

PHARMACEUTICAL COMPOSITIONS OF ANTI-IL-13 ANTIBODIES WITH AND WITHOUT C-TERMINAL LYSINE

Related Applications

[0001] This application claims the benefit of U.S. Provisional Patent Application No. 63/612900 (filed on December 20, 2023) the disclosure of which is incorporated by reference herein in its entirety.

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, compositions comprising anti-IL-13 antibodies suitable for administration to patients remains an unmet need.

Summary

[0004] Human IgG heavy chain sequences encode a C-terminal lysine residue. Due to the actions of cellular carboxypeptidases, most, but not all, mature antibody molecules recovered from recombinant cell culture production lack a C-terminal lysine on their heavy chains. Without wishing to be bound by theory, it is contemplated that the resulting heterogeneity of C-terminal lysine levels observed in recombinant monoclonal antibodies is due to incomplete processing (Owen *et al.* (2023) *J. Biotechnol.* 10;374:38-48). Following human or animal administration, the remaining C-terminal lysine is subject to additional cleavage by carboxypeptidases present in serum (Cai *et al.* (2011) *Biotechnol. Bioeng.* 108(2):404-412) so even lower levels are typically observed *in vivo*.

[0005] The level of C-terminal lysine in antibodies produced in recombinant cell lines can vary based on the cell line used and the cell culture process conditions (Dick *et al.* (2008) *Biotechnol. Bioeng.* 100(6):1132-1143; Shah *et al.* (2022) *J. Pharm. Sci.* 111(9):2445-2450). For example, C-terminal lysine levels in Chinese Hamster Ovary (CHO) cell lines are typically low (<20%) and often <5% of the original level.

[0006] In certain aspects, the present disclosure relates to a composition comprising a mixture of anti-interleukin 13 (IL-13) antibodies, wherein the mixture comprises a) C-terminal anti IL-13 antibodies comprising at least one heavy chain having a C-terminal lysine (also referred to herein as “C-terminal lysine antibodies” or “C-terminal antibodies”), and b) non-C-terminal anti IL-13 antibodies otherwise identical to the C-terminal anti IL-13 antibodies but lacking the C-terminal lysine (also referred to herein as “non-C-terminal lysine antibodies” or “non-C-terminal antibodies”), wherein each of the non-C-terminal and C-terminal antibodies 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 SEQ ID NOs: 58-99 and 121;

(b) CDR-H2 comprises a sequence selected from the sequences set forth in SEQ ID NOs: 100-111;

(c) CDR-H3 comprises a sequence selected from the sequences set forth in SEQ ID NOs: 112-120 and 130-140,

(d) CDR-L1 comprises a sequence selected from the sequences set forth in SEQ ID NOs: 141-144 and 149-152,

(e) CDR-L2 comprises a sequence selected from the sequences set forth in 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 SEQ ID NOs: 165-172, and

wherein each C-terminal antibody having a C-terminal lysine comprises a heavy chain constant domain comprising a sequence selected from the sequences set forth in SEQ ID NOs: 610-709.

[0007] In certain embodiments, between about 0.01% and about 50% of the antibodies are C-terminal antibodies. In certain embodiments, between about 0.1% and about 20% of the antibodies are C-terminal antibodies. In certain embodiments, between about 0.5% and about 10% of the antibodies are C-terminal antibodies. In certain embodiments, between about 1% and about 5% of the antibodies are C-terminal antibodies. In certain embodiments, between about 5% and about 10% of the antibodies are C-terminal antibodies. In certain embodiments, between about 5% and about 20% of the antibodies are C-terminal antibodies. In certain embodiments, between about 5% and about 30% of the antibodies are C-terminal antibodies.

[0008] In certain embodiments, the anti-IL-13 antibodies comprise a VH sequence selected from the sequences set forth in any one of SEQ ID NOs: 1-32. In certain embodiments, the anti-IL-13 antibodies comprise a VL sequence selected from the sequences set forth in any one of SEQ ID NOs: 33-57. In certain embodiments, the anti-IL-13 antibodies comprise 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. In certain embodiments, the anti-IL-13 antibodies comprise 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. In certain embodiments, the anti-IL-13 antibodies comprise a light chain constant region comprising SEQ ID NO: 469.

[0009] In certain embodiments, the composition further comprises one or more pharmaceutically acceptable excipients.

[0010] In another aspect, the disclosure relates to an anti-IL-13 antibody having a light chain comprising a VL comprising SEQ ID NO: 39 and a light chain constant region comprising SEQ ID NO: 469 and a heavy chain comprising a VH comprising SEQ ID NO: 3

and a heavy chain constant region comprising SEQ ID NO: 624. In certain embodiments, the composition further comprises an antibody having a light chain comprising a VL comprising SEQ ID NO: 39 and a light chain constant region comprising SEQ ID NO: 469 and a heavy chain comprising a VH comprising SEQ ID NO: 3 and a heavy chain constant region comprising SEQ ID NO: 439.

[0011] In certain embodiments, the antibodies are produced in a Chinese Hamster Ovary (CHO) cell line.

[0012] In another aspect, the disclosure relates to a vial comprising a composition described herein. In certain embodiments, the volume of the vial is between 1.0 mL and 3.0 mL. In certain embodiments, the volume of the vial is about 2.0 mL. In certain embodiments, the vial is a syringe. In certain embodiments, the syringe is a prefilled syringe.

[0013] In another aspect, the disclosure relates to a composition comprising a mixture of anti-interleukin 13 (IL-13) antibodies, wherein the mixture comprises a first IL-13 antibody and a second IL-13 antibody, wherein each antibody comprises at least one heavy chain, and wherein the first antibody and the second antibody are identical except that the first antibody comprises a lysine at the C-terminus of the at least one heavy chain, and the second antibody lacks the lysine at the C-terminus of the at least one heavy chain, wherein each 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 SEQ ID NOs: 58-99 and 121;
 - (b) CDR-H2 comprises a sequence selected from the sequences set forth in SEQ ID NOs: 100-111;
 - (c) CDR-H3 comprises a sequence selected from the sequences set forth in SEQ ID NOs: 112-120 and 130-140,
 - (d) CDR-L1 comprises a sequence selected from the sequences set forth in SEQ ID NOs: 141-144 and 149-152,
 - (e) CDR-L2 comprises a sequence selected from the sequences set forth in 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 SEQ ID NOs: 165-172, and

wherein the first antibody comprises a heavy chain constant domain comprising a sequence selected from the sequences set forth in SEQ ID NOs: 610-709.

[0014] In certain embodiments, each anti-IL-13 antibody comprises a VH sequence selected from the sequences set forth in any one of SEQ ID NOs: 1-32. In certain embodiments, each anti-IL-13 antibody comprises a VL sequence selected from the sequences set forth in any one of SEQ ID NOs: 33-57. In certain embodiments, each anti-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. In certain embodiments, each anti-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. In certain embodiments, each antibody comprises a light chain constant region comprising SEQ ID NO: 469.

[0015] In certain embodiments, the antibodies are produced in a Chinese Hamster Ovary (CHO) cell line.

[0016] In another aspect, the disclosure relates to a vial comprising a composition as described herein. In another aspect, the disclosure relates to a bag or a bottle comprising a composition as described herein. In certain embodiments, the 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.

[0017] In another aspect, the disclosure relates to a composition comprising a mixture of anti-interleukin 13 (IL-13) antibodies, wherein the mixture comprises

a) C-terminal anti IL-13 antibodies comprising a heavy chain having at least one C-terminal lysine, and

b) non-C-terminal anti IL-13 antibodies otherwise identical to the C-terminal anti IL-13 antibodies but lacking the at least one C-terminal lysine,

wherein each of the non-C-terminal and C-terminal antibodies 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 SEQ ID NOs: 58-99 and 121;

(b) CDR-H2 comprises a sequence selected from the sequences set forth in SEQ ID NOs: 100-111;

(c) CDR-H3 comprises a sequence selected from the sequences set forth in SEQ ID NOs: 112-120 and 130-140,

(d) CDR-L1 comprises a sequence selected from the sequences set forth in SEQ ID NOs: 141-144 and 149-152,

(e) CDR-L2 comprises a sequence selected from the sequences set forth in 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 SEQ ID NOs: 165-172, and

wherein each C-terminal antibody having at least one C-terminal lysine comprises a heavy chain constant domain having a means for enhancing the half-life of the C-terminal antibody.

Brief Description of the Drawings

[0018] **Figure 1** shows the imaged capillary isoelectric focusing (icIEF) profile and relative amounts of basic peaks for Construct 133 encoded without a C-terminal lysine from a 500L production culture. Basic peaks can be seen to the right of the main peak. The x-axis corresponds to pI, and the y-axis to absorbance.

[0019] **Figure 2** shows the icIEF profile and relative amounts of basic peaks for Construct 133 encoded with a C-terminal lysine from a 500L production culture. Basic peaks can be seen to the right of the main peak. The x-axis corresponds to pI, and the y-axis to absorbance.

Detailed Description

Definitions

[0020] 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.

[0021] As used herein, the singular form “a,” “an,” and “the” includes plural references unless indicated otherwise.

[0022] It is understood that aspects and embodiments of the invention described herein include “comprising,” “consisting,” and “consisting essentially of” aspects and embodiments.

[0023] 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.

[0024] An “effective amount” or “therapeutically effective amount” as used herein refers to an amount of therapeutic compound, such as an anti-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.

[0025] 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.

[0026] 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.

[0027] 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.

[0028] 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.

[0029] The terms “modulate” and “modulation” refer to reducing or inhibiting or, alternatively, activating or increasing, a recited variable.

[0030] 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.

[0031] 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.

[0032] 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).

[0033] For any of the structural and functional characteristics described herein, methods of determining these characteristics are known in the art.

[0034] The term “optionally” is meant, when used sequentially, to include from one to all of the enumerated combinations and contemplates all sub-combinations.

[0035] 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.

[0036] 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).

[0037] 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 k_{off} value.

[0038] The term “ k_a ” ($\text{M}^{-1}\times\text{sec}^{-1}$), as used herein, refers to the association rate constant of a particular antibody -antigen interaction. This value is also referred to as the k_{on} value.

[0039] 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.

[0040] The term “ K_A ” (M^{-1}), as used herein, refers to the association equilibrium constant of a particular antibody-antigen interaction. $K_A = k_a/k_d$.

[0041] 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.

[0042] 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.

[0043] The terms “C-terminal lysine antibody” and “C-terminal antibody” are used interchangeably herein to refer to an antibody which has a lysine at the C-terminus of at least one heavy chain. In certain embodiments, a C-terminal antibody has the following amino acid sequence at the C-terminus of at least one heavy chain: SLSLSPGK (SEQ ID NO: 710). In certain embodiments, a C-terminal antibody has a C-terminal lysine on at least one heavy chain. In certain embodiments, a C-terminal antibody has a C-terminal lysine on at least two heavy chains (e.g., both heavy chains in an antibody having two heavy chains).

[0044] The terms “non-C-terminal lysine antibody” and “non-C-terminal antibody” are used interchangeably herein to refer to an antibody which lacks a lysine at the C-terminus of each of its one or more heavy chains (e.g., both heavy chains in an antibody having two heavy chains). In certain embodiments, a non-C-terminal antibody may have the following amino acid sequence at the C-terminus of one or more heavy chains: SLSLSPG (SEQ ID NO: 711). In certain embodiments, a non-C-terminal antibody may have the following amino acid sequence at the C-terminus of one or more heavy chains: SLSLSP (SEQ ID NO: 712). In certain embodiments, the heavy chain of a non-C-terminal antibody is originally encoded with a C-terminal lysine, but the C-terminal lysine is removed by a carboxypeptidase in a production cell or in serum. In certain embodiments, the heavy chain of a non-C-terminal antibody is originally encoded without a C-terminal lysine and thus does not contain a C-terminal lysine to begin with.

[0045] The term “epitope” means a portion of an antigen that specifically binds to an antibody.

[0046] 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”).

[0047] The term “antigen-binding domain” means the portion of an antibody that is capable of specifically binding to an antigen or epitope.

[0048] 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.

[0049] 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.

[0050] 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.

[0051] 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.

[0052] 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.

[0053] 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.

[0054] 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.

[0055] 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.

[0056] “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.

[0057] “Fv” fragments comprise a non-covalently-linked dimer of one heavy chain variable domain and one light chain variable domain.

[0058] “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.

[0059] “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.

[0060] 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).

[0061] 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.

[0062] 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.

[0063] 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.

[0064] The term "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.

[0065] 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.

[0066] 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.

[0067] 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*).

[0068] 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.

[0069] 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.

[0070] In all the embodiments of the invention, “formulation,” “pharmaceutical formulation,” and “pharmaceutical composition” can also be referred to as “stable formulation” without any differentiation.

[0071] 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, or a syringe. In some embodiments, the vial may be a vial, *e.g.*, a glass vial or a pre-filled syringe.

Anti-IL-13 Antibodies

[0072] In some embodiments, the present disclosure provides compositions comprising (a) a therapeutically effective amount of an isolated antibody that binds interleukin 13 (IL-13) *e.g.*, 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 poloxamer, at pH 5.0 to 7.0.

[0073] In some embodiments, the present disclosure further provides formulations comprising: (a) a therapeutically effective amount of an isolated antibody that binds IL-13 *e.g.*, at a concentration of about 180 mg/mL; (b) a histidine buffer at a concentration of about 10 mM; (c) an arginine salt solution at a concentration of about 120 mM; (d) methionine at a concentration of about 10 mM; and (e) a polysorbate 80 or poloxamer at a concentration of about 0.05% w/v, at pH of about 5.8.

[0074] In some embodiments, the present disclosure further provides formulations comprising: (a) a therapeutically effective amount of an isolated antibody that binds IL-13 *e.g.*, at a concentration of about 180 mg/mL; (b) a histidine buffer at a concentration of about 10 mM; (c) an arginine salt solution at a concentration of about 80 mM; (d) methionine at a concentration of about 10 mM; and (e) a polysorbate 80 or poloxamer at a concentration of about 0.05% w/v, at pH of about 5.8.

[0075] In some embodiments, the present disclosure further provides formulations comprising: (a) a therapeutically effective amount of an isolated antibody that binds IL-13 *e.g.*, at a concentration of about 200 mg/mL; (b) a histidine buffer at a concentration of about 10 mM; (c) an arginine salt solution at a concentration of about 120 mM; (d) methionine at a concentration of about 10 mM; and (e) a polysorbate 80 or poloxamer at a concentration of about 0.05% w/v, at pH of about 5.8.

[0076] In certain embodiments, the formulation further comprises sucrose.

[0077] In certain embodiments, the poloxamer is poloxamer 188.

[0078] In certain embodiments, the formulation comprises the formulation comprises:

- (a) an interleukin 13 (IL-13) antibody present at a concentration between 140 mg/mL and 290 mg/mL (*e.g.*, at 180 mg/ml);
- (b) a histidine buffer, an acetate buffer, or a succinate buffer (*e.g.*, a histidine buffer at a concentration of 10 mM, wherein the histidine buffer comprises L-histidine and L-histidine HCl monohydrate);

- (c) arginine or a salt solution thereof (e.g., L-arginine salt solution at a concentration of 120 mM);
- (d) methionine or a salt solution thereof (e.g., L-methionine at a concentration of 10 mM);
- (e) a polysorbate (e.g., polysorbate 80 at a concentration of 0.05% w/v) or a poloxamer (e.g., poloxamer 188 at a concentration of 0.5 mg/ml); and
- (f) optionally, a metal ion chelator (e.g., EDTA-2Na at a concentration of 0.05 mM);

wherein the formulation is at pH 5.0 to 7.0 (e.g., pH 5.8 or pH 6.0).

[0079] In some embodiments, the antibody that binds IL-13 is a humanized, human, or chimeric antibody. In some embodiments, the antibody that binds IL-13 is a humanized antibody.

Anti-IL-13 Antibody Structure

[0080] The present application provides antibodies and formulations comprising an antibody which binds IL-13.

[0081] 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.

[0082] 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.

[0083] 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.

[0084] 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.

[0085] 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.

[0086] 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.

[0087] **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.

[0088] 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
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.

[0089] 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.

[0090] 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.

[0091] 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.

[0092] 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.

[0093] 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.

[0094] 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.

[0095] 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.

[0096] 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”).

[0097] 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.

[0098] In some embodiments the antibodies are monoclonal antibodies.

[0099] In some embodiments the antibodies are polyclonal antibodies.

[00100] 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.

[00101] 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.

[00102] 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.

[00103] 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.

[00104]

Sequences of IL-13 Antibodies

VH Domains

[00105] In some embodiments, the present disclosure further provides an isolated antibody that binds IL-13, comprising: (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.

[00106] In some embodiments, the present disclosure further provides an isolated antibody that binds IL-13, comprising: (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.

[00107] In some embodiments, an antibody provided herein comprises a VH sequence selected from SEQ ID NOs: 1-32. 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 a 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

[00108] In some embodiments, an antibody provided herein comprises a VL sequence selected from SEQ ID NOs: 33-57. 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 a 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

[00109] 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.

[00110] In certain aspects, any of SEQ ID NOs: 1-32 can be combined with any of SEQ ID NOs: 33-57.

[00111] 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.

[00112] 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.

[00113] 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 a 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 a 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.

[00114] 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

[illegible]

[illegible]

VH sequence set forth in SEQ ID NO: 19 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: 20 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: 21 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: 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.

[00115] In certain embodiments, the isolated 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 isolated 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.

[00116] In certain embodiments, the isolated 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 isolated 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.

