

**Engineered Antibodies and Immunoconjugates and Methods of Use****STATEMENT AS TO FEDERALLY SPONSORED RESEARCH**

[0001] None.

**REFERENCE TO RELATED APPLICATIONS**

5 [0002] This application claims the benefit of the priority dates of U.S. provisional application 63/608,173, filed December 8, 2023; U.S. provisional application 63/609,776, filed December 13, 2023; U.S. provisional application 63/566,200, filed March 15, 2024; U.S. provisional application 63/566,201, filed March 15, 2024; U.S. provisional application 63/724,852, filed November 25, 2024; and U.S. provisional application 63/724,854, filed November 25, 2024, the  
10 contents of which are incorporated herein in their entireties.

**BACKGROUND**

[0003] Antibody-drug conjugates (ADCs) represent a significant advance in cancer therapy. ADCs incorporate the specificity of monoclonal antibodies with the potency of cytotoxic drugs. By targeting cancer cells with high precision, ADCs reduce harm to healthy tissues. In an ADC,  
15 the monoclonal antibody is designed to bind to a specific antigen that is expressed on the surface of cancer cells. Once bound, the ADC is internalized into the cancer cell, where the cytotoxic agent is released to induce cell death. This targeted delivery allows for the use of highly potent drugs that might be too toxic if delivered systemically. ADCs have shown promise in treating various cancers, including breast, lung, and blood cancers. They represent a  
20 personalized and targeted cancer therapy.

**BRIEF DESCRIPTION OF THE DRAWINGS**

[0004] The accompanying drawings, which are incorporated herein and form a part of the specification, illustrate exemplary embodiments and, together with the description, further serve to enable a person skilled in the pertinent art to make and use these embodiments and others  
25 that will be apparent to those skilled in the art. The invention will be more particularly described in conjunction with the following drawings wherein:

[0005] FIG. 1 shows a format for a platform 1 antibody in a Fab-Fc-Fab (e.g., "IgG-Fab") format.

[0006] FIG. 2 shows a format for a platform 2 antibody in a Diabody-Fc-Fab format.

30 [0007] FIG. 3 shows a format for a platform 3 antibody in a Fab-Fab-Fc (e.g., "Fab-IgG") format.

[0008] FIG. 4 shows a format for a platform 4 antibody in a Fab-Diabody-Fc format.

[0009] FIGs. 5A-5D show four different configurations for paratopes in a bi-specific, tetravalent format, in this case, Fab-diabody-Fc format. 5A: Symmetric antibody in which the paratopes binding Epitope 1 (paratopes 1 and 2) are in the NW/NE positions, the paratopes binding Epitope 2 (paratopes 3 and 4) are in the SW/SE positions. 5B: Symmetric antibody in which the paratopes binding Epitope 2 (paratopes 1 and 2) are in the NW/NE positions and the paratopes binding Epitope 1 (paratopes 3 and 4) are in the SW/SE positions. 5C: Asymmetric antibody in which the paratopes binding Epitope 1 (paratopes 1 and 4) are in the NW/SE positions, and the paratopes binding Epitope 2 (paratopes 2 and 3) are in the SW/NE positions. 5D: Asymmetric antibody in which the paratopes binding epitope 1 (paratopes 1 and 3) are in the NW/SW positions, and the paratopes binding epitope 2 (paratopes 2 and 4) are in the NE/SE positions.

[00010] FIGs. 6A-6C show three different configurations for paratopes in a Fab-Diabody-Fc tri-specific and tetra-specific format. 6A: Paratopes binding Epitope 1 are in the NW/NE positions, the paratope binding epitope 2 is in the SE position, and the paratope binding epitope 3 is in the SW position. 6B: The paratope binding Epitope 1 is in the NW position; the paratope binding epitope 2 is in the NE position, and the two paratopes binding epitope 3 are in the SW/SE position. 6C: The paratope binding Epitope 1 is in the NW position, the paratope binding Epitope 2 is in the NE position, the paratope binding epitope 3 in the SW position, and the paratope binding epitope 4 is in the SE position.

[00011] FIGs. 7A to 7C show three different configurations for epitope-binding paratopes in a bi-specific, tetravalent format, in this case, diabody-Fc-Fab format. 7A: Symmetric antibody in which the two paratopes binding Epitope 1 are in the NW/NE positions, and the two paratopes binding epitope 2 are in the SW/SE positions. 7B: Symmetric antibody in which the two paratopes binding Epitope 2 are in the NW/NE positions and the two paratopes binding epitope 1 are in the SW/SE positions. 7C: Asymmetric antibody in which the two paratopes binding Epitope 1 are in the NW/SW positions, and the two paratopes binding epitope 2 are in the NE/SE positions.

[00012] FIGs. 8A-8C show three different configurations for paratopes in a Diabody-Fc-Fab tri-specific and tetra-specific format. 8A: The paratope binding Epitope 1 is in the NW position, the paratope binding epitope 2 is in the NE position, and the two paratopes binding epitope 3 are in the SW/SE positions. 8B: The two paratopes binding Epitope 1 are in the NW/NE positions, the paratope binding epitope 2 is in the SE position, and the paratope binding epitope 3 is in the SW position. 8C: The paratope binding Epitope 1 is in the NW position, the paratope binding epitope 2 is in the NE position, the paratope binding epitope 3 is in the SW position, and the paratope binding epitope 4 is in the SE position.

[00013] FIGs 9A-9E show that Bi-specific Tetravalent ADC showed Superior Potency over Mono-specific Bivalent or Tetravalent ADCs.

- [00014] FIG 10. shows a summary of CD30/PD-L1 IgG1 Binders.
- [00015] FIG 11. shows different CD30-PD-L1 Platform 1 Constructs.
- [00016] FIG 12. shows different CD30-PD-L1 Platform 2 and Platform 3 Constructs.
- [00017] FIG 13. shows different CD30-PD-L1 Platform 4 Constructs.
- 5 [00018] FIG 14. shows Biologic Production & Analytical QC Summary of various antibodies.
- [00019] FIG 15. shows binding of CD30/PD-L1 tetravalent antibodies to Karpas 299 cells by FACS analysis.
- [00020] FIG 16. shows CD30/PD-L1 tetravalent ADCs Displayed Potency in Both CD30 +ve and PD-L1 +ve Cells.
- 10 [00021] FIG 17. shows that CD30/PD-L1 biologics demonstrated functional activity equivalent to clinical PD-L1 antibodies Avelumab, Atezolizumab, and BMS936559.
- [00022] FIG 18. shows a size exclusion chromatography analysis of Tri-specific HER2/Trop2 Platform 2 ADC.
- [00023] FIG 19. shows tri-specific Her2-Trop2 Platform ADC displayed superior potency over  
15 mono-specific HER2 ADC in A431 and MCF7 cells.
- [00024] FIG 20. shows different HER2/Trop2 tetravalent constructs (AB607 is tri-specific).
- [00025] FIG 21. shows In Vitro Cell Potency of Platform 2 HER2/Trop2 in SKOV3 cells.
- [00026] FIG 22. shows In Vitro Cell Potency of Platform 4 HER2/Trop2 in SKOV3 cells.
- [00027] FIG 23. shows In Vitro Cell Potency of Platform 2 HER2/Trop2 in JIMT1 cells.
- 20 [00028] FIG 24. shows In Vitro Cell Potency of Platform 4 HER2/Trop2 in JIMT1 cells.
- [00029] FIG 25. shows In Vitro Cell Potency of Platform 2 HER2/Trop2 in OVCAR3 cells.
- [00030] FIG 26. shows In Vitro Cell Potency of Platform 4 HER2/Trop2 in OVCAR3 cells.
- [00031] Figs. 27A-27C show analysis of three bi-specific, tetravalent ADCs comprising binding sites for NaPi-2b and Muc16. Fig. 27A: Fab-diabody-Fc format. Fig. 27B: Fab-diabody-Fc format. Fig. 27C: diabody-Fc-Fab format. The data shows that the ADCs assemble in a  
25 homogenous fashion. All ADCs exhibit uniform 4 DAR via cysteine-engineered site specific conjugation
- [00032] Fig. 28 compares the effect of different ADCs on cell viability of OVCAR3 cells and provides inhibitory concentration 50% (IC50) values.
- 30 [00033] Fig. 29 compares the effect of different ADCs on viability of engineered OVCAR3-AV cells. OVCAR3 cells are a cell line derived from a human ovarian carcinoma, OVCAR3-AV cells

are mixtures of OVCAR3 wild type cells with OVCAR3 cells genetically modified to knock out Muc16 gene expression.

