG. 3A** and **FIG. 3B**, which show results for particles equal to or greater than 2 µm or 10 µm, respectively. The results for pH and PS80 stability are shown in **FIG. 4A** and **FIG. 4B**, respectively. The SEC data results are shown in **FIG. 5**, wherein the data has been normalized to 100% at T=0. The iCIEF data results are shown in **FIG. 6**, wherein the data has been normalized to 100% at T=0. The CE-SDS results are shown in **FIG. 7A** (non-reduced) and **FIG. 7B** (reduced). ELISA data for container closure compatibility are shown in **FIG. 8**. **Table 57**

summarizes the overall assessment of visual appearance, turbidity, concentration, subvisible particles, pH, PS80, SEC, iCIEF, CE-SDS-NR/R, and ELISA for the samples.

Table 57: Overall Scorecard for Tested Quality Parameters of Syringes and Plungers

PPM	Visual appearance	Turbidity	Concentration	Subvisible particles	pH	PS80	SEC	iCEF	CE-NR/R	ELISA
Vial Control	acceptable	acceptable	acceptable	acceptable	acceptable	acceptable	acceptable	acceptable	acceptable	acceptable
C+A	acceptable	acceptable	acceptable	acceptable	acceptable	acceptable	acceptable	acceptable	acceptable	acceptable
C+B	acceptable	acceptable	acceptable	acceptable	acceptable	acceptable	acceptable	acceptable	acceptable	acceptable
D+A	acceptable	acceptable	acceptable	unacceptable	acceptable	acceptable	acceptable	acceptable	acceptable	acceptable
D+B	acceptable	acceptable	acceptable	unacceptable	acceptable	acceptable	acceptable	acceptable	acceptable	acceptable

In summary, all biochemical assays and physicochemical assays showed a similar performance for the syringes and plunger combinations tested except for sub-visible particles, wherein certain syringes demonstrated a lower total particle load than others and thus are recommended for selection. The results of the studies demonstrated that the IL-13 antibody formulation is compatible with glass pre-filled syringes and rubber plunger stoppers and support a pre-filled syringe product presentation.

Example 12: Two Lead Formulation Candidates Confirmed through 3 Months Stability Data

Two lead formulation candidates from non-GMP development lots were tested for 3-month stability after storage at various conditions. The anti-IL-13 antibody (protein) used in this example was Construct 133. The formulations tested were:

- (1) 180 mg/mL IL-13 antibody, L-10 mM His/L-His-HCl, 120 mM L-Arg-HCl, 10 mM L-Met, 0.05 mM EDTA, 0.05% PS80, pH 6.0; and
- (2) 180 mg/mL IL-13 antibody, 10 mM L-His/L-His-HCl, 120 mM L-Arg-HCl, 10 mM L-Met, 0.5 mg/mL P188, pH 6.0

Formulations were tested for various quality parameters over time and at various temperatures as described in the previous examples according to the study plan set forth in **Table 58**. The Tg', viscosity, pH, osmolality and excipient concentration at time zero (T0) are shown in **Table 59**. The 5°C data is summarized in **Table 60**. The 25°C data is summarized in **Table 61**. The 40°C data is summarized in **Table 62**. The data for agitation is summarized in **Table 63**. The -70°C data is summarized in **Table 64**.

Abbreviations used in the tables are as follows: SY=slightly yellow, SO=slightly opalescent, FP = free of visible particles, ND = not detected, LMW= low molecular weight, HMW= high molecular weight, LC=light chain, HC= heavy chain, MP= main peak, AP=acidic peak, BP= basic peak, C= colorless, CL= clear.

Table 58: Study Plan

Formulation			Conditions		T0	Sampling Points and Assay													
F01: 180 mg/mL APG777, 10 mM L-His/L-His-HCl, 120 mM L-Arg-HCl, 10 mM L-Met, 0.05 mM EDTA, 0.05% (w/v) PS80, pH 6.0			2~8 °C (Inverted)		X, Y, Z, W	2 Weeks	4 Weeks	8 Weeks	3M	6M	9M	12M	18M	24M	Retain	Retain			
			25 °C (Inverted)			X, Z (except potency)	X, Y, Z	X, Y, Z	X, Y, Z	X, Y, Z	X, Y, Z	X, Y, Z	X, Y, Z	X, Y, Z	X, Y, Z	X, Y, Z	X, Y, Z	X, Y, Z	
			40 °C (Upright)			X, Z (except potency)	X, Y, Z	X, Y, Z	X, Y, Z	X, Y, Z	X, Y, Z	X, Y, Z	X, Y, Z	X, Y, Z	X, Y, Z	X, Y, Z	X, Y, Z	X, Y, Z	X, Y, Z
			Agitation (100 rpm, 25 °C) (Upright)			X, Z (except potency)	X, Y, Z	/	/	/	/	/	/	/	/	/	/	/	/
			1 Day													3 Days			
						X			X, Y										
X = Appearance, SE-UPLC, CE-SDS (NR & R), iCIEF Y = Sub-visible particles (HIAC) Z = Potency, PS80 W = Tg', Viscosity, protein concentration, pH, Osmolality, His & Arg con., Cl conc.																			

Table 59: Tg', Viscosity, pH, Osmolality and Excipient Concentration at T0

No.	Tg'(°C)	Viscosity, (cP)	pH	Osmo, (mOsm/kg)	Protein conc., (mg/mL)	His. Conc., (mM)	Cl ⁻ Conc., (mM)	Arg. Conc., (mM)	Met. Conc., (mM)
F01	-25.1	14.1	6.0	310	182.8	10.677	139.2	118.804	9.880

F02	-25.2	14.2	6.0	313	185.5	10,546	138.4	121.480	10.005
F03	/	/	6.0	236	/	/	/	/	/
F04	/	/	6.1	234	/	/	/	/	/

Table 60: 5°C Data Summary

No.	F01 (0.05 mM EDTA, 0.05% (w/v) PS80)					F02 (0.5 mg/mL P188)				
	T0	5C-2W	5C-4W	5C-8W	5C-3M	T0	5C-2W	5C-4W	5C-8W	5C-3M
Appearance	SY, SO, FP	SY, SO, FP	SY, SO, FP	SY, SO, FP	SY, SO, FP	SY, SO, FP	SY, SO, FP	SY, SO, FP	SY, SO, FP	SY, SO, FP
	≥2 um	NT	373	380	268	144	NT	234	339	121
	≥5 um		69	90	69	37	/	31	77	11
	≥10 um		12	6	5	11	/	4	9	1
	≥25 um		0	0	1	1	/	0	0	0
SE-UPLC	Normalized Monomer%	100.0	100.0	99.7	99.6	100.0	100.0	100.0	99.7	99.7
	Fold-change in IIMW	1.0	1.0	1.4	1.4	1.0	1.0	1.0	1.3	1.3
CE-NR	Purity%	96.7	96.8	96.8	96.6	96.8	96.9	96.8	96.7	96.7
	LMWs%	3.1	3.1	3.1	3.1	3.1	3.0	3.1	3.1	3.2
CE-R	LC+HC, %	97.1	97.2	97.2	97.0	97.1	97.3	97.2	97.2	97.1
	LMWs%	2.3	2.3	2.2	2.4	2.2	2.2	2.2	2.3	2.3
iCIEF	Normalized Main peak %	100.0	97.0	100.1	97.0	100.0	99.6	102.2	101.6	101.0

	Fold-change in Acidic peak	1.0	1.1	1.0	1.1	1.1	1.0	1.1	1.0	1.1	1.0	1.0	1.0	1.0
	Fold-change in Basic peak	1.0	1.1	1.0	1.0	1.0	1.0	1.0	0.9	0.9	0.9	0.9	0.9	0.9
PS80/P188, %		0.044	0.043	0.045	0.042	0.047	0.063	0.059	0.056	0.052	0.045			
Potency%		99	/	98	101	98	96	/	88	99	88			

Table 61: 25°C Data Summary

No.	F01 (0.05 mM EDTA, 0.05% (w/v) PS80)							F02 (0.5 mg/mL P188)							
	T0	25C-2W	25C-4W	25C-8W	25C-3M	T0	25C-2W	25C-4W	25C-8W	25C-3M	T0	25C-2W	25C-4W	25C-8W	25C-3M
Appearance	SY, SO, FP	SY, SO, FP	SY, SO, FP	SY, SO, FP	SY, SO, FP	SY, SO, FP	SY, SO, FP	SY, SO, FP	SY, SO, FP	SY, SO, FP	SY, SO, FP	SY, SO, FP	SY, SO, FP	SY, SO, FP	SY, SO, FP
	≥2 um	437	NT	181	406	194	144	NT	236	225	167				
	≥5 um	98		34	70	39	37	/	45	25	24				
	≥10 um	18		8	11	6	11	/	14	2	4				
	≥25 um	1		1	0	1	1	/	1	0	1				
SE-UPLC	Normalized Monomer%	100.0	99.8	99.7	99.3	99.1	100.0	99.8	99.8	99.4	99.1				
	Fold-change in HMW	1.0	1.3	1.4	1.6	1.8	1.0	1.3	1.3	1.6	1.9				
CE-NR	Purity%	96.7	96.5	96.6	96.1	95.5 (↓1.2)	96.8	96.7	96.6	96.1	95.7 (↓1.1)				
	LMW%	3.1	3.3	3.3	3.5	4.1	3.1	3.1	3.2	3.5	3.9				
CE-R	LC+HC, %	97.1	97.2	97.0	96.5	96.4	97.1	97.1	97.0	96.3	96.4				
	LMWs%	2.3	2.3	2.4	2.7	2.8	2.3	2.4	2.4	2.8	2.7				
iCIEF	Normalized Main peak %	100.0	98.1	97.1	93.8	90.4	100.0	102.4	97.6	96.7	94.5				
	Fold-change in Acidic peak	1.0	1.0	1.1	1.2	1.3	1.0	1.0	1.1	1.1	1.2				

	Fold-change in Basic peak	1.0	1.0	1.0	1.1	1.1	1.0	0.9	1.0	0.9	0.9
PS80/P188, %		0.044	0.045	0.043	0.040	0.042	0.063	0.057	0.057	0.054	0.045

Table 62: 40°C Data Summary

Testing items		F01 (0.05 mM EDTA, 0.05% (w/v) PS80)				F02 (0.5 mg/mL P188)				
		T0	40C-2W	40C-4W	T0	40C-2W	40C-4W	T0	40C-2W	40C-4W
Appearance		SY, SO, FP	SY, SO, FP	SY, SO, FP	SY, SO, FP	SY, SO, FP	SY, SO, FP	SY, SO, FP	SY, SO, FP	SY, SO, FP
Sub-visible particles by HIAC, particles/mL	≥2 um	437	NT	334	144	NT	92			
	≥5 um	98		45	37	/	18			
	≥10 um	18		9	11	/	6			
	≥25 um	1		1	1	/	1			
SE-UPLC	Normalized Monomer%	100.0	98.8	98.5	100.0	99.2	98.5			
	Fold-change in HMW	1.0	1.6	1.9	1.0	1.6	2.1			
CE-NR	Purity%	96.7	95.5 (↓1.2)	93.7 (↓3.0)	96.8	95.6 (↓1.2)	94.1 (↓2.7)			
	LMWs%	3.1	4.1	5.7	3.1	4.1	5.3			
CE-R	LC+HC, %	97.1	96.4	95.9 (↓1.2)	97.1	96.5	95.7 (↓1.4)			
	LMWs%	2.3	2.9	3.4	2.3	2.8	3.4			
iCIEF	Normalized Main peak %	100.0	87.8	75.3	100.0	88.5	75.6			
	Fold-change in Acidic peak	1.0	1.4	1.8	1.0	1.4	1.8			
	Fold-change in Basic peak	1.0	1.1	1.1	1.0	1.0	1.1			
PS80%		0.044	0.044	0.042	0.063	0.056	0.058			
Potency%		99	/	90	96	/	91			

Table 63: 1D/3D Agitation Data Summary

No.	Appearance	Sub-visible particles by HIAC, particles/mL				SE-UPLC		CE-NR		CE-R		iCIEF		
		≥2 um	≥5 um	≥10 um	≥25 um	Normalized Monomer %	Fold-change in HMW	Purity%	LMW%	LC+HC, %	LMW%	Normalized Main peak %	Fold- change in Acidic peak	Fold- change in Basic peak
F01 (0.05 mM EDTA, 0.05% (w/v) PS80)	T0	437	98	18	1	100.0	1.0	96.7	3.1	97.1	2.3	100.0	1.0	1.0
	A-1D	/	/	/	/	100.0	1.0	96.7	3.2	97.0	2.5	99.9	1.0	1.0
	A-3D	342	92	16	1	99.9	1.1	96.7	3.2	97.0	2.4	99.7	1.0	1.0
F02 (0.5 mg/mL P188)	T0	144	37	11	1	100.0	1.0	96.8	3.1	97.1	2.3	100.0	1.0	1.0
	A-1D	/	/	/	/	100.0	1.0	96.8	3.2	97.1	2.4	101.8	1.0	1.0
	A-3D	128	34	8	0	99.9	1.1	96.8	3.2	96.9	2.5	102.4	0.9	1.0

Table 64: -70°C Data Summary

Testing items	F03 (0.05 mM EDTA, 0.05% (w/v) PS80)				F04 (0.5 mg/mL P188)			
	T0	-70C-4W	-70C-8W	-70C-3M	T0	-70C-4W	-70C-8W	-70C-3M

Appearance	C, CL, FP	C, CL, FP	C, CL, FP	C, CL, FP	C, CL, FP	C, CL, FP	C, CL, FP	C, CL, FP	C, CL, FP
≥2 um	1226	140	260	376	51	192	200	231	
Sub-visible particles by H1AC, particles/mL	232	40	82	96	14	35	43	61	
≥5 um									
≥10 um	31	6	22	12	3	5	3	8	
≥25 um	0	0	0	1	0	0	0	0	
PS80/P188, %	0.042	0.041	0.039	0.041	0.061	0.059	0.058	0.048	

Analysis of SE-UPLC is presented as monomer peak normalized to T0 and high molecular weight species (HMW) are presented as a fold-change over T0. Values for low molecular weight (LMW) species for all tested samples at all conditions < 1.0%. Analysis of iCIEF is presented as main peak (MP) normalized to T0 and acidic peaks (AP) and basic peaks (BP) are presented as a fold-change over T0.

Regarding the data in **Table 60**, after three months of incubation at 5°C, all samples were slightly yellow and slightly opalescent but free of visible particles, similar to their appearance at time zero (T0). No substantial changes were observed in either tested formulation after three months of incubation at 5°C as compared to time zero (T0).

Regarding the data in **Table 61**, after three months of incubation at 25°C, all samples were slightly yellow and slightly opalescent but free of visible particles, similar to how they appeared at time zero (T0). No substantial changes were observed in either formulation in terms of sub-visible particles, SEC, CE-R purity, PS80/P188 content or potency after three months of incubation at 25°C. Slight decreases of CE-NR purity (1.1-1.2%) and iCIEF main peak percentages were observed in both formulations after three months incubation at 25°C as compared to time zero (T0).

Regarding the data in **Table 62**, after three months of incubation at 40°C, all samples were slightly yellow and slightly opalescent. Samples were free of visible particles at time zero (T0) and after four weeks of incubation at 40°C. There were no substantial changes in sub-visible particles, PS80 content or percent potency in either formulation after four weeks of incubation at 40°C. Slight decreases of SEC percent monomer, CE-NR percent purity (2.7-3.0%), and CE-R percent purity (1.2-1.4%), and substantial decreases of iCIEF main peak percentages were observed in both formulations after one month incubation at 40°C as compared with time zero (T0).

Regarding the data in **Table 63**, after three days of agitation all samples were slightly yellow, slightly opalescent and free of visible particles, just as they appeared at time zero (T0). There were no substantial changes observed in any test results after one day or three days of agitation as compared to at time zero (T0).

Regarding the data in **Table 64**, after storage for three months at -70°C, all samples were colorless, clear, and free of visible particles, just as they appeared at time zero (T0). No

substantial changes were observed in any test results after three months storage at -70°C as compared to at time zero (T0).