[00117] In certain embodiments, the isolated 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 LTMTNMDPVDTATYY CAGDGYYPYAMDNW GQGSLVTVSS (SEQ ID NO: 470)	DIVMTQSPDSLVSLSGER ATINCRASKSVDSYGNST MHWYQQKPGQPPLLIY LASNLESGVPDRFSGSGS GTDFTLTISSLQAEDVAV YYCQQNNEDPRTFGGGT KVEIK (SEQ ID NO: 471)

2	Lebrikizumab – HC; Lebrikizumab – LC; hIgG1- LAGA YTE; Human kappa LC	QVTLRESGPALVKPTQ TLTLTCTVSGFSLAYS VNWIRQPPGKALEWL AMIWGDGKIVYNSAL KSRLTISKDTSKNQVV LTMTNMDPVDATYY CAGDGYYPYAMDNW GQGS�VTVSS (SEQ ID NO: 470)	DIVMTQSPDSLVS�GER ATINCRASKSVDSYGNSF MHWYQQKPGQPPLLIY LASNLESGVPDRFSGSGS GTDFTLTISSLQAEDVAV 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 MHWYQQKPGQPPLLIY 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 MHWYQQKPGQPPLLIY LASNLESGVPARFSGSGS RTDFTLTIDPVEADDAAS YYCQQNNEDPRTFGGGT KLEIK (SEQ ID NO: 33)
5	HC1; LC2; hIgG1-LAGA YTE; Human kappa LC	EVQLQESGPGLVKPSE TSLTCTVSGFSLNAYS VNWIRQPPGKGLEWL GMIWGDGKIVYNSAL KSRLTISKDSSKNQVSL	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPPLLIY LASNLESGVPSRFSGSGS RTDFTLTISSLQPEDFATY

		KLSSVTAADTAVYYC AGDGYYPYAMDNDWG QGTTVTVSS (SEQ ID NO: 3)	YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 35)
6	HC2; LC2; hIgG1-LAGA YTE; Human kappa LC	EVQLVQSGAEVKKPG ASVKVSCASGFSNA YSVNWVRQAPGQGLE WLGMIWGDGKIVYNS ALKSRLTITKDSSTSTV YMELSSLRSEDVAVYY CAGDGYYPYAMDNDW QGTTVTVSS (SEQ ID NO: 4)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS RTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 35)
7	HC3; LC2; hIgG1-LAGA YTE; Human kappa LC	EVQLVQSGAEVKKPGS SVKVSCASGFSNAY SVNWVRQAPGQGLEW LGMIWGDGKIVYNSA LKSRLTITKDSSTSTVY MELSSLRSEDVAVYYC AGDGYYPYAMDNDWG QGTTVTVSS (SEQ ID NO: 5)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS RTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 35)
8	HC4; LC2; hIgG1-LAGA YTE; Human kappa LC	EVQLVESGGGLVKPG GSLRLSCAASGFSNA YSVNWVRQAPGKGLE WLGMIWGDGKIVYNS ALKSRLTISKDSSKNTV YLQMNSLKTEDTAVY YCAGDGYYPYAMDNDW WGQTTVTVSS (SEQ ID NO: 6)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS RTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 35)

9	HC5; LC2; hIgG1-LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNW 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	EVQLQESGPGLVKPS TSLTCTVSGFSLNAYS VNWIRQPPGKGLEWL GMIWGDGKIVYNSAL KSRLTISKDSSKNQVSL KLSSVTAADTAVYYC AGDGYYPYAMDNWG QGTTVTVSS (SEQ ID NO: 3)	EIVLTQSPATLSVSPGERA TLSCRASKSVDSYGNSF MHWYQQKPGQAPRLIY LASNLESGIPARFSGSGSR TEFTLTISSLQSEDFAVYY CQQNNEDPRTFGGGTKV EIK (SEQ ID NO: 36)
11	HC2; LC3; hIgG1-LAGA YTE; Human kappa LC	EVQLVQSGAEVKKPG ASVKVSCKASGFSLNA YSVNWVRQAPGQGLE WLGMIWGDGKIVYNS ALKSRLTITKDSSTSTV YMELSSLRSED TAVYY CAGDGYYPYAMDNW GQGTTVTVSS (SEQ ID NO: 4)	EIVLTQSPATLSVSPGERA TLSCRASKSVDSYGNSF MHWYQQKPGQAPRLIY LASNLESGIPARFSGSGSR TEFTLTISSLQSEDFAVYY CQQNNEDPRTFGGGTKV EIK (SEQ ID NO: 36)
12	HC3; LC3; hIgG1-LAGA YTE; Human kappa LC	EVQLVQSGAEVKKPGS SVKVSCKASGFSLNAY SVNWVRQAPGQGLEW LGMIWGDGKIVYNSA LKSRLTITKDSSTSTVY	EIVLTQSPATLSVSPGERA TLSCRASKSVDSYGNSF MHWYQQKPGQAPRLIY LASNLESGIPARFSGSGSR TEFTLTISSLQSEDFAVYY

		MELSSLRSED TAVYYC AGDGYYPYAMD NWG QGTTVT VSS (SEQ ID NO: 5)	CQQNNEDPRTFGGGTKV EIK (SEQ ID NO: 36)
13	HC4; LC3; hIgG1-LAGA YTE; Human kappa LC	EVQLVESGGGLVKPG GSLRLSCAASG FSLNA YSVNWVRQAPGKGLE WLGMIWGDGKIVYNS ALKSRLTISKDSSKNTV YLQMNSLKTEDTAVY YCAGDGYYPYAMD N WGQGTTVT VSS (SEQ ID NO: 6)	EIVLTQSPATLSVSPGERA TLSCRASKSVDSYGNSF MHWYQQKPGQAPRLLIY LASNLESGIPARFSGSGSR TEFTLTISSLQSEDFAVYY CQQNNEDPRTFGGGTKV EIK (SEQ ID NO: 36)
14	HC5; LC3; hIgG1-LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASG FSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMD NW GQGTTVT VSS (SEQ ID NO: 7)	EIVLTQSPATLSVSPGERA TLSCRASKSVDSYGNSF MHWYQQKPGQAPRLLIY LASNLESGIPARFSGSGSR TEFTLTISSLQSEDFAVYY CQQNNEDPRTFGGGTKV EIK (SEQ ID NO: 36)
15	HC1; LC6; hIgG1-LAGA YTE; Human kappa LC	EVQLQESGPGLVKPSE TSLTCTVSG FSLNAYS VNWIRQPPGKGLEWL GMIWGDGKIVYNSAL KSRLTISKDSSKNQVSL KLSSVTAADTAVYYC AGDGYYPYAMD NWG QGTTVT VSS (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 NWG QGTTVTVSS (SEQ ID NO: 713)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
17	HC3; LC6; hIgG1-LAGA YTE; Human kappa LC	EVQLVQSGAEVKKPGS SVKVSCKASGFSLNAY SVNWVRQAPGQGLEW LGMIWGDGKIVYNSA LKSRLTITKDSSTSTVY MELSSLRSED TAVYYC AGDGYYPYAMD NWG QGTTVTVSS (SEQ ID NO: 5)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
18	HC4; LC6; hIgG1-LAGA YTE; Human kappa LC	EVQLVESGGGLVKPG GSLRLSCAASGFSLNA YSVNWVRQAPGKGLE WLGMWGDGKIVYNS ALKSRLTISKDSSKNTV YLQMNSLKTEDTAVY YCAGDGYYPYAMD N WGQGTTVTVSS (SEQ ID NO: 6)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
19	HC5; LC6; hIgG1-LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY

		LQMNSLRAEDTAVYY CAGDGYYPYAMDNW QGTTVTVSS (SEQ ID NO: 7)	YCQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
20	HC1; LC7; hIgG1-LAGA YTE; Human kappa LC	EVQLQESGPGLVKPSE TSLTCTVSGFSLNAYS VNWIRQPPGKGLEWL GMIWGDGKIVYNSAL KSRLTISKDSSKNQVSL KLSSVTAADTAVYYC AGDGYYPYAMDNWG QGTTVTVSS (SEQ ID NO: 3)	EIVLTQSPATLSVSPGERA TLSCRASKSVDSYGNSF MHWYQQKPGQAPRLLIY LASNLESGIPARFSGSGSG TEFTLTISSLQSEDAVYY CQNNEDPRTFGGGTKV EIK (SEQ ID NO: 40)
21	HC2; LC7; hIgG1-LAGA YTE; Human kappa LC	EVQLVQSGAEVKKPGS SVKVSCKASGFSLNAY SVNWVRQAPGQGLEW LGMIWGDGKIVYNSA LKSRLTITKDSSTSTVY MELSSLRSEDVAVYYC AGDGYYPYAMDNWG QGTTVTVSS (SEQ ID NO: 713)	EIVLTQSPATLSVSPGERA TLSCRASKSVDSYGNSF MHWYQQKPGQAPRLLIY LASNLESGIPARFSGSGSG TEFTLTISSLQSEDAVYY CQNNEDPRTFGGGTKV EIK (SEQ ID NO: 40)
22	HC3; LC7; hIgG1-LAGA YTE; Human kappa LC	EVQLVQSGAEVKKPGS SVKVSCKASGFSLNAY SVNWVRQAPGQGLEW LGMIWGDGKIVYNSA LKSRLTITKDSSTSTVY MELSSLRSEDVAVYYC AGDGYYPYAMDNWG QGTTVTVSS (SEQ ID NO: 5)	EIVLTQSPATLSVSPGERA TLSCRASKSVDSYGNSF MHWYQQKPGQAPRLLIY LASNLESGIPARFSGSGSG TEFTLTISSLQSEDAVYY CQNNEDPRTFGGGTKV EIK (SEQ ID NO: 40)

23	HC4; LC7; hIgG1-LAGA YTE; Human kappa LC	EVQLVESGGGLVKPG GSLRLSCAASGFSLN YSVNWVRQAPGKGLE WLGMIWGDGKIVYNS ALKSRLTISKDSSKNTV YLQMNSLKTEDTAVY YCAGDGYYPYAMD WGQGTTVTVSS (SEQ ID NO: 6)	EIVLTQSPATLSVSPGERA TLSCRASKSVDSYGNSF MHWYQQKPGQAPRLLIY LASNLESGIPARFSGSGS TEFTLTISLQSEDAVYY CQQNNEDPRTFGGGTKV EIK (SEQ ID NO: 40)
24	HC5; LC7; hIgG1-LAGA YTE; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMD GQGTTVTVSS (SEQ ID NO: 7)	EIVLTQSPATLSVSPGERA TLSCRASKSVDSYGNSF MHWYQQKPGQAPRLLIY LASNLESGIPARFSGSGS TEFTLTISLQSEDAVYY CQQNNEDPRTFGGGTKV EIK (SEQ ID NO: 40)
25	HC6; LC9; hIgG1-LAGA YTE; Human kappa LC	EVQLQESGPGLVKPSE TSLTCTVSGGSLNAY SVNWVRQPPGKGLEW LGMIWGDGKIVYNSA LKSRLTISLDTSKSQVF LKMSSLTAADTAVYY CARDGYYPYAMD 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 LGYIYGDGKTNYPAL KSRLTISLDTSKSQVFL	DIVLTQSPASLAVSPGER ATISCRASQSVDSNGNNF LHWYQQKPGQPPKLLIY LASNRESGVPDRFSGSGS GTDFTLTISRVEADDAV

		KMSSLTAADTAVYYC ARDGYYYYYAMDVWG QGTTVTVSS (SEQ ID NO: 9)	YYCQNNHTPRTFGGGT KLEIK (SEQ ID NO: 43)
90	HC5; LC6; hIgG1-LAGA YTE; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNW GQGTTVTVSS (SEQ ID NO: 7)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
91	HC5; LC6_m1; hIgG1-LAGA YTE; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNW GQGTTVTVSS (SEQ ID NO: 7)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSR MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQNNEDPRTFGGGTK VEIK (SEQ ID NO: 44)
92	HC5; LC6_m2; hIgG1-LAGA YTE; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNW GQGTTVTVSS (SEQ ID NO: 7)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSS MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQNNEDPRTFGGGTK VEIK (SEQ ID NO: 45)

93	HC5; LC6_m3; hIgG1-LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNW GQGTTVTVSS (SEQ ID NO: 7)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIR LASNLESGVPSRFSGSGS GTDFTLTISSLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 46)
94	HC5; LC6_m4; hIgG1-LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNW GQGTTVTVSS (SEQ ID NO: 7)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIF LASNLESGVPSRFSGSGS GTDFTLTISSLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 47)
95	HC5; LC6_m5; hIgG1-LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG 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	EVQLLES GGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASDLESGVPSRFSGSGS GTDFTLTISSLQPEDFATY

		LQMNSLRAEDTAVYY CAGDGYYPYAMDNW GQGTTVTVSS (SEQ ID NO: 7)	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 GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 50)
98	HC5; LC6_m8; hIgG1-LAGA YTE; 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)
99	HC5; LC6_m9; hIgG1-LAGA YTE; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNW GQGTTVTVSS (SEQ ID NO: 7)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNHEDPRTFGGGTK VEIK (SEQ ID NO: 52)

100	HC5; LC6_m10; hIgG1-LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNW 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 CAGDGYYPYAMDNW 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 GTDFTLTISSLQPEDFATY YCQQNNRDPRTFGGGTK VEIK (SEQ ID NO: 55)
103	HC5; LC6_m13; hIgG1-LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISSLQPEDFATY

		LQMNSLRAEDTAVYY CAGDGYYPYAMDNW GQGTTVTVSS (SEQ ID NO: 7)	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 CAGDGYYPYAMDNW GQGTTVTVSS (SEQ ID NO: 10)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
106	HC5_m2; LC6; hIgG1- LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFSLRAY 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	EVQLLES GGGLVQPGG SLRLSCAASGFS LHAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMD NW 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	EVQLLES GGGLVQPGG SLRLSCAASGFS LDAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMD NW GQGTTVTVSS (SEQ ID NO: 13)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
109	HC5_m5; LC6; hIgG1- LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFS LYAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMD NW GQGTTVTVSS (SEQ ID NO: 14)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
110	HC5_m6; LC6; hIgG1- LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFS LSAYS VNWVRQAPGKGLEWL GMIWGDGKIVYNSAL KSRLTISKDSSKNTVYL	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY

		QMNSLRAEDTAVYYC AGDGYYPYAMDNDWG QGTTVTVSS (SEQ ID NO: 15)	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 GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
112	HC5_m8; LC6; hIgG1- LAGA YTE; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFSLNRY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNDW GQGTTVTVSS (SEQ ID NO: 17)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
113	HC5_m9; LC6; hIgG1- LAGA YTE; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFSLNHY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNDW 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 LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMDNW GQTTVTVSS (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 AGDGYYPYAMDNWG QGTTVTVSS (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 AGDGYYPYAMDNWG QGTTVTVSS (SEQ ID NO: 21)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
117	HC5_m13; LC6; hIgG1- LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFSLNYY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY

		LQMNSLRAEDTAVYY CAGDGYYPYAMD NW GQGT TVTVSS (SEQ ID NO: 22)	YCQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
118	HC5_m14; LC6; hIgG1- LAGA YTE; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFS LNAES VNWVRQAPGKGLEW L GMIWGDGKIVYNSAL KSR LTISKDSSKNTVYL QMNSLRAEDTAVYYC AGDGYYPYAMD NW G QGT TVTVSS (SEQ ID NO: 23)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGN SF MHWYQQKPGKAPKLLIY LASNLESGVPSRFS GSGS GTDFTLTIS SLQPEDFATY YCQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
119	HC5_m15; LC6; hIgG1- LAGA YTE; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFS LNAY SVNWVRQAPGKGLEW L LGMIWSDGKIVYNSAL KSR LTISKDSSKNTVYL QMNSLRAEDTAVYYC AGDGYYPYAMD NW G QGT TVTVSS (SEQ ID NO: 24)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGN SF MHWYQQKPGKAPKLLIY LASNLESGVPSRFS GSGS GTDFTLTIS SLQPEDFATY YCQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)
120	HC5_m16; LC6; hIgG1- LAGA YTE; Human kappa LC	EVQLLESGGGLVQPGG SLRLSCAASGFS LNAY SVNWVRQAPGKGLEW L LGMIWADGKIVYNSA L KSR LTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDGYYPYAMD NW G QGT TVTVSS (SEQ ID NO: 25)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGN SF MHWYQQKPGKAPKLLIY LASNLESGVPSRFS GSGS GTDFTLTIS SLQPEDFATY YCQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)

121	HC5_m17; LC6; hIgG1- LAGA YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGHGYYPYAMDNW 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	EVQLLES GGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDLYYPYAMDNW 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	EVQLLES GGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY LQMNSLRAEDTAVYY CAGDKYYPYAMDNW 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	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY

		LQMNSLRAEDTAVYY CAGDGYGYAMDNDW GQGTTVTVSS (SEQ ID NO: 29)	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 CAGDGYTYAMDNDW GQGTTVTVSS (SEQ ID NO: 32)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASNLESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 39)

128	Lebrikizumab – HC; Lebrikizumab – LC; hIgG4- YTE; Human kappa LC	QVTLRESGPALVKPTQ TLTLTCTVSGFSLAYS VNWIRQPPGKALEWL AMIWGDGKIVYNSAL KSRLTISKDTSKNQVV LTMTNMDPVDATATYY CAGDGYYPYAMDNDW GQGS�VTVSS (SEQ ID NO: 470)	DIVMTQSPDSLVS�GER ATINCRASKSVDSYGNSF MHWYQQKPGQPPLLIY LASNLESGVPDRFSGSGS GTDFTLTISSLQAEDVAV YYCQQNNEDPRTFGGGT KVEIK (SEQ ID NO: 471)
129	Lebrikizumab – HC; Lebrikizumab – LC; hIgG4- LS; Human kappa LC	QVTLRESGPALVKPTQ TLTLTCTVSGFSLAYS VNWIRQPPGKALEWL AMIWGDGKIVYNSAL KSRLTISKDTSKNQVV LTMTNMDPVDATATYY CAGDGYYPYAMDNDW GQGS�VTVSS (SEQ ID NO: 470)	DIVMTQSPDSLVS�GER ATINCRASKSVDSYGNSF MHWYQQKPGQPPLLIY LASNLESGVPDRFSGSGS GTDFTLTISSLQAEDVAV YYCQQNNEDPRTFGGGT KVEIK (SEQ ID NO: 471)
130	Lebrikizumab – HC; Lebrikizumab – LC; hIgG1- LALA-YTE; Human kappa LC	QVTLRESGPALVKPTQ TLTLTCTVSGFSLAYS VNWIRQPPGKALEWL AMIWGDGKIVYNSAL KSRLTISKDTSKNQVV LTMTNMDPVDATATYY CAGDGYYPYAMDNDW GQGS�VTVSS (SEQ ID NO: 470)	DIVMTQSPDSLVS�GER ATINCRASKSVDSYGNSF MHWYQQKPGQPPLLIY LASNLESGVPDRFSGSGS GTDFTLTISSLQAEDVAV YYCQQNNEDPRTFGGGT KVEIK (SEQ ID NO: 471)
131	Lebrikizumab – HC; Lebrikizumab – LC; hIgG1- LALA-LS;	QVTLRESGPALVKPTQ TLTLTCTVSGFSLAYS VNWIRQPPGKALEWL AMIWGDGKIVYNSAL KSRLTISKDTSKNQVV	DIVMTQSPDSLVS�GER ATINCRASKSVDSYGNSF MHWYQQKPGQPPLLIY LASNLESGVPDRFSGSGS GTDFTLTISSLQAEDVAV

	Human kappa LC	LTMTNMDPVDATATYY CAGDGYYPYAMDNDW GQGS�VTVSS (SEQ ID NO: 470)	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 GTDFTLTISLQPEDFATY 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 GTDFTLTISLQPEDFATY 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 GTDFTLTISLQPEDFATY 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 GTDFTLTISSLQPEDFATY 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 GTDFTLTISSLQPEDFATY 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 GTDFTLTISSLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 51)
138	HC5; LC6_m8; hIgG4-YTE; Human kappa LC	EVQLLES GGGLVQPGG SLRLSCAASGFSLNAY SVNWVRQAPGKGLEW LGMIWGDGKIVYNSA LKSRLTISKDSSKNTVY	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASELESGVPSRFSGSGS GTDFTLTISSLQPEDFATY

		LQMNSLRAEDTAVYY CAGDGYYPYAMD NW 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 CAGDGYYPYAMD NW 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 CAGDGYYPYAMD NW 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 AGDGYYPYAMD NW GQGTTVTVSS (SEQ ID NO: 3)	DIQLTQSPSSLSASVGDR VTITCRASKSVDSYGNSF MHWYQQKPGKAPKLLIY LASELESGVPSRFSGSGS GTDFTLTISLQPEDFATY YCQQNNEDPRTFGGGTK VEIK (SEQ ID NO: 51)

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

*Names correspond with name in informal sequence listing

[00118] 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 anti-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 heavy chain constant (HC) domain comprising a sequence selected from any one of SEQ ID NOs: 435-468, 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. 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.