5 [00034] Figs. 30A-30B compare the effect of different ADCs binding Muc16 and NaPi-2b on cell viability of Muc16 knock-out OVCAR3 cells (Fig. 30A) and NaPi-2b knock-out OVCAR3 cells (Fig. 30B) and provides a table with IC50 values and DAR.

[00035] Figs. 31A-31D show cell viability assays with varying ratio of OVCAR3 WT and Muc16-KO cells, which compare the effect of different ADCs binding Muc16 and NaPi-2b on cell viability of cell mixtures. OVCAR3-AV1 cells comprise OVCAR3 Muc16 knockouts and OVCAR3 wild type in a ratio of 60:40. OVCAR3-AV2 cells comprise OVCAR3 Muc16 knockouts and OVCAR3 wild type in a ratio of 70:30. OVCAR3-AV3 cells comprise OVCAR3 Muc16 knockouts and OVCAR3 wild type in a ratio of 80:20. OVCAR3-AV4 cells comprise OVCAR3 Muc16 knockouts and OVCAR3 wild type in a ratio of 90:10. Accordingly, all the OVCAR3-AV cell mixtures have constant expression levels of NaPi2b, and different levels of expression of Muc16. This mimics the expression of both targets to that of patient tumors. 31A: 60% Muc16 knock-out, 40% OVCAR3 wild type. 31B: 70% Muc16 knock-out, 30% OVCAR3 wild type. 31C: 80% Muc16 knock-out, 20% OVCAR3 wild type. 31D: 90% Muc16 knock-out, 10% OVCAR3 wild type. OVCAR3-AV cells have varying levels of Muc16 expression with NaPi-2b expression being constant to mimic the expression of both targets to that of patient tumors. Table shows IC50 values of different cell ratios.

20 [00036] Fig. 32 compares the effect of different ADCs on cell viability of a mixture of OVCAR3-AV cells having varying different levels of expression of Muc16 and NaPi-2b. (20% of the cells were expression positive for both target antigens while 60% were expression positive for only NaPi-2b, and 20% were expression-positive for only MUC-16.)

25 [00037] Fig. 33A and 33B show manufacturability of various antibody formats. Fab-Diabody-Fc format and Diabody-Fc-Fab format demonstrate highest yields. Antibodies identified by hashtag have lowest manufacture yields.

[00038] Figs. 34A-34C show *in vivo* efficacy of ADCs in the OVCAR3 ovarian xenograft tumor model using female CB.17 SCID mice: A. study design; Tumor growth curves (B) and Bodyweight changes (C) in mice upon treatment with ADCs. Tetravalent, bi-specific ADCs displayed superior *in vivo* efficacy compared to mono-specific ADCs. No body weight changes were observed across all ADC dosing groups.

[00039] Fig. 35 compares the effect of different ADCs on cell viability of OVCAR3 cells and provides inhibitory concentration 50% (IC50) values.

35 [00040] Fig. 36A-36D show *in vivo* efficacy of ADCs (40 nmole dose comparison) in the OVCAR3 ovarian xenograft tumor model: A. study design; B. Tumor growth curves vs number of days; C. Tumor growth observed in various ADC treatment groups on day 32; D. p-values



observed among treatment groups at day 32. All groups are dosed with 40 nmoles of ADC (single dose on Day1 when the tumor size was 100-150 mm<sup>3</sup>).

[00041] Fig. 37A-37D show *in vivo* efficacy of ADCs (AB301 vs AB309) in the OVCAR3 ovarian xenograft tumor model: A. study design; B. Tumor growth curves vs number of days; C. Tumor growth observed in various ADC treatment groups on day 32; D. p-values observed among treatment groups.

[00042] Fig. 38A-38D show *in vivo* efficacy of ADCs (AB312 vs AB309) in the OVCAR3 ovarian xenograft tumor model: A. study design; B. Tumor growth curves vs number of days; C. Tumor growth observed in various ADC treatment groups on day 32; D. p-values observed among treatment groups.

[00043] Fig. 39 compares bodyweight changes in mice upon treatment with ADCs.

[00044] Fig. 40 shows pharmacokinetic characterization of AB304 and AB309 antibodies in non-human primates.

[00045] Fig. 41 compares the effect of AB304 and AB306 ADCs on cell viability of OVCAR3 cells and provides inhibitory concentration 50% (IC50) values.

[00046] Fig. 42 compares the effect of different ADCs on cell viability of OVCAR3 cells and provides IC50 values.

[00047] FIG 43. shows that Bi-specific bivalent Her2/Her2 ADC (AB105 ADC) showed Superior Potency over Mono-specific Bivalent ADC (AB103 ADC) in both Her2 high copy number cell line (SKBr) and low copy number cell line (JIMT1).

[00048] FIG 44. depicts different Her2-PD-L1 Platform 4 Constructs with different spacer variations.

[00049] FIG 45. describes different Her2-PD-L1 Platform 2 & 4 Constructs with different spacer variations.

[00050] FIG 46. shows different multi-specific Her2-PD-L1 Platform 2 & 4 Constructs with different spacer variations.

[00051] FIG 47. describes different bi-specific Her2-Her2 Platform 4 Constructs with different spacer variations.

[00052] FIG 48. depicts different bi-specific Her2-Her2 Platform 2 Constructs with varying G4S spacer size.

[00053] FIG 49. describes CD30-PD-L1 multi-specific tetravalent ADCs Displayed Superior Potency in Karpus 299-AV (mixed cell population of CD30-KO and PD-L1 KO Cells) cells.

[00054] FIG 50. depicts different multi-specific CD30-PD-L1 Platform 2 & 4 Constructs.

[00055] FIG 51. shows In Vitro Cell Potency of Platform 4 multi-specific tetravalent (AB612 bi-specific tetravalent) HER2/Trop2 in SKOV3 and JMIT1 cells.

[00056] FIG 52. shows multi-specific tetravalent ADCs (AB616 and AB618 ADCs) Displayed Superior Potency over mono-specific or bi-specific bivalent ADCs in SKOV3 cells. All paratopes of AB616 and AB618 ADCs are functional.

[00057] FIG 53. describes all paratopes of AB616 and AB618 ADCs are functional in NCI-N87 cell line.

[00058] FIG 54. depicts different multi-specific Her2-Trop2 Platform 2 & 4 Constructs with two different Trop2 paratopes (Trop2-17487 and H1D3).

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## SUMMARY

[00059] Provided herein are tetravalent antibody architectures that may be mono-specific, bi-specific, tri-specific or tetra-specific. Paratopes can be formed from Fab regions, diabodies, and scFv regions. In the instance of multi-specific antibodies, paratopes binding particular epitopes can be positioned at any of the four positions in the tetravalent antibody. Certain embodiments comprise two identical heavy chains and two identical light chains. In other embodiments, the antibodies can have asymmetric heavy chains. In other instances, paratopes binding different epitopes can have identical light chain variable regions and different heavy chain variable regions. The antibodies of this disclosure have superior manufacturability and potency. The antibodies can be formulated as immunoconjugates, e.g., with toxic or detectable payloads, for therapeutic and diagnostic uses.