Informal sequence listing

Description	Sequence	SEQ ID NO
Heavy Chain Variable domain HC0	QVQLQESGPGLVAPSQSL SITCTVSGFSLNAYS VNWVRQP PGKGLEWLGMIWGDGKIVYNSALKSRLNISKDSSKSQVFL KMSSLQSDDTARYYCAGDGYYPYAMD NWGHGTSVTVSS	SEQ ID NO: 1
Heavy Chain Variable domain HC0_M	QVQLQESGPGLVAPSQSL SITCTVSGFSLNAYS VNWVRQP PGKGLEWLGMIWGDGKIVYNSALKSRLTISKDSSKSQVFL KMSSLQSDDTARYYCAGDGYYPYAMD NWGHGTSVTVSS	SEQ ID NO: 2
Heavy Chain Variable domain HC1	EVQLQESGPGLVKPSETLSLTCTVSGFSLNAYS VNWIRQPP GKGLEWLGMIWGDGKIVYNSALKSRLTISKDSSKNQVSLK LSSVTAADTAVYYCAGDGYYPYAMD NWGQGTTVTVSS	SEQ ID NO: 3
Heavy Chain Variable domain HC2	EVQLVQSGAEVKKPGASVKVSCKASGFSLNAYS VNWVR QAPGQGLEWLGMIWGDGKIVYNSALKSRLTITKDSSTSTV YMELSSLRSED TAVYYCAGDGYYPYAMD NWGQGTTVTV SS	SEQ ID NO: 4
Heavy Chain Variable domain HC3	EVQLVQSGAEVKKPGSSVKVSCKASGFSLNAYS VNWVRQ APGQGLEWLGMIWGDGKIVYNSALKSRLTITKDSSTSTVY MELSSLRSED TAVYYCAGDGYYPYAMD NWGQGTTVTVS S	SEQ ID NO: 5

Heavy Chain Variable domain HC4	EVQLVESGGGLVKPGGSLRLSCAASGFSLNAYSVNWVRQ APGKGLEWLGMIWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLKTEDTAVYYCAGDGYYPYAMDNWGQGTTVTV SS	SEQ ID NO: 6
Heavy Chain Variable domain HC5	EVQLLES GGGLVQPGGSLRLSCAASGFSLNAYSVNWVRQ APGKGLEWLGMIWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMDNWGQGTTVTV SS	SEQ ID NO: 7
Heavy Chain Variable domain HC6	EVQLQESGPGLVKPSETLSLTCTVSGGSLNAYSVNWVRQP PGKGLEWLGMIWGDGKIVYNSALKSRLTISLDTSKSQVFL KMSSLTAADTAVYYCARDGYYPYAMDNWGQGTTVTVSS	SEQ ID NO: 8
Heavy Chain Variable domain HC7	QVQLQESGPGLVKPSETLSLTCTVSGGSLNAYSWNWVRQ PPGKGLEWLGYYIGDGKTNYPALKSRLTISLDTSKSQVF LKMSSLTAADTAVYYCARDGYYYYAMDVWGQGTTVTV SS	SEQ ID NO: 9
Heavy Chain Variable domain HC5m1	EVQLLES GGGLVQPGGSLRLSCAASGYSLNAYSVNWVRQ APGKGLEWLGMIWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMDNWGQGTTVTV SS	SEQ ID NO: 10
Heavy Chain Variable domain HC5m2	EVQLLES GGGLVQPGGSLRLSCAASGFSLRAYSVNWVRQ APGKGLEWLGMIWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMDNWGQGTTVTV SS	SEQ ID NO: 11

Heavy Chain Variable domain HC5m3	EVQLLES GGGLVQP GGS LRLSCAASG FSLHAYS VNWVRQ APGKGLEWLGM IWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMD NWGQGTTVT V SS	SEQ ID NO: 12
Heavy Chain Variable domain HC5m4	EVQLLES GGGLVQP GGS LRLSCAASG FSLDAYSVNWVRQ APGKGLEWLGM IWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMD NWGQGTTVT V SS	SEQ ID NO: 13
Heavy Chain Variable domain HC5m5	EVQLLES GGGLVQP GGS LRLSCAASG FSLYAYS VNWVRQ APGKGLEWLGM IWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMD NWGQGTTVT V SS	SEQ ID NO: 14
Heavy Chain Variable domain HC5m6	EVQLLES GGGLVQP GGS LRLSCAASG FSLSAYS VNWVRQ APGKGLEWLGM IWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMD NWGQGTTVT V SS	SEQ ID NO: 15
Heavy Chain Variable domain HC5m7	EVQLLES GGGLVQP GGS LRLSCAASG FSLNRYSVNWVRQ APGKGLEWLGM IWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMD NWGQGTTVT V SS	SEQ ID NO: 16
Heavy Chain Variable domain HC5m8	EVQLLES GGGLVQP GGS LRLSCAASG FSLNKYS VNWVRQ APGKGLEWLGM IWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMD NWGQGTTVT V SS	SEQ ID NO: 17

Heavy Chain Variable domain HC5m9	EVQLLESGGGLVQPGGSLRLSCAASGFSLNHYSVNWVRQ APGKGLEWLGMIWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMDNDWGQGTTVT SS	SEQ ID NO: 18
Heavy Chain Variable domain HC5m10	EVQLLESGGGLVQPGGSLRLSCAASGFSLNQYSVNWVRQ APGKGLEWLGMIWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMDNDWGQGTTVT SS	SEQ ID NO: 19
Heavy Chain Variable domain HC 5m11	EVQLLESGGGLVQPGGSLRLSCAASGFSLNEYSVNWVRQ APGKGLEWLGMIWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMDNDWGQGTTVT SS	SEQ ID NO: 20
Heavy Chain Variable domain HC 5m12	EVQLLESGGGLVQPGGSLRLSCAASGFSLNSYSVNWVRQ APGKGLEWLGMIWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMDNDWGQGTTVT SS	SEQ ID NO: 21
Heavy Chain Variable domain HC5m13	EVQLLESGGGLVQPGGSLRLSCAASGFSLNYSVNWVRQ APGKGLEWLGMIWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMDNDWGQGTTVT SS	SEQ ID NO: 22
Heavy Chain Variable domain HC5m14	EVQLLESGGGLVQPGGSLRLSCAASGFSLNAESVNWVRQ APGKGLEWLGMIWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMDNDWGQGTTVT SS	SEQ ID NO: 23

Heavy Chain Variable domain HC 5m15	EVQLLES GGGLVQP GGS LRLSCAASG FSLNAYS VNWVRQ APGKGLEWL GMIWSDG KIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMD NWGQGTTVTV SS	SEQ ID NO: 24
Heavy Chain Variable domain HC5m16	EVQLLES GGGLVQP GGS LRLSCAASG FSLNAYS VNWVRQ APGKGLEWL GMIWADG KIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMD NWGQGTTVTV SS	SEQ ID NO: 25
Heavy Chain Variable domain HC5m17	EVQLLES GGGLVQP GGS LRLSCAASG FSLNAYS VNWVRQ APGKGLEWL GMIWGDG KIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGHGYYPYAMD NWGQGTTVTV SS	SEQ ID NO: 26
Heavy Chain Variable domain HC5m18	EVQLLES GGGLVQP GGS LRLSCAASG FSLNAYS VNWVRQ APGKGLEWL GMIWGDG KIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDLYYPYAMD NWGQGTTVTVS S	SEQ ID NO: 27
Heavy Chain Variable domain HC5m19	EVQLLES GGGLVQP GGS LRLSCAASG FSLNAYS VNWVRQ APGKGLEWL GMIWGDG KIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDKYYPYAMD NWGQGTTVTV SS	SEQ ID NO: 28
Heavy Chain Variable domain HC5m20	EVQLLES GGGLVQP GGS LRLSCAASG FSLNAYS VNWVRQ APGKGLEWL GMIWGDG KIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYGYAMD NWGQGTTVTV SS	SEQ ID NO: 29

Heavy Chain Variable domain HC5m21	EVQLLES GGGLVQPGGSLRLSCAASG FSLNAYS VNWVRQ APGKGLEWLGMIWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGY YAYAMD NWGQGTTVTV SS	SEQ ID NO: 30
Heavy Chain Variable domain HC5m22	EVQLLES GGGLVQPGGSLRLSCAASG FSLNAYS VNWVRQ APGKGLEWLGMIWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGY YSYAMD NWGQGTTVTV SS	SEQ ID NO: 31
Heavy Chain Variable domain HC5m23	EVQLLES GGGLVQPGGSLRLSCAASG FSLNAYS VNWVRQ APGKGLEWLGMIWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGY YTYAMD NWGQGTTVTV SS	SEQ ID NO: 32
Light Chain Variable domain LC0	NIVLTQSPASLAVSLGQRATISCRASKSVDSYGNSFMHWY QQKPGQPPKLLIYLASNLESGV PARFSGSGSRTDFTLTIDPV EADDAASYCQ QNNEDPRTFGGGTKLEIK	SEQ ID NO: 33
Light Chain Variable domain LC1	DIQLTQSPSSLSASVGDRVITICRASKSVDSYGNSFMHWY QQKPGKAPKLLIYLASNLESGVPSRFSGSGSRTDFTLTISL QPEDFATYYCQ QNNEDPRTFGGGTKVEIK	SEQ ID NO: 34
Light Chain Variable domain LC2	DIQLTQSPSSLSASVGDRVITICRASKSVDSYGNSFMHWY QQKPGKAPKLLIYLASNLESGVPSRFSGSGSRTDFTLTISL QPEDFATYYCQ QNNEDPRTFGGGTKVEIK	SEQ ID NO: 35
Light Chain Variable domain LC3	EIVLTQSPATLSVSPGERATLSCRASKSVDSYGNSFMHWY QQKPGQAPRLLIYLASNLESGIPARFSGSGSRTEFTLTISL QSEDFAVYYCQ QNNEDPRTFGGGTKVEIK	SEQ ID NO: 36

Light Chain Variable domain LC4	DIVLTQSPLSLPVTGPGEPAISCRASKSVDSYGNSFMHWYL QKPGQSPQLLIYLASNLESGVPDRFSGSGSRTDFTLKISRVE AEDVGYYCQNNEDPRTFGGGTKVEIK	SEQ ID NO: 37
Light Chain Variable domain LC5	DIVLTQSPDSLAVSLGERATINCRASKSVDSYGNSFMHWY QQKPGQPPKLLIYLASNLESGVPDRFSGSGSGTDFTLTISL QAEDVAVYYCQNNEDPRTFGGGTKVEIK	SEQ ID NO: 38
Light Chain Variable domain LC6	DIQLTQSPSSLSASVGDRVITTCRASKSVDSYGNSFMHWY QQKPGKAPKLLIYLASNLESGVPSRFSGSGSGTDFTLTISL QPEDFATYYCQNNEDPRTFGGGTKVEIK	SEQ ID NO: 39
Light Chain Variable domain LC7	EIVLTQSPATLSVSPGERATLSCRASKSVDSYGNSFMHWY QQKPGQAPRLIYLASNLESGIPARFSGSGSGTEFTLTISL QSEDFAVYYCQNNEDPRTFGGGTKVEIK	SEQ ID NO: 40
Light Chain Variable domain LC8	DIVLTQSPLSLPVTGPGEPAISCRASKSVDSYGNSFMHWYL QKPGQSPQLLIYLASNLESGVPDRFSGSGSGTDFTLKISRVE AEDVGYYCQNNEDPRTFGGGTKVEIK	SEQ ID NO: 41
Light Chain Variable domain LC9	DIVLTQSPASLAVSPGERATISCRASKSVDSYGNSFMHWY QQKPGQPPKLLIYLASNLESGVPDRFSGSGSGTDFTLTISR EADDVAVYYCQNNEDPRTFGGGTKLEIK	SEQ ID NO: 42
Light Chain Variable domain LC10	DIVLTQSPASLAVSPGERATISCRASQSVDSNGNNFLHWY QQKPGQPPKLLIYLASNRESGVPDRFSGSGSGTDFTLTISR VEADDVAVYYCQNNHTPRTFGGGTKLEIK	SEQ ID NO: 43
Light Chain Variable domain	DIQLTQSPSSLSASVGDRVITTCRASKSVDSYGNSRMHWY QQKPGKAPKLLIYLASNLESGVPSRFSGSGSGTDFTLTISL QPEDFATYYCQNNEDPRTFGGGTKVEIK	SEQ ID NO: 44

LC6_m1		
Light Chain Variable domain LC6_m2	DIQLTQSPSSLSASVGDRVITITCRASKSVDSYGNSSMHWY QQKPGKAPKLLIYLASNLESGVPSRFSGSGSGTDFTLTISL QPEDFATYYCQQNNEDPRTFGGGTKVEIK	SEQ ID NO: 45
Light Chain Variable domain LC6_m3	DIQLTQSPSSLSASVGDRVITITCRASKSVDSYGNFSMHWY QQKPGKAPKLLIRLASNLESGVPSRFSGSGSGTDFTLTISL QPEDFATYYCQQNNEDPRTFGGGTKVEIK	SEQ ID NO: 46
Light Chain Variable domain LC6_m4	DIQLTQSPSSLSASVGDRVITITCRASKSVDSYGNFSMHWY QQKPGKAPKLLIFLASNLESGVPSRFSGSGSGTDFTLTISL QPEDFATYYCQQNNEDPRTFGGGTKVEIK	SEQ ID NO: 47
Light Chain Variable domain LC6_m5	DIQLTQSPSSLSASVGDRVITITCRASKSVDSYGNFSMHWY QQKPGKAPKLLIYLASHLESGVPSRFSGSGSGTDFTLTISL QPEDFATYYCQQNNEDPRTFGGGTKVEIK	SEQ ID NO: 48
Light Chain Variable domain LC6_m6	DIQLTQSPSSLSASVGDRVITITCRASKSVDSYGNFSMHWY QQKPGKAPKLLIYLASDLESGVPSRFSGSGSGTDFTLTISL QPEDFATYYCQQNNEDPRTFGGGTKVEIK	SEQ ID NO: 49
Light Chain Variable domain LC6_m7	DIQLTQSPSSLSASVGDRVITITCRASKSVDSYGNFSMHWY QQKPGKAPKLLIYLASQLESGVPSRFSGSGSGTDFTLTISL QPEDFATYYCQQNNEDPRTFGGGTKVEIK	SEQ ID NO: 50
Light Chain Variable domain LC6_m8	DIQLTQSPSSLSASVGDRVITITCRASKSVDSYGNFSMHWY QQKPGKAPKLLIYLASELESGVPSRFSGSGSGTDFTLTISL QPEDFATYYCQQNNEDPRTFGGGTKVEIK	SEQ ID NO: 51

Light Chain Variable domain LC6_m9	DIQLTQSPSSLSASVGDRVITICRASKSVDSYGNSFMHWY QQKPGKAPKLLIYLASNLESGVPSRFSGSGSGTDFTLTISL QPEDFATYYCQQNHEDPRTFGGGTKVEIK	SEQ ID NO: 52
Light Chain Variable domain LC6_m10	DIQLTQSPSSLSASVGDRVITICRASKSVDSYGNSFMHWY QQKPGKAPKLLIYLASNLESGVPSRFSGSGSGTDFTLTISL QPEDFATYYCQQNYEDPRTFGGGTKVEIK	SEQ ID NO: 53
Light Chain Variable domain LC6_m11	DIQLTQSPSSLSASVGDRVITICRASKSVDSYGNSFMHWY QQKPGKAPKLLIYLASNLESGVPSRFSGSGSGTDFTLTISL QPEDFATYYCQQNSEDPTFGGGTKVEIK	SEQ ID NO: 54
Light Chain Variable domain LC6_m12	DIQLTQSPSSLSASVGDRVITICRASKSVDSYGNSFMHWY QQKPGKAPKLLIYLASNLESGVPSRFSGSGSGTDFTLTISL QPEDFATYYCQQNNRDPRTFGGGTKVEIK	SEQ ID NO: 55
Light Chain Variable domain LC6_m13	DIQLTQSPSSLSASVGDRVITICRASKSVDSYGNSFMHWY QQKPGKAPKLLIYLASNLESGVPSRFSGSGSGTDFTLTISL QPEDFATYYCQQNDDPRTFGGGTKVEIK	SEQ ID NO: 56
Light Chain Variable domain LC6_m14	DIQLTQSPSSLSASVGDRVITICRASKSVDSYGNSFMHWY QQKPGKAPKLLIYLASNLESGVPSRFSGSGSGTDFTLTISL QPEDFATYYCQQNNQDPRTFGGGTKVEIK	SEQ ID NO: 57
Parental Kabat HCDR1	AYSVN	SEQ ID NO: 58
HC5_m7 Kabat HCDR1	RYSVN	SEQ ID NO: 59