[00119] In certain embodiments, the HC domain includes IgG4-SP, hIgG1-LALA-YTE, hIgG1-LAGA YTE, hIgG1-LALA-LS, IgG4-YTE HC, and IgG4-LS.

[00120] In some embodiments, such an IgG4-SP HC constant domain has the sequence:
ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ
SSGLYSLSVVTPSSSLGKTYTCNVDPKPSNTKVDKRVESKYGPPCPPCPAPEFLG
GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTKPRE
EQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVY
TLPDSQESDEGHKPSQTLSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF
FLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLSPG (SEQ ID NO: 427).

[00121] In some embodiments, such a hIgG1-LALA-YTE HC constant domain has the sequence:

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
QSSGLYSLSVVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP
EAAGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
SFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPG (SEQ ID NO: 439).

[00122] In some embodiments, such a hIgG1-LAGA YTE HC constant domain has the sequence:

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
QSSGLYSLSVVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP
ELAGAPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
SFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPG (SEQ ID NO: 440).

[00123] In some embodiments, such a hIgG1-LALA-LS HC constant domain has the sequence:

[00124] ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPG (SEQ ID NO: 446).

[00125] In some embodiments, such an IgG4-YTE HC constant domain has the sequence: ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVDHKPSNTKVDKRVESKYGPPCPSCAPEFLGPSVFLFPPKPKDTLYITREPEVTCVVDVVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK (SEQ ID NO: 457).

[00126] In some embodiments, such an IgG4-LS HC constant domain has the sequence: ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVDHKPSNTKVDKRVESKYGPPCPSCAPEFLGPSVFLFPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVLHEALHSYTQKSLSLSLGK (SEQ ID NO: 460).

[00127] In some embodiments, such a hIgG1-LALA-YTE HC C-terminal lysine variant constant domain has the sequence:

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLYITREPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 624).

[00128] In some embodiments, such a hIgG1-LAGA YTE HC C-terminal lysine variant constant domain has the sequence:

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

[00129] In some embodiments, such a hIgG1-LALA-LS HC C-terminal lysine variant constant domain has the sequence:

[00130] ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV
HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT
CPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPGK (SEQ
ID NO: 631).

[00131] 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
EQDSKDSSTLSSTLTLSKADYEEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID
NO: 469).

CDRs

[00132] 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.

[00133] 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.

[00134] 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.

[00135] 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.

[00136] 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.

[00137] 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.

[00138] 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.

[00139] 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.

[00140] 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.

[00141] 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.

[00142] 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.

[00143] 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.

[00144] 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.

[00145] 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.

[00146] 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.

[00147] 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.

[00148] 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.

[00149] 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.

[00150] 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:	CDR3	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 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 PPGKG 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 PPGKG 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	WIRQP 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	RLTISK 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 PPGKG LEWLG	256	YIYGD GKTNY NPALK S	101	RLTISL DTSKS QVFLK MSSLT AADTA VYYCA R	319	DGYYP YYAM DV	113	WGQG TTVTV 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 TTVTV 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 TTVTV 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 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 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 GFSL\$	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	DGYY GYAM DN	117	WGQG TTVTV 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	DGYY AYAM DN	118	WGQG TTVTV 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	DGYY YAMD N	119	WGQG TTVTV 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	DGYY YAMD N	120	WGQG TTVTV 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	GFSL 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:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
4	HC0_M	QVQLQ ESGPG LVAPS QSLST CTVS	543	GFSLN AY	68	SVNW VRQPP GKGLE WLGMI	551	WGDG K	104	IVYNS ALKSR LTISKD SSKSQ VFLKM SSLQS DDTAR YYCAG	558	DGYYP YAMD N	112	WGHG TSVTV SS	369
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:	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	546	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
8, 13, 18, and 23	HC4	EVQLV ESGGG LVKPG GSLRL SCAAS	547	GFSLN AY	68	SVNW VRQAP GKGLE 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 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:	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 TTVTV SS	371
26	HC7	QVQLQ ESGPG LVKPS ETLSL TCTVS	549	GGSLN AY	69	SWNW VRQPP GKGLE WLGVI	555	YGDG K	105	TNYNP ALKSR LTISLD TSKSQ VFLKM SSLTA ADTAV YYCAR	564	DGYYP YYAM DV	113	WGQG TTVTV 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 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:
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	GFSLH 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:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
109	HC5_m5	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLY AY	75	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
110	HC5_m6	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLS AY	67	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
111	HC5_m7	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN RY	76	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:	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	548	GFSLN KY	77	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
113	HC5_m9	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN HY	78	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
114	HC5_m10	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN QY	79	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:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
115	HC5_m11	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN EY	80	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
116	HC5_m12	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN SY	81	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
117	HC5_m13	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN YY	82	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:	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:	CDR1	SEQ ID NO:	FR2	SEQ ID NO:	CDR2	SEQ ID NO:	FR3	SEQ ID NO:	CDR3	SEQ ID NO:	FR4	SEQ ID NO:
121	HC5_m17	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	HGYYP YAMD N	114	WGQG TTVTV SS	371
122	HC5_m18	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	DLYYP YAMD N	115	WGQG TTVTV SS	371
123	HC5_m19	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	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	548	GFSLN AY	68	SVNW VRQAP GKGLE WLGMI	554	WGDG K	104	IVYNS ALKSR LTISKD SSKNT VYLQ MNSLR AEDTA VYYCA G	562	DGYY 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	DGYY 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	DGYTY YAMD N	120	WGQG TTVT V 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 (lebrikizu mab), 2, and 128-131	Lebrikizum ab - HC	QVTLR ESGPA LVKPT QTLTL TCTVS	542	GFSLS AYS	84	VNWIR QPPGK ALEWL AM	566	IWGDG KI	108	VYNSA LKSRL TISKDT SKNQV VLTMT NMDP VDTAT YYC	572	AGDG YYPYA MDN	130	WGQG SLVT V 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 CTVS	543	GFSLN AYS	85	VNWV RQPPG KGLE WLGW	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 QSLST CTVS	543	GFSLN AYS	85	VNWV RQPPG KGLE WLGW	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	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:
6, 11, 16, and 21	HC2	EVQLV QSGAE VKKPG ASVKV SCKAS	545	GFSLN AYS	85	VNWV RQAPG QGLE WLGW	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 WLGW	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 WLGW	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 WLG M	570	IWGDG KI	108	VYNSA 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 WLG M	567	IWGDG KI	108	VYNSA 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	VNWV RQPPG KGLE WLG Y	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 WLGW	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 WLGW	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 WLGW	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 WLG M	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 WLG M	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 WLG M	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 WLGW	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 WLGW	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 WLGW	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 WLG M	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 WLG M	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 WLG M	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 WLGW	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 WLGW	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 WLGW	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 WLG M	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 WLG M	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 WLG M	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 WLG M	570	IWGDG KI	108	VYNSA LKSRL TISKDS SKNTV YLQM NSLRA EDTAV YYC	578	AGDK YYPYA MDN	135	WGQG TTVTV SS	371
124	HC5_m20	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN AYS	85	VNWV RQAPG KGLE WLG M	570	IWGDG KI	108	VYNSA LKSRL TISKDS SKNTV YLQM NSLRA EDTAV YYC	578	AGDG YGY AMDN	136	WGQG TTVTV SS	371
125	HC5_m21	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN AYS	85	VNWV RQAPG KGLE WLG M	570	IWGDG KI	108	VYNSA LKSRL TISKDS SKNTV YLQM NSLRA EDTAV YYC	578	AGDG YYAY AMDN	137	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:
126	HC5_m22	EVQLL ESGGG LVQPG GSLRL SCAAS	548	GFSLN AYS	85	VNWV RQAPG KGLE WLG M	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 WLG M	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	Lebrikizum ab - LC	DIVMT QSPDS LSVSL GERAT INC	581	RASKS VDSYG NSFMH	141	WYQQ KPGQP PKLLIY	286	LASNL ES	153	GVPCR 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	LASNL ES	153	GVPAR FSGSG SRTDF TLTIDP VEADD AASY C	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	715	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

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 PRLLIY	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	WYVQ 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	WYVQ 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	WYVQ 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 PRLLIY	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	714	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	LASNL ES	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	LASNL 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 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 (lebrikizu mab), 2, and 128-131	Lebrikizum ab - LC	DIVMT QSPDS LSVSL GERAT INC	581	RASKS VDSYG NSFMH	141	WYQQ KPGQP PKLLIY	286	LASNL ES	153	GVPPDR 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 FATYYC	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 FATYYC	345	QQNNE DPRT	165	FGGGT KVEIK	400
10-14	LC3	EIVLT QSPAT LSVSP GERAT LSC	233	RASKS VDSYG NSFMH	141	WYQQ KPGQA PRLLIY	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	WYVQ KPGQS PQLLIY	291	LASNLS 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	WYVQ KPGQP PKLLIY	286	LASNLS 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	WYVQ KPGKA PKLLIY	288	LASNLS ES	153	GVPSR FSGSG SGTDF TLTISS LQPED FATYY C	349	QQNNE DPRT	165	FGGGT KVEIK	400
20-24	LC7	EIVLT QSPAT LSVSP GERAT LSC	233	RASKS VDSYG NSFMH	141	WYVQ KPGQA PRLIY	290	LASNLS 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 QSPLS 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	LASNR 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	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:
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	QQNHE 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	QQNVE 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
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	LASNL 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	SEQ ID NO:	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	596	NLESG VPDRF SGSGS GTDFT LTISSL QAEDV AVYYC	165	QQNNE DPRT	400	FGGGT KVEIK	400
3 and 4	LC0	NIVLT QSPAS LAVSL GQRAT ISCRAS	583	KSVDS YGNSF	149	MHWY QQKPG QPPKL LIY	589	LAS	597	NLESG VPARF SGSGS RTDFT LTIDPV EADDA ASYVC	165	QQNNE DPRT	401	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 SEDF 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 SEDFG 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 YGNSF	149	MHWY QQKPG QPPKL LIY	589	LAS	NLESG VPDRF SGSGS GTDFT LTISR V EADDV AVYYC	604	QQNNE DPRT	165	FGGGT KLEIK	401
26	LC10	DIVLT QSPAS LAVSP GERAT ISCRAS	588	QSVDS NGNIF	150	LHWY QQKPG QPPKL LIY	593	LAS	NLESG VPDRF SGSGS GTDFT LTISR V EADDV AVYYC	605	QQNN HTPRT	166	FGGGT KLEIK	401
91	LC6_m1	DIQLT QSPSSL SASVG DRVTI TCRAS	584	KSVDS YGNSR	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 YGNS	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	QQNHE 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.

[00151] In some embodiments, antibody that binds IL-13 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.

10 [00152] In some embodiments, antibody that binds IL-13 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.

15 **Fc Region**

[00153] 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.

20 [00154] 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.

- [00155] 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
- 5 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
- 10 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
- 15 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)).
- [00156] Modifications in the CH2 domain can affect the binding of FcRs to the Fc. A number
- 20 of amino acid modifications in the Fc region are known in the art for selectively altering the affinity of the Fc for different Fcγgamma receptors. In some aspects, the Fc comprises one or more modifications to promote selective binding of Fc-gamma receptors.
- [00157] Exemplary mutations that alter the binding of FcRs to the Fc are listed below:
- [00158] S298A/E333A/K334A, S298A/E333A/K334A/K326A (Lu Y, Vernes JM, Chiang N,
- 25 *et al. J Immunol Methods.* 2011 Feb 28;365(1-2):132-41);
- [00159] 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);
- [00160] F243L (Stewart R, Thom G, Levens M, *et al. Protein Eng Des Sel.* 2011
- 30 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);

[00161] 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);

[00162] S239D/S267E, S267E/L328F (Chu SY, Vostiar I, Karki S, *et al. Mol Immunol.* 2008 Sep;45(15):3926-33);

5 [00163] 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.

10 [00164] 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.

[00165] 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.

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30 [00166] 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	Modification(s)	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
Stavenhagen, 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

- 5 **[00167]** 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
- 10 (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.

[00168] 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**:

5 **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

[00169] 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
10 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.

[00170] 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).

[00171] 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.

[00172] 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.

[00173] 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.

[00174] 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.

[00175] 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.

[00176] 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.

[00177] In certain embodiments, the heavy chain comprises a constant heavy chain sequence set forth in SEQ ID NO: 439 or SEQ ID NO: 624.

[00178] In certain embodiments, the isolated antibody described herein comprises a constant light chain sequence set forth in SEQ ID NO: 469.

[00179] In certain embodiments, the isolated antibody comprises a constant heavy chain sequence selected from SEQ ID NO: 439 and 624 and a constant light chain sequence

comprising 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.

5 [00180] In certain embodiments, the isolated antibody comprises a constant heavy chain sequence selected from SEQ ID NO: 439 and 624 and a constant light chain sequence comprising 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.

15 [00181] In certain embodiments, the anti-IL-13 antibody comprises a light chain comprising a VL comprising SEQ ID NO: 39 and a light chain constant region comprising SEQ ID NO: 469 and a heavy chain comprising a VH comprising SEQ ID NO: 3 and a heavy chain constant region comprising SEQ ID NO: 624. In certain embodiments, the composition further comprises an antibody having a light chain comprising a VL comprising SEQ ID NO: 39 and a light chain constant region comprising SEQ ID NO: 469 and a heavy chain comprising a VH comprising SEQ ID NO: 3 and a heavy chain constant region comprising SEQ ID NO: 439.

20 [00182] 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.

25 [00183] 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);

5 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;

10 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,

15 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.

[00184] 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

20 embodiments, the antibodies described herein comprise the heavy and light chain variable regions of Construct 133 and an Fc region comprising YTE mutations at positions 253, 255 and 257, respectively and with LALA mutations at positions 235 and 236, respectively.

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[00185] 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

30 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.

- 5 [00186] 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 Substitutions

- 10 [00187] In certain embodiments, the fragment crystallizable region (Fc region) of the anti-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 (also referred to herein as YTE mutations)
- 15 can 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 mutations confer greater FcRn-IgG binding, prolonging the IgG serum half-life compared to an unmodified IgG.

LALA Substitutions

- 20 [00188] In certain embodiments, the anti-IL-13 antibodies described herein additionally carry Fc region amino acid substitutions L234A/L235A or L235A/L236A in the IgG1 heavy chain, commonly called LALA substitutions or LALA mutations. These changes can impair Fc receptor binding to IgG and prevent undesired effector cell activation.

Binding

- 25 [00189] In certain embodiments, an anti-IL-13 antibody described herein is a high-affinity IgG1 humanized monoclonal antibody (mAb) that binds IL-13. In certain embodiments, the anti-IL-13 antibody described herein comprises a IgG1 constant region comprising YTE substitutions and LALA substitutions.

[00190] Without wishing to be bound by theory, the binding of the anti-IL-13 antibodies described herein to IL-13 is believed to 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.

[00191] 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®).

[00192] 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 anti-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 anti-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 anti-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 anti-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 anti-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 anti-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 anti-IL-13 antibody for a non-target molecule is less than about 0.1% of the affinity for IL-13.

[00193] 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 anti-IL-13 antibody, after which a second anti-IL-13 antibody is added. In another
5 exemplary assay, a first anti-IL-13 antibody is coated on a surface and contacted with IL-13, and then a second anti-IL-13 antibody is added. If the presence of the first anti-IL-13 antibody reduces binding of the second anti-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
10 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
15 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
20 (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.

[00194] 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,
25 *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
30 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%.

5 [00195] In certain embodiments, the antibody binds an IL-13 sequence set forth in SEQ ID NOs: 472-475.

[00196] 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).

[00197] 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.

[00198] 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.

[00199] 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, 1.9-1.5, 1.5-1, 1-0.8, 1-0.5, 0.9-0.6, 0.7-0.4, 0.6-0.2, 0.5-0.3, 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.

Antibody Compositions

[00200] Human IgG typically is produced with a C-terminal lysine, given that IgG heavy chain genes encode a C-terminal lysine. However, the C-terminal lysine is often cleaved off by intracellular carboxypeptidases during antibody bioproduction in cell culture. C-terminal lysine clipping is also observed in serum (Cai et al., *Biotechnol. Bioeng.* 2011;108:404-12). While the absence of the C-terminal lysine reportedly does not induce conformational changes to antibody structure and was thought to have no impact on activity (e.g., CDC), recent studies suggest that antibodies lacking the C-terminal lysine had higher CDC activity compared to the corresponding antibody with the C-terminal lysine (van den Bremer ET. *MAbs* 2015;7:672; Tang et al., *MAbs* 2013;5:114; *Biotechnol. J.* 2018;13:1700476). Binding of antibodies to FcγRIIIa-Val176 and human FcRn does not appear to be altered by C-terminal lysine clipping (Faid et al., *Eur. J. Pharm. Sci.* 2021;159:105730). In certain contexts, the expression of antibodies in recombinant cells lines with a heavy chain that does not encode a C-terminal lysine have been shown to have lower specific productivities compared to cell lines that express a heavy chain that encode a C-terminal lysine, potentially due to slower heavy chain synthesis and faster antibody degradation (Hu et al., *Biotechnol. Prog.* 2017;33:786-94) or altered interactions between C-terminal amino acid sequences and ribosomes (Owen et al., *J. Biotechnol.* 2023;374:38-48).

[00201] The level of C-terminal lysine in antibodies produced in recombinant cell lines can vary based on the cell line used and the cell culture process conditions (Dick et al. (2008) *Biotechnol. Bioeng.* 100(6):1132-1143; Shah et al. (2022) *J. Pharm. Sci.* 111(9):2445-2450). For example, C-terminal lysine levels in Chinese Hamster Ovary (CHO) cell lines are typically low (<20%) and often <5% of the original level.

[00202] Theoretically, an antibody heavy chain can have no C-terminal lysine (e.g., both heavy chains lacking a C-terminal lysine in an antibody having two heavy chains), one C-terminal lysine on either heavy chain, or a C-terminal lysine on both heavy chains (i.e., two C-

terminal lysines). When a batch of antibody has <5% C-terminal lysine, antibodies with two C-terminal lysines are rare; the predominant species of lysine-containing antibody in such batches is an antibody with one C-terminal lysine. When C-terminal lysine is being quantified, depending on the method used, the result may not differentiate between one lysine and two
5 lysines, but rather whether the antibody has a C-terminal lysine or not. Methods to differentiate between different C-terminal lysine containing species of antibody include, e.g., charged based analytical methods such as ion exchange chromatography (e.g., IEF, cIEF, CEX) (see, e.g., WO2013/158273, the contents of which are herein incorporated by reference in its entirety). Methods such as mass spectrometry and peptide mapping including those described in the
10 Examples, e.g., LC-MS/MS, are also suitable for analyzing whether C-terminal lysines are present on heavy chains.