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## DETAILED DESCRIPTION

### I. Antibodies

[00060] An “antibody” is a protein or protein complex comprising a framework region from an immunoglobulin gene, which protein or protein complex binds to a target epitope. The framework region of an immunoglobulin gene refers to relatively conserved sequences within the variable region of the immunoglobulin (Ig) heavy chain and light chain. Accordingly, the term “antibody” includes the intact tetrameric antibody, which includes two heavy immunoglobulin chains and two light immunoglobulin chains. The term also includes any binding fragment of a tetrameric antibody. The term also includes engineered antibodies in which various immunoglobulin domains are rearranged, or are added to immunoglobulin chains, for example, to create antibodies with more than two binding sites, as described herein. Antibodies described herein may bear names with an “AB” prefix. Such antibody names may be given as “AB101 antibody.” These names may refer to antibody drug conjugates depending on context. For example, an ADC of AB101 might be referred to as “AB101-ADC.”

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**A. Antibody Structure**

**[00061]** An exemplary antibody structure is an intact tetrameric antibody. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one “light” chain (about 25 kD) and one “heavy” chain (about 50-70 kD). Antibodies can be of (i) any of the five major classes of immunoglobulins, based on the identity of their heavy-chain constant domains – alpha (IgA), delta (IgD), epsilon (IgE), gamma (IgG) and mu (IgM), or (ii) subclasses (isotypes) thereof (e.g., IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2). The light chains can be either lambda or kappa. In an intact antibody, a light chain comprises, from N-terminus to C-terminus, a light chain variable (VL) region and a light chain constant (CL) region. In an intact antibody, a heavy chain comprises, from N-terminus to C-terminus, a heavy chain variable (VH) region, a heavy chain constant 1 (CH1) region, a hinge region, a heavy chain constant 2 (CH2) region, and a heavy chain constant 3 (CH3) region. Two light chains associate with the heavy chain portions comprising a VH region and a CH1 region, to form two Fab (Fragment antigen-binding) regions. The light chains and heavy chains are connected by a covalent bond (e.g., a disulfide bond) and by non-covalent interactions. The combination of a VL region and a VH region forms the antigen binding domain of the antibody, also referred to as a “paratope”. The combination of the hinge, CH2 and CH3 regions are referred to collectively as the Fc (“fragment crystallizable”) region.

**[00062]** In the formation of antibodies, different chains or portions of chains interact with each other to form higher order structures. In this way, antibody chains or portions of them can be said to associate to form these structures. For example and without limitation, a heavy chain and light chain can associate to form a paratope. Two heavy chains can associate to form an Fc dimer. Heavy chain variable regions and light chain variable regions in an scFv molecule, or in a diabody can associate to form one or more paratopes. The association can be effected through a variety of covalent and non-covalent interactions. This includes, without limitation, disulfide bonds, which can connect heavy chains with each other and light chains with heavy chains, as well as hydrogen bonding, hydrophobic interactions, and van der Waals forces. Association between chains or portions of them can occur naturally, so that the higher order structures self-assemble.

**[00063]** Paratopes can be formed through the association of various light chain variable regions and heavy chain variable regions in a variety of formats, discussed in more detail herein. For example, the association of a light chain and a polypeptide containing a heavy chain variable region and heavy chain constant 1 region form an Fab that comprises a paratope. A single chain comprising a heavy chain variable region and a light chain variable region can associate to form an scFv that comprises a paratope. Two chains, each comprising a heavy chain variable region and a light chain variable region can associate to form a diabody that comprises two paratopes. As used herein, the phrases, “an Fab comprising a paratope,”

“an scFv comprising a paratope,” and “a diabody comprising two paratopes,” (and so forth) can be equivalently expressed as “a paratope comprised in an Fab,” “a paratope comprised in an scFv,” and “two paratopes comprised in a diabody.”

5 [00064] The variable regions of both light and heavy chains in antibodies are composed of framework regions and complementarity-determining regions (“CDRs”) (also called “hypervariable” regions). There are three CDRs in each variable region, labeled CDR1, CDR2, and CDR3. They typically have lengths between about seven and 25 amino acids. The CDRs play a role in antigen recognition. Framework regions are interspersed between the CDRs and provide structural integrity, contributing to proper conformation of the CDRs for antigen binding.

10 [00065] The phrase “CDR sequence set” refers to the 3 heavy chain and/or 3 light chain CDRs of a particular antibody. A “light chain” CDR sequence set refers to the light chain CDR sequences. A “heavy chain” CDR sequence set refers to the heavy chain CDR sequences. A “full” CDR sequence set refers to both heavy chain and light chain CDR sequences. CDRs can be predicted based on, for example, IMGT sequence alignment. (The international  
15 ImMunoGeneTics information system.)

[00066] The constant region interacts with other immune cells of the body. Between the Fab and Fc regions of IgG, IgD, and IgA, is the hinge region that provides flexibility to articulate antigen binding.

#### B. Antibody Nomenclature

20 [00067] Antibodies can exist in natural or genetically modified forms such as humanized, human, single-chain, chimeric, synthetic, recombinant, hybrid, mutated, grafted, and in vitro generated antibodies.

[00068] As used herein, the term “monoclonal antibody” refers to a clonal preparation or composition of antibodies with a single binding specificity and affinity for a given epitope on an  
25 antigen (“monoclonal antibody composition”). A “polyclonal antibody” refers to a preparation or composition of antibodies that are raised against a single antigen, but with different binding specificities and affinities (“polyclonal antibody composition”).

[00069] As used herein, the term “chimeric antibody” refers to an antibody having amino acid sequences derived from two or more species. In one embodiment, the variable region of both  
30 light and heavy chains correspond to the variable region of antibodies derived from one species of mammal (e.g., mouse, rat, rabbit, etc.) with the desired specificity, affinity and capability, while the constant region contains amino acid sequences derived from another species (typically in the subject receiving the therapy, e.g., human) to avoid eliciting an immune response.

[00070] As used herein, the term “humanized antibody” refers to a chimeric antibody in which  
35 the CDRs, obtained from the VH and VL regions of a non-human antibody having the desired specificity, affinity and capability are grafted to a human framework sequence. In one

embodiment, the framework residues of the humanized antibody are modified to refine and optimize the antibody specificity, affinity and capability. Humanization, i.e., substitution of non-human CDR sequences for the corresponding sequences of a human antibody, can be performed following the methods described in, e.g., U.S. Patent Nos. 5,545,806; 5,569,825; 5,633,425; 5,661,016; Riechmann et al., *Nature* 332:323-327 (1988); Marks et al., *Bio/Technology* 10:779-783 (1992); Morrison, *Nature* 368:812-13 (1994); Fishwild et al., *Nature Biotechnology* 14:845-51 (1996).

**[00071]** As used herein, the term “human antibody” refers to an antibody produced by a human or an antibody having an amino acid sequence corresponding thereto made by any technique known in the art.

**[00072]** As used herein, the term “immunoassay” refers to a method for detecting an analyte by detecting binding between the analyte and an antibody that recognizes the analyte.

**[00073]** Amino acid sequences of antibody drugs can be found, for example, at [go.drugbank.com/drugs](http://go.drugbank.com/drugs), as well as at [opig.stats.ox.ac.uk/webapps/sabdab-sabpred/](http://opig.stats.ox.ac.uk/webapps/sabdab-sabpred/) and [opig.stats.ox.ac.uk/webapps/sabdab-sabpred/therasabdab/](http://opig.stats.ox.ac.uk/webapps/sabdab-sabpred/therasabdab/), Raybould et al. *Nucleic Acids Res.* 48:D383-D388, (2020).

**[00074]** As used herein, the term “polypeptide” refers to a molecule having a sequence of natural and/or unnatural amino acids connected through peptide bonds. The term “peptide” refers to a short polypeptide, typically no more than 30 amino acids long. The amino acid sequence of a polypeptide is referred to as its “primary structure.” The term “protein” refers to a polypeptide having a secondary, tertiary and/or quaternary structure, e.g., structures stabilized by hydrogen bonds, relationships between secondary structures and structures formed of more than one protein. Proteins can be further modified by other attached moieties such as carbohydrate (glycoproteins), lipids (lipoproteins) phosphate groups (phosphoproteins) and the like.