HC5_m8 Kabat HCDR1	KYSVN	SEQ ID NO: 60
HC5_m9 Kabat HCDR1	HYSVN	SEQ ID NO: 61
HC5_m10 Kabat HCDR1	QYSVN	SEQ ID NO: 62
HC5_m11 Kabat HCDR1	EYSVN	SEQ ID NO: 63
HC5_m12 Kabat HCDR1	SYSVN	SEQ ID NO: 64
HC5_m13 Kabat HCDR1	YYSVN	SEQ ID NO: 65
HC5_m14 Kabat HCDR1	AESVN	SEQ ID NO: 66
Lebrikizuma b Chothia HCDR1	GFSLSAY	SEQ ID NO: 67
Parental Chothia HCDR1	GFSLNAY	SEQ ID NO: 68
HC6 Chothia HCDR1	GGSLNAY	SEQ ID NO: 69

HC7 Chothia HCDR1	GGSLNAY	SEQ ID NO: 70
HC5_m1 Chothia HCDR1	GYSLNAY	SEQ ID NO: 71
HC5_m2 Chothia HCDR1	GFSRLAY	SEQ ID NO: 72
HC5_m3 Chothia HCDR1	GFSLHAY	SEQ ID NO: 73
HC5_m4 Chothia HCDR1	GFSLDAY	SEQ ID NO: 74
HC5_m5 Chothia HCDR1	GFSLYAY	SEQ ID NO: 75
HC5_m7 Chothia HCDR1	GFSLNRY	SEQ ID NO: 76
HC5_m8 Chothia HCDR1	GFSLNKY	SEQ ID NO: 77
HC5_m9 Chothia HCDR1	GFSLNHY	SEQ ID NO: 78
HC5_m10 Chothia HCDR1	GFSLNQY	SEQ ID NO: 79

HC5_m11 Chothia HCDR1	GFSLNEY	SEQ ID NO: 80
HC5_m12 Chothia HCDR1	GFSLNSY	SEQ ID NO: 81
HC5_m13 Chothia HCDR1	GFSLNYY	SEQ ID NO: 82
HC5_m14 Chothia HCDR1	GFSLNAE	SEQ ID NO: 83
Lebrikizuma b IMGT HCDR1	GFSLSAYS	SEQ ID NO: 84
Parental IMGT HCDR1	GFSLNAYS	SEQ ID NO: 85
HC6 IMGT HCDR1	GGSLNAYS	SEQ ID NO: 86
HC5_m1 IMGT HCDR1	GYSLNAYS	SEQ ID NO: 87
HC5_m2 IMGT HCDR1	GFSLRAYS	SEQ ID NO: 88
HC5_m3 IMGT HCDR1	GFSLHAYS	SEQ ID NO: 89

HC5_m4 IMGT HCDR1	GFSLDAYS	SEQ ID NO: 90
HC5_m5 IMGT HCDR1	GFSLYAYS	SEQ ID NO: 91
HC5_m6 IMGT HCDR1	GFSLSAYS	SEQ ID NO: 92
HC5_m7 IMGT HCDR1	GFSLNRYS	SEQ ID NO: 93
HC5_m8 IMGT HCDR1	GFSLNKYS	SEQ ID NO: 94
HC5_m9 IMGT HCDR1	GFSLNHYS	SEQ ID NO: 95
HC5_m10 IMGT HCDR1	GFSLNQYS	SEQ ID NO: 96
HC5_m11 IMGT HCDR1	GFSLNEYS	SEQ ID NO: 97
HC5_m13 IMGT HCDR1	GFSLNYYs	SEQ ID NO: 98
HC5_m14 IMGT HCDR1	GFSLNAES	SEQ ID NO: 99

Parental Kabat HCDR2	MIWGDGKIVYNSALKS	SEQ ID NO: 100
HC7 Kabat HCDR2	YIYGDGKTNYPALKS	SEQ ID NO: 101
HC5_m15 Kabat HCDR2	MIWSDGKIVYNSALKS	SEQ ID NO: 102
HC5_m16 Kabat HCDR2	MIWADGKIVYNSALKS	SEQ ID NO: 103
Parental Chothia HCDR2	WGDGK	SEQ ID NO: 104
HC7 Chothia HCDR2	YGDGK	SEQ ID NO: 105
HC5_m15 Chothia HCDR2	WSDGK	SEQ ID NO: 106
HC5_m16 Chothia HCDR2	WADGK	SEQ ID NO: 107
Parental IMGT HCDR2	IWGDGKI	SEQ ID NO: 108
HC7 IMGT HCDR2	IYGDGKT	SEQ ID NO: 109

HC5_m15 IMGT HCDR2	IWSDGKI	SEQ ID NO: 110
HC5_m16 IMGT HCDR2	IWADGKI	SEQ ID NO: 111
Parental Kabat and Chothia HCDR3	DGYYPYAMDN	SEQ ID NO: 112
HC7 Kabat and Chothia HCDR3	DGYYYYAMDV	SEQ ID NO: 113
HC5_m17 Kabat and Chothia HCDR3	HGYYPYAMDN	SEQ ID NO: 114
HC5_m18 Kabat and Chothia HCDR3	DLYYPYAMDN	SEQ ID NO: 115
HC5_m19 Kabat and Chothia HCDR3	DKYYPYAMDN	SEQ ID NO: 116
HC5_m20 Kabat and Chothia HCDR3	DGYGYAMDN	SEQ ID NO: 117

HC5_m21 Kabat and Chothia HCDR3	DGYAYAMDN	SEQ ID NO: 118
HC5_m22 Kabat and Chothia HCDR3	DGYYSYAMDN	SEQ ID NO: 119
HC5_m23 Kabat and Chothia HCDR3	DGYITYAMDN	SEQ ID NO: 120
HC5_m12 IMGT HCDR1	GNSLNSYS	SEQ ID NO: 121
		SEQ ID NO: 122
		SEQ ID NO: 123
		SEQ ID NO: 124
		SEQ ID NO: 125
		SEQ ID NO: 126
		SEQ ID NO: 127
		SEQ ID NO: 128

		SEQ ID NO: 129
Parental IMGT HCDR3	AGDGYYPYAMDN	SEQ ID NO: 130
HC6 IMGT HCDR3	ARDGYYPYAMDN	SEQ ID NO: 131
HC7 IMGT HCDR3	ARDGYYYYAMDV	SEQ ID NO: 132
HC5_m17 IMGT HCDR3	AGHGYYPYAMDN	SEQ ID NO: 133
HC5_m18 IMGT HCDR3	AGDLYYPYAMDN	SEQ ID NO: 134
HC5_m19 IMGT HCDR3	AGDKYYPYAMDN	SEQ ID NO: 135
HC5_m20 IMGT HCDR3	AGDGYYGYAMDN	SEQ ID NO: 136
HC5_m21 IMGT HCDR3	AGDGYYAYAMDN	SEQ ID NO: 137
HC5_m22 IMGT HCDR3	AGDGYYSYAMDN	SEQ ID NO: 138
HC5_m23 IMGT	AGDGYYTYAMDN	SEQ ID NO: 139

HCDR3		
HC1_m6 IMGT HCDR3	AGDGYYPYAMDN	SEQ ID NO: 140
Parental Kabat and Chothia LCDR1	RASKSVDSYGNSFMH	SEQ ID NO: 141
LC10 Kabat and Chothia LCDR1	RASQSVDSNGNNFLH	SEQ ID NO: 142
LC6_m1 Kabat and Chothia LCDR1	RASKSVDSYGNSRMH	SEQ ID NO: 143
LC6_m2 Kabat and Chothia LCDR1	RASKSVDSYGNSSMH	SEQ ID NO: 144
		SEQ ID NO: 145
		SEQ ID NO: 146
		SEQ ID NO: 147
		SEQ ID NO: 148
Parental IMGT LCDR1	KSVDSYGNSF	SEQ ID NO: 149

LC10 IMGT LCDR1	QSVDSNGNNF	SEQ ID NO: 150
LC6_m1 IMGT LCDR1	KSVDSYGNSR	SEQ ID NO: 151
LC6_m2 IMGT LCDR1	KSVDSYGNSS	SEQ ID NO: 152
Parental Kabat and Chothia LCDR2	LASNLES	SEQ ID NO: 153
LC6_m5 Kabat and Chothia LCDR2	LASHLES	SEQ ID NO: 154
LC6_m6 Kabat and Chothia LCDR2	LASDLES	SEQ ID NO: 155
LC6_m7 Kabat and Chothia LCDR2	LASQLES	SEQ ID NO: 156
LC6_m8 Kabat and Chothia LCDR2	LASELES	SEQ ID NO: 157
LC10	LASNRES	SEQ ID NO: 158

Kabat and Chothia LCDR2		
		SEQ ID NO: 159
		SEQ ID NO: 160
		SEQ ID NO: 161
		SEQ ID NO: 162
		SEQ ID NO: 163
		SEQ ID NO: 164
Parental Kabat, Chothia and IMGT LCDR3	QQNNEDPRT	SEQ ID NO: 165
LC10 Kabat, Chothia and IMGT LCDR3	QQNNHTPRT	SEQ ID NO: 166
LC6_m9 Kabat, Chothia and IMGT LCDR3	QQNHEDPRT	SEQ ID NO: 167

LC6_m10 Kabat, Chothia and IMGT LCDR3	QQNYEDPRT	SEQ ID NO: 168
LC6_m11 Kabat, Chothia and IMGT LCDR3	QQNSEDPR	SEQ ID NO: 169
LC6_m12 Kabat, Chothia and IMGT LCDR3	QQNNRDPRT	SEQ ID NO: 170
LC6_m13 Kabat, Chothia and IMGT LCDR3	QQNNDDPRT	SEQ ID NO: 171
LC6_m14 Kabat, Chothia and IMGT LCDR3	QQNNQDPRT	SEQ ID NO: 172
		SEQ ID NO: 173
		SEQ ID NO: 174
		SEQ ID NO: 175

		SEQ ID NO: 176
		SEQ ID NO: 177
		SEQ ID NO: 178
		SEQ ID NO: 179
		SEQ ID NO: 180
		SEQ ID NO: 181
		SEQ ID NO: 182
		SEQ ID NO: 183
		SEQ ID NO: 184
		SEQ ID NO: 185
		SEQ ID NO: 186
		SEQ ID NO: 187
		SEQ ID NO: 188
HC Framework Region 1 HC0 Kabat	QVQLQESGPGLVAPSQSL SITCTVSGFSLN	SEQ ID NO: 198

HC Framework Region 1 HC0_M Kabat	QVQLQESGPGLVAPSQSLTCTVSGFSLN	SEQ ID NO: 198
HC Framework Region 1 HC1 Kabat	EVQLQESGPGLVKPSETLSLTCTVSGFSLN	SEQ ID NO: 200
HC Framework Region 1 HC2 Kabat	EVQLVQSGAEVKKPGASVKVSCKASGFSLN	SEQ ID NO: 201
HC Framework Region 1 HC3 Kabat	EVQLVQSGAEVKKPGSSVKVSCKASGFSLN	SEQ ID NO: 202
HC Framework Region 1 HC4 Kabat	EVQLVESGGGLVKPGGSLRLSCAASGFSLN	SEQ ID NO: 203
HC Framework Region 1 HC5 Kabat	EVQLLESGGGLVQPGGSLRLSCAASGFSLN	SEQ ID NO: 204
HC Framework Region 1 HC6 Kabat	EVQLQESGPGLVKPSETLSLTCTVSGGSLN	SEQ ID NO: 205

HC Framework Region 1 HC7 Kabat	QVQLQESGPGLVKPSETLSLTCTVSGGSLN	SEQ ID NO: 206
HC Framework Region 1 HC5_m1 Kabat	EVQLLESGGGLVQPGGSLRLSCAASGYSLN	SEQ ID NO: 207
HC Framework Region 1 HC5_m2 Kabat	EVQLLESGGGLVQPGGSLRLSCAASGFSLR	SEQ ID NO: 208
HC Framework Region 1 HC5_m3 Kabat	EVQLLESGGGLVQPGGSLRLSCAASGFSLH	SEQ ID NO: 209
HC Framework Region 1 HC5_m4 Kabat	EVQLLESGGGLVQPGGSLRLSCAASGFSLD	SEQ ID NO: 210
HC Framework Region 1 HC5_m5 Kabat	EVQLLESGGGLVQPGGSLRLSCAASGFSLY	SEQ ID NO: 211

HC Framework Region 1 HC5_m6 Kabat	EVQLLESGGGLVQPGGSLRLSCAASGFSLS	SEQ ID NO: 212
HC Framework Region 1 HC5_m7 Kabat	EVQLLESGGGLVQPGGSLRLSCAASGFSLN	SEQ ID NO: 204
HC Framework Region 1 HC5_m8 Kabat	EVQLLESGGGLVQPGGSLRLSCAASGFSLN	SEQ ID NO: 204
HC Framework Region 1 HC5_m9 Kabat	EVQLLESGGGLVQPGGSLRLSCAASGFSLN	SEQ ID NO: 204
HC Framework Region 1 HC5_m10 Kabat	EVQLLESGGGLVQPGGSLRLSCAASGFSLN	SEQ ID NO: 204
HC Framework Region 1 HC5_m11 Kabat	EVQLLESGGGLVQPGGSLRLSCAASGFSLN	SEQ ID NO: 204

HC Framework Region 1 HC5_m12 Kabat	EVQLLESGGGLVQPGGSLRLSCAASGFSLN	SEQ ID NO: 204
HC Framework Region 1 HC5_m13 Kabat	EVQLLESGGGLVQPGGSLRLSCAASGFSLN	SEQ ID NO: 204
HC Framework Region 1 HC5_m14 Kabat	EVQLLESGGGLVQPGGSLRLSCAASGFSLN	SEQ ID NO: 204
HC Framework Region 1 HC5_m15 Kabat	EVQLLESGGGLVQPGGSLRLSCAASGFSLN	SEQ ID NO: 204
HC Framework Region 1 HC5_m16 Kabat	EVQLLESGGGLVQPGGSLRLSCAASGFSLN	SEQ ID NO: 204
HC Framework Region 1 HC5_m17 Kabat	EVQLLESGGGLVQPGGSLRLSCAASGFSLN	SEQ ID NO: 204

HC Framework Region 1 HC5_m18 Kabat	EVQLLESGGGLVQPGGSLRLSCAASGFSLN	SEQ ID NO: 204
HC Framework Region 1 HC5_m19 Kabat	EVQLLESGGGLVQPGGSLRLSCAASGFSLN	SEQ ID NO: 204
HC Framework Region 1 HC5_m20 Kabat	EVQLLESGGGLVQPGGSLRLSCAASGFSLN	SEQ ID NO: 204
HC Framework Region 1 HC5_m21 Kabat	EVQLLESGGGLVQPGGSLRLSCAASGFSLN	SEQ ID NO: 204
HC Framework Region 1 HC5_m22 Kabat	EVQLLESGGGLVQPGGSLRLSCAASGFSLN	SEQ ID NO: 204
HC Framework Region 1 HC5_m24 Kabat	EVQLLESGGGLVQPGGSLRLSCAASGFSLN	SEQ ID NO: 204

LC Framework Region 1LC0 Kabat	NIVLTQSPASLAVSLGQRATISC	SEQ ID NO: 230
LC Framework Region 1 LC1 Kabat	DIQLTQSPSSLSASVGDRVITIC	SEQ ID NO: 231
LC Framework Region 1 LC2 Kabat	DIQLTQSPSSLSASVGDRVITIC	SEQ ID NO: 231
LC Framework Region 1 LC3 Kabat	EIVLTQSPATLSVSPGERATLSC	SEQ ID NO: 233
LC Framework Region 1 LC4 Kabat	DIVLTQSPLSLPVTPGEPASISC	SEQ ID NO: 234
LC Framework Region 1 LC5 Kabat	DIVLTQSPDSLAVSLGERATINC	SEQ ID NO: 235
LC Framework Region 1 LC6 Kabat	DIQLTQSPSSLSASVGDRVITIC	SEQ ID NO: 231
LC Framework Region 1	EIVLTQSPATLSVSPGERATLSC	SEQ ID NO: 233