[00203] In certain aspects, the present disclosure relates to compositions comprising a mixture of anti-interleukin 13 (IL-13) antibodies, wherein a portion of the anti-IL-13 antibodies comprise a C-terminal lysine (“C-terminal lysine antibodies” or “C-terminal antibodies”) and a portion
15 lack a C-terminal lysine (“non-C-terminal lysine antibodies” or “non-C-terminal antibodies”). The percentage of C-terminal lysine antibodies and non-C-terminal lysine antibodies can vary depending upon the cell line used and the cell culture process conditions. For example, in certain embodiments, between about 0.01% and about 50% of the antibodies are C-terminal antibodies, between about 0.01% and about 20% of the antibodies are C-terminal antibodies, between
20 about 0.01% and about 10% of the antibodies are C-terminal antibodies, between about 0.01% and about 1% of the antibodies are C-terminal antibodies, between about 0.1% and about 50% of the antibodies are C-terminal antibodies, between about 0.1% and about 30% of the antibodies are C-terminal antibodies, between about 0.1% and about 20% of the antibodies are C-terminal antibodies, between about 0.1% and about 10% of the antibodies are C-terminal antibodies,
25 between about 0.1% and about 1% of the antibodies are C-terminal antibodies, between about 0.5% and about 50% of the antibodies are C-terminal antibodies, between about 0.5% and about 30% of the antibodies are C-terminal antibodies, between about 0.5% and about 20% of the antibodies are C-terminal antibodies, between about 0.5% and about 10% of the antibodies are C-terminal antibodies, between about 0.5% and about 5% of the antibodies are C-terminal
30 antibodies, between about 0.5% and about 1% of the antibodies are C-terminal antibodies, between about 1% and about 50% of the antibodies are C-terminal antibodies, between about 1%

and about 30% of the antibodies are C-terminal antibodies, between about 1% and about 20% of the antibodies are C-terminal antibodies between about 1% and about 10% of the antibodies are C-terminal antibodies, or between about 1% and about 5% of the antibodies are C-terminal antibodies, between about 5% and about 50% of the antibodies are C-terminal antibodies, between about 5% and about 30% of the antibodies are C-terminal antibodies, between about 5% and about 20% of the antibodies are C-terminal antibodies between about 5% and about 10% of the antibodies are C-terminal antibodies, between about 10% and about 50% of the antibodies are C-terminal antibodies, between about 10% and about 30% of the antibodies are C-terminal antibodies, or between about 10% and about 20% of the antibodies are C-terminal antibodies.

5 [00204] Some antibodies have high retention of C-terminal lysine, e.g., depending on the conditions of preparation or cell culture conditions used. For example, PCT Publication WO2013/158273, the contents of which are herein incorporated by reference in its entirety, describes a percentage range of C-terminal lysine containing adalimumab of about 7.2% up to about 26.6% (19.5% Lys1 and 7.1% Lys2 from Figure 17 of WO2013/158273) based on

10 different cell lines and cell culture conditions (e.g., different concentrations of arginine). Accordingly, in certain embodiments, a batch of antibody is made with a C-terminal lysine on the input sequence and the resulting output is a mixture of antibody containing greater than 5%, greater than 6%, greater than 7%, greater than 8%, greater than 9%, greater than 10%, greater than 11%, greater than 12%, greater than 13%, greater than 14%, greater than 15%, greater than

15 16%, greater than 17%, greater than 18%, greater than 19%, greater than 20%, greater than 21%, greater than 22%, greater than 23%, greater than 24%, greater than 25%, greater than 26%, greater than 27%, greater than 28%, greater than 29%, or greater than 30% of antibody having a C-terminal lysine. In another embodiment, the output mixture contains 5-30%, 5-25%, 5-20%, 5-15%, 5-10%, 10-30%, 10-25%, 10-20%, 10-15%, 15-30%, 15-25%, 15-20%, 20-30%, 20-

20 25%, or 25-30% of antibody having a C-terminal lysine. In another embodiment, the output mixture contains about 6%, about 7%, about 8%, about 9%, about 10%, about 11%, about 12%, about 13%, about 14%, about 15%, about 16%, about 17%, about 18%, about 19%, about 20%, about 21%, about 22%, about 23%, about 24%, about 25%, about 26%, about 27%, about 28%, about 29%, or about 30% of antibody having a C-terminal lysine. In another embodiment, the

25 output mixture contains 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%,

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18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, or 30% of antibody having a C-terminal lysine.

[00205] In certain embodiments, each of the non-C-terminal and C-terminal antibodies comprises:

- 5 (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 SEQ
10 ID NOs: 58-99 and 121;
- (b) CDR-H2 comprises a sequence selected from the sequences set forth in SEQ ID NOs: 100-111;
- (c) CDR-H3 comprises a sequence selected from the sequences set forth in SEQ ID NOs: 112-120 and 130-140,
- 15 (d) CDR-L1 comprises a sequence selected from the sequences set forth in SEQ ID NOs: 141-144 and 149-152,
- (e) CDR-L2 comprises a sequence selected from the sequences set forth in 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 SEQ
20 ID NOs: 165-172.

[00206] In certain embodiments, each C-terminal antibody comprises a heavy chain constant domain comprising a sequence selected from the sequences set forth in SEQ ID NOs: 610-709.

In certain embodiments, each C-terminal antibody comprises a heavy chain constant domain comprising a sequence selected from the sequences set forth in SEQ ID NOs: 610, 614-641, and
25 651-709.

[00207] In certain embodiments, the anti-IL-13 antibodies comprise a VH sequence selected from the sequences set forth in any one of SEQ ID NOs: 1-32. In certain embodiments, the anti-IL-13 antibodies comprise a VL sequence selected from the sequences set forth in any one of SEQ ID NOs: 33-57. In certain embodiments, the anti-IL-13 antibodies comprise a VH sequence
30 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. In certain

embodiments, the anti-IL-13 antibodies comprise 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. In certain embodiments, the anti-IL-13 antibodies comprise a light chain constant region comprising SEQ ID NO: 469. In certain embodiments, the heavy chain constant region of the C-terminal antibody is SEQ ID NO: 624, and the heavy chain constant region of the non-C-terminal antibody is SEQ ID NO: 439.

[00208] In certain embodiments, the composition comprises an anti-IL-13 antibody having a light chain comprising a VL comprising SEQ ID NO: 39 and a light chain constant region comprising SEQ ID NO: 469 and a heavy chain comprising a VH comprising SEQ ID NO: 3 and a heavy chain constant region comprising SEQ ID NO: 624. In certain embodiments, the composition further comprises an antibody having a light chain comprising a VL comprising SEQ ID NO: 39 and a light chain constant region comprising SEQ ID NO: 469 and a heavy chain comprising a VH comprising SEQ ID NO: 3 and a heavy chain constant region comprising SEQ ID NO: 439.

[00209] In another aspect, the disclosure relates to a composition comprising a mixture of anti-interleukin 13 (IL-13) antibodies, wherein the mixture comprises a first IL-13 antibody and a second IL-13 antibody. In certain embodiments, each antibody comprises at least one heavy chain, and the first antibody and the second antibody are identical except that the first antibody comprises a lysine at the C-terminus of the at least one heavy chain, and the second antibody lacks the lysine at the C-terminus of the at least one heavy chain. In certain embodiments, each 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 SEQ ID NOs: 58-99 and 121;

(b) CDR-H2 comprises a sequence selected from the sequences set forth in SEQ ID NOs: 100-111;

(c) CDR-H3 comprises a sequence selected from the sequences set forth in SEQ ID NOs: 112-120 and 130-140,

(d) CDR-L1 comprises a sequence selected from the sequences set forth in SEQ ID NOs: 141-144 and 149-152,

(e) CDR-L2 comprises a sequence selected from the sequences set forth in SEQ ID NOs: 153-158 and the amino acid sequence LAS; and

5 (f) CDR-L3 comprises a sequence selected from the sequences set forth in SEQ ID NOs: 165-172.

[00210] In certain embodiments, the first antibody comprises a heavy chain constant domain comprising a sequence selected from the sequences set forth in SEQ ID NOs: 610-709. In certain embodiments, each C-terminal antibody comprises a heavy chain constant domain
10 comprising a sequence selected from the sequences set forth in SEQ ID NOs: 610, 614-641, and 651-709. In certain embodiments, each C-terminal antibody having at least one C-terminal lysine comprises a heavy chain constant domain having a means for enhancing the half-life of the C-terminal antibody.

[00211] In certain embodiments, each anti-IL-13 antibody comprises a VH sequence selected
15 from the sequences set forth in any one of SEQ ID NOs: 1-32. In certain embodiments, each anti-IL-13 antibody comprises a VL sequence selected from the sequences set forth in any one of SEQ ID NOs: 33-57. In certain embodiments, each anti-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. In certain
20 embodiments, each anti-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. In certain embodiments, each antibody comprises a light chain constant region comprising SEQ ID NO: 469.

Pharmaceutical Formulations

25 [00212] 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 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,

osmolarity, viscosity, clarity, color, isotonicity, odor, sterility, stability, rate of dissolution or release, adsorption, or penetration.

Excipients and pH

[00213] Excipients may be selected for their suitability for intravenous or subcutaneous
5 administration, providing the necessary stabilizing, buffering capacity, and tonicity. The
formulation can improve the stability of the anti-IL-13 and can provide a sterile solution suitable
for subcutaneous or intravenous administration. In some embodiments the excipients contained
in the formulation are pharmacopoeial grade excipients. In some embodiments, the excipients in
the formulation comprise a histidine buffer, an acetate buffer, or a succinate buffer; arginine
10 and/or methionine or a salt solution thereof; and a polysorbate. In some embodiments, the
formulation further comprises a sugar or sugar alcohol.

[00214] 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
15 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.

[00215] In certain embodiments, the buffer or buffer system, such as a histidine buffer, acetate
20 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 6.5 (*e.g.*, between 5.6 and 6.4, 5.7 and 6.3, 5.6
and 5.9, and 5.7 and 5.8). In some embodiments, the pH is between 5.6 and 5.9. In some
embodiments, the pH is between 5.7 and 5.8.

[00216] In some embodiments, the buffer has a pH of about 5.5. In some embodiments, the
25 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. 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.

[00217] In some embodiments, the histidine buffer, acetate buffer, or succinate buffer is at a
30 concentration between 5 mM and 15 mM (*e.g.*, between 6 mM and 14 mM, 7 mM and 13 mM, 8

mM and 12 mM, 9 mM and 11 mM, and about 10 mM). In some embodiments, the histidine buffer, acetate buffer, or succinate buffer is at a concentration between 6 mM and 14 mM. In some embodiments, the histidine buffer, acetate buffer, or succinate buffer is at a concentration between 7 mM and 13 mM. In some embodiments, the histidine buffer, acetate buffer, or succinate buffer is at a concentration between 8 mM and 12 mM. In some embodiments, the histidine buffer, acetate buffer, or succinate buffer is at a concentration between 9 mM and 11 mM.

[00218] In some embodiments, the histidine 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.

[00219] In some embodiments the formulation comprises a histidine buffer, acetate buffer, or succinate buffer. In some embodiments the formulation comprises a histidine buffer. In some embodiments the formulation comprises an acetate buffer. In some embodiments, the formulation comprises a succinate buffer.

[00220] In some embodiments, a histidine buffer (*e.g.*, L-histidine, 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 histidine HCl monohydrate.

5 [00221] In some embodiments, the formulation comprises methionine.

[00222] In some embodiments, the methionine is at a concentration between 5 mM and 50 mM (*e.g.*, between 5 mM and 40 mM, between 5 mM and 30 mM, between 5 mM and 20 mM, between 5 mM and 10 mM, between 10 mM and 50 mM, between 10 mM and 40 mM, between 10 mM and 30 mM, between 10 mM and 20 mM, between 20 mM and 50 mM, between 20 mM and 40 mM, between 20 mM and 30 mM, between 30 mM and 50 mM, between 30 mM and 40 mM, between 40 mM and 50 mM, between 6 mM and 14 mM, 7 mM and 13 mM, 8 mM and 12 mM, 9 mM and 11 mM, and about 10 mM). In some embodiments, the methionine is at a concentration between 6 mM and 14 mM. In some embodiments, the methionine is at a concentration between 7 mM and 13 mM. In some embodiments, the methionine is at a concentration between 8 mM and 12 mM. In some embodiments, the methionine is at a concentration between 9 mM and 11 mM.

[00223] In some embodiments, the methionine is at a concentration of about 1 mM. In some embodiments, the methionine is at a concentration of about 2 mM. In some embodiments, the methionine is at a concentration of about 3 mM. In some embodiments, the methionine is at a concentration of about 4 mM. In some embodiments, the methionine is at a concentration of about 5 mM. In some embodiments, the methionine is at a concentration of about 6 mM. In some embodiments, the methionine is at a concentration of about 7 mM. In some embodiments, the methionine is at a concentration of about 8 mM. In some embodiments, the methionine is at a concentration of about 9 mM. In some embodiments, the methionine is at a concentration of about 10 mM. In some embodiments, the methionine is at a concentration of about 11 mM. In some embodiments, the methionine is at a concentration of about 12 mM. In some embodiments, the methionine is at a concentration of about 13 mM. In some embodiments, the methionine is at a concentration of about 14 mM. In some embodiments, the methionine is at a concentration of about 15 mM.

30 [00224] In some embodiments, the formulation comprises arginine. In some embodiments, the formulation comprises an arginine salt solution. In some embodiments, the arginine or arginine

salt solution acts as a viscosity modulator. In some embodiments, the arginine salt solution salt solution comprises HCl monohydrate.

[00225] In some embodiments, the 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). In some embodiments, the arginine salt solution is at a concentration of about 80 mM. In some embodiments, the arginine salt solution is at a concentration of about 40 mM, 50 mM, 60 mM, 70 mM, 80 mM, 90 mM, 100 mM, 120 mM, 125 mM, 150 mM, 200 mM, or 250 mM.

[00226] 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.

[00227] In some embodiments, the pharmaceutical formulation comprises a poloxamer. In some embodiments, the poloxamer is poloxamer 188. In some embodiments, the concentration of poloxamer 188 in the pharmaceutical formulation is between 0.4 mg/mL to 1.5 mg/mL, between 0.4 mg/mL to 1.0 mg/mL, between 0.4 mg/mL to 0.6 mg/mL, between 0.5 mg/mL to 1.5 mg/mL, between 0.5 mg/mL to 1.0 mg/mL, between 0.5 mg/mL to 0.6 mg/mL, between 0.8 mg/mL to 1.5 mg/mL, between 0.8 mg/mL to 1.2 mg/mL, between 1.0 mg/mL to 1.5 mg/mL, or between 1.0 mg/mL to 1.2 mg/mL. In some embodiments, the concentration of poloxamer 188

in the pharmaceutical formulation is about 0.5 mg/mL. In some embodiments, the concentration of poloxamer 188 in the pharmaceutical formulation is about 1.0 mg/mL. In some embodiments, the concentration of poloxamer 188 in the pharmaceutical formulation is 0.5 mg/mL. In some embodiments, the concentration of poloxamer 188 in the pharmaceutical formulation is 1.0 mg/mL.

[00228] In some embodiments, a polysorbate acts as a stabilizer. In some embodiments, the polysorbate is at a concentration 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 is at a concentration between 0.02% and 0.14%. In some embodiments, the polysorbate is at a concentration between 0.03% and 0.13%. In some embodiments, the polysorbate is at a concentration between 0.04% and 0.12%. In some embodiments, the polysorbate is at a concentration between 0.05% and 0.11%.

[00229] In some embodiments, the polysorbate is at a concentration of about 0.01% w/v, about 0.02% w/v, about 0.03% w/v, about 0.04% w/v, about 0.05% w/v, about 0.06% w/v, about 0.07% w/v, about 0.08% w/v, about 0.09% w/v, about 0.1% w/v, about 0.11% w/v, about 0.12%, about 0.13% w/v, about 0.14% w/v, or about 0.15% w/v.

[00230] 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.

[00231] The one or more excipients in the pharmaceutical formulation of the present invention further comprises 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.

[00232] 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 10% w/v (*e.g.*, between 3% w/v and 10% w/v, between 5% w/v and 10% w/v, between 8% w/v and 10% w/v, between 3% and 8% w/v, or between 5% w/v and 8% w/v). In some embodiments, the
5 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. In some embodiments, the sugar or sugar alcohol is at a concentration of about 1%, about 2%, about 3%, about 4%, about 5% w/v, about 6% w/v, about 7% w/v, about 8% w/v, about 9% w/v, or about 10% w/v. In some embodiments, the
10 sugar or sugar alcohol is a disaccharide. In some embodiments, the disaccharide is sucrose.

[00233] In some embodiments, the formulation is adjusted to final volume in water for injection (WFI).

[00234] 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
15 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).

20 *Dosage Forms*

[00235] Prior to pharmaceutical use, the pharmaceutical formulation can be diluted in an aqueous carrier if suitable for the route of administration. 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
25 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
30 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.

[00236] The pharmaceutical formulation comprises the anti-IL-13 antibody or mixture of anti-IL-13 antibodies at a concentration suitable for storage. In certain embodiments, the pharmaceutical formulation comprises the anti-IL-13 antibody or mixture of anti-IL-13 antibodies at a concentration between 160 mg/mL and 220 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 anti-IL-13 antibody is at a concentration between 170 mg/mL and 210 mg/mL. In some embodiments, the anti-IL-13 antibody or mixture of anti-IL-13 antibodies is at a concentration between 180 mg/mL and 200 mg/mL.

[00237] In some embodiments, the anti-IL-13 antibody or mixture of anti-IL-13 antibodies is at a concentration of about 160 mg/mL, about 170 mg/mL, about 180 mg/mL, about 190 mg/mL, about 200 mg/mL, about 210 mg/mL, about 220 mg/mL, about 230 mg/mL, about 240 mg/mL, or about 250 mg/mL.

[00238] Formulations described herein may be included in *e.g.*, a vial. In some embodiments, the vial is a syringe. In some embodiments, the syringe is a prefilled syringe.

[00239] In some embodiments, the extractable volume of the vial is between 1.0 mL and 3.0 mL. In some embodiments, the volume of the vial is about 2.0 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.

[00240] In certain embodiments, the pharmaceutical formulation is delivered using a bag, an autoinjector, or an on-body delivery device. In certain embodiments, the pharmaceutical formulation is packaged in a vial (*e.g.*, a vial, bottle, bag, 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%.