**[00075]** As used herein, an amino acid sequence “consists of” only the amino acids in that sequence.

**[00076]** As used herein, a first amino acid sequence “consists essentially of” a second amino acid sequence if the first amino acid sequence (1) comprises the second amino sequence and (2) is no more than 1, no more than 2 or no more than 3 amino acids longer than the second amino acid sequence.

**[00077]** As used herein, a first amino acid sequence is a “fragment” of a second amino acid sequence if the second amino acid sequence comprises the first amino acid sequence. In certain embodiments, a first amino acid sequence that is a fragment of a second amino acid sequence may have no more than any of 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 fewer amino acids than the second amino acid sequence.

[00078] As used herein, a “functional equivalent” of a reference amino acid sequence is a sequence that is not identical to the reference sequence, but that contains minor alterations such as, for example, insertion, deletion or substitution of one or a few amino acids. A functionally equivalent sequence retains the function (e.g., antigen binding, immunogenicity) of the reference sequence to which it is equivalent. If a functionally equivalent amino acid sequence contains substitution of one or more amino acids with respect to the reference sequence, these will generally be conservative amino acid substitutions.

[00079] The term “cross-linked” with respect to an antibody refers to attachment of the antibody to a solid or semisolid matrix (e.g., Sepharose, beads, microtiter plate), or to another protein or antibody. For example, an antibody can be multimerized to create an antibody complex with multiple (more than 2) antigen-binding sites. The antibody can be multimerized by expressing the antibody as a high-valency isotype (e.g., IgA or IgM, which typically form complexes of 2 or 5 antibodies, respectively). Antibody multimerization can also be carried out by using a cross-linker comprising a reactive group capable of linking proteins (e.g., carbodiimide, NHS esters, etc.). Methods and compositions for cross-linking an antibody to a matrix are described, e.g., in the Abcam and New England Biolab catalogs and websites (available at abcam.com and neb.com). Cross-linker compounds with various reactive groups are described, e.g., in Thermo Fisher Scientific catalog and website (available at piercenet.com).

### C. Antibody Binding

[00080] The specificity of antibody binding can be expressed in terms of the dissociation constant ( $K_d$ ) of the complex between the antibody (or other targeting moiety) and its target, as compared to the dissociation constant of a complex between the antibody and a non-target molecule. A larger (higher)  $K_d$  is a  $K_d$  that describes a lower affinity interaction. Conversely a smaller (lower)  $K_d$  is a  $K_d$  that describes a higher affinity interaction or tighter binding. By way of example only, the  $K_d$  for an antibody specifically binding to a target may be femtomolar, picomolar, nanomolar, or micromolar and the  $K_d$  for the antibody binding to unrelated material may be millimolar or higher. Binding affinity can be in the nanomole range ( $K_d = 10^{-7}$  M to  $10^{-9}$  M), picomole range ( $K_d = 10^{-10}$  M to  $10^{-12}$  M), or femtomole range  $K_d = 10^{-13}$  M to  $10^{-15}$  M).

[00081] As used herein, an antibody “specifically binds” or “is specific for” an antigen or epitope of an antigen if it binds the antigen or epitope with a  $K_d$  of less than  $10^{-7}$  M (i.e., in the nanomolar range). This includes, for example, less than any of  $1 \times 10^{-7}$  M,  $1 \times 10^{-8}$  M,  $1 \times 10^{-9}$  M,  $1 \times 10^{-10}$  M,  $1 \times 10^{-11}$  M, or  $1 \times 10^{-12}$  M. Typically, specific binding is characterized by binding the antigen with sufficient affinity that the antibody is useful as a diagnostic to detect the antigen or epitope and/or as a therapeutic agent in targeting the antigen or epitope.

[00082] The term “binds” with respect to a cell type (e.g., an antibody that binds cancer cells), typically indicates that an agent binds a majority of the cells in a pure population of those cells. For example, an antibody that binds a given cell type typically binds to at least 2/3 of the cells in a population of the indicated cells (e.g., 67, 75, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100% of the cells in the population). In some cases, binding of an antibody to a polypeptide can be assayed by comparing binding of the antibody to a cell that presents the polypeptide, to the binding (or lack thereof) of the antibody to a cell that does not express the polypeptide. One of skill will recognize that some variability will arise depending on the method and/or threshold of determining binding. Affinity of an antibody for a target can be determined according to methods known in the art, e.g., as reviewed in Ernst *et al.* Determination of Equilibrium Dissociation Constants, *Therapeutic Monoclonal Antibodies* (Wiley & Sons ed. 2009).

[00083] As used herein, the term “greater affinity” refers to a relative degree of antibody binding where an antibody X binds to target Y more strongly, and/or with a lower dissociation constant, than to target Z, and in this context antibody X has a greater affinity for target Y than for Z. Likewise, the term “lesser affinity” herein refers to a degree of antibody binding where an antibody X binds to target Y less strongly and/or with a higher dissociation constant than to target Z, and in this context antibody X has a lesser affinity for target Y than for Z. The affinity of binding between an antibody and its target antigen, can be expressed as  $K_A$  equal to  $1/K_d$  where  $K_d$  is equal to  $k_{off}/k_{on}$ . The  $k_{on}$  and  $k_{off}$  values can be measured using surface plasmon resonance technology, for example, using a Molecular Affinity Screening System (MASS-1) (Sierra Sensors GmbH, Hamburg, Germany).

[00084] An antagonist or blocking antibody is an antibody that partially or fully blocks, inhibits or neutralizes a biological activity related to the target antigen relative to the activity under similar physiological conditions when the antibody is not present. Antagonists can be competitive, non-competitive or irreversible. A competitive antagonist is a substance that binds to a natural ligand or receptor at the same site as is used in the natural ligand-receptor interaction or binds allosterically in a manner that induces a change to prevent normal binding of the natural ligand. A non-competitive antagonist binds at a different site, on either the ligand or the receptor, than is used in the natural ligand-receptor interaction, but increases the  $K_d$  of the interaction, or lowers a signal resulting from the interaction. An irreversible inhibitor causes, e.g., covalent modifications to the receptor or to the natural ligand which prevent binding of the natural ligand to the receptor.

[00085] As used herein, the term “avidity” refers to the overall stability of the binding complex between the antibody and the target antigen. It is governed by three factors, (i) the intrinsic affinity of the antibody for the antigen, (2) the valency of the antibody, and (3) the geometric arrangement of the interacting components. Affinity is the strength of the interaction between

the antibody and a single target, whereas avidity is an accumulated strength of multiple affinities.

**[00086]** As used herein, an antibody “preferentially binds” binds a first antigen relative to a second antigen if it binds the first antigen with greater affinity than it does the second antigen.

5 Preferential binding can be at least any of 2-fold, 5-fold, 9-fold, 10-fold, 20-fold, 30-fold, 40-fold, 50-fold, 100-fold, 500-fold or 1000-fold greater affinity.

**[00087]** As used herein, an antibody “blocks” or “antagonizes” the binding of a ligand to receptor when it reduces or prevents interaction of the ligand with the receptor. In embodiments, the measured level of reduction can be at least any of 5%, 10%, 25%, 50%, 80%, 90%, 95%,

10 97.5%, 99%, 99.5%, or 99.9% of a control) ligand-receptor complex (i.e., a ligand-receptor complex in the absence of the antibody).

**[00088]** The term “captures” with respect to an antibody target (e.g., antigen, analyte, immune complex), typically indicates that an antibody binds a majority of the antibody targets in a pure population (assuming appropriate molar ratios). For example, an antibody that binds a

15 given antibody target typically binds to at least 2/3 of the antibody targets in a solution (e.g., at least any of 67, 75, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100% of the targets). One of skill will recognize that some variability will arise depending on the method and/or threshold of determining binding.

#### D. Antibody Formats

20 **[00089]** The following are a non-exhaustive list of different antibody formats, all retaining antigen binding activity:

(1) whole immunoglobulins (also referred to as “intact” antibodies) (two light chains and two heavy chains, e.g., a tetramer, e.g., IgG, IgA, IgD, IgE and fragments of IgM).

(2) an immunoglobulin polypeptide (a light chain or a heavy chain).