LC7 Kabat		
LC Framework Region 1 LC8 Kabat	DIVLTQSPLSLPVTPGEPASISC	SEQ ID NO: 234
LC Framework Region 1 LC9 Kabat	DIVLTQSPASLAVSPGERATISC	SEQ ID NO: 239
LC Framework Region 1 LC10 Kabat	DIVLTQSPASLAVSPGERATISC	SEQ ID NO: 239
LC Framework Region 1 LC6_m1 Kabat	DIQLTQSPSSLSASVGDRVITIC	SEQ ID NO: 231
LC Framework Region 1 LC6_m2 Kabat	DIQLTQSPSSLSASVGDRVITIC	SEQ ID NO: 231
LC Framework Region 1 LC6_m3 Kabat	DIQLTQSPSSLSASVGDRVITIC	SEQ ID NO: 231
LC Framework Region 1	DIQLTQSPSSLSASVGDRVITIC	SEQ ID NO: 231

LC6_m4 Kabat		
LC Framework Region 1 LC6_m5 Kabat	DIQLTQSPSSLSASVGDRVITIC	SEQ ID NO: 231
LC Framework Region 1 LC6_m6 Kabat	DIQLTQSPSSLSASVGDRVITIC	SEQ ID NO: 231
LC Framework Region 1 LC6_m7 Kabat	DIQLTQSPSSLSASVGDRVITIC	SEQ ID NO: 231
LC Framework Region 1 LC6_m8 Kabat	DIQLTQSPSSLSASVGDRVITIC	SEQ ID NO: 231
LC Framework Region 1 LC6_m9 Kabat	DIQLTQSPSSLSASVGDRVITIC	SEQ ID NO: 231
LC Framework Region 1	DIQLTQSPSSLSASVGDRVITIC	SEQ ID NO: 231

LC6_m10 Kabat		
LC Framework Region 1 LC6_m11 Kabat	DIQLTQSPSSLSASVGDRVITIC	SEQ ID NO: 231
LC Framework Region 1 LC6_m12 Kabat	DIQLTQSPSSLSASVGDRVITIC	SEQ ID NO: 231
LC Framework Region 1 LC6_m13 Kabat	DIQLTQSPSSLSASVGDRVITIC	SEQ ID NO: 231
LC Framework Region 1 LC6_m14 Kabat	DIQLTQSPSSLSASVGDRVITIC	SEQ ID NO: 231
Lebrikizuma b - HC	WIRQPPGKALEWLA	SEQ ID NO: 255
HC Framework Region 2 HC0	WVRQPPGKGLEWLG	SEQ ID NO: 256

HC Framework Region 2 HC0_M Kabat	WVRQPPGKGLEWLG	SEQ ID NO: 256
HC Framework Region 2 HC1 Kabat	WIRQPPGKGLEWLG	SEQ ID NO: 258
HC Framework Region 2 HC2 Kabat	WVRQAPGQGLEWLG	SEQ ID NO: 259
HC Framework Region 2 HC3 Kabat	WVRQAPGQGLEWLG	SEQ ID NO: 259
HC Framework Region 2 HC4 Kabat	WVRQAPGKGLEWLG	SEQ ID NO: 262
HC Framework Region 2 HC5 Kabat	WVRQAPGKGLEWLG	SEQ ID NO: 262
HC Framework Region 2 HC6 Kabat	WVRQPPGKGLEWLG	SEQ ID NO: 263

HC Framework Region 2 HC7 Kabat	WVRQPPGKGLEWLG	SEQ ID NO: 263
HC Framework Region 2 HC5_m1 Kabat	WVRQAPGKGLEWLG	SEQ ID NO: 262
HC Framework Region 2 HC5_m2 Kabat	WVRQAPGKGLEWLG	SEQ ID NO: 262
HC Framework Region 2 HC5_m3 Kabat	WVRQAPGKGLEWLG	SEQ ID NO: 262
HC Framework Region 2 HC5_m4 Kabat	WVRQAPGKGLEWLG	SEQ ID NO: 262
HC Framework Region 2 HC5_m5 Kabat	WVRQAPGKGLEWLG	SEQ ID NO: 262

HC Framework Region 2 HC5_m6 Kabat	WVRQAPGKGLEWLG	SEQ ID NO: 262
HC Framework Region 2 HC5_m7 Kabat	WVRQAPGKGLEWLG	SEQ ID NO: 262
HC Framework Region 2 HC5_m8 Kabat	WVRQAPGKGLEWLG	SEQ ID NO: 262
HC Framework Region 2 HC5_m9 Kabat	WVRQAPGKGLEWLG	SEQ ID NO: 262
HC Framework Region 2 HC5_m10 Kabat	WVRQAPGKGLEWLG	SEQ ID NO: 262
HC Framework Region 2 HC5_m11 Kabat	WVRQAPGKGLEWLG	SEQ ID NO: 262

HC Framework Region 2 HC5_m12 Kabat	WVRQAPGKGLEWLG	SEQ ID NO: 262
HC Framework Region 2 HC5_m13 Kabat	WVRQAPGKGLEWLG	SEQ ID NO: 262
HC Framework Region 2 HC5_m14 Kabat	WVRQAPGKGLEWLG	SEQ ID NO: 262
HC Framework Region 2 HC5_m15 Kabat	WVRQAPGKGLEWLG	SEQ ID NO: 262
HC Framework Region 2 HC5_m16 Kabat	WVRQAPGKGLEWLG	SEQ ID NO: 262
HC Framework Region 2 HC5_m17 Kabat	WVRQAPGKGLEWLG	SEQ ID NO: 262

HC Framework Region 2 HC5_m18 Kabat H	WVRQAPGKGLEWLG	SEQ ID NO: 262
HC Framework Region 2 HC5_m19 Kabat	WVRQAPGKGLEWLG	SEQ ID NO: 262
HC Framework Region 2 HC5_m20 Kabat	WVRQAPGKGLEWLG	SEQ ID NO: 262
HC Framework Region 2 HC5_m21 Kabat	WVRQAPGKGLEWLG	SEQ ID NO: 262
HC Framework Region 2 HC5_m22 Kabat	WVRQAPGKGLEWLG	SEQ ID NO: 262
HC Framework Region 2 HC5_m24 Kabat	WVRQAPGKGLEWLG	SEQ ID NO: 262

Lebrikizuma b - LC	WYQQKPGQPPKLLIY	SEQ ID NO: 286
LC Framework Region 2 LC0 Kabat	WYQQKPGQPPKLLIY	SEQ ID NO: 286
LC Framework Region 2 LC1 Kabat	WYQQKPGKAPKLLIY	SEQ ID NO: 288
LC Framework Region 2 LC2 Kabat	WYQQKPGKAPKLLIY	SEQ ID NO: 288
LC Framework Region 2 LC3 Kabat	WYQQKPGQAPRLLIY	SEQ ID NO: 290
LC Framework Region 2 LC4 Kabat	WYLQKPGQSPQLLIY	SEQ ID NO: 291
LC Framework Region 2 LC5 Kabat	WYQQKPGQPPKLLIY	SEQ ID NO: 286
LC Framework Region 2 LC6 Kabat	WYQQKPGKAPKLLIY	SEQ ID NO: 288

LC Framework Region 2 LC7 Kabat	WYQQKPGQAPRLLIY	SEQ ID NO: 290
LC Framework Region 2 LC8 Kabat	WYLQKPGQSPQLLIY	SEQ ID NO: 291
LC Framework Region 2 LC9 Kabat	WYQQKPGQPPKLLIY	SEQ ID NO: 292
LC Framework Region 2 LC10 Kabat	WYQQKPGQPPKLLIY	SEQ ID NO: 286
LC Framework Region 2 LC6_m1 Kabat	WYQQKPGKAPKLLIY	SEQ ID NO: 288
LC Framework Region 2 LC6_m2 Kabat	WYQQKPGKAPKLLIY	SEQ ID NO: 288
LC Framework Region 2 LC6_m3 Kabat	WYQQKPGKAPKLLIR	SEQ ID NO: 300

LC Framework Region 2 LC6_m4 Kabat	WYQQKPGKAPKLLIF	SEQ ID NO: 301
LC Framework Region 2 LC6_m5 Kabat	WYQQKPGKAPKLLIY	SEQ ID NO: 288
LC Framework Region 2 LC6_m6 Kabat	WYQQKPGKAPKLLIY	SEQ ID NO: 288
LC Framework Region 2 LC6_m7 Kabat	WYQQKPGKAPKLLIY	SEQ ID NO: 288
LC Framework Region 2 LC6_m8 Kabat	WYQQKPGKAPKLLIY	SEQ ID NO: 288
LC Framework Region 2 LC6_m9 Kabat	WYQQKPGKAPKLLIY	SEQ ID NO: 288

LC Framework Region 2 LC6_m10 Kabat	WYQQKPGKAPKLLIY	SEQ ID NO: 288
LC Framework Region 2 LC6_m11 Kabat	WYQQKPGKAPKLLIY	SEQ ID NO: 288
LC Framework Region 2 LC6_m12 Kabat	WYQQKPGKAPKLLIY	SEQ ID NO: 288
LC Framework Region 2 LC6_m13 Kabat	WYQQKPGKAPKLLIY	SEQ ID NO: 288
LC Framework Region 2 LC6_m14 Kabat	WYQQKPGKAPKLLIY	SEQ ID NO: 288
Lebrikizuma b - HC	RLTISKDTSKNQVVLMTNMDPVDTATYYCAG	SEQ ID NO: 311
HC Framework Region 3 HC0 Kabat	RLNISKDSSKSQVFLKMSSLQSDDTARYYCAG	SEQ ID NO: 312

HC Framework Region 3 HC0_M Kabat	RLTISKDSSKSQVFLKMSSLQSDDTARYYCAG	SEQ ID NO: 313
HC Framework Region 3 HC1 Kabat	RLTISKDSSKNQVSLKLSSVTAADTAVYYCAG	SEQ ID NO: 314
HC Framework Region 3 HC2 Kabat	RLTITKDSSTSTVYMELSSLRSED TAVYYCAG	SEQ ID NO: 315
HC Framework Region 3 HC3 Kabat	RLTITKDSSTSTVYMELSSLRSED TAVYYCAG	SEQ ID NO: 315
HC Framework Region 3 HC4 Kabat	RLTISKDSSKNTVYLQMNSLKTED TAVYYCAG	SEQ ID NO: 317
HC Framework Region 3 HC5 Kabat	RLTISKDSSKNTVYLQMNSLRAED TAVYYCAG	SEQ ID NO: 318
HC Framework Region 3 HC6 Kabat	RLTISLDTSKSQVFLKMSSLTAADTAVYYCAR	SEQ ID NO: 319

HC Framework Region 3 HC7 Kabat	RLTISLDTSKSQVFLKMSSLTAADTAVYYCAR	SEQ ID NO: 319
HC Framework Region 3 HC5_m1 Kabat	RLTISKDSSKNTVYLMNSLRAEDTAVYYCAG	SEQ ID NO: 318
HC Framework Region 3 HC5_m2 Kabat	RLTISKDSSKNTVYLMNSLRAEDTAVYYCAG	SEQ ID NO: 318
HC Framework Region 3 HC5_m3 Kabat	RLTISKDSSKNTVYLMNSLRAEDTAVYYCAG	SEQ ID NO: 318
HC Framework Region 3 HC5_m4 Kabat	RLTISKDSSKNTVYLMNSLRAEDTAVYYCAG	SEQ ID NO: 318
HC Framework Region 3 HC5_m5 Kabat	RLTISKDSSKNTVYLMNSLRAEDTAVYYCAG	SEQ ID NO: 318

HC Framework Region 3 HC5_m6 Kabat	RLTISKDSSKNTVYLMNSLRAEDTAVYYCAG	SEQ ID NO: 318
HC Framework Region 3 HC5_m7 Kabat	RLTISKDSSKNTVYLMNSLRAEDTAVYYCAG	SEQ ID NO: 318
HC Framework Region 3 HC5_m8 Kabat	RLTISKDSSKNTVYLMNSLRAEDTAVYYCAG	SEQ ID NO: 318
HC Framework Region 3 HC5_m9 Kabat	RLTISKDSSKNTVYLMNSLRAEDTAVYYCAG	SEQ ID NO: 318
HC Framework Region 3 HC5_m10 Kabat	RLTISKDSSKNTVYLMNSLRAEDTAVYYCAG	SEQ ID NO: 318
HC Framework Region 3 HC5_m11 Kabat	RLTISKDSSKNTVYLMNSLRAEDTAVYYCAG	SEQ ID NO: 318

HC Framework Region 3 HC5_m12 Kabat	RLTISKDSSKNTVYLMNSLRAEDTAVYYCAG	SEQ ID NO: 318
HC Framework Region 3 HC5_m13 Kabat	RLTISKDSSKNTVYLMNSLRAEDTAVYYCAG	SEQ ID NO: 318
HC Framework Region 3 HC5_m14 Kabat	RLTISKDSSKNTVYLMNSLRAEDTAVYYCAG	SEQ ID NO: 318
HC Framework Region 3 HC5_m15 Kabat	RLTISKDSSKNTVYLMNSLRAEDTAVYYCAG	SEQ ID NO: 318
HC Framework Region 3 HC5_m16 Kabat	RLTISKDSSKNTVYLMNSLRAEDTAVYYCAG	SEQ ID NO: 318
HC Framework Region 3 HC5_m17 Kabat	RLTISKDSSKNTVYLMNSLRAEDTAVYYCAG	SEQ ID NO: 318

HC Framework Region 3 HC5_m18 Kabat	RLTISKDSSKNTVYLMNSLRAEDTAVYYCAG	SEQ ID NO: 318
HC Framework Region 3 HC5_m19 Kabat	RLTISKDSSKNTVYLMNSLRAEDTAVYYCAG	SEQ ID NO: 318
HC Framework Region 3 HC5_m20 Kabat	RLTISKDSSKNTVYLMNSLRAEDTAVYYCAG	SEQ ID NO: 318
HC Framework Region 3 HC5_m21 Kabat	RLTISKDSSKNTVYLMNSLRAEDTAVYYCAG	SEQ ID NO: 318
HC Framework Region 3 HC5_m22 Kabat	RLTISKDSSKNTVYLMNSLRAEDTAVYYCAG	SEQ ID NO: 318
HC Framework Region 3 HC5_m24 Kabat	RLTISKDSSKNTVYLMNSLRAEDTAVYYCAG	SEQ ID NO: 318

Lebrikizuma b - LC	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC	SEQ ID NO: 343
LC Framework Region 3 LC0 Kabat	GVPARFSGSGSRTDFTLTIDPVEADDAASYC	SEQ ID NO: 344
LC Framework Region 3 LC1 Kabat	GVPSRFSGSGSRTDFTLTISSLQPEDFATYYC	SEQ ID NO: 345
LC Framework Region 3 LC2 Kabat	GVPSRFSGSGSRTDFTLTISSLQPEDFATYYC	SEQ ID NO: 345
LC Framework Region 3 LC3 Kabat	GIPARFSGSGSRTEFTLTISSLQSEDFAVYYC	SEQ ID NO: 347
LC Framework Region 3 LC4 Kabat	GVPDRFSGSGSRTDFTLKISRVEAEDVGVYYC	SEQ ID NO: 348
LC Framework Region 3 LC6 Kabat	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC	SEQ ID NO: 713
LC Framework Region 3 LC7 Kabat	GIPARFSGSGSGTEFTLTISSLQSEDFAVYYC	SEQ ID NO: 351