[00241] In certain embodiments, the formulation may be a liquid formulation. In certain embodiments, the amount of anti-IL-13 antibody in the container is suitable for administration as a single dose. In certain embodiments, the amount of anti-IL-13 antibody in the container is suitable for administration in multiple doses. In certain embodiments, the pharmaceutical formulation comprises the anti-IL-13 antibody in an amount of 0.1 to 200 mg. In certain embodiments, the pharmaceutical formulation comprises the anti-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, 5 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 anti-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, 10 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

15 **[00242]** In some embodiments, the present application also provides compositions comprising a formulation, vial (e.g. pre-filled syringe) described herein for use in methods of treating an inflammatory disorder or disease, 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 20 year. In certain embodiments, the patient is a pediatric patient.

[00243] 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 25 ≥ 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 $\geq 10\%$.

[00244] 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.

[00245] 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.

[00246] 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.

[00247] 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.

[00248] 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.

[00249] 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.

[00250] 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.

[00251] 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:

- 5 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,
- 10 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
- 15 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).

- [00252]** In certain embodiments, a patient described herein is determined to have one or more
- 20 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
- 25 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
- 30 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

5 Quality Index (DLQI) at baseline and during and after the induction period.

[00253] In an aspect, the present application provides methods of contacting IL-13 with an anti-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.

[00254] In an aspect, the present application provides compositions comprising a formulation,

10 vial, or bag described herein for use in the treatment 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-

15 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), or Chronic Obstructive Pulmonary Disease (COPD).

20 **[00255]** 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, vial, or bag described herein.

[00256] In some embodiments, the inflammatory disorder or disease is atopic dermatitis.

25 **[00257]** In some embodiments, the inflammatory disorder or disease is 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

30 (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), or Chronic Obstructive Pulmonary Disease (COPD).

[00258] In some embodiments, the inflammatory disorder or disease is asthma. In some
5 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
10 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
15 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
20 (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
25 disease is Chronic Obstructive Pulmonary Disease (COPD).

[00259] 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 or vial described herein.

30 **[00260]** 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 or vial described herein.

[00261] 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
5 to the mammalian subject a therapeutically effective amount of the formulation or vial described herein.

[00262] 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
10 amount of the formulation or vial described herein.

[00263] 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 or vial described herein.

15 [00264] In some embodiments, the formulation or vial is administered subcutaneously or intravenously.

Examples

Example 1: Peptide Mapping by LC-MS/MS to Determine Presence and Approximate Amounts of Antibody Retaining a C-Terminal Lysine (500 L production culture)

20 [00265] Peptide mapping was used to identify and approximate the amounts of C-terminal lysine retained in a batch of anti-IL-13 antibodies.

[00266] The anti-IL-13 antibodies used in this experiment were generated from stable CHO cell lines transfected with expression vectors encoding the sequences for Construct 133 (which has the VH and VL sequences of SEQ ID NOs: 3 and 39, respectively, the light chain constant
25 region sequence of SEQ ID NO: 469, and the heavy chain constant region sequence of SEQ ID NO: 439 (lacks C-terminal lysine) or SEQ ID NO: 624) and express the antibody. The cell lines were serially expanded in vessels of increasing size and volume to reach a cell number sufficient to seed the 500L production bioreactor. The production bioreactor step involved a fed-batch process of approximately 14 days followed by a harvest step where the cell culture was clarified.
30 The clarified harvest was purified using three chromatography steps: protein A capture, anion

exchange, and cation exchange chromatography. Purified products were then concentrated, diafiltered, and formulated.

[00267] The purified antibodies were then denatured with guanidine hydrochloride (Gdn-HCl) and reduced by dithiothreitol (DTT), followed by cysteine-alkylation with iodoacetamide (IAM).

5 Proteolytic digestion was performed with endoproteinase Lys-C/Trypsin and thermolysin. The peptides were separated by reversed phase liquid chromatography with detection at 214 nm, and by a mass spectrometer operating with full MS scan followed by tandem mass spectrometry (MS/MS) scans. Peptide sequences were assigned by comparing masses to theoretical sequences of Construct 133, and the presence of C-terminal lysine was determined; all masses agreed with
10 theoretical within 10.0 ppm. Quantitation of antibodies with C-terminal lysine was determined by its relative area in extracted ion chromatograms (EICs).

[00268] Table 11 shows that, for Construct 133 encoded with the C-terminal lysine on the input sequence, about 3% to 4% of the output sequences included a C-terminal lysine. The remaining antibody species (96.3%) lacked the C-terminal lysine.

15

Table 11. Output sequences having a C-terminal lysine, no C-terminal lysine, or some other species at the C-terminus when the input sequence is with or without the C-terminal lysine.

Species	500L Lot without C-terminal lysine input	500L Lot with C-terminal lysine input
With C-terminal lysine (SLSLSPGK; SEQ ID NO: 710)	N/A	~3-4%
Without C-terminal lysine (SLSLSPG; SEQ ID NO: 711)	98.1%	94.5%
With other species at C-terminus (SLSLSP; SEQ ID NO: 712)	1.9%	1.8%

20 **Example 2: Quantitative Analysis of Antibody Retaining the C-Terminal Lysine via iCIEF (500 L production culture)**

[00269] Imaged capillary isoelectric focusing (iCIEF) is a charge heterogeneity analysis method used to monitor the percentage of charge variant species. The isoelectric point (pI) is an intrinsic property of a specific protein molecule and is the pH at which the protein molecule does

not carry net electrical charge. Under an external electric field, the charge variants move along a continuous pH gradient formed by ampholytes and stop where the pH equals its pI, since the protein carries no net electrical charge and would not be attracted by either electrode. Different antibody species with different pI values are focused and separated in different positions, thereby resolving charge-based isoforms. pI values and relative abundance of the resolved peaks are quantified using chromatographic software, and the relative abundance of the main peak as well as acidic and basic peak groups are reported. In this Example, iCIEF was used to monitor and quantify the presence/absence of C-terminal lysine on Construct 133 from a 500L production culture.

[00270] Briefly, Construct 133 encoded without a C-terminal lysine or with a C-terminal lysine, generated using the 500 L production culture described in Example 1, were mixed with a master mixture to generate a loading mixture, which contained Pharmalyte 8-10.5, Pharmalyte 3-10, 1% MC, pI marker 7.05, pI marker 9.22, urea, and ultrapure water at a final product concentration of 0.2 mg/mL. The loading mixture was loaded into a Maurice CIEF cartridge and analyzed with a Maurice Capillary Isoelectric Focusing Analyzer with a whole-column detection camera.

[00271] **Figure 1** shows the iCIEF profile for Construct 133 encoded without a C-terminal lysine. **Figure 2** shows the iCIEF profile for Construct 133 encoded with a C-terminal lysine. Results showed that the basic peak at about pI 8.3 was larger in **Figure 2** than in **Figure 1**. This larger peak in **Figure 2** is due to the presence of C-terminal lysine, which is a basic amino acid.

[00272] Next, the percentage of Construct 133 with a C-terminal lysine was quantified. Since basic peaks reflect the antibody with retained C-terminal lysine in addition to other modifications which can lead to basic peaks, the percentage of antibody with C-terminal lysine can be estimated by subtracting basic peaks of the sample treated with carboxypeptidase B (CPB), which removes the residual C-terminal lysine, from the basic peaks of the sample not treated with CPB.

[00273] The basic peaks of Construct 133 encoded without a C-terminal lysine (shown in **Figure 1** and referred to as reference standard ("RS") in **Table 12**) were quantified. As shown in **Table 12**, this sample had about 4.2% basic peaks, corresponding to basic peaks resulting from modifications other than C-terminal lysine since the encoded antibody does not include a C-terminal lysine.

[00274] Next, a portion of Construct 133 encoded with a C-terminal lysine was treated with CPB to remove any residual C-terminal lysine. As shown in **Table 13**, this resulted in about 8.0% basic peaks. When Construct 133 encoding a C-terminal lysine was treated with CPB, this yielded about 5.0% basic peaks. Accordingly, the amount of remaining C-terminal lysine in

5 Construct 133 was about 3.0% (i.e., 8.0% minus 5.0%).

Table 12. Percentage of Basic Peaks in Construct 133 encoded without a C-Terminal Lysine

	Sample	pI	% acidic peaks	% main peak	% basic peaks
	RS-1	8.1	19.5	76.3	4.2
	RS-2	8.1	19.6	76.1	4.3
	RS-3	8.1	19.6	76.3	4.1
	RS-4	8.1	20.1	75.8	4.1
Mean		8.1	19.7	76.1	4.2
SD		0.0	0.3	0.2	0.1
% RSD		0.0	1.3	0.3	2.8

10

Table 13: Percentage of Basic Peaks in Construct 133 encoded with a C-Terminal Lysine treated with or without carboxypeptidase B

	Main Peak %	Acidic Peaks %	Basic Peaks %
Without CPB	69.4	22.6	8.0
With CPB	72.5	22.5	5.0

15 **Example 3: Quantitative Analysis of Antibody Retaining the C-Terminal Lysine via iCIEF (2000 L production culture)**

[00275] In this Example, iCIEF was used to monitor and quantify the presence/absence of C-terminal lysine on Construct 133 from a 2000 L production culture.

[00276] Samples were prepared and processed essentially as described in Examples 1 and 2, but upscaled to a 2000 L production culture.

20 [00277] The basic peaks of Construct 133 encoded without a C-terminal lysine or with a C-terminal lysine treated either with or without CPB were quantified. **Tables 14** and **15** summarize the results for no treatment or treatment with CPB, respectively, of Construct 133 encoded

without a C-terminal lysine. **Table 16** summarizes the results for no treatment or treatment with CPB of Construct 133 encoded with a C-terminal lysine.

[00278] Without CPB treatment, % basic peaks of Construct 133 encoded without a C-terminal lysine was 3.5-4.1% (**Table 14**), whereas with CPB treatment, % basic peaks was about 3.9%-4.9% (**Table 15**). This difference in % basic peaks between with and without CPB treatment was likely due to analytical variability; % basic peaks did not decrease after CPB treatment because there is no C-terminal lysine to remove from the antibody.

[00279] With respect to Construct 133 encoded with a C-terminal lysine, without CPB treatment, % basic peaks was 7.5%, whereas with CPB treatment, % basic peaks was 3.8% (**Table 16**). This suggests that the sample had about 3.7% Construct 133 with a C-terminal lysine (i.e., 7.5% minus 3.8%). Given this relatively low level, the C-terminal lysine would likely be predominantly on one heavy chain, with very low amounts of the antibody having the C-terminal lysine on both heavy chains. This value (i.e., 3.7%) using the 2000 L production lot is similar to that obtained using the 500L production lot (~3%) based on the same analytical approach.

Table 14. Percentage of Basic Peaks in Construct 133 encoded without a C-Terminal Lysine without carboxypeptidase B treatment

	Sample	pI	% acidic peaks	% main peak	% basic peaks
	RS-1	8.1	20.9	75.2	3.9
	RS-2	8.1	20.3	75.6	4.1
	RS-3	8.1	21.3	74.7	4.0
Mean		8.1	20.9	75.2	4.0
SD		0.0	0.5	0.4	0.1
% RSD		0.0	2.4	0.6	2.5
	RS-X*	8.1	20.9	75.6	3.5

*The data for RS-X is from a separate experiment than those of RS-1 to RS-3.

Table 15. Percentage of Basic Peaks in Construct 133 encoded without a C-Terminal Lysine with carboxypeptidase B treatment

	Sample	pI	% acidic peaks	% main peak	% basic peaks
	RS-1	8.1	18.9	76.3	4.8
	RS-2	8.1	20.3	75.8	3.9
	RS-3	8.1	19.4	76.4	4.2
Mean		8.1	19.5	76.2	4.3
SD		0.0	0.7	0.3	0.4
% RSD		0.0	3.6	0.4	9.9
	RS-X*	8.1	20.2	75.0	4.9

*The data for RS-X is from a separate experiment than those of RS-1 to RS-3.

5 Table 16. Percentage of Basic Peaks in Construct 133 encoded with a C-Terminal Lysine with or without carboxypeptidase B treatment

Sample	pI	% acidic peaks	% main peak	% basic peaks
Without CPB	8.1	22.0	70.4	7.5
With CPB	8.1	19.5	76.6	3.8

Informal sequence listing

Description	Sequence	SEQ ID NO
Heavy Chain Variable domain HC0	QVQLQESGPGLVAPSQSL SITCTVSGFSLNAYS VNWVRQP PGKGLEWLGMIWGDGKIVYNSALKSRLNISKDSSKSQVFL KMSSLQSDDTARYYCAGDGYYPYAMDNWGHGTSVTVSS	SEQ ID NO: 1
Heavy Chain Variable domain HC0_M	QVQLQESGPGLVAPSQSL SITCTVSGFSLNAYS VNWVRQP PGKGLEWLGMIWGDGKIVYNSALKSRLTISKDSSKSQVFL KMSSLQSDDTARYYCAGDGYYPYAMDNWGHGTSVTVSS	SEQ ID NO: 2

Heavy Chain Variable domain HC1	EVQLQESGPGLVKPSETLSLTCTVSGFSLNAYSVNWIRQPP GKGLEWLGMIWGDGKIVYNSALKSRLTISKDSSKNQVSLK LSSVTAADTAVYYCAGDGYYPYAMDNWGQGTTVTVSS	SEQ ID NO: 3
Heavy Chain Variable domain HC2	EVQLVQSGAEVKKPGASVKVSCKASGFSLNAYSVNWVR QAPGQGLEWLGMIWGDGKIVYNSALKSRLTITKDSSTSTV YMELSSLRSED TAVYYCAGDGYYPYAMDNWGQGTTVTV SS	SEQ ID NO: 4
Heavy Chain Variable domain HC3	EVQLVQSGAEVKKPGSSVKVSCKASGFSLNAYSVNWVRQ APGQGLEWLGMIWGDGKIVYNSALKSRLTITKDSSTSTVY MELSSLRSED TAVYYCAGDGYYPYAMDNWGQGTTVTVS S	SEQ ID NO: 5
Heavy Chain Variable domain HC4	EVQLVESGGGLVKPGGSLRLSCAASGFSLNAYSVNWVRQ APGKGLEWLGMIWGDGKIVYNSALKSRLTISKDSSKNQTVY LQMNSLKTED TAVYYCAGDGYYPYAMDNWGQGTTVTV SS	SEQ ID NO: 6
Heavy Chain Variable domain HC5	EVQLLES GGGLVQPGGSLRLSCAASGFSLNAYSVNWVRQ APGKGLEWLGMIWGDGKIVYNSALKSRLTISKDSSKNQTVY LQMNSLRAED TAVYYCAGDGYYPYAMDNWGQGTTVTV SS	SEQ ID NO: 7
Heavy Chain Variable domain HC6	EVQLQESGPGLVKPSETLSLTCTVSGGSLNAYSVNWVRQP PGKGLEWLGMIWGDGKIVYNSALKSRLTISLDTSKSQVFL KMSSLTAADTAVYYCARDGYYPYAMDNWGQGTTVTVSS	SEQ ID NO: 8

Heavy Chain Variable domain HC7	QVQLQESGPGLVKPSETLSLTCTVSGGSLNAYSWNWVRQ PPGKGLEWLGYYIGDGKTNYNPALKSRLTISLDTSKSQVF LKMSSLTAADTAVYYCARDGYYYYAMDVWGQGTTTVTV SS	SEQ ID NO: 9
Heavy Chain Variable domain HC5m1	EVQLLESGGGLVQPGGSLRLSCAASGYSLNAYSVNWVRQ APGKGLEWLGMIWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMDNWGQGTTTVTV SS	SEQ ID NO: 10
Heavy Chain Variable domain HC5m2	EVQLLESGGGLVQPGGSLRLSCAASGFSRLAYSVNWVRQ APGKGLEWLGMIWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMDNWGQGTTTVTV SS	SEQ ID NO: 11
Heavy Chain Variable domain HC5m3	EVQLLESGGGLVQPGGSLRLSCAASGFSLHAYSVNWVRQ APGKGLEWLGMIWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMDNWGQGTTTVTV SS	SEQ ID NO: 12
Heavy Chain Variable domain HC5m4	EVQLLESGGGLVQPGGSLRLSCAASGFSLDAYSVNWVRQ APGKGLEWLGMIWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMDNWGQGTTTVTV SS	SEQ ID NO: 13
Heavy Chain Variable domain HC5m5	EVQLLESGGGLVQPGGSLRLSCAASGFSLYAYSVNWVRQ APGKGLEWLGMIWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMDNWGQGTTTVTV SS	SEQ ID NO: 14

Heavy Chain Variable domain HC5m6	EVQLLES GGGLVQP GGSRLRLSCAASGFSL SAYSVNWVRQ APGKGLEWLGM IWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMD NWGQGTTVTV SS	SEQ ID NO: 15
Heavy Chain Variable domain HC5m7	EVQLLES GGGLVQP GGSRLRLSCAASGFSLN RYSVNWVRQ APGKGLEWLGM IWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMD NWGQGTTVTV SS	SEQ ID NO: 16
Heavy Chain Variable domain HC5m8	EVQLLES GGGLVQP GGSRLRLSCAASGFSLN KYSVNWVRQ APGKGLEWLGM IWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMD NWGQGTTVTV SS	SEQ ID NO: 17
Heavy Chain Variable domain HC5m9	EVQLLES GGGLVQP GGSRLRLSCAASGFSLN HYSVNWVRQ APGKGLEWLGM IWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMD NWGQGTTVTV SS	SEQ ID NO: 18
Heavy Chain Variable domain HC5m10	EVQLLES GGGLVQP GGSRLRLSCAASGFSLN QYSVNWVRQ APGKGLEWLGM IWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMD NWGQGTTVTV SS	SEQ ID NO: 19
Heavy Chain Variable domain HC 5m11	EVQLLES GGGLVQP GGSRLRLSCAASGFSLN EYSVNWVRQ APGKGLEWLGM IWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMD NWGQGTTVTV SS	SEQ ID NO: 20

Heavy Chain Variable domain HC 5m12	EVQLLES GGGLVQP GGSRLRLSCAASG FSLNSYSVNWVRQ APGKGLEWLGM IWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMD NWGQGTTTVTV SS	SEQ ID NO: 21
Heavy Chain Variable domain HC5m13	EVQLLES GGGLVQP GGSRLRLSCAASG FSLNYYSVNWVRQ APGKGLEWLGM IWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMD NWGQGTTTVTV SS	SEQ ID NO: 22
Heavy Chain Variable domain HC5m14	EVQLLES GGGLVQP GGSRLRLSCAASG FSLNAESVNWVRQ APGKGLEWLGM IWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMD NWGQGTTTVTV SS	SEQ ID NO: 23
Heavy Chain Variable domain HC 5m15	EVQLLES GGGLVQP GGSRLRLSCAASG FSLNAYSVNWVRQ APGKGLEWLGM IWSDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMD NWGQGTTTVTV SS	SEQ ID NO: 24
Heavy Chain Variable domain HC5m16	EVQLLES GGGLVQP GGSRLRLSCAASG FSLNAYSVNWVRQ APGKGLEWLGM IWADGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYPYAMD NWGQGTTTVTV SS	SEQ ID NO: 25
Heavy Chain Variable domain HC5m17	EVQLLES GGGLVQP GGSRLRLSCAASG FSLNAYSVNWVRQ APGKGLEWLGM IWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGHGYYPYAMD NWGQGTTTVTV SS	SEQ ID NO: 26