25 (3) an antibody fragment, including rearranged binding regions. These include, for example:

- Fv (a monovalent or bi-valent variable region fragment, and can encompass only the variable regions (e.g.,  $V_L$  and/or  $V_H$ ),
- Fab ( $V_L C_L V_H C_H$ ),
- 30 • F(ab')<sub>2</sub>,
- Fv ( $V_L V_H$ ),
- scFv (single chain Fv) (a polypeptide comprising a  $V_L$  and  $V_H$  joined by a spacer, e.g., a peptide spacer),
- (scFv)<sub>2</sub>, (optionally bi-specific),
- 35 • sc(Fv)<sub>2</sub> (optionally bi-specific),



- minibody (sc(Fv)<sub>2</sub> fused to CH3 domain)
- diabody (noncovalent dimer of heavy chain variable (VH) and light chain variable (VL) regions connected by a peptide spacer) (It is understood that while the VH and VL regions on a first chain can be in any order, the order of these regions on the second chain is reversed relative to the order of these regions on the first chain.)
- triabody: trivalent sc(Fv)<sub>3</sub> or tri-specific sc(Fv)<sub>3</sub>.
- Antibody fragments further include Fd (the portion of the heavy chain included in the Fab fragment) and single domain antibodies. A single domain antibody (sdAb) is a variable domain of either a heavy chain or a light chain, produced by recombinant methods.

(4) a multi-specific antibody (an antibody comprising at least two paratopes that bind to different epitopes).

(5) a multivalent antibody (an antibody having two or more paratopes, including bivalent, trivalent and tetravalent antibodies).

(6) a fusion protein comprising a binding portion of an immunoglobulin fused to another amino acid sequence (such as a fluorescent protein).

**[00090]** Any of these formats can be mono-specific, or multi-specific, e.g., bi-specific, tri-specific or tetra-specific.

#### **E. Antibody Symmetry**

**[00091]** Antibodies comprising two heavy chains, typically, can be symmetric or asymmetric. A symmetric antibody has mirror-image parts. Typically, this will involve having identical heavy chains. An asymmetric antibody is not formatted as a mirror image. In this case, typically, the heavy chains are not identical.

**[00092]** An asymmetric antibody typically has two non-identical heavy chains. Usually, paratopes in the same relative position will bind different epitopes. A challenge in producing such antibodies is ensuring that the two different heavy chains pair correctly and selectively without mismatching. Mismatch can produce a mixture of mono-specific and bi-specific antibodies. Such chains may not stably associate with one another. Knobs-into-holes or Knob and Holes ("KIHS") technology addresses this problem. KIHS involves engineering CH3 domains to create a "knob" in a first heavy chain and a "hole" in a second heavy chain to promote heterodimerization between the first and second heavy chains. In asymmetric antibodies as disclosed herein, the paratopes can be in either orientation, that is, on a chain comprising a knob or on a chain comprising a hole.

[00093] In this approach a 'knob' variant can be obtained by replacement of a small amino acid (e.g., threonine) with a larger one (e.g., tyrosine) in the CH3 domain of an antibody (e.g., T366Y). The knob is designed to insert into a 'hole' in the CH3 domain of another antibody. In one embodiment, a 'hole' is created by replacement of a large residue (e.g., tyrosine) with a smaller one (e.g., threonine), such as in Y407T.

[00094] When protein domains or subdomain interact, a knob is a bulky side chain that protrudes into the opposite ("hole") domain where it is aligned with a small side chain that makes such invasion possible. In this approach, knob and hole variants were anticipated to heterodimerize by virtue of the knob inserting into an appropriately designed hole on the partner CH3 domain. Knobs were constructed by replacing small side chains with the largest side chains, tyrosine or tryptophan. Holes of identical or similar size to the knobs were created by replacing large side chains with the smaller ones, in this case alanine or threonine. This way, two heavy chains that are knob variants cannot homoassociate because of side chain clashes, and the homoassociation of two hole variants is less favored because of the absence of a stabilizing side-chain interaction. Subsequently, a disulfide bond was introduced near the C-terminus of the CH3 domain to further stabilize the assembled bi-specific antibodies. See, for example, U.S. Pat. No. 7,183,076, incorporated herein by reference.

#### F. Spacer Moieties

[00095] Engineered antibodies disclosed herein comprise functional portions attached to each other. This includes, for example, variable regions attached to each other in an scFv or diabody format, different paratope configurations (e.g., Fab, diabody, scFv) attached to each other, or paratopes attached to an Fc region, either on the amino side or the carboxy side. These regions or portions can be attached through spacer moieties. For example, for a tetravalent antibody of Platform 4, the C-terminal portion of an CH1 region of a heavy chain is attached to the N-terminal portion of a diabody region. The N-terminus of a diabody can be either a VL or VH region, depending on the format of the diabody region. The C-terminus of the diabody region also can be a VH or a VL region. It is attached to the N-terminal region of an Fc region. The borders of these regions can be determined from the sequences herein and from antibody sequences well known in the art.

[00096] Spacers can be, for example, 0 (no spacer) to 50 amino acids, e.g., 1 to 50 amino acids long. The spacer can have, for example, any 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, or 50 amino acids. For example, the polypeptide spacer can have between any of 1 to 50, 5 to 50, 1 to 30, 1 to 25, 5 to 25, 5 to 20, 5 to 15, 5 to 10, 15, 20, 1-10 or 1-5 amino acids. In one embodiment, the spacer is a monomer or polymer of the sequence (GGGGS)<sub>n</sub> (SEQ ID NO:170), (GGGGA)<sub>n</sub> (SEQ ID NO:171), or (GGGGG)<sub>n</sub> (SEQ ID NO:173), wherein n is any of 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10. An embodiment of a spacer has

the sequence GGGSGGGGSEPKSSDKTHT (SEQ ID NO: 173) (e.g., to link a diabody region with an Fc region). Another embodiment of a spacer has the sequence GGGSGGGSGGGSGGGSGSTG (SEQ ID NO: 174) (e.g., to link an Fc region with an Fab region). Other exemplary spacers have the sequence: LEDKTHTKVEPKSS (SEQ ID NO: 175), SGSETPGTSESATPESGGG (SEQ ID NO: 176) or GTTAASGSSGGSSSGA (SEQ ID NO: 177).

**[00097]** As used herein regions or portions of an engineered antibody are connected “directly” if no spacer (0 amino acids) link them. Regions or portions of an engineered antibody are connected “substantially directly” (“substantially no spacer”) if they are connected by a spacer of one or two amino acids. Antibodies of Platform 2 comprise a diabody region attached to an Fc region, and an Fc region attached to an Fab region. In certain embodiments, these regions are attached directly or substantially directly (i.e., 0, 1 or 2 amino acids). That is, the C-terminus of the variable region of the diabody is directly connected to the N terminus of the CH2 of the Fc region, and the C-terminus of the Fc region is directly connected to N terminus of the light chain variable region. Reference to attachment to the CH2 region contemplates attachment to the hinge connected to CH2.

**[00098]** Antibodies of Platform 4 comprise an Fab region attached to diabody region, and a diabody region attached to an Fc region.