LC Framework Region 3 LC8 Kabat	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	SEQ ID NO: 352
LC Framework Region 3 LC9 Kabat	GVPDRFSGSGSGTDFTLTISRVEADDVAVYYC	SEQ ID NO: 353
LC Framework Region 3 LC10 Kabat	GVPDRFSGSGSGTDFTLTISRVEADDVAVYYC	SEQ ID NO: 353
LC Framework Region 3 LC6_m1 Kabat	GVPSRFSGSGSGTDFTLTISLQPEDFATYYC	SEQ ID NO: 349
LC Framework Region 3 LC6_m2 Kabat	GVPSRFSGSGSGTDFTLTISLQPEDFATYYC	SEQ ID NO: 349
LC Framework Region 3 LC6_m3 Kabat	GVPSRFSGSGSGTDFTLTISLQPEDFATYYC	SEQ ID NO: 349
LC Framework Region 3	GVPSRFSGSGSGTDFTLTISLQPEDFATYYC	SEQ ID NO: 349

LC6_m4 Kabat		
LC Framework Region 3 LC6_m5 Kabat	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	SEQ ID NO: 349
LC Framework Region 3 LC6_m6 Kabat	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	SEQ ID NO: 349
LC Framework Region 3 LC6_m7 Kabat	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	SEQ ID NO: 349
LC Framework Region 3 LC6_m8 Kabat	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	SEQ ID NO: 349
LC Framework Region 3 LC6_m9 Kabat	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	SEQ ID NO: 349
LC Framework Region 3	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	SEQ ID NO: 349

LC6_m10 Kabat		
LC Framework Region 3 LC6_m11 Kabat	GVPSRFSGSGSGTDFTLTISLQPEDFATYYC	SEQ ID NO: 349
LC Framework Region 3 LC6_m12 Kabat	GVPSRFSGSGSGTDFTLTISLQPEDFATYYC	SEQ ID NO: 349
LC Framework Region 3 LC6_m13 Kabat	GVPSRFSGSGSGTDFTLTISLQPEDFATYYC	SEQ ID NO: 349
LC Framework Region 3 LC6_m14 Kabat	GVPSRFSGSGSGTDFTLTISLQPEDFATYYC	SEQ ID NO: 349
Lebrikizuma b - HC	WGQGS�VTVSS	SEQ ID NO: 368
HC Framework Region 4 HC0	WGHGTSVTVSS	SEQ ID NO: 369
HC Framework Region 4	WGHGTSVTVSS	SEQ ID NO: 369

HC0_M Kabat		
HC Framework Region 4 HC1 Kabat	WGQGTTVTVSS	SEQ ID NO: 371
HC Framework Region 4 HC2 Kabat	WGQGTTVTVSS	SEQ ID NO: 371
HC Framework Region 4 HC3 Kabat	WGQGTTVTVSS	SEQ ID NO: 371
HC Framework Region 4 HC4 Kabat	WGQGTTVTVSS	SEQ ID NO: 371
HC Framework Region 4 HC5 Kabat	WGQGTTVTVSS	SEQ ID NO: 371
HC Framework Region 4 HC6 Kabat	WGQGTTVTVSS	SEQ ID NO: 371
HC Framework Region 4 HC7 Kabat	WGQGTTVTVSS	SEQ ID NO: 371

HC Framework Region 4 HC5_m1 Kabat	WGQGTTVTVSS	SEQ ID NO: 371
HC Framework Region 4 HC5_m2 Kabat	WGQGTTVTVSS	SEQ ID NO: 371
HC Framework Region 4 HC5_m3 Kabat	WGQGTTVTVSS	SEQ ID NO: 371
HC Framework Region 4 HC5_m4 Kabat	WGQGTTVTVSS	SEQ ID NO: 371
HC Framework Region 4 HC5_m5 Kabat	WGQGTTVTVSS	SEQ ID NO: 371
HC Framework Region 4 HC5_m6 Kabat	WGQGTTVTVSS	SEQ ID NO: 371

HC Framework Region 4 HC5_m7 Kabat	WGQGTTVTVSS	SEQ ID NO: 371
HC Framework Region 4 HC5_m8 Kabat	WGQGTTVTVSS	SEQ ID NO: 371
HC Framework Region 4 HC5_m9 Kabat	WGQGTTVTVSS	SEQ ID NO: 371
HC Framework Region 4 HC5_m10 Kabat	WGQGTTVTVSS	SEQ ID NO: 371
HC Framework Region 4 HC5_m11 Kabat	WGQGTTVTVSS	SEQ ID NO: 371
HC Framework Region 4 HC5_m12 Kabat	WGQGTTVTVSS	SEQ ID NO: 371

HC Framework Region 4 HC5_m13 Kabat	WGQGTTVTVSS	SEQ ID NO: 371
HC Framework Region 4 HC5_m14 Kabat	WGQGTTVTVSS	SEQ ID NO: 371
HC Framework Region 4 HC5_m15 Kabat	WGQGTTVTVSS	SEQ ID NO: 371
HC Framework Region 4 HC5_m16 Kabat	WGQGTTVTVSS	SEQ ID NO: 371
HC Framework Region 4 HC5_m17 Kabat	WGQGTTVTVSS	SEQ ID NO: 371
HC Framework Region 4 HC5_m18 Kabat	WGQGTTVTVSS	SEQ ID NO: 371

HC Framework Region 4 HC5_m19 Kabat	WGQGTTVTVSS	SEQ ID NO: 371
HC Framework Region 4 HC5_m20 Kabat	WGQGTTVTVSS	SEQ ID NO: 371
HC Framework Region 4 HC5_m21 Kabat	WGQGTTVTVSS	SEQ ID NO: 371
HC Framework Region 4 HC5_m22 Kabat	WGQGTTVTVSS	SEQ ID NO: 371
HC Framework Region 4 HC5_m24 Kabat	WGQGTTVTVSS	SEQ ID NO: 371
Lebrikizuma b - LC	FGGGTKVEIK	SEQ ID NO: 400
LC Framework Region 4 LC0 Kabat	FGGGTKLEIK	SEQ ID NO: 401

LC Framework Region 4 LC1 Kabat	FGGGTKVEIK	SEQ ID NO: 400
LC Framework Region 4 LC2 Kabat	FGGGTKVEIK	SEQ ID NO: 400
LC Framework Region 4 LC3 Kabat	FGGGTKVEIK	SEQ ID NO: 400
LC Framework Region 4 LC4 Kabat	FGGGTKVEIK	SEQ ID NO: 400
LC Framework Region 4 LC5 Kabat	FGGGTKVEIK	SEQ ID NO: 400
LC Framework Region 4 LC6 Kabat	FGGGTKVEIK	SEQ ID NO: 400
LC Framework Region 4 LC7 Kabat	FGGGTKVEIK	SEQ ID NO: 400
LC Framework Region 4	FGGGTKVEIK	SEQ ID NO: 400

LC8 Kabat		
LC Framework Region 4 LC9 Kabat	FGGGTKLEIK	SEQ ID NO: 401
LC Framework Region 4 LC10 Kabat	FGGGTKLEIK	SEQ ID NO: 401
LC Framework Region 4 LC6_m1 Kabat	FGGGTKVEIK	SEQ ID NO: 400
LC Framework Region 4 LC6_m2 Kabat	FGGGTKVEIK	SEQ ID NO: 400
LC Framework Region 4 LC6_m3 Kabat	FGGGTKVEIK	SEQ ID NO: 400
LC Framework Region 4 LC6_m4 Kabat	FGGGTKVEIK	SEQ ID NO: 400
LC Framework	FGGGTKVEIK	SEQ ID NO: 400

Region 4 LC6_m5 Kabat		
LC Framework Region 4 LC6_m6 Kabat	FGGGTKVEIK	SEQ ID NO: 400
LC Framework Region 4 LC6_m7 Kabat	FGGGTKVEIK	SEQ ID NO: 400
LC Framework Region 4 LC6_m8 Kabat	FGGGTKVEIK	SEQ ID NO: 400
LC Framework Region 4 LC6_m9 Kabat	FGGGTKVEIK	SEQ ID NO: 400
LC Framework Region 4 LC6_m10 Kabat	FGGGTKVEIK	SEQ ID NO: 400
LC Framework Region 4	FGGGTKVEIK	SEQ ID NO: 400

LC6_m11 Kabat		
LC Framework Region 4 LC6_m12 Kabat	FGGGTKVEIK	SEQ ID NO: 400
LC Framework Region 4 LC6_m13 Kabat	FGGGTKVEIK	SEQ ID NO: 400
LC Framework Region 4 LC6_m14 Kabat	FGGGTKVEIK	SEQ ID NO: 400
Heavy Chain hIgG1	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 425
Heavy Chain hIgG4	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYT CNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYK	SEQ ID NO: 426

	CKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKS LSLSLGK	
Heavy Chain IgG4-SP	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTKYT CNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKS LSLSLGK	SEQ ID NO: 427
Heavy Chain IgG4-SPLE	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTKYT CNVDHKPSNTKVDKRVESKYGPPCPPCPAPEELGGPSVFL FPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKS LSLSLGK	SEQ ID NO: 428
Heavy Chain IgG2	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYT CNVDHKPSNTKVDKTVKCCVECPAPPVAGPSVFLF PPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDG EVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKC KVSNGKLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPMLDSDG SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSP	SEQ ID NO: 429

Heavy Chain hIgG1-N297A	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 430
Heavy Chain hIgG1-D265A	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 431
Heavy Chain hIgG1-LALA	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 432
Heavy Chain hIgG1-LAGA	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW	SEQ ID NO: 433

	YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	
Heavy Chain hIgG1- LALAGA	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 434
Heavy Chain hIgG1- LALAPG	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP PVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPG	SEQ ID NO: 435
Heavy Chain hIgG1-YTE	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLYITREPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP	SEQ ID NO: 436

	VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	
Heavy Chain hIgG1- N297A/YT E	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 437
Heavy Chain hIgG1- D265A/YT E	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLYITREPEVTCVVVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 438
Heavy Chain hIgG1- LALA/YTE	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 439
Heavy Chain	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT	SEQ ID NO: 440

hIgG1-LAGA/YTE	YICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	
Heavy Chain hIgG1-LALAGA/YTE	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 441
Heavy Chain hIgG1-LALAPG/YTE	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP PVLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPG	SEQ ID NO: 442
Heavy Chain hIgG1-LS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD	SEQ ID NO: 443

	ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFCVSLHEALHSH YTQKSLSLSPG	
Heavy Chain hIgG1- N297A/LS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFCVSLHEALHSH YTQKSLSLSPG	SEQ ID NO: 444
Heavy Chain hIgG1- D265A/LS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFCVSLHEALHSH YTQKSLSLSPG	SEQ ID NO: 445
Heavy Chain hIgG1- LALA/LS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAEEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFCVSLHEALHSH YTQKSLSLSPG	SEQ ID NO: 446

Heavy Chain hIgG1-LAGA/LS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSH YTQKSLSLSPG	SEQ ID NO: 447
Heavy Chain hIgG1-LALAGA/LS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSH YTQKSLSLSPG	SEQ ID NO: 448
Heavy Chain hIgG1-LALAPG/LS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP PVLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSH YTQKSLSLSPG	SEQ ID NO: 449
Heavy Chain hIgG1-DHS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW	SEQ ID NO: 450

	YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVDHHDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHSH YTQKSLSLSPG	
Heavy Chain hIgG1- N297A/DH S	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLTVDHHDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHSH YTQKSLSLSPG	SEQ ID NO: 451
Heavy Chain hIgG1- D265A/DH S	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVDHHDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHSH YTQKSLSLSPG	SEQ ID NO: 452
Heavy Chain hIgG1- LALA/DHS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVDHHDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP	SEQ ID NO: 453

	VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHSH YTQKSLSLSP	
Heavy Chain hIgG1- LAGA/DHS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVDHHDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHSH YTQKSLSLSPG	SEQ ID NO: 454
Heavy Chain hIgG1- LALAGA/D HS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVDHHDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHSH YTQKSLSLSPG	SEQ ID NO: 455
Heavy Chain hIgG1- LALAPG/D HS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVDHHDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHS HYTQKSLSLSPG	SEQ ID NO: 456
Heavy Chain	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGKTYT	SEQ ID NO: 457

IgG4-YTE	CNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFL FPPKPKDTLYITREPEVTCVVVDVSQEDPEVQFNWYVDGV EVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKC KVSNGKLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSL SLSLGK	
Heavy Chain IgG4- SP/YTE	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTKYT CNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFL FPPKPKDTLYITREPEVTCVVVDVSQEDPEVQFNWYVDGV EVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKC KVSNGKLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSL SLSLGK	SEQ ID NO: 458
Heavy Chain IgG4- SPLE/YTE	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTKYT CNVDHKPSNTKVDKRVESKYGPPCPSCPAPEELGGPSVFL FPPKPKDTLYITREPEVTCVVVDVSQEDPEVQFNWYVDGV EVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKC KVSNGKLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSL SLSLGK	SEQ ID NO: 459
Heavy Chain IgG4-LS	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTKYT CNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNGKLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN	SEQ ID NO: 460

	QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVLHEALHSYTQKSLS LSLGK	
Heavy Chain IgG4-SP/LS	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGKTKYT CNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVLHEALHSHYTQKSL SLSLGK	SEQ ID NO: 461
Heavy Chain IgG4- SPLE/LS	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGKTKYT CNVDHKPSNTKVDKRVESKYGPPCPPCPAPEELGGPSVFL FPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVLHEALHSHYTQKSL SLSLGK	SEQ ID NO: 462
Heavy Chain IgG4-DHS	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGKTKYT CNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVDHHDWLNGKEY KCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS DGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHSHYTQK SLSLSLGK	SEQ ID NO: 463

Heavy Chain IgG4-SP/DHS	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTKTYT CNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVDHHDLNGLKEY KCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSRLTVDKSRWQEGNVFSCSVMEALHSHYTQKSLSLSLGK	SEQ ID NO: 464
Heavy Chain IgG4-SPLE/DHS	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTKTYT CNVDHKPSNTKVDKRVESKYGPPCPPCPAPEELGGPSVFL FPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVDHHDLNGLKEY KCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSRLTVDKSRWQEGNVFSCSVMEALHSHYTQKSLSLSLGK	SEQ ID NO: 465
Heavy Chain IgG2-YTE	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSNFGTQTYT CNVDHKPSNTKVDKTVKCCVECPAPPVAGPSVFLF PPKPKDTLYITREPEVTCVVVDVSHEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTFRVVSVLTVVHQDNLNGLKEYKCK VSNKGLPAIEKTISKTKGQPREPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGS FFLYSKLTVDKSRWQQGNVFCVSLHEALHSHYTQKSLSLSP	SEQ ID NO: 466
Heavy Chain IgG2-LS	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSNFGTQTYT CNVDHKPSNTKVDKTVKCCVECPAPPVAGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGV	SEQ ID NO: 467

	EVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKC KVSNGKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPMLDSDG SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSP	
Heavy Chain IgG2-DHS	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSNFGTQTYT CNVDHKPSNTKVDKTVKCCVECPPCAPPVAGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGV EVHNAKTKPREEQFNSTFRVVSVLTVDHHDWLNGKEYKC KVSNGKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPMLDSDG SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHSHYTQKSL SLSP	SEQ ID NO: 468
Light Chain Human kappa LC	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ WKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC	SEQ ID NO: 469
Lebrikizuma b Heavy Chain Variable Region	QVTLRSGPALVKPTQTLTCTVSGFSLAYSVNWIRQPP GKALEWLAMIWGDGKIVYNSALKSRLTISKDTSKNQVVL TMTNMDPVDATYYCAGDGYYPYAMDNWGQGS�VTVS S	SEQ ID NO: 470
Lebrikizuma b Light Chain Variable Region	DIVMTQSPDLSVSLGERATINCRASKSVDSYGNSFMHWY QQKPGQPPKLLIYLASNLESGVPDRFSGSGSGTDFTLTISL QAEDVAVYYCQNNEDPRTFGGGTKVEIK	SEQ ID NO: 471
Human IL- 13	MHPLLNPLLLALGLMALLTTVIALTCLGGFASPGVPPST ALRELIEELVNITQNQKAPLCNGSMVWSINLTAGMYCAAL	SEQ ID NO: 472