Heavy Chain Variable domain HC5m18	EVQLLES GGGLVQP GGSRLRLSCAASGFSLNAYS VNWVRQ APGKGLEWLGM IWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDLYYPYAMD NWGQGTTTVTS S	SEQ ID NO: 27
Heavy Chain Variable domain HC5m19	EVQLLES GGGLVQP GGSRLRLSCAASGFSLNAYS VNWVRQ APGKGLEWLGM IWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDKYYPYAMD NWGQGTTTVT SS	SEQ ID NO: 28
Heavy Chain Variable domain HC5m20	EVQLLES GGGLVQP GGSRLRLSCAASGFSLNAYS VNWVRQ APGKGLEWLGM IWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYGYAMD NWGQGTTTVT SS	SEQ ID NO: 29
Heavy Chain Variable domain HC5m21	EVQLLES GGGLVQP GGSRLRLSCAASGFSLNAYS VNWVRQ APGKGLEWLGM IWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYAYAMD NWGQGTTTVT SS	SEQ ID NO: 30
Heavy Chain Variable domain HC5m22	EVQLLES GGGLVQP GGSRLRLSCAASGFSLNAYS VNWVRQ APGKGLEWLGM IWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYYSYAMD NWGQGTTTVT SS	SEQ ID NO: 31
Heavy Chain Variable domain HC5m23	EVQLLES GGGLVQP GGSRLRLSCAASGFSLNAYS VNWVRQ APGKGLEWLGM IWGDGKIVYNSALKSRLTISKDSSKNTVY LQMNSLRAEDTAVYYCAGDGYITYAMD NWGQGTTTVT SS	SEQ ID NO: 32

Light Chain Variable domain LC0	NIVLTQSPASLAVSLGQRATISCRASKSVDSYGNSFMHWY QQKPGQPPKLLIYLASNLESGVPARFSGSGSRTDFTLTIDPV EADDAASYCQNNEDPRTFGGGTKLEIK	SEQ ID NO: 33
Light Chain Variable domain LC1	DIQLTQSPSSLASVGDRVTITCRASKSVDSYGNSFMHWY QQKPGKAPKLLIYLASNLESGVPSRFSGSGSRTDFTLTISL QPEDFATYYCQNNEDPRTFGGGTKVEIK	SEQ ID NO: 34
Light Chain Variable domain LC2	DIQLTQSPSSLASVGDRVTITCRASKSVDSYGNSFMHWY QQKPGKAPKLLIYLASNLESGVPSRFSGSGSRTDFTLTISL QPEDFATYYCQNNEDPRTFGGGTKVEIK	SEQ ID NO: 35
Light Chain Variable domain LC3	EIVLTQSPATLSVSPGERATLSCRASKSVDSYGNSFMHWY QQKPGQAPRLIYLASNLESGIPARFSGSGSRTEFTLTISL QSEDFAVYYCQNNEDPRTFGGGTKVEIK	SEQ ID NO: 36
Light Chain Variable domain LC4	DIVLTQSPSLPVTPGEPASISCRASKSVDSYGNSFMHWY QKPGQSPQLLIYLASNLESGVPDRFSGSGSRTDFTLKISRVE AEDVGVYYCQNNEDPRTFGGGTKVEIK	SEQ ID NO: 37
Light Chain Variable domain LC5	DIVLTQSPDSLAVSLGERATINCRASKSVDSYGNSFMHWY QQKPGQPPKLLIYLASNLESGVPDRFSGSGSGTDFTLTISL QAEDVAVYYCQNNEDPRTFGGGTKVEIK	SEQ ID NO: 38
Light Chain Variable domain LC6	DIQLTQSPSSLASVGDRVTITCRASKSVDSYGNSFMHWY QQKPGKAPKLLIYLASNLESGVPSRFSGSGSGTDFTLTISL QPEDFATYYCQNNEDPRTFGGGTKVEIK	SEQ ID NO: 39
Light Chain Variable domain	EIVLTQSPATLSVSPGERATLSCRASKSVDSYGNSFMHWY QQKPGQAPRLIYLASNLESGIPARFSGSGSGTEFTLTISL QSEDFAVYYCQNNEDPRTFGGGTKVEIK	SEQ ID NO: 40

LC7		
Light Chain Variable domain LC8	DIVLTQSPSLSPVTPGEPASISCRASKSVDSYGNSFMHWYL QKPGQSPQLLIYLASNLESGVPDRFSGSGSGTDFTLKISRVE AEDVGVYYCQQNNEDPRTFGGGTKVEIK	SEQ ID NO: 41
Light Chain Variable domain LC9	DIVLTQSPASLAVSPGERATISCRASKSVDSYGNSFMHWY QQKPGQPPKLLIYLASNLESGVPDRFSGSGSGTDFTLTISR EADDVAVYYCQQNNEDPRTFGGGTKLEIK	SEQ ID NO: 42
Light Chain Variable domain LC10	DIVLTQSPASLAVSPGERATISCRASQSVDSNGNNFLHWY QQKPGQPPKLLIYLASNRESGVPDRFSGSGSGTDFTLTISR VEADDVAVYYCQQNNHTPRTFGGGTKLEIK	SEQ ID NO: 43
Light Chain Variable domain LC6_m1	DIQLTQSPSSLSASVGDRVITTCRASKSVDSYGNSRMHWY QQKPGKAPKLLIYLASNLESGVPSRFSGSGSGTDFTLTISL QPEDFATYYCQQNNEDPRTFGGGTKVEIK	SEQ ID NO: 44
Light Chain Variable domain LC6_m2	DIQLTQSPSSLSASVGDRVITTCRASKSVDSYGNSSMHWY QQKPGKAPKLLIYLASNLESGVPSRFSGSGSGTDFTLTISL QPEDFATYYCQQNNEDPRTFGGGTKVEIK	SEQ ID NO: 45
Light Chain Variable domain LC6_m3	DIQLTQSPSSLSASVGDRVITTCRASKSVDSYGNSFMHWY QQKPGKAPKLLIRLASNLESGVPSRFSGSGSGTDFTLTISL QPEDFATYYCQQNNEDPRTFGGGTKVEIK	SEQ ID NO: 46
Light Chain Variable domain LC6_m4	DIQLTQSPSSLSASVGDRVITTCRASKSVDSYGNSFMHWY QQKPGKAPKLLIFLASNLESGVPSRFSGSGSGTDFTLTISL QPEDFATYYCQQNNEDPRTFGGGTKVEIK	SEQ ID NO: 47

Light Chain Variable domain LC6_m5	DIQLTQSPSSLSASVGDRVITICRASKSVDSYGNSFMHWY QQKPGKAPKLLIYLASHLESGVPSRFSGSGSGTDFTLTISL QPEDFATYYCQQNNEDPRTFGGGTKVEIK	SEQ ID NO: 48
Light Chain Variable domain LC6_m6	DIQLTQSPSSLSASVGDRVITICRASKSVDSYGNSFMHWY QQKPGKAPKLLIYLASDLESGVPSRFSGSGSGTDFTLTISL QPEDFATYYCQQNNEDPRTFGGGTKVEIK	SEQ ID NO: 49
Light Chain Variable domain LC6_m7	DIQLTQSPSSLSASVGDRVITICRASKSVDSYGNSFMHWY QQKPGKAPKLLIYLASQLESGVPSRFSGSGSGTDFTLTISL QPEDFATYYCQQNNEDPRTFGGGTKVEIK	SEQ ID NO: 50
Light Chain Variable domain LC6_m8	DIQLTQSPSSLSASVGDRVITICRASKSVDSYGNSFMHWY 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 QPEDFATYYCQQNSEDPRTFGGGKVEIK	SEQ ID NO: 54

Light Chain Variable domain LC6_m12	DIQLTQSPSSLSASVGDRVTITCRASKSVDSYGNSFMHWY QQKPGKAPKLLIYLASNLESGVPSRFSGSGSGTDFTLTISL QPEDFATYYCQQNNRDPRTFGGGTKVEIK	SEQ ID NO: 55
Light Chain Variable domain LC6_m13	DIQLTQSPSSLSASVGDRVTITCRASKSVDSYGNSFMHWY QQKPGKAPKLLIYLASNLESGVPSRFSGSGSGTDFTLTISL QPEDFATYYCQQNNDDPRTFGGGTKVEIK	SEQ ID NO: 56
Light Chain Variable domain LC6_m14	DIQLTQSPSSLSASVGDRVTITCRASKSVDSYGNSFMHWY 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	GFSLHAY	SEQ ID NO: 73

HCDR1		
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	GFSLNAE	SEQ ID NO: 83

HCDR1		
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	GFS LHAYS	SEQ ID NO: 89
HC5_m4 IMGT HCDR1	GFS LDAYS	SEQ ID NO: 90
HC5_m5 IMGT HCDR1	GFS LYAYS	SEQ ID NO: 91
HC5_m6 IMGT HCDR1	GFS LSAYS	SEQ ID NO: 92

HC5_m7 IMGT HCDR1	GFSLNRYYS	SEQ ID NO: 93
HC5_m8 IMGT HCDR1	GFSLNKYYS	SEQ ID NO: 94
HC5_m9 IMGT HCDR1	GFSLNHYYS	SEQ ID NO: 95
HC5_m10 IMGT HCDR1	GFSLNQYYS	SEQ ID NO: 96
HC5_m11 IMGT HCDR1	GFSLNEYYS	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	YIYGDGKTNYNPALKS	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	DGYYPYAMDN	SEQ ID NO: 112

HCDR3		
HC7 Kabat and Chothia HCDR3	DGYYYAMDV	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 HCDR3	AGDGYYTYAMDN	SEQ ID NO: 139
HC1_m6 IMGT HCDR3	AGDGYYPYAMDN	SEQ ID NO: 140
Parental Kabat and Chothia	RASKSVDSYGNSFMH	SEQ ID NO: 141

LCDR1		
LC10 Kabat and Chothia LCDR1	RASQSVDSNGNNFLH	SEQ ID NO: 142
LC6_m1 Kabat and Chothia LCDR1	RASKSVDSYGN SRMH	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 Kabat and Chothia LCDR2	LASNRES	SEQ ID NO: 158
		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	QQNSEDPRT	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	QVQLQESGPGLVAPSQSL SITCTVSGFSLN	SEQ ID NO: 198

HC0_M Kabat		
HC Framework Region 1 HC1 Kabat	EVQLQESGPGLVKPSSETLSLTCTVSGFSLN	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	EVQLVESGGGLVKGPGSLRLSCAASGFSLN	SEQ ID NO: 203
HC Framework Region 1 HC5 Kabat	EVQLLESGGGLVQPGGSLRLSCAASGFSLN	SEQ ID NO: 204
HC Framework Region 1 HC6 Kabat	EVQLQESGPGLVKPSSETLSLTCTVSGGSLN	SEQ ID NO: 205
HC Framework Region 1 HC7 Kabat	QVQLQESGPGLVKPSSETLSLTCTVSGGSLN	SEQ ID NO: 206

HC Framework Region 1 HC5_m1 Kabat	EVQLLES GGGLVQPGGSLRLSCAASGYSLN	SEQ ID NO: 207
HC Framework Region 1 HC5_m2 Kabat	EVQLLES GGGLVQPGGSLRLSCAASGFSLR	SEQ ID NO: 208
HC Framework Region 1 HC5_m3 Kabat	EVQLLES GGGLVQPGGSLRLSCAASGFSLH	SEQ ID NO: 209
HC Framework Region 1 HC5_m4 Kabat	EVQLLES GGGLVQPGGSLRLSCAASGFSLD	SEQ ID NO: 210
HC Framework Region 1 HC5_m5 Kabat	EVQLLES GGGLVQPGGSLRLSCAASGFSLY	SEQ ID NO: 211
HC Framework Region 1 HC5_m6 Kabat	EVQLLES GGGLVQPGGSLRLSCAASGFSLS	SEQ ID NO: 212

HC Framework Region 1 HC5_m7 Kabat	EVQLLES GGGLVQPGGSLRLSCAASG FSLN	SEQ ID NO: 204
HC Framework Region 1 HC5_m8 Kabat	EVQLLES GGGLVQPGGSLRLSCAASG FSLN	SEQ ID NO: 204
HC Framework Region 1 HC5_m9 Kabat	EVQLLES GGGLVQPGGSLRLSCAASG FSLN	SEQ ID NO: 204
HC Framework Region 1 HC5_m10 Kabat	EVQLLES GGGLVQPGGSLRLSCAASG FSLN	SEQ ID NO: 204
HC Framework Region 1 HC5_m11 Kabat	EVQLLES GGGLVQPGGSLRLSCAASG FSLN	SEQ ID NO: 204
HC Framework Region 1 HC5_m12 Kabat	EVQLLES GGGLVQPGGSLRLSCAASG FSLN	SEQ ID NO: 204

HC Framework Region 1 HC5_m13 Kabat	EVQLLES GGGLVQPGGSLRLSCAASG FSLN	SEQ ID NO: 204
HC Framework Region 1 HC5_m14 Kabat	EVQLLES GGGLVQPGGSLRLSCAASG FSLN	SEQ ID NO: 204
HC Framework Region 1 HC5_m15 Kabat	EVQLLES GGGLVQPGGSLRLSCAASG FSLN	SEQ ID NO: 204
HC Framework Region 1 HC5_m16 Kabat	EVQLLES GGGLVQPGGSLRLSCAASG FSLN	SEQ ID NO: 204
HC Framework Region 1 HC5_m17 Kabat	EVQLLES GGGLVQPGGSLRLSCAASG FSLN	SEQ ID NO: 204
HC Framework Region 1 HC5_m18 Kabat	EVQLLES GGGLVQPGGSLRLSCAASG FSLN	SEQ ID NO: 204

HC Framework Region 1 HC5_m19 Kabat	EVQLLES GGGLVQPGGSLRLSCAASG FSLN	SEQ ID NO: 204
HC Framework Region 1 HC5_m20 Kabat	EVQLLES GGGLVQPGGSLRLSCAASG FSLN	SEQ ID NO: 204
HC Framework Region 1 HC5_m21 Kabat	EVQLLES GGGLVQPGGSLRLSCAASG FSLN	SEQ ID NO: 204
HC Framework Region 1 HC5_m22 Kabat	EVQLLES GGGLVQPGGSLRLSCAASG FSLN	SEQ ID NO: 204
HC Framework Region 1 HC5_m24 Kabat	EVQLLES GGGLVQPGGSLRLSCAASG FSLN	SEQ ID NO: 204
LC Framework Region 1LC0 Kabat	NIVLTQSPASLAVSLGQRATISC	SEQ ID NO: 230

LC Framework Region 1 LC1 Kabat	DIQLTQSPSSLSASVGDRVTITC	SEQ ID NO: 231
LC Framework Region 1 LC2 Kabat	DIQLTQSPSSLSASVGDRVTITC	SEQ ID NO: 231
LC Framework Region 1 LC3 Kabat	EIVLTQSPATLSVSPGERATLSC	SEQ ID NO: 233
LC Framework Region 1 LC4 Kabat	DIVLTQSPSLPVTGPGEPAISIC	SEQ ID NO: 234
LC Framework Region 1 LC5 Kabat	DIVLTQSPDSLAVSLGERATINC	SEQ ID NO: 235
LC Framework Region 1 LC6 Kabat	DIQLTQSPSSLSASVGDRVTITC	SEQ ID NO: 231
LC Framework Region 1 LC7 Kabat	EIVLTQSPATLSVSPGERATLSC	SEQ ID NO: 233

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	WYQQKPGKAPKLLIR	SEQ ID NO: 300

LC6_m3 Kabat		
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	WYQQKPGKAPKLLIY	SEQ ID NO: 288

LC6_m9 Kabat		
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	RLTISKDTSKNQVVLMTNMDPVDATYYCAG	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	RLTISKDSSKNTVY LQMNSLKTED TAVYYCAG	SEQ ID NO: 317
HC Framework Region 3 HC5 Kabat	RLTISKDSSKNTVY LQMNSLRAED 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	RLTISKDSSKNTVYLQMNSLRAEDTAVYYCAG	SEQ ID NO: 318
HC Framework Region 3 HC5_m6 Kabat	RLTISKDSSKNTVYLQMNSLRAEDTAVYYCAG	SEQ ID NO: 318
HC Framework Region 3 HC5_m7 Kabat	RLTISKDSSKNTVYLQMNSLRAEDTAVYYCAG	SEQ ID NO: 318
HC Framework Region 3 HC5_m8 Kabat	RLTISKDSSKNTVYLQMNSLRAEDTAVYYCAG	SEQ ID NO: 318
HC Framework Region 3 HC5_m9 Kabat	RLTISKDSSKNTVYLQMNSLRAEDTAVYYCAG	SEQ ID NO: 318
HC Framework Region 3 HC5_m10 Kabat	RLTISKDSSKNTVYLQMNSLRAEDTAVYYCAG	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	RLTISKDSSKNTVYLQMNSLRAEDTAVYYCAG	SEQ ID NO: 318
HC Framework Region 3 HC5_m18 Kabat	RLTISKDSSKNTVYLQMNSLRAEDTAVYYCAG	SEQ ID NO: 318
HC Framework Region 3 HC5_m19 Kabat	RLTISKDSSKNTVYLQMNSLRAEDTAVYYCAG	SEQ ID NO: 318
HC Framework Region 3 HC5_m20 Kabat	RLTISKDSSKNTVYLQMNSLRAEDTAVYYCAG	SEQ ID NO: 318
HC Framework Region 3 HC5_m21 Kabat	RLTISKDSSKNTVYLQMNSLRAEDTAVYYCAG	SEQ ID NO: 318
HC Framework Region 3 HC5_m22 Kabat	RLTISKDSSKNTVYLQMNSLRAEDTAVYYCAG	SEQ ID NO: 318

HC Framework Region 3 HC5_m24 Kabat	RLTISKDSSKNTVYLMNSLRAEDTAVYYCAG	SEQ ID NO: 318
Lebrikizuma b - LC	GVPDRFSGSGSGTDFTLTISLQAEDVAVYYC	SEQ ID NO: 343
LC Framework Region 3 LC0 Kabat	GVPARFSGSGSRTDFTLTIDPVEADDAASYC	SEQ ID NO: 344
LC Framework Region 3 LC1 Kabat	GVPSRFSGSGSRTDFTLTISLQPEDFATYYC	SEQ ID NO: 345
LC Framework Region 3 LC2 Kabat	GVPSRFSGSGSRTDFTLTISLQPEDFATYYC	SEQ ID NO: 345
LC Framework Region 3 LC3 Kabat	GIPARFSGSGSRTEFTLTISLQSEDFAVYYC	SEQ ID NO: 347
LC Framework Region 3 LC4 Kabat	GVPDRFSGSGSRTDFTLKISRVEAEDVGVYYC	SEQ ID NO: 348
LC Framework Region 3	GVPDRFSGSGSGTDFTLTISLQAEDVAVYYC	SEQ ID NO: 716