**[00099]** Tables 3 and 4 shows spacers between functional portions of engineered antibodies. “G4S” refers to the sequence “GGGGS” (SEQ ID NO: 170). The number refers to the number of repetitions. Thus, for example, “(G4S)2” refers to the sequence GGGSGGGGS (SEQ ID NO: 178). A number of “0” means no spacer, or a spacer of 0 amino acids. In any of these antibodies, spacer (G4S)<sub>n</sub> can be substituted with (G4A)<sub>n</sub>, (G5)<sub>n</sub>, or an amino acid sequence comprising an equivalent number of amino acids, which need not be an exact multiple of 5, but could be any of (X5)<sub>n</sub> + 1, 2, 3 or 4, wherein n is 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

| Table 3                           |                       |                   |
|-----------------------------------|-----------------------|-------------------|
| Platform 2                        | Spacer 1 – Diabody-Fc | Spacer 2 – Fc-Fab |
| AB123; AB125; AB136; AB620; AB625 | (G4S)0                | (G4S)0            |
| AB143                             | (G4S)2                | (G4S)4            |
| AB142                             | (G4S)2                | (G4S)2            |
| AB141                             | (G4S)2                | (G4S)1            |
| AB140                             | (G4S)2                | (G4S)0            |
| AB139                             | (G4S)1                | (G4S)4            |
| AB138                             | (G4S)1                | (G4S)0            |
| AB137                             | (G4S)0                | (G4S)4            |

|                            |        |        |
|----------------------------|--------|--------|
| AB136                      | (G4S)0 | (G4S)0 |
| AB122; AB124; AB144; AB624 | (G4S)2 | (G4S)4 |

|                                             |                        |                       |
|---------------------------------------------|------------------------|-----------------------|
| Table 4                                     |                        |                       |
| Platform 4                                  | Spacer 3 – Fab-Diabody | Spacer 4 – Diabody-Fc |
| AB119; AB121; AB127; AB128;<br>AB618; AB623 | (G4S)0                 | (G4S)0                |
| AB106; AB113; AB120; AB126;<br>AB616; AB622 | (G4S)4                 | (G4S)2                |
| AB135                                       | (G4S)4                 | (G4S)1                |
| AB134                                       | (G4S)4                 | (G4S)0                |
| AB114; AB133                                | (G4S)3                 | (G4S)2                |
| AB115; AB132                                | (G4S)2                 | (G4S)2                |
| AB116; AB131; AB617                         | (G4S)1                 | (G4S)2                |
| AB117; AB130                                | (G4S)0                 | (G4S)2                |
| AB118; AB129                                | (G4S)0                 | (G4S)1                |

## II. Multivalent Antibody Platform Architectures

5 [000100] “Multivalent” antibodies have more than one antigen binding site or paratope. For example, an antibody that has two binding sites is bivalent, an antibody with three binding sites is trivalent, and an antibody with four binding sites is tetravalent.

[000101] Contemplated herein are a variety of formats for multi-specific, multivalent antibodies. Variables include the degree of valency, the format of the paratopes, and the arrangement of binding sites for particular epitopes.

10 [000102] A multivalent antibody can have a plurality of binding sites that bind the same epitope as well as one or more binding sites that bind different epitopes. Antibodies in nature, such as IgG molecules, are typically mono-specific and bivalent. An antibody is “mono-specific” if all of its antigen binding sites bind to the same epitope. A multi-specific antibody has at least two different antigen binding sites which each bind to a different epitope or antigen. So, for  
15 example, if a bivalent antibody has antigen binding sites that each bind to a different epitope, then the antibody is bi-specific. A trivalent antibody can be mono-specific, bi-specific or tri-specific. A tetravalent antibody can be mono-specific, bi-specific, tri-specific or tetra-specific.

20 [000103] In describing antibodies herein, the orientation of various functional portions of a heavy chain or light chain is described from amino terminus to carboxy terminus, unless explicitly provided otherwise.

[000104] In antibodies that have more than one light chain associated with a heavy chain, there is the issue of whether the paratopes formed by these associations bind the same or a different epitope. For example, in the antibodies shown schematically in Figs. 5A and 5B, paratopes 1 and 2 bind the same epitope. However, in the antibodies shown schematically in Figs. 5C and 5D, paratopes 1 and 2 bind different epitopes. Where the paratopes bind the same epitope, and the antibody is symmetric, a single light chain and a single heavy chain expressed in a cell can assemble to form the antibody. Where the paratopes bind different epitopes, and the antibody is asymmetric, the following approaches to antibody assembly can be used. In one approach, each different light chain/heavy chain pair can be expressed in a different cell, and the antibody can be assembled in vitro. In another approach, each heavy chain variable region pairs with a common light chain variable region. Such approaches are well known in the art. See, for example, U.S. Patent 8,642,745 ("Method for making multi-specific antibodies having heteromultimeric and common components"); U.S. Patent 11,033,009 ("Transgenic chicken for production of antibodies having a common light chain"); U.S. Patent 9,303,081 ("Recombinant production of mixtures of antibodies"); and U.S. Patent 11,325,982 ("Biparatopic and multiparatopic antibodies with common light chain and method of use").

[000105] Diabodies comprise a pair of chains that associate to form two paratopes. (See, e.g., Figs. 2 and 4.) Each chain comprises VL and VH regions linked to each other. This combination is referred to as a "diabody region." These regions can be arranged in any order, provided the regions of each partner chain are in an order consistent with formation of the diabody. In certain antibody architectures, such as shown in Figs. 5A, 5B and 6B, both paratopes of a diabody bind the same epitope. In this configuration, each diabody region can comprise VL and VH regions directed to the same epitope. In other architectures, such as shown in Figs. 5C, 5D, 6A and 6C; the paratopes bind different epitopes. In this configuration, the diabody region of a first chain includes a light or heavy chain variable region that binds a first epitope, and a heavy or light chain variable region (respectively) that binds a second epitope. In this way, each variable region can associate with the appropriate variable region on the diabody region of the other chain.

[000106] It is understood that references to "first," "second," "third," and "fourth" regions or portions of antibodies are for nomenclature purposes only, and do not necessarily indicate specific positions of these regions or portions in an antibody, for example, specific positions in the compass rose, or equivalence between different antibody formats.

#### A. Targeted Epitopes

[000107] Antibodies of this disclosure can target any epitope for which an antibody can be made. This includes, without limitation, any cell surface marker, e.g., on a cancer cell or other pathological cell. Functional portions of antibodies against any epitope, such as light chains

and variable regions thereof, heavy chain portions or regions comprising heavy chain variable regions and heavy chain constant 1 regions, and Fc portions of antibodies, can be assembled into the antibody architectures described here. So, for example, portions of different antibodies directed against different epitopes can be incorporated as Fabs, diabodies or scFvs into

5 tetraivalent, bi-specific antibodies of this disclosure. Exemplary antibodies of this disclosure comprise paratopes that specifically bind to epitopes of HER2 (epitope 1), HER2 (epitope 2), CD30, PD-L1 (epitope 1), PD-L1 (epitope 2), PD-L1 (epitope 3), PD-L1 (epitope 4), and Trop2.

[000108] In one embodiment, an antibody of this disclosure comprises paratopes that bind two different epitopes of HER2. In certain embodiments, one of these epitopes is an epitope bound  
10 by the antibody Trastuzumab. In certain embodiments, one of these epitopes is an epitope bound by the antibody Pertuzumab.

[000109] In another embodiment, an antibody of this disclosure comprises at least one paratope that binds to CD30, and at least one paratope that binds to an epitope of PD-L1. Alternatively, the antibody can comprise a paratope that binds to CD30, paratope that binds to a  
15 first epitope of PD-L1, and at least one paratope that binds to a second epitope of PD-L1.

[000110] In another embodiment, an antibody of this disclosure comprises at least one paratope that binds Trop2, and at least one paratope that binds to an epitope of HER2. Alternatively, the antibody can comprise a paratope that binds to Trop2, a paratope that binds to a first epitope of HER2, and a paratope that binds to a second epitope of HER2.

20 [000111] In another embodiment, an antibody of this disclosure comprises at least one paratope that binds to Muc16, and at least one paratope that binds to an epitope of NaPi2b.

[000112] In another embodiment, an antibody of this disclosure comprises paratopes that bind different epitopes of Her2 and at least one paratope that binds to an epitope of PD-L1.

[000113] In another embodiment, an antibody of this disclosure comprises paratopes that bind  
25 different epitopes of PD-L1 and at least one paratope that binds to an epitope of CD30.

[000114] In another embodiment, an antibody of this disclosure comprises paratopes that bind different epitopes of Her2 and at least one paratope that binds to an epitope of Trop2.

[000115] In another embodiment, an antibody of this disclosure comprises paratopes that bind different epitopes of Her2 and paratopes that binds to different epitopes of PD-L1.