Full sequence	ESLINVSGCSAIEKTQRMLSGFCPHKVSAGQFSSLHVRDTK IEVAQFVKDLLLLHLKKLFREGRFN	
Cynomolgus Monkey IL-13 Full sequence	MALLLTMVIALTCLGGFASPPVPPSTALKELIEELVNITQN QKAPLCNGSMVWSINLTAGVYCAALESLINVSGCSAIEKT QRMLNGFCPHKVSAGQFSSLRVDRDTKIEVAQFVKDLLVH LKKLFREGQFN	SEQ ID NO: 473
Mouse IL-13 Full sequence	MALWVTAVLALACLGGLAAPGPVPRSVSLPLTLKELIEEL SNITQDQTPLCNGSMVWSVDLAAGGFCVALDSL TNISNCN AIYRTQRILHGLCNRKAPTTVSSLPDTKIEVAHFITKLLSYT KQLFRHGPF	SEQ ID NO: 474
Rat IL-13 Full sequence	MALWVTAVLALACLGGLATPGPVRRSTSPVALRELIEEL SNITQDQKTS LCNSSMVWSVDLTAGGFCAALESLTNISSC NAIHRTQRILNGLCNQKASDVASSPPDTKIEVAQFISKLLN YSKQLFRYGH	SEQ ID NO: 475
Human IL-13 Leader sequence	MHPLLNP LLLALGLMALLLT TVIA	SEQ ID NO: 476
Cynomolgus Monkey IL-13 Leader sequence	MALLLT MVIALTCLGGFA	SEQ ID NO: 477
Mouse IL-13 Leader sequence	MALWVTAVLALACLGGLA	SEQ ID NO: 478
Rat IL-13 Leader sequence	MALWVTAVLALACLGGLA	SEQ ID NO: 479

Human IL-13 Main chain sequence	LTCLGGFASPGVPPSTALRELIEELVNITQNQKAPLCNGS MVWSINLTAGMYCAALESINVS GC SAIEKTQRMLSGFCP HKVSAGQFSSLHVRDTKIEVAQFVKDLLLHLKKLFREGRF N	SEQ ID NO: 480
Cynomolgus Monkey IL-13 Main chain sequence	SPSPVPPSTALKELIEELVNITQNQKAPLCNGSMVWSINLT AGVYCAALESINVS GC SAIEKTQRMLNGFCPHKVSAGQF SSLRVRDTKIEVAQFVKDLLVHLKKLFREGQFN	SEQ ID NO: 481
Mouse IL-13 Main chain sequence	APGPVPRSVSLPLTLKELIEELS NITQDQTPLCNGSMVWSV DLAAGGFCVALDSL TNISNCNAIYRTQRILHGLCNRKAPTT VSSLPDTKIEVAHFITKLLSYTKQLFRHGPF	SEQ ID NO: 482
Rat IL-13 Main chain sequence	TPGPVRRSTSPVALRELIEELS NITQDQKTS LCNSSMVWS VDLTAGGFCAALES LTNISSCNAIHRTQRILNGLCNQKASD VASSPPDTKIEVAQFISKLLNYSKQLFRYGH	SEQ ID NO: 483
hIgG1-LA	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDS DGSFFLYSKLTVDKSRWQQGNV FSCSVLHEALHAH YTQKSLSLSPG	SEQ ID NO: 484
hIgG1-N297A/LA	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD	SEQ ID NO: 485

	ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHAH YTQKSLSLSPG	
hIgG1- D265A/LA	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVAVVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHAH YTQKSLSLSPG	SEQ ID NO: 486
hIgG1- LALA/LA	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHAH YTQKSLSLSPG	SEQ ID NO: 487
hIgG1- LAGA/LA	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHAH YTQKSLSLSPG	SEQ ID NO: 488

hIgG1- LALAGA/L A	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHAH YTQKSLSLSPG	SEQ ID NO: 489
hIgG1- LALAPG/L A	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHA HYTQKSLSLSPG	SEQ ID NO: 490
hIgG1- N434A	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHAH YTQKSLSLSPG	SEQ ID NO: 491
hIgG1- N297A/ N434A	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW	SEQ ID NO: 492

	YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHAH YTQKSLSLSPG	
hIgG1- D265A/ N434A	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVAVVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHAH YTQKSLSLSPG	SEQ ID NO: 493
hIgG1- LALA/ N434A	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHAH YTQKSLSLSPG	SEQ ID NO: 494
hIgG1- LAGA/ N434A	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP	SEQ ID NO: 495

	VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHAH YTQKSLSLSPG	
hIgG1- LALAGA/ N434A	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHAH YTQKSLSLSPG	SEQ ID NO: 496
hIgG1- LALAPG/ N434A	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP PVLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHA HYTQKSLSLSPG	SEQ ID NO: 497
hIgG1- N434W	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHW HYTQKSLSLSPG	SEQ ID NO: 498
hIgG1- N297A/ N434W	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT	SEQ ID NO: 499

	YICNVNHKPSNTKVDDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHW HYTQKSLSLSPG	
hIgG1- D265A/ N434W	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHW HYTQKSLSLSPG	SEQ ID NO: 500
hIgG1- LALA/ N434W	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHW HYTQKSLSLSPG	SEQ ID NO: 501
hIgG1- LAGA/ N434W	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD	SEQ ID NO: 502

	ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHW HYTQKSLSLSPG	
hIgG1- LALAGA/ N434W	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHW HYTQKSLSLSPG	SEQ ID NO: 503
hIgG1- LALAPG/ N434W	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP PVLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHW HYTQKSLSLSPG	SEQ ID NO: 504
hIgG1/DQ	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 505

hIgG1- N297A/DQ	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLQVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 506
hIgG1- D265A/DQ	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 507
hIgG1- LALA/DQ	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 508
hIgG1- LAGA/DQ	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW	SEQ ID NO: 509

	YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	
hIgG1- LALAGA/D Q	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 510
hIgG1- LALAPG/D Q	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP PVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPG	SEQ ID NO: 511
hIgG1/DW	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLWVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP	SEQ ID NO: 512

	VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	
hIgG1- N297A/DW	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLWV LHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 513
hIgG1- D265A/DW	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVVA VSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLWV LHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 514
hIgG1- LALA/DW	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLWV LHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 515
hIgG1- LAGA/DW	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT	SEQ ID NO: 516

	YICNVNHHKPSNTKVDDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRDEPVTCTVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLWVHLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	
hIgG1- LALAGA/D W	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHHKPSNTKVDDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRDEPVTCTVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLWVHLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 517
hIgG1- LALAPG/D W	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHHKPSNTKVDDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRDEPVTCTVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLWVHLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP PVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPG	SEQ ID NO: 518
hIgG1/YD	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHHKPSNTKVDDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLYISRDEPVTCTVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD	SEQ ID NO: 519

	ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNH YTQKSLSLSPG	
hIgG1- N297A/YD	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLYISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 520
hIgG1- D265A/YD	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLYISRDPEVTCVVVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 521
hIgG1- LALA/YD	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAEEAAGG PSVFLFPPKPKDTLYISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 522

hIgG1-LAGA/YD	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLYISRDPETCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 523
hIgG1-LALAGA/YD	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLYISRDPETCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 524
hIgG1-LALAPG/YD	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLYISRDPETCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP PVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPG	SEQ ID NO: 525
hIgG1/QVV	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW	SEQ ID NO: 526

	YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	
hIgG1- N297A/QV V	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLQVLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 527
hIgG1- D265A/QV V	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 528
hIgG1- LALA/QVV	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTTPP	SEQ ID NO: 529

	VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	
hIgG1- LAGA/QV V	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVHLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTTPP VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 530
hIgG1- LALAGA/Q VV	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVHLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTTPP VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 531
hIgG1- LALAPG/Q VV	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVHLHVDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTTP PVLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPG	SEQ ID NO: 532
hIgG1/DDR VV	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT	SEQ ID NO: 533

	YICNVNHKPSNTKVDDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVDNAKTKPREEQYNSTYRVVSVLRLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	
hIgG1- N297A/DD RVV	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVDNAKTKPREEQYASTYRVVSVLRLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 534
hIgG1- D265A/DD RVV	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVVAVSHEDPEVKFNW YVDGVEVDNAKTKPREEQYNSTYRVVSVLRLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 535
hIgG1- LALA/DDR VV	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVDNAKTKPREEQYNSTYRVVSVLRLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD	SEQ ID NO: 536

	ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	
hIgG1- LAGA/DD RVV	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVDNAKTKPREEQYNSTYRVVSVLRLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 537
hIgG1- LALAGA/D DRVV	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVDNAKTKPREEQYNSTYRVVSVLRLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 538
hIgG1- LALAPG/D DRVV	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVDNAKTKPREEQYNSTYRVVSVLRLHVDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTPP PVLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPG	SEQ ID NO: 539

Heavy Chain hIgG1 c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 610
Heavy Chain hIgG4 c-terminal lysine variant	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTKYT CNVDHKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFCFSVMHEALHNHNTQKS LSLSLGKK	SEQ ID NO: 611
Heavy Chain IgG4-SP c-terminal lysine variant	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTKYT CNVDHKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFCFSVMHEALHNHNTQKS LSLSLGKK	SEQ ID NO: 612
Heavy Chain IgG4-SPLE c-terminal	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTKYT CNVDHKPSNTKVDKRVESKYGPPCPCPAPEELGGPSVFL FPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDG	SEQ ID NO: 613

lysine variant	VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKSLSLSLGKK	
Heavy Chain IgG2 c-terminal lysine variant	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTWSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSNFGTQTYTCNVDPKPSNTKVDKTKVERKCCVECPPEPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVS VLT VVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPK	SEQ ID NO: 614
Heavy Chain hIgG1-N297A c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGPPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV MHEALHNHYTQKSLSLSPGK	SEQ ID NO: 615
Heavy Chain hIgG1-D265A c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGPPSVFLFPPKPKDTLMISRTPEVTCVVA VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP	SEQ ID NO: 616

	VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	
Heavy Chain hIgG1-LALA c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHCPCPAPEAAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 617
Heavy Chain hIgG1-LAGA c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHCPCPAPELAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 618
Heavy Chain hIgG1-LALAGA c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHCPCPAPEAAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 619
Heavy Chain	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT	SEQ ID NO: 620

hIgG1-LALAPG c-terminal lysine variant	YICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP PVLDSDGSEFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	
Heavy Chain hIgG1-YTE c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 621
Heavy Chain hIgG1-N297A/YTE c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 622
Heavy Chain hIgG1-D265A/YTE c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLYITREPEVTCVVVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD	SEQ ID NO: 623

	ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNH YTQKSLSLSPGK	
Heavy Chain hIgG1- LALA/YTE c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 624
Heavy Chain hIgG1- LAGA/YTE c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 625
Heavy Chain hIgG1- LALAGA/Y TE c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 626

Heavy Chain hIgG1-LALAPG/Y TE c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP PVLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	SEQ ID NO: 627
Heavy Chain hIgG1-LS c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSH YTQKSLSLSPGK	SEQ ID NO: 628
Heavy Chain hIgG1-N297A/LS c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSH YTQKSLSLSPGK	SEQ ID NO: 629
Heavy Chain hIgG1-D265A/LS c-terminal	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVAVSHEDPEVKFNW	SEQ ID NO: 630

lysine variant	YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFCSSVLHEALHSH YTQKSLSLSPGK	
Heavy Chain hIgG1- LALA/LS c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFCSSVLHEALHSH YTQKSLSLSPGK	SEQ ID NO: 631
Heavy Chain hIgG1- LAGA/LS c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFCSSVLHEALHSH YTQKSLSLSPGK	SEQ ID NO: 632
Heavy Chain hIgG1- LALAGA/L S c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP	SEQ ID NO: 633

	VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSH YTQKSLSLSPGK	
Heavy Chain hIgG1-LALAPG/L S c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP PVLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSH YTQKSLSLSPGK	SEQ ID NO: 634
Heavy Chain hIgG1-DHS c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVDHHDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSH YTQKSLSLSPGK	SEQ ID NO: 635
Heavy Chain hIgG1-N297A/DH S c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLTVDHHDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSH YTQKSLSLSPGK	SEQ ID NO: 636
Heavy Chain	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT	SEQ ID NO: 637

hIgG1-D265A/DH S c-terminal lysine variant	YICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVAVVAVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVDHHDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHSHYTQKSLSLSPGK	
Heavy Chain hIgG1-LALA/DHS c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVDHHDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHSHYTQKSLSLSPK	SEQ ID NO: 638
Heavy Chain hIgG1-LAGA/DHS c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVDHHDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHSHYTQKSLSLSPGK	SEQ ID NO: 639
Heavy Chain hIgG1-LALAGA/DHS c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVDHHDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD	SEQ ID NO: 640

	ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHSHYTQKSLSLSPGK	
Heavy Chain hIgG1-LALAPG/D HS c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSGLVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVDHHDLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHSHTYQKSLSLSPGK	SEQ ID NO: 641
Heavy Chain IgG4-YTE c-terminal lysine variant	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTWNSGALTSGLVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYCNVDHKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFLFPPKPKDTLYITREPEVTCVVDVVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLGGK	SEQ ID NO: 642
Heavy Chain IgG4-SP/YTE c-terminal lysine variant	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTWNSGALTSGLVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYCNVDHKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFLFPPKPKDTLYITREPEVTCVVDVVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLGGK	SEQ ID NO: 643

Heavy Chain IgG4-SPLE/YTE c-terminal lysine variant	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTKTYT CNVDHKPSNTKVDKRVESKYGPPCPPCPAPEELGGPSVFL FPPKPKDTLYITREPEVTCVVVDVSQEDPEVQFNWYVDGV EVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKC KVSNGKLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSRLTVDKSRWQEGNVFSCSVMHREALHNHYTQKSL SLSLGKK	SEQ ID NO: 644
Heavy Chain IgG4-LS c-terminal lysine variant	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTKTYT CNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNGKLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVLHEALHSYTQKSLS LSLGKK	SEQ ID NO: 645
Heavy Chain IgG4-SP/LS c-terminal lysine variant	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTKTYT CNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNGKLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVLHEALHSHYTQKSL SLSLGKK	SEQ ID NO: 646
Heavy Chain IgG4-SPLE/LS c-	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTKTYT CNVDHKPSNTKVDKRVESKYGPPCPPCPAPEELGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG	SEQ ID NO: 647

terminal lysine variant	VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS GSFFLYSRLTVDKSRWQEGNVFSCSVLHEALHSHYTQKSL SLSLGKK	
Heavy Chain IgG4-DHS c-terminal lysine variant	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGKTKYT CNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVDHHDWLNGKEY KCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS DGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHSHYTQK SLSLSLGKK	SEQ ID NO: 648
Heavy Chain IgG4- SP/DHS c- terminal lysine variant	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGKTKYT CNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVDHHDWLNGKEY KCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS DGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHSHYTQK SLSLSLGKK	SEQ ID NO: 649
Heavy Chain IgG4- SPLE/DHS c-terminal lysine variant	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGKTKYT CNVDHKPSNTKVDKRVESKYGPPCPSCPAPEELGGPSVFL FPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVDHHDWLNGKEY KCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS	SEQ ID NO: 650

	DGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHSHYTQK SLSLSLGKK	
Heavy Chain IgG2-YTE c-terminal lysine variant	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYT CNVDHKPSNTKVDKTVKCCVECPAPPVAGPSVFLF PPKPKDTLYITREPEVTCVVVDVSHEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTFRVVSVLTVVHQQDWLNGKEYKCK VSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPMLDSDGS FFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSL SPK	SEQ ID NO: 651
Heavy Chain IgG2-LS c- terminal lysine variant	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYT CNVDHKPSNTKVDKTVKCCVECPAPPVAGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGV EVHNAKTKPREEQFNSTFRVVSVLTVVHQQDWLNGKEYKC KVSNNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPMLDSDG SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPK	SEQ ID NO: 652
Heavy Chain IgG2-DHS c-terminal lysine variant	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYT CNVDHKPSNTKVDKTVKCCVECPAPPVAGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGV EVHNAKTKPREEQFNSTFRVVSVLTVDHHDWLNGKEYKC KVSNNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPMLDSDG SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHSHYTQKSL SLSPK	SEQ ID NO: 653
hIgG1-LA c-terminal	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQT	SEQ ID NO: 654

lysine variant	YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHAH YTQKSLSLSPGK	
hIgG1- N297A/LA c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHAH YTQKSLSLSPGK	SEQ ID NO: 655
hIgG1- D265A/LA c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHAH YTQKSLSLSPGK	SEQ ID NO: 656
hIgG1- LALA/LA c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD	SEQ ID NO: 657

	ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHAH YTQKSLSLSPGK	
hIgG1- LAGA/LA c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHAH YTQKSLSLSPGK	SEQ ID NO: 658
hIgG1- LALAGA/L A c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHAH YTQKSLSLSPGK	SEQ ID NO: 659
hIgG1- LALAPG/L A c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP PVLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHA HYTQKSLSLSPGK	SEQ ID NO: 660

hIgG1- N434A c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHAH YTQKSLSLSPGK	SEQ ID NO: 661
hIgG1- N297A/ N434A c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHAH YTQKSLSLSPGK	SEQ ID NO: 662
hIgG1- D265A/ N434A c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHAH YTQKSLSLSPGK	SEQ ID NO: 663
hIgG1- LALA/ N434A c- terminal	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW	SEQ ID NO: 664

lysine variant	YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHAH YTQKSLSLSPGK	
hIgG1- LAGA/ N434A c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHAH YTQKSLSLSPGK	SEQ ID NO: 665
hIgG1- LALAGA/ N434A c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHAH YTQKSLSLSPGK	SEQ ID NO: 666
hIgG1- LALAPG/ N434A c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP	SEQ ID NO: 667

	PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHA HYTQKSLSLSPGK	
hIgG1- N434W c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHW HYTQKSLSLSPGK	SEQ ID NO: 668
hIgG1- N297A/ N434W c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHW HYTQKSLSLSPGK	SEQ ID NO: 669
hIgG1- D265A/ N434W c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHW HYTQKSLSLSPGK	SEQ ID NO: 670
hIgG1- LALA/	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT	SEQ ID NO: 671

N434W c-terminal lysine variant	YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHW HYTQKSLSLSPGK	
hIgG1-LAGA/ N434W c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHW HYTQKSLSLSPGK	SEQ ID NO: 672
hIgG1-LALAGA/ N434W c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHW HYTQKSLSLSPGK	SEQ ID NO: 673
hIgG1-LALAPG/ N434W c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR	SEQ ID NO: 674

	DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHW HYTQKSLSLSPGK	
hIgG1/DQ c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 675
hIgG1- N297A/DQ c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLQVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 676
hIgG1- D265A/DQ c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 677

hIgG1- LALA/DQ c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVHLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 678
hIgG1- LAGA/DQ c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVHLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 679
hIgG1- LALAGA/D Q c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVHLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 680
hIgG1- LALAPG/D Q c-terminal	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW	SEQ ID NO: 681

lysine variant	YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP PVLDSGDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHN HYTQKSLSLSPGK	
hIgG1/DW c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLWVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 682
hIgG1- N297A/DW c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLWVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 683
hIgG1- D265A/DW c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLWVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP	SEQ ID NO: 684

	VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	
hIgG1- LALA/DW c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLWV LHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 685
hIgG1- LAGA/DW c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLWV LHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 686
hIgG1- LALAGA/D W c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLWV LHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 687
hIgG1- LALAPG/D	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT	SEQ ID NO: 688

W c-terminal lysine variant	YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLWV LHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP PVLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	
hIgG1/YD c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLYISRDEPVTCTVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 689
hIgG1-N297A/YD c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLYISRDEPVTCTVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 690
hIgG1-D265A/YD c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLYISRDEPVTCTVVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN	SEQ ID NO: 691

	GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	
hIgG1- LALA/YD c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLYISRDEPVTCTVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 692
hIgG1- LAGA/YD c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLYISRDEPVTCTVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 693
hIgG1- LALAGA/Y D c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLYISRDEPVTCTVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 694

hIgG1- LALAPG/Y D c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLYISRDEPVTCTVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP PVLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	SEQ ID NO: 695
hIgG1/QVV c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 696
hIgG1- N297A/QV V c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLQVLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 697
hIgG1- D265A/QV V c-terminal	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVAVSHEDPEVKFNW	SEQ ID NO: 698

lysine variant	YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	
hIgG1- LALA/QVV c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 699
hIgG1- LAGA/QV V c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 700
hIgG1- LALAGA/Q VV c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTPP	SEQ ID NO: 701

	VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	
hIgG1- LALAPG/Q VV c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHVDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTPP PVLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	SEQ ID NO: 702
hIgG1/DDR VV c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVDVSHEDPEVKFNW YVDGVEVDNAKTKPREEQYNSTYRVVSVLRVLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTPP VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 703
hIgG1- N297A/DD RVV c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVDVSHEDPEVKFNW YVDGVEVDNAKTKPREEQYASTYRVVSVLRVLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTPP VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 704
hIgG1- D265A/DD	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT	SEQ ID NO: 705

RVV c-terminal lysine variant	YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRDPEVTCVVVAVSHEDPEVKFNWYVDGVEVDNAKTKPREEQYNSTYRVVSVLRLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	
hIgG1-LALA/DDR VV c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVDNAKTKPREEQYNSTYRVVSVLRLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 706
hIgG1-LAGA/DD RVV c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVDNAKTKPREEQYNSTYRVVSVLRLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 707
hIgG1-LALAGA/D DRVV c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVDNAKTKPREEQYNSTYRVVSVLRLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD	SEQ ID NO: 708

	ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTTPP VLDS DGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNH YTQKSLSLSPGK	
hIgG1- LALAPG/D DRVV c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVDNAKTKPREEQYNSTYRVVSVLRLHVDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTTP PVLDS DGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHN HYTQKSLSLSPGK	SEQ ID NO: 709

WHAT IS CLAIMED IS:

1. A formulation comprising:

- (a) an interleukin 13 (IL-13) antibody present at a concentration between 140 mg/mL and 290 mg/mL;
 - (b) a histidine buffer, an acetate buffer, or a succinate buffer;
 - (c) arginine and/or methionine or a salt solution thereof; and
 - (d) a polysorbate or a poloxamer,
- wherein the formulation is at pH 5.0 to 7.0.

2. A formulation comprising:

- (a) an IL-13 antibody present at a concentration between 140 mg/mL and 290 mg/mL;
 - (b) a histidine buffer, an acetate buffer, or a succinate buffer;
 - (c) arginine and/or methionine or a salt solution thereof; and
 - (d) a polysorbate or a poloxamer,
- wherein the formulation is at pH 5.0 to 7.0, and
- wherein the IL-13 antibody comprises:
- (i) a variable heavy (VH) chain sequence comprising three heavy chain CDR sequences, CDR-H1, CDR-H2, and CDR-H3; and
 - (ii) a variable light (VL) chain sequence comprising three light chain CDR sequences, CDR-L1, CDR-L2, and CDR-L3; wherein:
 - a. CDR-H1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 58-99 and 121;
 - b. CDR-H2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 100-111;
 - c. CDR-H3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 112-120 and 130-140,
 - d. CDR-L1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 141-144 and 149-152,

- e. CDR-L2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 153-158 and the amino acid sequence LAS; and
- f. CDR-L3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 165-172.

3. A formulation comprising:

- (a) an IL-13 antibody present at a concentration between 140 mg/mL and 290 mg/mL;
 - (b) a histidine buffer, an acetate buffer, or a succinate buffer;
 - (c) arginine and/or methionine or a salt solution thereof; and
 - (d) a polysorbate or a poloxamer,
- wherein the formulation is at pH 5.0 to 7.0,
- wherein the IL-13 antibody comprises:
- (i) a variable heavy (VH) chain sequence comprising three heavy chain CDR sequences, CDR-H1, CDR-H2, and CDR-H3; and
 - (ii) a variable light (VL) chain sequence comprising three light chain CDR sequences, CDR-L1, CDR-L2, and CDR-L3; wherein:
 - a. CDR-H1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 58, SEQ ID NO: 68, and SEQ ID NO: 85;
 - b. CDR-H2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 100, SEQ ID NO: 104, and SEQ ID NO: 108;
 - c. CDR-H3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 112 and SEQ ID NO: 130,
 - d. CDR-L1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 141 and SEQ ID NO: 149,
 - e. CDR-L2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 153 and SEQ ID NO: 164; and
 - f. CDR-L3 comprises the sequence set forth in SEQ ID NO: 165.

4. A formulation comprising:

- (a) an IL-13 antibody present at a concentration between 140 mg/mL and 290 mg/mL;
- (b) a histidine buffer, an acetate buffer, or a succinate buffer;
- (c) arginine and/or methionine or a salt solution thereof; and
- (d) a polysorbate or a poloxamer,

wherein the formulation is at pH 5.0 to 7.0,

wherein the IL-13 antibody comprises:

(i) a variable heavy (VH) chain sequence comprising three heavy chain CDR sequences, CDR-H1, CDR-H2, and CDR-H3; and

(ii) a variable light (VL) chain sequence comprising three light chain CDR sequences, CDR-L1, CDR-L2, and CDR-L3; wherein:

- a. CDR-H1 comprises the sequence set forth in SEQ ID NO: 58 or 67;
- b. CDR-H2 comprises the sequence set forth in SEQ ID NO: 100 or 104;
- c. CDR-H3 comprises the sequence set forth in SEQ ID NO: 112;
- d. CDR-L1 comprises the sequence set forth in SEQ ID NO: 141 or 149;
- e. CDR-L2 comprises the sequence set forth in SEQ ID NO: 153 or 596; and
- f. CDR-L3 comprises the sequence set forth in SEQ ID NO: 165.

5. The formulation of any one of the above claims, wherein the IL-13 antibody has a means for extending the half-life of the IL-13 antibody.

6. The formulation of claim 5, wherein the means comprises at least one amino acid modification in the IL-13 antibody.

7. The formulation of any one of the above claims, wherein the formulation further comprises a metal ion chelator.

8. The formulation of claim 7, wherein the metal ion chelator is EDTA or salt thereof.
9. The formulation of any one of the above claims, wherein the formulation further comprises a sugar or sugar alcohol.
10. The formulation of any one of the above claims, wherein the IL-13 antibody is present at a concentration between 160 mg/mL and 250 mg/mL.
11. The formulation of claim 10, wherein the IL-13 antibody is present at a concentration of about 180 mg/mL.
12. The formulation of claim 10, wherein the IL-13 antibody is present at a concentration of about 200 mg/mL.
13. The formulation of any one of the above claims, wherein the histidine buffer, acetate buffer, or succinate buffer is at a concentration between 5 mM and 20 mM.
14. The formulation of any one of the above claims, wherein the histidine buffer, acetate buffer, or succinate buffer is at a concentration of about 10 mM.
15. The formulation of any one of the above claims, wherein the histidine buffer comprises a histidine and a histidine salt.
16. The formulation of claim 15, wherein the histidine is L-histidine.
17. The formulation of claim 15 or 16, wherein the histidine salt is L-histidine HCl monohydrate.
18. The formulation of any one of the above claims, wherein the formulation comprises methionine, and wherein the methionine is L-methionine.

19. The formulation of claim 18, wherein the L-methionine is at a concentration between 1 mM and 15 mM.
20. The formulation of claim 19, wherein the L-methionine is at a concentration of about 10 mM.
21. The formulation of any one of the above claims, wherein the formulation comprises arginine, and wherein the arginine is L-arginine.
22. The formulation of claim 21, wherein the formulation comprises an L-arginine salt solution.
23. The formulation of claim 22, wherein the L-arginine salt solution comprises HCl monohydrate.
24. The formulation of claim 22 or 23, wherein the L-arginine salt solution is at a concentration between 40 mM and 250 mM.
25. The formulation of claim 24, wherein the L-arginine salt solution is at a concentration of about 80 mM.
26. The formulation of claim 24, wherein the L-arginine salt solution is at a concentration of about 120 mM.
27. The formulation of any one of the above claims, wherein the formulation comprises a polysorbate, and wherein the polysorbate is at a concentration between 0.005% w/v and 0.15% w/v.
28. The formulation of any one of the above claims, wherein the polysorbate is at a concentration of about 0.05% w/v.

29. The formulation of any one of the above claims, wherein the polysorbate is polysorbate 20, polysorbate 40, polysorbate 60, or polysorbate 80.
30. The formulation of claim 29, wherein the polysorbate is polysorbate 80.
31. The formulation of any one of the above claims, wherein the formulation comprises a poloxamer, and wherein the poloxamer is poloxamer 188.
32. The formulation of any one of the above claims, wherein the pH is between 5.5 and 7.0.
33. The formulation of any one of the above claims, wherein the pH is between 5.5 and 6.5.
34. The formulation of claim 33, wherein the pH is about 5.8 or about 6.0.
35. A formulation comprising:
- (a) an IL-13 antibody present at a concentration of about 180 mg/mL;
 - (b) a histidine buffer at a concentration of about 10 mM, wherein the histidine buffer comprises L-histidine and L-histidine HCl monohydrate;
 - (c) an L-arginine salt solution at a concentration of about 120 mM;
 - (d) L-methionine at a concentration of about 10 mM; and
 - (e) polysorbate 80 at a concentration of about 0.05% w/v,
- wherein the formulation is at a pH of about 5.8.
36. A formulation comprising:
- (a) an IL-13 antibody present at a concentration of about 180 mg/mL;
 - (b) a histidine buffer at a concentration of about 10 mM, wherein the histidine buffer comprises L-histidine and L-histidine HCl monohydrate;
 - (c) an L-arginine salt solution at a concentration of about 80 mM;
 - (d) L-methionine at a concentration of about 10 mM; and
 - (e) polysorbate 80 at a concentration of about 0.05% w/v,
- wherein the formulation is at a pH of about 5.8.

37. A formulation comprising:
- (a) an IL-13 antibody present at a concentration of about 200 mg/mL;
 - (b) a histidine buffer at a concentration of about 10 mM, wherein the histidine buffer comprises L-histidine and L-histidine HCl monohydrate;
 - (c) an L-arginine salt solution at a concentration of about 120 mM;
 - (d) L-methionine at a concentration of about 10 mM; and
 - (e) polysorbate 80 at a concentration of about 0.05% w/v, wherein the formulation is at a pH of about 5.8.
38. The formulation of claim 0, wherein the formulation further comprises:
- (f) a sugar or sugar alcohol.
39. The formulation of any one of claims 9-38, wherein the sugar or sugar alcohol is at a concentration between 1% w/v and 8% w/v.
40. The formulation of claim 39, wherein the sugar or sugar alcohol is at a concentration of about 3% w/v.
41. The formulation of any one of claims 9-40, wherein the sugar or sugar alcohol is a disaccharide.
42. The formulation of claim 41, wherein the disaccharide is sucrose.
43. The formulation of any one of claims 1 and 5-42 wherein the IL-13 antibody comprises:
- (a) a variable heavy (VH) chain sequence comprising three heavy chain CDR sequences, CDR-H1, CDR-H2, and CDR-H3; and
 - (b) a variable light (VL) chain sequence comprising three light chain CDR sequences, CDR-L1, CDR-L2, and CDR-L3; wherein:
 - a. CDR-H1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 58-99 and 121;

- b. CDR-H2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 100-111;
- c. CDR-H3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 112-120 and 130-140,
- d. CDR-L1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 141-144 and 149-152,
- e. CDR-L2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 153-158 and the amino acid sequence LAS; and
- f. CDR-L3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 165-172.

44. The formulation of claim 43, wherein:

- a. CDR-H1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 58, SEQ ID NO: 68, and SEQ ID NO: 85;
- b. CDR-H2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 100, SEQ ID NO: 104, and SEQ ID NO: 108;
- c. CDR-H3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 112 and SEQ ID NO: 130,
- d. CDR-L1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 141 and SEQ ID NO: 149,
- e. CDR-L2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 153 and SEQ ID NO: 164; and
- f. CDR-L3 comprises the sequence set forth in SEQ ID NO: 165.

45. The formulation of claim 43, wherein the IL-13 antibody comprises:

- a. CDR-H1 comprising a sequence selected from the sequences set forth in any one of SEQ ID NOs: 58-66;
- b. CDR-H2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 100-103;
- c. CDR-H3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 112-120,

- d. CDR-L1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 141-144,
 - e. CDR-L2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 153-158; and
 - f. CDR-L3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 165-172.
46. The formulation of claim 43, wherein the IL-13 antibody comprises:
- a. CDR-H1 comprising a sequence selected from the sequences set forth in any one of SEQ ID NOs: 67-83;
 - b. CDR-H2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 104-107;
 - c. CDR-H3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 112-120,
 - d. CDR-L1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 141-144,
 - e. CDR-L2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 153-158; and
 - f. CDR-L3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 165-172.
47. The formulation of claim 43, wherein the IL-13 antibody comprises:
- a. CDR-H1 comprising a sequence selected from the sequences set forth in any one of SEQ ID NOs: 84-99 and 121;
 - b. CDR-H2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 108-111;
 - c. CDR-H3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 130-140,
 - d. CDR-L1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 149-152,
 - e. CDR-L2 comprises the amino acid sequence LAS; and

f. CDR-L3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 165-172.