LC6 Kabat		
LC Framework Region 3 LC7 Kabat	GIPARFSGSGSGTEFTLTISLQSEDFAVYYC	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	GVPSRFSGSGSGTDFTLTISLQPEDFATYYC	SEQ ID NO: 349

Region 3 LC6_m3 Kabat		
LC Framework Region 3 LC6_m4 Kabat	GVPSRFSGSGSGTDFTLTISLQPEDFATYYC	SEQ ID NO: 349
LC Framework Region 3 LC6_m5 Kabat	GVPSRFSGSGSGTDFTLTISLQPEDFATYYC	SEQ ID NO: 349
LC Framework Region 3 LC6_m6 Kabat	GVPSRFSGSGSGTDFTLTISLQPEDFATYYC	SEQ ID NO: 349
LC Framework Region 3 LC6_m7 Kabat	GVPSRFSGSGSGTDFTLTISLQPEDFATYYC	SEQ ID NO: 349
LC Framework Region 3 LC6_m8 Kabat	GVPSRFSGSGSGTDFTLTISLQPEDFATYYC	SEQ ID NO: 349
LC Framework	GVPSRFSGSGSGTDFTLTISLQPEDFATYYC	SEQ ID NO: 349

Region 3 LC6_m9 Kabat		
LC Framework Region 3 LC6_m10 Kabat	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	SEQ ID NO: 349
LC Framework Region 3 LC6_m11 Kabat	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	SEQ ID NO: 349
LC Framework Region 3 LC6_m12 Kabat	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	SEQ ID NO: 349
LC Framework Region 3 LC6_m13 Kabat	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	SEQ ID NO: 349
LC Framework Region 3 LC6_m14 Kabat	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	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 HC0_M Kabat	WGHGTSVTVSS	SEQ ID NO: 369
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	FGGGTKVEIK	SEQ ID NO: 400

LC5 Kabat		
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 LC8 Kabat	FGGGTKVEIK	SEQ ID NO: 400
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	FGGGTKVEIK	SEQ ID NO: 400

LC6_m2 Kabat		
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 Region 4 LC6_m5 Kabat	FGGGTKVEIK	SEQ ID NO: 400
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	FGGGTKVEIK	SEQ ID NO: 400

LC6_m8 Kabat		
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 LC6_m11 Kabat	FGGGTKVEIK	SEQ ID NO: 400
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	FGGGTKVEIK	SEQ ID NO: 400

LC6_m14 Kabat		
Heavy Chain hIgG1	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPG	SEQ ID NO: 425
Heavy Chain hIgG4	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGKTKYT CNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKS LSLSLGK	SEQ ID NO: 426
Heavy Chain IgG4-SP	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGKTKYT CNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKS LSLSLGK	SEQ ID NO: 427

Heavy Chain IgG4-SPLE	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGKTYT CNVDHKPSNTKVDKRVESKYGPPCPPCPAPEELGGPSVFL FPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKS LSLSLGK	SEQ ID NO: 428
Heavy Chain IgG2	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVPSSNFGTQTYT CNVDHKPSNTKVDKTKVERKCCVECPAPPVAGPSVFLF PPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGV EVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKC KVSNGKLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIA VEWESNGQPENNYKTPPMLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSP	SEQ ID NO: 429
Heavy Chain hIgG1- N297A	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPG	SEQ ID NO: 430
Heavy Chain	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG	SEQ ID NO: 431

hIgG1-D265A	PSVFLFPPKPKDTLMISRTPEVTCVVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPG	
Heavy Chain hIgG1-LALA	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPG	SEQ ID NO: 432
Heavy Chain hIgG1-LAGA	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPG	SEQ ID NO: 433
Heavy Chain hIgG1-LALAGA	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD	SEQ ID NO: 434

	ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPG	
Heavy Chain hIgG1- LALAPG	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP PVLDSGDSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPG	SEQ ID NO: 435
Heavy Chain hIgG1-YTE	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLYITREPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPG	SEQ ID NO: 436
Heavy Chain hIgG1- N297A/YT E	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLYITREPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPG	SEQ ID NO: 437

Heavy Chain hIgG1-D265A/YTE	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLYITREPEVTCVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPG	SEQ ID NO: 438
Heavy Chain hIgG1-LALA/YTE	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLYITREPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPG	SEQ ID NO: 439
Heavy Chain hIgG1-LAGA/YTE	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLYITREPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPG	SEQ ID NO: 440
Heavy Chain	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA	SEQ ID NO: 441

hIgG1-LALAGA/YTE	PSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPG	
Heavy Chain hIgG1-LALAPG/YTE	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP PVLDSGDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPG	SEQ ID NO: 442
Heavy Chain hIgG1-LS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSC SVLHEALHSHYTQKSLSLSPG	SEQ ID NO: 443
Heavy Chain hIgG1-N297A/LS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD	SEQ ID NO: 444

	ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSC SVLHEALHSHYTQKSLSLSPG	
Heavy Chain hIgG1- D265A/LS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSC SVLHEALHSHYTQKSLSLSPG	SEQ ID NO: 445
Heavy Chain hIgG1- LALA/LS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSC SVLHEALHSHYTQKSLSLSPG	SEQ ID NO: 446
Heavy Chain hIgG1- LAGA/LS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSC SVLHEALHSHYTQKSLSLSPG	SEQ ID NO: 447

Heavy Chain hIgG1-LALAGA/LS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSC SVLHEALHSHYTQKSLSLSPG	SEQ ID NO: 448
Heavy Chain hIgG1-LALAPG/LS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP PVLDSGDGSFFLYSKLTVDKSRWQQGNVFSC SVLHEALHSHYTQKSLSLSPG	SEQ ID NO: 449
Heavy Chain hIgG1-DHS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVDHHDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHSHYTQKSLSLSPG	SEQ ID NO: 450
Heavy Chain	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG	SEQ ID NO: 451

hIgG1- N297A/DH S	PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLTVDHHDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHSHYTQKSLSLSPG	
Heavy Chain hIgG1- D265A/DH S	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVDHHDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHSHYTQKSLSLSPG	SEQ ID NO: 452
Heavy Chain hIgG1- LALA/DHS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVDHHDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHSHYTQKSLSLSP	SEQ ID NO: 453
Heavy Chain hIgG1- LAGA/DHS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVDHHDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD	SEQ ID NO: 454

	ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHSHYTQKSLSLSPG	
Heavy Chain hIgG1- LALAGA/D HS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVDHHDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHSHYTQKSLSLSPG	SEQ ID NO: 455
Heavy Chain hIgG1- LALAPG/D HS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVDHHDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP PVLDSGDSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHSHYTQKSLSLSPG	SEQ ID NO: 456
Heavy Chain IgG4-YTE	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYT CNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFL FPPKPKDTLYITREPEVTCVVDVVSQEDPEVQFNWYVDGV EVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKC KVSNGKLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDG SFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSL SLSLGK	SEQ ID NO: 457

Heavy Chain IgG4-SP/YTE	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTKTYT CNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLYITREPEVTCVVDVDSQEDPEVQFNWYVDGV EVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKC KVSNGKLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDG SFFLYSRLTVDKSRWQEGNVFSCSVMHREALHNHYTQKSL LSLGK	SEQ ID NO: 458
Heavy Chain IgG4-SPLE/YTE	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTKTYT CNVDHKPSNTKVDKRVESKYGPPCPPCPAPEELGGPSVFL FPPKPKDTLYITREPEVTCVVDVDSQEDPEVQFNWYVDGV EVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKC KVSNGKLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDG SFFLYSRLTVDKSRWQEGNVFSCSVMHREALHNHYTQKSL LSLGK	SEQ ID NO: 459
Heavy Chain IgG4-LS	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTKTYT CNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNGKLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVLHEALHSYTQKSLS LSLGK	SEQ ID NO: 460
Heavy Chain IgG4-SP/LS	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTKTYT CNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFL	SEQ ID NO: 461

	FPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVLHEALHSHYTQKSL SLSLGK	
Heavy Chain IgG4- SPLE/LS	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTKTYT CNVDHKPSNTKVDKRVESKYGPPCPPCPAPEELGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVLHEALHSHYTQKSL SLSLGK	SEQ ID NO: 462
Heavy Chain IgG4-DHS	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTKTYT CNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVDHHDWLNGKEY KCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD DGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHSHYTQK SLSLSLGK	SEQ ID NO: 463
Heavy Chain IgG4- SP/DHS	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTKTYT CNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVDHHDWLNGKEY KCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK	SEQ ID NO: 464

	NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDS DGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHSHYTQK SLSLSLGK	
Heavy Chain IgG4- SPLE/DHS	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTKTYT CNVDHKPSNTKVDKRVESKYGPPCPPCAPEELGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVDHHDLNGLKEY KCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSSEEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDS DGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHSHYTQK SLSLSLGK	SEQ ID NO: 465
Heavy Chain IgG2-YTE	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYT CNVDHKPSNTKVDKTVKCCVECPAPPVAGPSVFLF PPKPKDTLYITREPEVTCVVVDVSHEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCK VSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQV SLTCLVKGFYPSDIA VEWESNGQPENNYKTPPMLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVLHEALHSHYTQKSLSLSP	SEQ ID NO: 466
Heavy Chain IgG2-LS	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSNFGTQTYT CNVDHKPSNTKVDKTVKCCVECPAPPVAGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGV EVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKC KVSNGKLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPMLDSDG SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSP	SEQ ID NO: 467

Heavy Chain IgG2-DHS	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYT CNVDHKPSNTKVDKTKVERKCCVECPPCAPPVAGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGV EVHNAKTKPREEQFNSTFRVVSFLTVDHHDWLNGKEYKC KVSNGKLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPMLDSDG SFFLYSKLTVDKSRWQQGNVFCFSVMHEALHSHYTQKSL SLSP	SEQ ID NO: 468
Light Chain Human kappa LC	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ WKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC	SEQ ID NO: 469
Lebrikizuma b Heavy Chain Variable Region	QVTLRSGPALVKPTQTLTLCTVSGFSLAYSVNWIRQPP GKALEWLAMIWGDGKIVYNSALKSRLTISKDTSKNQVVL TMTNMDPVDATYYCAGDGYYPYAMDNWGQGS�VTVS S	SEQ ID NO: 470
Lebrikizuma b Light Chain Variable Region	DIVMTQSPDSLVSLSGERATINCRASKSVDSYGNSFMHWY QQKPGQPPLLIYLASNLESGVPDRFSGSGSGTDFTLTISL QAEDVAVYYCQQNNEDPRTFGGGTKVEIK	SEQ ID NO: 471
Human IL-13 Full sequence	MHPLLNPLLLALGLMALLTTVIALTCLGGFASPGPVPPST ALRELIEELVNITQNQKAPLCNGSMVWSINLTAGMYCAAL ESLINVSGCSAIEKTQRMLSGFCPHKVSAGQFSSLHVRDTK IEVAQFVKDLLHLKKLFREGRFN	SEQ ID NO: 472

Cynomolgus Monkey IL- 13 Full sequence	MALLLTMVIALTCLGGFASPSPVPPSTALKELIEELVNITQN QKAPLCNGSMVWSINLTAGVYCAALESINVSGCSAIEKT QRMLNGFCPHKVSAGQFSSLRVRDTKIEVAQFVKDLLVH 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 LCN SSMVWSVDLTAGGFCAALES LTNIS SC NAIHRTQRILNGLCNQKASDVASSPPDTKIEVAQFISKLLN YSKQLFRYGH	SEQ ID NO: 475
Human IL- 13 Leader sequence	MHPLLNPLLLALGLMALLLTTVIA	SEQ ID NO: 476
Cynomolgus Monkey IL- 13 Leader sequence	MALLLTMVIALTCLGGFA	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 LTNISSCNAIHR TQRILNGLCNQKASD VASSPPDTKIEVAQFISKLLNYSKQLFRYGH	SEQ ID NO: 483
hIgG1-LA	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSV VTPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDS DGSFFLYSKLTVDKSRWQQGNV FSCSVLHEALHAH YTQKSLSLSPG	SEQ ID NO: 484
hIgG1-N297A/LA	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSV VTPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLN	SEQ ID NO: 485

	GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHAH YTQKSLSLSPG	
hIgG1- D265A/LA	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHAH YTQKSLSLSPG	SEQ ID NO: 486
hIgG1- LALA/LA	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHAH YTQKSLSLSPG	SEQ ID NO: 487
hIgG1- LAGA/LA	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP	SEQ ID NO: 488

	VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHAH YTQKSLSLSPG	
hIgG1- LALAGA/L A	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHAH YTQKSLSLSPG	SEQ ID NO: 489
hIgG1- LALAPG/L A	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP PVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHA HYTQKSLSLSPG	SEQ ID NO: 490
hIgG1- N434A	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHAH YTQKSLSLSPG	SEQ ID NO: 491

hIgG1- N297A/ N434A	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHAH YTQKSLSLSPG	SEQ ID NO: 492
hIgG1- D265A/ N434A	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVAVSHEDPEVKFNW 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	SEQ ID NO: 495

	PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHAH YTQKSLSLSPG	
hIgG1- LALAGA/ N434A	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHAH YTQKSLSLSPG	SEQ ID NO: 496
hIgG1- LALAPG/ N434A	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP PVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHA HYTQKSLSLSPG	SEQ ID NO: 497
hIgG1- N434W	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD	SEQ ID NO: 498

	ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHW HYTQKSLSLSPG	
hIgG1- N297A/ N434W	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHW HYTQKSLSLSPG	SEQ ID NO: 499
hIgG1- D265A/ N434W	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHW HYTQKSLSLSPG	SEQ ID NO: 500
hIgG1- LALA/ N434W	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHW HYTQKSLSLSPG	SEQ ID NO: 501

hIgG1-LAGA/ N434W	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHW HYTQKSLSLSPG	SEQ ID NO: 502
hIgG1-LALAGA/ N434W	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHW HYTQKSLSLSPG	SEQ ID NO: 503
hIgG1-LALAPG/ N434W	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP PVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHW HYTQKSLSLSPG	SEQ ID NO: 504
hIgG1/DQ	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG	SEQ ID NO: 505

	PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	
hIgG1- N297A/DQ	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLQVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 506
hIgG1- D265A/DQ	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 507
hIgG1- LALA/DQ	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHQDWLN	SEQ ID NO: 508

	GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	
hIgG1- LAGA/DQ	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVHLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 509
hIgG1- LALAGA/D Q	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVHLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 510
hIgG1- LALAPG/D Q	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVHLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP	SEQ ID NO: 511

	PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPG	
hIgG1/DW	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLWVHLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 512
hIgG1- N297A/DW	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLWVHLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 513
hIgG1- D265A/DW	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLWVHLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 514

hIgG1- LALA/DW	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLWV LHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 515
hIgG1- LAGA/DW	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLWV LHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 516
hIgG1- LALAGA/D W	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLWV LHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 517
hIgG1- LALAPG/D W	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG	SEQ ID NO: 518

	PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLWV LHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP PVLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPG	
hIgG1/YD	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLYISRDP E VTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 519
hIgG1- N297A/YD	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLYISRDP E VTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 520
hIgG1- D265A/YD	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLYISRDP E VTCVVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN	SEQ ID NO: 521

	GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	
hIgG1- LALA/YD	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLYISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 522
hIgG1- LAGA/YD	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLYISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 523
hIgG1- LALAGA/Y D	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLYISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP	SEQ ID NO: 524

	VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	
hIgG1- LALAPG/Y D	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLYISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP PVLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPG	SEQ ID NO: 525
hIgG1/QVV	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTPP VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 526
hIgG1- N297A/QV V	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLQVLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTPP VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 527

hIgG1-D265A/QV V	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVHLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 528
hIgG1-LALA/QVV	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVHLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 529
hIgG1-LAGA/QV V	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVHLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 530
hIgG1-LALAGA/Q VV	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA	SEQ ID NO: 531

	PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	
hIgG1- LALAPG/Q VV	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHVDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTTP PVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPG	SEQ ID NO: 532
hIgG1/DDR VV	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVDNAKTKPREEQYNSTYRVVSVLRVLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 533
hIgG1- N297A/DD RVV	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVDNAKTKPREEQYASTYRVVSVLRVLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD	SEQ ID NO: 534

	ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNH YTQKSLSLSPG	
hIgG1- D265A/DD RVV	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVVAVSHEDPEVKFNW YVDGVEVDNAKTKPREEQYNSTYRVVSVLRLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 535
hIgG1- LALA/DDR VV	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVDNAKTKPREEQYNSTYRVVSVLRLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNH YTQKSLSLSPG	SEQ ID NO: 536
hIgG1- LAGA/DD RVV	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVDNAKTKPREEQYNSTYRVVSVLRLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNH 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 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSC SVMHEALHNHYTQKSLSLSPGK	SEQ ID NO: 610
Heavy Chain hIgG4 c- terminal	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYT CNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFL	SEQ ID NO: 611

lysine variant	FPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKS LSLSLGKK	
Heavy Chain IgG4-SP c-terminal lysine variant	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTKYT CNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKS LSLSLGKK	SEQ ID NO: 612
Heavy Chain IgG4-SPLE c-terminal lysine variant	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTKYT CNVDHKPSNTKVDKRVESKYGPPCPPCPAPEELGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSV MHEALHNHYTQKS LSLSLGKK	SEQ ID NO: 613
Heavy Chain IgG2 c-terminal lysine variant	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSNFGTQTYT CNVDHKPSNTKVDKTVKCCVECPAPPVAGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGV EVHNAKTKPREEQFNSTFRVSVLTVVHQDWLNGKEYKC KVSNGKLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQ	SEQ ID NO: 614

	VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDS DG SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPK	
Heavy Chain hIgG1- N297A c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 615
Heavy Chain hIgG1- D265A c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVA VSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 616
Heavy Chain hIgG1- LALA c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 617

Heavy Chain hIgG1-LAGA c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 618
Heavy Chain hIgG1-LALAGA c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 619
Heavy Chain hIgG1-LALAPG c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP PVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	SEQ ID NO: 620
Heavy Chain hIgG1-YTE c-terminal	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG	SEQ ID NO: 621

lysine variant	PSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	
Heavy Chain hIgG1-N297A/YT E c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 622
Heavy Chain hIgG1-D265A/YT E c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLYITREPEVTCVVVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 623
Heavy Chain hIgG1-LALA/YTE c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD	SEQ ID NO: 624

	ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP VLDSGDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNH YTQKSLSLSPGK	
Heavy Chain hIgG1- LAGA/YTE c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP VLDSGDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 625
Heavy Chain hIgG1- LALAGA/Y TE c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP VLDSGDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 626
Heavy Chain hIgG1- LALAPG/Y TE c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP PVLDSGDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHN HYTQKSLSLSPGK	SEQ ID NO: 627