30 [000116] In another embodiment, an antibody of this disclosure comprises paratopes that bind different epitopes of Her2, a paratope that binds to an epitope of PD-L1, and a paratope that binds to an epitope of Trop2.

[000117] Exemplary sequences of antibodies that bind such epitopes are presented in Table  
2.

**B. Tetraivalent, Multi-specific (e.g., Bi-specific, Tri-specific and Tetra-specific) Antibodies**

[000118] A bi-specific, tetraivalent antibody can have two paratopes directed to a first epitope, and two paratopes directed to a second epitope; or three paratopes directed to a first epitope and one paratope directed to a second epitope. The epitopes can be on different antigen molecules (that is, the antibody binds two different molecules) or the epitopes can be different epitopes on the same antigen. The paratopes can be placed in any arrangement of the four compass positions consistent with the bi-specific nature of the antibody.

[000119] The four paratopes of a tetraivalent antibody can be described as being positioned on a compass rose at “northwest,” “northeast,” “southeast,” and “southwest” positions. Antibodies typically have an asymmetric shape that can be said to include an “east” side (first heavy chain), a “west” side (second heavy chain), a “north” (toward the N-terminus) side, and a “south” (toward the C-terminus) side. In a tetraivalent antibody, for example, binding site positions could be characterized as “northeast,” “northwest,” “southeast,” and “southwest.” Accordingly, two binding sites that bind the same epitope could be related as “northwest-northeast,” “southwest-southeast,” “northeast-southeast,” “northwest-southwest,” “northwest-southeast,” and “northeast-southwest.” See, for example, Figs. 5A-5D.

[000120] Specific sequences of these configurations are provided in Table 2.

**1. Platform 1: Fab-Fc-Fab Antibody**

[000121] A schematic of an antibody having a Platform 1 configuration of Fab-Fc-Fab is presented in **Figure 1**. The antibody comprises a tetraivalent antibody comprising, e.g., one or more payloads conjugated thereto, wherein the antibody comprises first, second, third, and fourth light chains, and first and second heavy chains, and comprises, from N-terminus to C-terminus: a) a first pair of paratopes comprised in Fab regions; b) an Fc region; and c) a second pair of paratopes, comprised in Fab regions. An Fab attached directly to an Fc (Fab-Fc) is typically referred to as “IgG” (or other immunoglobulin format), but the Fab could be attached through a spacer.

[000122] By way of description, the antibody comprises first, second, third and fourth light chains, and first and second heavy chains, wherein: a) the first light chain comprises, from N-terminus to C-terminus, a first light chain variable (VL) region and a first light chain constant (CL) region; b) the second light chain comprises, from N-terminus to C-terminus, a second VL region and a second CL region; c) the third light chain comprises, from N-terminus to C-terminus, a third light chain variable (VL) region and a third light chain constant (CL) region; d) the fourth light chain comprises, from N-terminus to C-terminus, a fourth VL region and a fourth CL region; e) the first heavy chain comprises, from N-terminus to C-terminus: (i) a first heavy chain portion comprising a first heavy chain variable (VH) region and a first heavy chain

constant 1 (CH1) region; (ii) a first Fc region comprising a first heavy chain constant 2 (CH2) region and a first heavy chain constant 3 (CH3) region; (iii) a second heavy chain portion comprising a second heavy chain variable (VH) region and a second heavy chain constant 1 (CH1) region; and f) the second heavy chain comprises, from N-terminus to C-terminus: (i) a third heavy chain portion comprising a third heavy chain variable (VH) region and a third heavy chain constant 1 (CH1) region; (ii) a second Fc region comprising a second heavy chain constant 2 (CH2) region and a second heavy chain constant 3 (CH3) region; and (iii) a fourth heavy chain portion comprising a fourth heavy chain variable (VH) region and a fourth heavy chain constant 1 (CH1) region; and wherein: the first light chain and the first heavy chain portion form a first Fab portion comprising a first paratope; the second light chain and the second heavy chain portion form a second Fab portion comprising a second paratope; the third light chain and the third heavy chain portion form a third Fab portion comprising a third paratope; and the fourth light chain and the fourth heavy chain portion form a fourth Fab portion comprising a fourth paratope.

## 2. Platform 2: Diabody-Fc-Fab Antibody

**[000123]** A schematic of an antibody having a Platform 2 configuration of Diabody-Fc-Fab is presented in **Figure 2**. The antibody comprises a tetravalent antibody comprising, e.g., one or more payloads conjugated thereto, wherein the antibody comprises first and second light chains, and first and second heavy chains, and comprises, from N-terminus to C-terminus: a) a first pair of paratopes, comprised in a diabody; b) an Fc region; and c) a second pair of paratopes comprised in Fab regions.

**[000124]** By way of description, the antibody comprises first and second light chains and first and second heavy chains, wherein: a) the first light chain comprises, from N-terminus to C-terminus, a first light chain variable (VL) region and a first light chain constant (CL) region; b) the second light chain comprises, from N-terminus to C-terminus, a second VL region and a second CL region; c) the first heavy chain comprises, from N-terminus to C-terminus: (i) a first diabody region comprising a first VH region and a third VL region, in either order; (ii) a first Fc region comprising a first heavy chain constant 2 (CH2) region and a first heavy chain constant 3 (CH3) region; (iii) a first heavy chain portion comprising a second heavy chain variable (VH) region and a first heavy chain constant 1 (CH1) region; d) the second heavy chain comprises, from N-terminus to C-terminus: (i) a second diabody region comprising a third VH region and a fourth VL region, in either order; and (ii) a second Fc region comprising a second heavy chain constant 2 (CH2) region and a second heavy chain constant 3 (CH3) region; (iii) a second heavy chain portion comprising a fourth heavy chain variable (VH) region and a second heavy chain constant 1 (CH1) region; wherein: the first light chain and the first heavy chain portion form a first Fab portion comprising a first paratope; and the second light chain and the second heavy chain portion form a second Fab portion comprising a second paratope; the first and



second diabody regions form a diabody forming a third paratope comprising the third VL region and the third VH region, and a fourth paratope comprising the fourth VL region and the first VH region.

### 3. Platform 3: Fab-Fab-Fc Antibody

5 [000125] A schematic of an antibody having a Platform 3 configuration of Fab-Fab-Fc is presented in **Figure 3**. The antibody comprises a tetravalent antibody comprising, e.g., one or more payloads conjugated thereto, wherein the antibody comprises first, second, third, and fourth light chains, and first and second heavy chains, and comprises, from N-terminus to C-terminus: a) a first pair of paratopes comprised in Fab regions; b) a second pair of paratopes, 10 comprised in Fab regions; and c) an Fc region.

[000126] By way of description, the antibody comprises first, second, third and fourth light chains, and first and second heavy chains, wherein: a) the first light chain comprises, from N-terminus to C-terminus, a first light chain variable (VL) region and a first light chain constant (CL) region; b) the second light chain comprises, from N-terminus to C-terminus, a second VL 15 region and a second CL region; c) the third light chain comprises, from N-terminus to C-terminus, a third light chain variable (VL) region and a third light chain constant (CL) region; d) the fourth light chain comprises, from N-terminus to C-terminus, a fourth VL region and a fourth CL region; e) the first heavy chain comprises, from N-terminus to C-terminus: (i) a first heavy chain portion comprising a first heavy chain variable (VH) region and a first heavy chain constant 1 (CH1) region; (ii) a second heavy chain portion comprising a second heavy chain variable (VH) region and a second heavy chain constant 1 (CH1) region; and (iii) a first Fc region comprising a first heavy chain constant 2 (CH2) region and a first heavy chain constant 3 (CH3) region; f) the second heavy chain comprises, from N-terminus to C-terminus: (i) a third 20 heavy chain portion comprising a third heavy chain variable (VH) region and a third heavy chain constant 1 (CH1) region; (ii) a fourth heavy chain portion comprising a fourth heavy chain variable (VH) region and a fourth heavy chain constant 1 (CH1) region; and (iii) a second Fc region comprising a second heavy chain constant 2 (CH2) region and a second heavy chain constant 3 (CH3) region; wherein: the first light chain and the first heavy chain portion form a first Fab portion comprising a first paratope; and the second light chain and the second heavy chain portion form a second Fab portion comprising a second paratope; the third light chain and the third heavy chain portion form a third Fab portion comprising a third paratope; and the fourth light chain and the fourth heavy chain portion form a fourth Fab portion comprising a fourth 30 paratope.