48. The formulation of claim 43, wherein the IL-13 antibody does not comprise:

- (a) CDR-H1 set forth in SEQ ID NO: 58; CDR-H2 set forth in SEQ ID NO: 100; CDR-H3 set forth in SEQ ID NO: 112; CDR-L1 set forth in SEQ ID NO: 141; CDR-L2 set forth in SEQ ID NO: 153; and CDR-L3 set forth in SEQ ID NO: 165; or
- (b) CDR-H1 set forth in SEQ ID NO: 67; CDR-H2 set forth in SEQ ID NO: 104; CDR-H3 set forth in SEQ ID NO: 112; CDR-L1 set forth in SEQ ID NO: 141; CDR-L2 set forth in SEQ ID NO: 153; and CDR-L3 set forth in SEQ ID NO: 165; or
- (c) CDR-H1 set forth in SEQ ID NO: 84; CDR-H2 set forth in SEQ ID NO: 108; CDR-H3 set forth in SEQ ID NO: 130; CDR-L1 set forth in SEQ ID NO: 149; CDR-L2 set forth in the amino acid sequence LAS; and CDR-L3 set forth in SEQ ID NO: 165.

49. The formulation of claim 43, wherein the IL-13 antibody present does not comprise any combination of:

- (a) a CDR-H1 set forth in any of SEQ ID NOs: 58, 67, or 84;
- (b) a CDR-H2 set forth in any of SEQ ID NOs: 100, 104, or 108;
- (c) a CDR-H3 set forth in any of SEQ ID NOs: 112 or 130;
- (d) a CDR-L1 set forth in any of SEQ ID NOs: 141 or 149;
- (e) a CDR-L2 set forth in any of SEQ ID NOs: 153 or 154; and
- (f) a CDR-L3 set forth in SEQ ID NO: 165.

50. The formulation of claim 43, wherein the IL-13 antibody comprises a VH sequence having at least 90%, 95%, 96%, 97%, 98%, 99% or 100% identity to an amino acid sequence set forth in SEQ ID NOs: 1-32.

51. The formulation of claim 43, wherein the IL-13 antibody comprises a VL sequence having at least 90%, 95%, 96%, 97%, 98%, 99% or 100% identity to an amino acid sequence set forth in SEQ ID NOs: 33-57.

52. The formulation of claim 43, wherein the IL-13 antibody comprises a VH sequence having at least 90%, 95%, 96%, 97%, 98%, 99% or 100% identity to an amino acid sequence set forth in SEQ ID NOs: 1-32 and a VL sequence having at least 90%, 95%, 96%, 97%, 98%, 99% or 100% identity to an amino acid sequence set forth in of SEQ ID NOs: 33-57.

53. The formulation of any one of the above claims, wherein the IL-13 antibody comprises a VH comprising an amino acid sequence having at least 90%, 95%, 96%, 97%, 98%, 99% or 100% identity to an amino acid sequence set forth in SEQ ID NO: 3 and a VL comprising an amino acid sequence having at least 90%, 95%, 96%, 97%, 98%, 99% or 100% identity to an amino acid sequence set forth in SEQ ID NO: 39.

54. The formulation of any one of the above claims, wherein the IL-13 antibody is a humanized, human, or chimeric antibody.

55. The formulation of claim 54, wherein the IL-13 antibody is a humanized antibody.

56. The formulation of any one of the above claims, wherein the IL-13 antibody comprises a heavy chain human constant region of a class selected from IgG, IgA, IgD, IgE, and IgM.

57. The formulation of any one of the above claims, wherein the IL-13 antibody comprises a human Fc region comprising a human heavy chain constant region of the class IgG and a subclass selected from IgG1, IgG2, IgG3, and IgG4.

58. The formulation of claim 57, wherein the human Fc region comprises a human IgG1 Fc.

59. The formulation of claim 57, wherein the human Fc region comprises a human IgG4 Fc.

60. The formulation of claim 57, wherein the human Fc region comprises a human IgG2 Fc.

61. The formulation of any one of the above claims, wherein the IL-13 antibody comprises a heavy chain comprising a constant heavy chain sequence selected from the sequences set forth in

any one of SEQ ID NOs: 425-468, 484-539, and 610-709, optionally wherein the IL-13 antibody comprises a heavy chain comprising a constant heavy chain sequence selected from the sequences set forth in any one of SEQ ID NOs: 610, 615-641, and 654-709.

62. The formulation of any one of the above claims, wherein the IL-13 antibody comprises an Fc region comprising one or more amino acid substitutions, wherein the one or more substitutions result in a change in antibody half-life, ADCC activity, ADCP activity, or CDC activity as compared to an otherwise equivalent antibody comprising an Fc without the one or more substitutions.

63. The formulation of any one of the above claims, wherein the IL-13 antibody comprises an Fc region, and wherein the Fc region binds to Neonatal Fc receptor (FcRn).

64. The formulation of any one of the above claims, wherein the IL-13 antibody is a monoclonal antibody.

65. The formulation of any one of the above claims, wherein the IL-13 antibody binds an IL-13 sequence selected from a sequence set forth in any one of SEQ ID NOs: 472-475.

66. The formulation of any one of the above claims, wherein the IL-13 antibody does not have a heavy chain variable region sequence set forth in SEQ ID NO: 470.

67. A vial, bag, or bottle comprising the formulation of any one of claims 1-66.

68. The vial of claim 67, wherein the vial is a prefilled syringe or injector cartridge.

69. The vial of claim 67 or 68, wherein an extractable volume of the vial is between 1.0 mL and 10.0 mL.

70. The vial of claim 69, wherein the extractable volume of the vial is about 3.0-5.5 mL.

71. A composition comprising the formulation or vial of any one of the above claims for use in the treatment of an inflammatory disorder or disease.
72. The composition of claim 71, for use in the treatment of atopic dermatitis.
73. The composition of claim 72, wherein the treatment reduces disease severity in a subject, and wherein disease severity is assessed by an Atopic Dermatitis Disease Severity Outcome Measure.
74. The composition of claim 71, for use in the treatment of an inflammatory disorder or disease selected from the group consisting of asthma, idiopathic pulmonary fibrosis, alopecia areata, chronic sinusitis with nasal polyps, Chronic Rhinosinusitis without Nasal Polyps (CRSsNP), eosinophilic esophagitis (EoE), an Eosinophilic gastrointestinal disorder or disease (ENID) selected from the group consisting of Eosinophilic Gastritis (EoG), Eosinophilic Enteritis (EoN), Eosinophilic Colitis (EoC), and Eosinophilic Gastroenteritis (EGE), Churg-Strauss syndrome/Eosinophilic granulomatosis with polyangiitis (EGPA), Prurigo Nodularis (PN), of Chronic Spontaneous Urticaria (CSU), Chronic Pruritis of Unknown Origin (CPUO), Bullous Pemphigoid (BP), Cold Inducible Urticaria (ColdU), Allergic Fungal Rhinosinusitis (AFRS), Allergic Bronchopulmonary Aspergillosis (ABPA), and Chronic Obstructive Pulmonary Disease (COPD).
75. A method for treating an inflammatory disorder or disease in a mammalian subject in need thereof, the method comprising administering to the mammalian subject a therapeutically effective amount of the formulation of any one of claims 1-66 or the vial of any one of claims 67-70.
76. The method of claim 75, wherein the inflammatory disorder or disease is atopic dermatitis.
77. The method of claim 75, wherein the inflammatory disorder or disease is selected from the group consisting of asthma, idiopathic pulmonary fibrosis, alopecia areata, chronic sinusitis with nasal polyps, Chronic Rhinosinusitis without Nasal Polyps (CRSsNP), eosinophilic esophagitis

(EoE), an Eosinophilic gastrointestinal disorder or disease (ENID) selected from the group consisting of Eosinophilic Gastritis (EoG), Eosinophilic Enteritis (EoN), Eosinophilic Colitis (EoC), and Eosinophilic Gastroenteritis (EGE), Churg-Strauss syndrome/Eosinophilic granulomatosis with polyangiitis (EGPA), Prurigo Nodularis (PN), of Chronic Spontaneous Urticaria (CSU), Chronic Pruritis of Unknown Origin (CPUO), Bullous Pemphigoid (BP), Cold Inducible Urticaria (ColdU), Allergic Fungal Rhinosinusitis (AFRS), Allergic Bronchopulmonary Aspergillosis (ABPA), and Chronic Obstructive Pulmonary Disease (COPD).

78. A method for treating a pathology associated with elevated levels of IL-13 in a mammalian subject in need thereof, the method comprising administering to the mammalian subject a therapeutically effective amount of the formulation of any one of claims 1-66 or the vial of any one of claims 67-70.

79. A diafiltration buffer comprising:

- (a) a histidine buffer; and
 - (b) arginine or a salt solution thereof,
- wherein the diafiltration buffer is at pH of from 5.2 to 6.1.

80. The diafiltration buffer of claim 79, wherein the histidine buffer comprises a histidine and a histidine salt.

81. The diafiltration buffer of claim 80, wherein the histidine is L-histidine.

82. The diafiltration buffer of claim 80 or 81, wherein the histidine salt is L-histidine HCl monohydrate.

83. The diafiltration buffer of any one of claims 79-82, wherein the formulation comprises arginine, and wherein the arginine is L-arginine.

84. The diafiltration buffer of claim 83, wherein the formulation comprises an L-arginine salt solution.

85. The diafiltration buffer of claim 84, wherein the L-arginine salt solution salt solution comprises HCl monohydrate.

86. The diafiltration buffer of claim 84 or 85, wherein the L-arginine salt solution is at a concentration between 40 mM and 200 mM.

87. The diafiltration buffer of 86, wherein the L-arginine salt solution is at a concentration of about 50 mM.

88. The diafiltration buffer of 86, wherein the L-arginine salt solution is at a concentration of about 100 mM.

89. The diafiltration buffer of 86, wherein the L-arginine salt solution is at a concentration of about 120 mM.

90. The diafiltration buffer of any one of claims 79-89, wherein the pH is from about 5.5 to about 7.0.

91. The diafiltration buffer of claim 90, wherein the pH is about 5.8 or 6.0.

92. A method of manufacturing an intermediate preparation of an interleukin 13 (IL-13) antibody comprising:

- (a) obtaining a purified preparation of the IL-13 antibody; and
- (b) adjusting the matrix of the purified preparation of step (a), wherein adjusting the matrix comprises performing Ultrafiltration and Diafiltration (UFDF) with the diafiltration buffer of any one of claims 80-92, thereby obtaining the intermediate preparation of the IL-13 antibody.

93. The method of manufacturing of claim 92, wherein the intermediate preparation of the IL-13 antibody has a higher concentration of the IL-13 antibody relative to the purified preparation.

94. The method of manufacturing of claim 92 or 93, wherein the method of manufacturing further comprises:

(c) formulating the intermediate preparation to obtain a formulation of the IL-13 antibody.

95. The method of manufacturing of claim 94, wherein the formulation of the IL-13 antibody comprises the formulation of any one of claims 1-66.

96. A formulation comprising:

- (a) an interleukin 13 (IL-13) antibody present at a concentration between 140 mg/mL and 290 mg/mL;
 - (b) a histidine buffer, an acetate buffer, or a succinate buffer;
 - (c) arginine and/or methionine or a salt solution thereof;
 - (d) a polysorbate or a poloxamer; and
 - (e) a metal ion chelator,
- wherein the formulation is at pH 5.0 to 7.0.

97. The formulation of claim 96, which comprises:

- (a) an interleukin 13 (IL-13) antibody present at a concentration of about 180 mg/mL;
 - (b) a histidine buffer at a concentration of about 10 mM, wherein the histidine buffer comprises L-histidine and L-histidine HCl monohydrate;
 - (c) an L-arginine salt solution at a concentration of about 120 mM;
 - (d) L-methionine at a concentration of about 10 mM;
 - (e) polysorbate 80 at a concentration of about 0.05% w/v; and
 - (f) EDTA or salt thereof at a concentration of about 0.05 mM,
- wherein the formulation is at a pH of about 6.0

98. A formulation comprising:

- (a) an interleukin 13 (IL-13) antibody present at a concentration between 140 mg/mL and 290 mg/mL;
 - (b) a histidine buffer, an acetate buffer, or a succinate buffer;
 - (c) arginine and/or methionine or a salt solution thereof; and
 - (d) a poloxamer;
- wherein the formulation is at pH 5.0 to 7.0.

99. The formulation of claim 98, which comprises:

- (a) an interleukin 13 (IL-13) antibody present at a concentration of about 180 mg/mL;
 - (b) a histidine buffer at a concentration of about 10 mM, wherein the histidine buffer comprises L-histidine and L-histidine HCl monohydrate;
 - (c) an L-arginine salt solution at a concentration of about 120 mM;
 - (d) L-methionine at a concentration of about 10 mM; and
 - (e) poloxamer 188 at a concentration of about 0.5 mg/ml;
- wherein the formulation is at a pH of about 6.0.

100. The formulation of any one of claims 96-99, wherein the IL-13 antibody comprises:

- (i) a variable heavy (VH) chain sequence comprising three heavy chain CDR sequences, CDR-H1, CDR-H2, and CDR-H3; and
- (ii) a variable light (VL) chain sequence comprising three light chain CDR sequences, CDR-L1, CDR-L2, and CDR-L3; wherein:
 - a. CDR-H1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 58-99 and 121;
 - b. CDR-H2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 100-111;
 - c. CDR-H3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 112-120 and 130-140,
 - d. CDR-L1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 141-144 and 149-152,

- e. CDR-L2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 153-158 and the amino acid sequence LAS; and
- f. CDR-L3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NOs: 165-172.

101. The formulation of any one of claims 96-99, wherein the IL-13 antibody comprises:

- (i) a variable heavy (VH) chain sequence comprising three heavy chain CDR sequences, CDR-H1, CDR-H2, and CDR-H3; and
- (ii) a variable light (VL) chain sequence comprising three light chain CDR sequences, CDR-L1, CDR-L2, and CDR-L3; wherein:
 - a. CDR-H1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 58, SEQ ID NO: 68, and SEQ ID NO: 85;
 - b. CDR-H2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 100, SEQ ID NO: 104, and SEQ ID NO: 108;
 - c. CDR-H3 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 112 and SEQ ID NO: 130,
 - d. CDR-L1 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 141 and SEQ ID NO: 149,
 - e. CDR-L2 comprises a sequence selected from the sequences set forth in any one of SEQ ID NO: 153 and SEQ ID NO: 164; and
 - f. CDR-L3 comprises the sequence set forth in SEQ ID NO: 165.

102. The formulation of any one of claims 96-99, wherein the IL-13 antibody comprises:

- (i) a variable heavy (VH) chain sequence comprising three heavy chain CDR sequences, CDR-H1, CDR-H2, and CDR-H3; and
- (ii) a variable light (VL) chain sequence comprising three light chain CDR sequences, CDR-L1, CDR-L2, and CDR-L3; wherein:
 - a. CDR-H1 comprises the sequence set forth in SEQ ID NO: 58 or 67;

- b. CDR-H2 comprises the sequence set forth in SEQ ID NO: 100 or 104;
- c. CDR-H3 comprises the sequence set forth in SEQ ID NO: 112;
- d. CDR-L1 comprises the sequence set forth in SEQ ID NO: 141 or 149;
- e. CDR-L2 comprises the sequence set forth in SEQ ID NO: 153 or 596; and
- f. CDR-L3 comprises the sequence set forth in SEQ ID NO: 165.

103. The formulation of claim 102, wherein the IL-13 antibody comprises a means for extending the half-life of the IL-13 antibody.

104. The formulation of claim 103, wherein the means comprises at least one amino acid modification in the IL-13 antibody.

105. The formulation of any one of claims 96-104, wherein the formulation further comprises a sugar or sugar alcohol.