Heavy Chain hIgG1-LS c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSH YTQKSLSLSPGK	SEQ ID NO: 628
Heavy Chain hIgG1-N297A/LS c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSC SVLHEALHSHYTQKSLSLSPGK	SEQ ID NO: 629
Heavy Chain hIgG1-D265A/LS c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSH YTQKSLSLSPGK	SEQ ID NO: 630
Heavy Chain hIgG1-LALA/LS	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG	SEQ ID NO: 631

c-terminal lysine variant	PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSH YTQKSLSLSPGK	
Heavy Chain hIgG1- LAGA/LS c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSH YTQKSLSLSPGK	SEQ ID NO: 632
Heavy Chain hIgG1- LALAGA/L S c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSH YTQKSLSLSPGK	SEQ ID NO: 633
Heavy Chain hIgG1- LALAPG/L S c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR	SEQ ID NO: 634

	DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP PVLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSH YTQKSLSLSPGK	
Heavy Chain hIgG1-DHS c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVDHHDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSDGDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSH YTQKSLSLSPGK	SEQ ID NO: 635
Heavy Chain hIgG1- N297A/DH S c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLTVDHHDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSDGDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSH YTQKSLSLSPGK	SEQ ID NO: 636
Heavy Chain hIgG1- D265A/DH S c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVDHHDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSDGDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHSH YTQKSLSLSPGK	SEQ ID NO: 637

Heavy Chain hIgG1-LALA/DHS c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVDHHDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHSH YTQKSLSLSPK	SEQ ID NO: 638
Heavy Chain hIgG1-LAGA/DHS c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVDHHDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHSH YTQKSLSLSPGK	SEQ ID NO: 639
Heavy Chain hIgG1-LALAGA/DHS c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVDHHDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHSH YTQKSLSLSPGK	SEQ ID NO: 640
Heavy Chain hIgG1-LALAPG/D	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG	SEQ ID NO: 641

HS c-terminal lysine variant	PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVDHHDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PVLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHS HYTQKSLSLSPGK	
Heavy Chain IgG4-YTE c-terminal lysine variant	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTKTYT CNVDHKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFL FPPKPKDTLYITREPEVTCVVVDVSQEDPEVQFNWYVDGV EVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKC KVSNGKLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGD SFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSS LSLGKK	SEQ ID NO: 642
Heavy Chain IgG4-SP/YTE c-terminal lysine variant	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTKTYT CNVDHKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSVFL FPPKPKDTLYITREPEVTCVVVDVSQEDPEVQFNWYVDGV EVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKC KVSNGKLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGD SFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSL SLSLGKK	SEQ ID NO: 643
Heavy Chain IgG4-SPLE/YTE c-terminal	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTKTYT CNVDHKPSNTKVDKRVESKYGPPCPCPAPEELGGPSVFL FPPKPKDTLYITREPEVTCVVVDVSQEDPEVQFNWYVDGV EVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKC KVSNGKLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQ	SEQ ID NO: 644

lysine variant	VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG SFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKSL SLSLGKK	
Heavy Chain IgG4-LS c- terminal lysine variant	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTKYT CNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVSVLTVTLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVLHEALHSYTQKSLS LSLGKK	SEQ ID NO: 645
Heavy Chain IgG4-SP/LS c-terminal lysine variant	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTKYT CNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVSVLTVTLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVLHEALHSHYTQKSL SLSLGKK	SEQ ID NO: 646
Heavy Chain IgG4- SPLE/LS c- terminal lysine variant	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTKYT CNVDHKPSNTKVDKRVESKYGPPCPPCPAPEELGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVSVLTVTLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVLHEALHSHYTQKSL SLSLGKK	SEQ ID NO: 647

Heavy Chain IgG4-DHS c-terminal lysine variant	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTKTYT CNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVDHHDWLNGKEY KCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS DGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHSHYTQK SLSLSLGKK	SEQ ID NO: 648
Heavy Chain IgG4- SP/DHS c- terminal lysine variant	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTKTYT CNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVDHHDWLNGKEY KCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS DGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHSHYTQK SLSLSLGKK	SEQ ID NO: 649
Heavy Chain IgG4- SPLE/DHS c-terminal lysine variant	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTKTYT CNVDHKPSNTKVDKRVESKYGPPCPPCPAPEELGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVDHHDWLNGKEY KCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS DGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHSHYTQK SLSLSLGKK	SEQ ID NO: 650
Heavy Chain	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVPSSNFGTQTYT CNVDHKPSNTKVDKTVKCCVECPPCAPPVAGPSVFLF	SEQ ID NO: 651

IgG2-YTE c-terminal lysine variant	PPKPKDTLYITREPEVTCVVVDVSHEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCK VSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQ SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPMLDSDGS FFLYSKLTVDKSRWQQGNVFCVSLHEALHSHYTQKSLSL SPK	
Heavy Chain IgG2-LS c- terminal lysine variant	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYT CNVDHKPSNTKVDKTKVERKCCVECPAPPCAPPVAGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGV EVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCK KVSNGGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPMLDSDG SFFLYSKLTVDKSRWQQGNVFCVSMHEALHNHYTQKSL SLSPK	SEQ ID NO: 652
Heavy Chain IgG2-DHS c-terminal lysine variant	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYT CNVDHKPSNTKVDKTKVERKCCVECPAPPCAPPVAGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGV EVHNAKTKPREEQFNSTFRVVSVLTVDHHDWLNGKEYKCK KVSNGGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPMLDSDG SFFLYSKLTVDKSRWQQGNVFCVSMHEALHSHYTQKSL SLSPK	SEQ ID NO: 653
hIgG1-LA c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD	SEQ ID NO: 654

	ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHAH YTQKSLSLSPGK	
hIgG1- N297A/LA c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHAH YTQKSLSLSPGK	SEQ ID NO: 655
hIgG1- D265A/LA c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHAH YTQKSLSLSPGK	SEQ ID NO: 656
hIgG1- LALA/LA c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHAH YTQKSLSLSPGK	SEQ ID NO: 657

hIgG1- LAGA/LA c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHAH YTQKSLSLSPGK	SEQ ID NO: 658
hIgG1- LALAGA/L A c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHAH YTQKSLSLSPGK	SEQ ID NO: 659
hIgG1- LALAPG/L A c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP PVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVLHEALHA HYTQKSLSLSPGK	SEQ ID NO: 660
hIgG1- N434A c- terminal	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG	SEQ ID NO: 661

lysine variant	PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHAH YTQKSLSLSPGK	
hIgG1- N297A/ N434A c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHAH YTQKSLSLSPGK	SEQ ID NO: 662
hIgG1- D265A/ N434A c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHAH YTQKSLSLSPGK	SEQ ID NO: 663
hIgG1- LALA/ N434A c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD	SEQ ID NO: 664

	ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHAH YTQKSLSLSPGK	
hIgG1- LAGA/ N434A c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHAH YTQKSLSLSPGK	SEQ ID NO: 665
hIgG1- LALAGA/ N434A c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHAH YTQKSLSLSPGK	SEQ ID NO: 666
hIgG1- LALAPG/ N434A c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP PVLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHA HYTQKSLSLSPGK	SEQ ID NO: 667

hIgG1- N434W c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHW HYTQKSLSLSPGK	SEQ ID NO: 668
hIgG1- N297A/ N434W c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHW HYTQKSLSLSPGK	SEQ ID NO: 669
hIgG1- D265A/ N434W c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHW HYTQKSLSLSPGK	SEQ ID NO: 670
hIgG1- LALA/ N434W c-	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG	SEQ ID NO: 671

terminal lysine variant	PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHW HYTQKSLSLSPGK	
hIgG1- LAGA/ N434W c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHW HYTQKSLSLSPGK	SEQ ID NO: 672
hIgG1- LALAGA/ N434W c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHW HYTQKSLSLSPGK	SEQ ID NO: 673
hIgG1- LALAPG/ N434W c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR	SEQ ID NO: 674

	DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP PVLDSGDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHW HYTQKSLSLSPGK	
hIgG1/DQ c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVHLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSDGDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 675
hIgG1- N297A/DQ c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLQVHLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSDGDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 676
hIgG1- D265A/DQ c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVHLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP	SEQ ID NO: 677

	VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	
hIgG1- LALA/DQ c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 678
hIgG1- LAGA/DQ c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 679
hIgG1- LALAGA/D Q c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 680

hIgG1- LALAPG/D Q c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP PVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	SEQ ID NO: 681
hIgG1/DW c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLWVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 682
hIgG1- N297A/DW c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLWVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 683
hIgG1- D265A/DW	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT	SEQ ID NO: 684

c-terminal lysine variant	YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLWVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	
hIgG1- LALA/DW c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLWVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 685
hIgG1- LAGA/DW c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLWVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 686
hIgG1- LALAGA/D W c- terminal	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLWVLHQDWLN	SEQ ID NO: 687

lysine variant	GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	
hIgG1- LALAPG/D W c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLWV LHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP PVLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	SEQ ID NO: 688
hIgG1/YD c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLYISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 689
hIgG1- N297A/YD c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLYISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP	SEQ ID NO: 690

	VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	
hIgG1- D265A/YD c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLYISRDPEVTCVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 691
hIgG1- LALA/YD c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLYISRDPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 692
hIgG1- LAGA/YD c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLYISRDPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 693

hIgG1- LALAGA/Y D c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLYISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 694
hIgG1- LALAPG/Y D c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLYISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP PVLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	SEQ ID NO: 695
hIgG1/QVV c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 696
hIgG1- N297A/QV	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT	SEQ ID NO: 697

V c-terminal lysine variant	YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYASTYRVVSVLQVLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	
hIgG1- D265A/QV V c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVAVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 698
hIgG1- LALA/QVV c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTTPP VLDSGDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 699
hIgG1- LAGA/QV V c-terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVLHVDWLN	SEQ ID NO: 700

	GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	
hIgG1- LALAGA/Q VV c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVHLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 701
hIgG1- LALAPG/Q VV c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLQVHLHVDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTTP PVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	SEQ ID NO: 702
hIgG1/DDR VV c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVDVSHEDPEVKFNW YVDGVEVDNAKTKPREEQYNSTYRVVSVLRVLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTTPP	SEQ ID NO: 703

	VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	
hIgG1- N297A/DD RVV c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVDNAKTKPREEQYASTYRVVSVLRVLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 704
hIgG1- D265A/DD RVV c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRDPEVTCVVAVSHEDPEVKFNW YVDGVEVDNAKTKPREEQYNSTYRVVSVLRVLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 705
hIgG1- LALA/DDR VV c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAEEAAGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVDNAKTKPREEQYNSTYRVVSVLRVLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 706

hIgG1- LAGA/DD RVV c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELAGA PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVDNAKTKPREEQYNSTYRVVSVLRLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 707
hIgG1- LALAGA/D DRVV c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGA PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVDNAKTKPREEQYNSTYRVVSVLRLHVDWLN GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD ELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTPP VLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH YTQKSLSLSPGK	SEQ ID NO: 708
hIgG1- LALAPG/D DRVV c- terminal lysine variant	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGG PSVFLFPPKPKDTLMISRDPEVTCVVVDVSHEDPEVKFNW YVDGVEVDNAKTKPREEQYNSTYRVVSVLRLHVDWLN GKEYKCKVSNKALGAPIEKTISKAKGQPREPQVYTLPPSR DELTKNQVSLTCLVKGFYPSDIVVEWESNGQPENNYKTPP PVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK	SEQ ID NO: 709
C-terminal end	SLSLSPGK	710

C-terminal end	SLSLSPG	711
C-terminal end	SLSLSP	712

WHAT IS CLAIMED IS:

1. A composition comprising a mixture of anti-interleukin 13 (IL-13) antibodies, wherein the mixture comprises
- 5 a) C-terminal anti IL-13 antibodies comprising a heavy chain having at least one C-terminal lysine, and
- b) non-C-terminal anti IL-13 antibodies otherwise identical to the C-terminal anti IL-13 antibodies but lacking the at least one C-terminal lysine,
- wherein each of the non-C-terminal and C-terminal antibodies comprises:
- 10 (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 SEQ
- 15 ID NOs: 58-99 and 121;
- (b) CDR-H2 comprises a sequence selected from the sequences set forth in SEQ ID NOs: 100-111;
- (c) CDR-H3 comprises a sequence selected from the sequences set forth in SEQ ID NOs: 112-120 and 130-140,
- 20 (d) CDR-L1 comprises a sequence selected from the sequences set forth in SEQ ID NOs: 141-144 and 149-152,
- (e) CDR-L2 comprises a sequence selected from the sequences set forth in 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 SEQ
- 25 ID NOs: 165-172, and
- wherein each C-terminal antibody having at least one C-terminal lysine comprises a heavy chain constant domain comprising a sequence selected from the sequences set forth in SEQ ID NOs: 624, 610-623, and 625-709.
2. The composition of claim 1, wherein between about 0.01% and about 50% of the antibodies
- 30 are C-terminal antibodies.

3. The composition of claim 1, wherein between about 0.1% and about 20% of the antibodies are C-terminal antibodies.
4. The composition of claim 1, wherein between about 0.5% and about 10% of the antibodies are C-terminal antibodies.
- 5 5. The composition of claim 1, wherein between about 1% and about 5% of the antibodies are C-terminal antibodies.
6. The composition of claim 1, wherein between about 5% and about 30% of the antibodies are C-terminal antibodies.
7. The composition of any one of claims 1-6, wherein the anti-IL-13 antibodies comprise a VH
10 sequence selected from the sequences set forth in any one of SEQ ID NOs: 3, 1, 2, and 4-32.
8. The composition of any one of claims 1-7, wherein the anti-IL-13 antibodies comprise a VL sequence selected from the sequences set forth in any one of SEQ ID NOs: 39, 33-38, and 40-57.
9. The composition of any one of claims 1-6, wherein the anti-IL-13 antibodies comprise a VH sequence selected from the sequences set forth in any one of SEQ ID NOs: 3, 1, 2, and 4-32 and
15 a VL sequence selected from the sequences set forth in any one of SEQ ID NOs: 39, 33-38, and 40-57.
10. The composition of claim 9, wherein the anti-IL-13 antibodies comprise 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.
- 20 11. The composition of any one of claims 1-10, wherein the anti-IL-13 antibodies comprise a light chain constant region comprising SEQ ID NO: 469.
12. The composition of any one of claims 1-11, further comprising one or more pharmaceutically acceptable excipients.

13. An anti-IL-13 antibody having a light chain comprising a VL comprising SEQ ID NO: 39 and a light chain constant region comprising SEQ ID NO: 469 and a heavy chain comprising a VH comprising SEQ ID NO: 3 and a heavy chain constant region comprising SEQ ID NO: 624.
14. A composition comprising the antibody of claim 12 and an antibody having a light chain
5 comprising a VL comprising SEQ ID NO: 39 and a light chain constant region comprising SEQ ID NO: 469 and a heavy chain comprising a VH comprising SEQ ID NO: 3 and a heavy chain constant region comprising SEQ ID NO: 439.
15. The composition of any one of claims 1-12 and 14, wherein the antibodies were produced in a Chinese Hamster Ovary (CHO) cell line.
- 10 16. A vial comprising the composition of any one of claims 1-12, 14, and 15.
17. The vial of claim 16, wherein the extractable volume of the vial is between 1.0 mL and 3.0 mL.
18. The vial of claim 17, wherein the extractable volume of the vial is about 2.0 mL.
19. The vial of any one of claims 16-18, wherein the vial is a syringe.
- 15 20. The vial of claim 19, wherein the syringe is a prefilled syringe.
21. A composition comprising a mixture of anti-interleukin 13 (IL-13) antibodies, wherein
the mixture comprises a first IL-13 antibody and a second IL-13 antibody, wherein each antibody comprises at least one heavy chain, and wherein
the first antibody and the second antibody are identical except that the first antibody
20 comprises a lysine at the C-terminus of the at least one heavy chain, and the second antibody lacks the lysine at the C-terminus of the at least one heavy chain, wherein
each 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 SEQ ID NOs: 58-99 and 121;
- 5 (b) CDR-H2 comprises a sequence selected from the sequences set forth in SEQ ID NOs: 100-111;
- (c) CDR-H3 comprises a sequence selected from the sequences set forth in SEQ ID NOs: 112-120 and 130-140,
- (d) CDR-L1 comprises a sequence selected from the sequences set forth in SEQ ID NOs: 141-144 and 149-152,
- 10 (e) CDR-L2 comprises a sequence selected from the sequences set forth in 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 SEQ ID NOs: 165-172, and
- 15 wherein the first antibody comprises a heavy chain constant domain comprising a sequence selected from the sequences set forth in SEQ ID NOs: 624, 610-623, and 625-709.
22. The composition of claim 21, wherein each anti-IL-13 antibody comprises a VH sequence selected from the sequences set forth in any one of SEQ ID NOs: 3, 1, 2, and 4-32.
23. The composition of claim 21 or claim 22, wherein each anti-IL-13 antibody comprises a VL sequence selected from the sequences set forth in any one of SEQ ID NOs: 39, 33-38, and 40-57.
- 20 24. The composition of claim 21, wherein each anti-IL-13 antibody comprises a VH sequence selected from the sequences set forth in any one of SEQ ID NOs: 3, 1, 2, and 4-32 and a VL sequence selected from the sequences set forth in any one of SEQ ID NOs: 39, 33-38, and 40-57.
- 25 25. The composition of any one of claims 21-24, wherein each anti-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.
26. The composition of any one of claims 21-25, wherein each antibody comprises a light chain constant region comprising SEQ ID NO: 469.

27. The composition of any one of claims 24-26, wherein the antibodies were produced in a Chinese Hamster Ovary (CHO) cell line.
28. A vial comprising the composition of any one of claims 21-27.
29. The vial of claim 28, wherein the extractable volume of the vial is between 1.0 mL and 3.0 mL.
30. The vial of claim 29, wherein the volume of the vial is about 2.0 mL.
31. The vial of any one of claims 28-30, wherein the vial is a syringe.
32. The vial of claim 31, wherein the syringe is a prefilled syringe.
33. A composition comprising a mixture of anti-interleukin 13 (IL-13) antibodies, wherein the mixture comprises
- a) C-terminal anti IL-13 antibodies comprising a heavy chain having at least one C-terminal lysine, and
- b) non-C-terminal anti IL-13 antibodies otherwise identical to the C-terminal anti IL-13 antibodies but lacking the at least one C-terminal lysine,
- wherein each of the non-C-terminal and C-terminal antibodies 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 SEQ ID NOs: 58-99 and 121;
- (b) CDR-H2 comprises a sequence selected from the sequences set forth in SEQ ID NOs: 100-111;
- (c) CDR-H3 comprises a sequence selected from the sequences set forth in SEQ ID NOs: 112-120 and 130-140,
- (d) CDR-L1 comprises a sequence selected from the sequences set forth in SEQ ID NOs: 141-144 and 149-152,

(e) CDR-L2 comprises a sequence selected from the sequences set forth in 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 SEQ ID NOs: 165-172, and

- 5 wherein each C-terminal antibody having at least one C-terminal lysine comprises a heavy chain constant domain having a means for enhancing the half-life of the C-terminal antibody.