### 4. Platform 4: Fab-Diabody-Fc Platform

35 [000127] A schematic of an antibody having a Platform 4 configuration of Fab-Diabody-Fc is presented in **Figure 4**. The antibody comprises a tetravalent antibody comprising, e.g., one or

more payloads conjugated thereto, wherein the antibody comprises first and second light chains, and first and second heavy chains, and comprises, from N-terminus to C-terminus: a) a first pair of paratopes comprised in Fab regions; b) a second pair of paratopes, comprised in a diabody; and c) an Fc region.

- 5 **[000128]** By way of description, the antibody comprises first and second light chains, wherein:
- a) the first light chain comprises, from N-terminus to C-terminus, a first light chain variable (VL) region and a first light chain constant (CL) region; b) the second light chain comprises, from N-terminus to C-terminus, a second VL region and a second CL region; c) the first heavy chain comprises, from N-terminus to C-terminus: (i) a first heavy chain portion comprising a first
- 10 heavy chain variable (VH) region and a first heavy chain constant 1 (CH1) region; (ii) a first diabody region comprising a second VH region and a third VL region, in either order; and (iii) a first Fc region comprising a first heavy chain constant 2 (CH2) region and a first heavy chain constant 3 (CH3) region; d) the second heavy chain comprises, from N-terminus to C-terminus:
- 15 (i) a second heavy chain portion comprising a third VH region and a second CH1 region; (ii) a second diabody region comprising a fourth VH region and a fourth VL region, in either order; and (iii) a second Fc region comprising a second CH2 region and a second CH3 region;
- wherein: the first light chain and the first heavy chain portion form a first Fab portion comprising a first paratope; and the second light chain and the second heavy chain portion form a second Fab portion comprising a second paratope; the first and second diabody regions form a diabody
- 20 forming a third paratope comprising the fourth VL region and the second VH region, and a fourth paratope comprising the third VL region and the fourth VH region.

**[000129]** These regions can be attached to each other spacer moieties, directly (no spacer moiety) or substantially directly.

### C. Specific Targets

- 25 **[000130]** The following exemplary targeting strategies are specifically contemplated. Antibodies comprising such targeting strategies can be in ADC or non-ADC format.

#### 1. Her2/Her2

- [000131]** Her2 is an antigen expressed on a number of different types of cancer cells including, in particular, breast cancer and ovarian cancer. Antibodies, such as trastuzumab and
- 30 pertuzumab are directed to this antigen.

**[000132]** A tetravalent, mono-specific antibody of this disclosure comprises first, second, third, and fourth paratopes directed to the same epitope of HER2.

- [000133]** A tetravalent, bi-specific antibody of this disclosure comprises first and second paratopes directed to the same first epitope of HER2 and third and fourth paratopes directed to
- 35 the same second epitope of HER2. In one embodiment the paratopes directed to the same epitopes can be arranged in the NW/NE positions and SW/SE positions. In another embodiment

the paratopes directed to the same epitopes can be arranged in the NW/SW and NE/SE positions.

[000134] In certain embodiments, there is no spacer or substantially no spacer between the Fab regions and the diabody, and between the diabody and the Fc region. In another embodiment, there is a spacer of about 15 amino acids between the Fab regions and the diabody and a spacer of about 10 amino acids between the diabody and the Fc region.

## 2. CD30/PD-L1

[000135] A tetravalent, bi-specific antibody of this disclosure comprises first and second paratopes directed to CD30 and third and fourth paratopes directed to PD-L1. In another embodiment, the antibody comprises first, second and third paratopes directed to CD30 and a fourth paratope directed to PD-L1. In another embodiment, the antibody comprises first, second and third paratopes directed to PD-L1 and a fourth paratope directed to CD30.

[000136] CD30 is a cell membrane protein predominantly found on activated T and B cells, playing a role in regulating cell proliferation and death. It is related to, particularly Hodgkin's lymphoma and some non-Hodgkin lymphomas, as well as other lymphoproliferative disorders. In these cancers, CD30 is often overexpressed on the surface of malignant cells. This overexpression makes CD30 a valuable therapeutic target.

[000137] PD-L1 (Programmed Death-Ligand 1) is a checkpoint inhibitor that can be targeted as an anticancer therapy. Some cancers, such as melanoma, non-small cell lung cancer, and certain types of bladder, kidney, and head and neck cancers can be treated by targeting this marker.

## 3. Her2/Trop2

[000138] A tetravalent, bi-specific antibody of this disclosure comprises first and second paratopes directed to Her2 and third and fourth paratopes directed to Trop2. In another embodiment, the antibody comprises first, second and third paratopes directed to Her2 and a fourth paratope directed to Trop2. In another embodiment, the antibody comprises first, second and third paratopes directed to Trop2 and a fourth paratope directed to Her2.

[000139] TROP2, also known as EpCAM (Epithelial Cell Adhesion Molecule), is a transmembrane glycoprotein primarily expressed on the surface of epithelial cells and has a role in cell adhesion, migration, and proliferation. Its significance in the field of oncology stems from its overexpression in a wide variety of human carcinomas, including breast, colon, prostate, and ovarian cancers. This overexpression is often associated with increased tumor aggressiveness, poor prognosis, and reduced patient survival, making TROP2 a valuable biomarker for cancer diagnosis and prognosis. Moreover, TROP2's consistent overexpression on the surface of many cancer cells compared to normal tissues has made it an attractive target for cancer

therapy, underscoring the importance of TROP2 as both a cancer marker and a therapeutic target.

5 [000140] In another embodiment, a tetravalent antibody comprises first and second paratopes directed to the same epitope of HER2, and third and fourth paratopes directed to the same epitope of Trop2. The paratopes that bind the same epitope of HER2 can be positioned in the NW/NE positions, SW/SE positions, or the NW/SW positions.

10 [000141] In another embodiment, a tetravalent antibody comprises a first paratope directed to a first epitope of Her2, a second paratope directed to a second epitope of Her2 and third and fourth paratopes directed to the same epitope of Trop2. The two paratopes that bind the same epitope of Trop2 can be positioned in the NE/SE positions.

#### 4. Muc16/NaPi2b

15 [000142] A tetravalent, bi-specific antibody of this disclosure comprises first and second paratopes directed to Muc16 and third and fourth paratopes directed to NaPi-2b. In another embodiment, the antibody comprises first, second and third paratopes directed to Muc16 and a fourth paratope directed to NaPi-2b. In another embodiment, the antibody comprises first, second and third paratopes directed to NaPi-2b and a fourth paratope directed to Muc16.

20 [000143] "Mucin-16, cell surface associated", also referred to as Muc16 and CA125, is a member of the mucin family of proteins. These are large glycoproteins which have a role in forming mucus, which serves as a protective barrier in epithelial tissues. Muc16 is a membrane-associated mucin that possesses a single transmembrane domain. Muc16 is primarily found in the epithelial cells of the respiratory, digestive, and reproductive tracts.

[000144] Aberrant overexpression of Muc16 has been observed in several human malignancies, including ovarian, pancreatic, breast, and lung cancers. Muc16 is also thought to participate in cell-to-cell interactions that enable the metastasis of tumor cells.

25 [000145] Elevated levels of Muc16 in blood serum are often used as a biomarker in the diagnosis and monitoring of certain types of cancers, particularly ovarian cancer. Elevated Muc16 expression is also associated with small cell cancer of the lung and lung oat cell carcinoma.

30 [000146] Muc16 has the UniProt accession number Q8WXI7. The protein is encoded by the Muc16 gene, which is located on chromosome 19p13.2.

[000147] Antibodies known to specifically bind Muc16 include, for example, sofituzumab. Antibodies that specifically bind Muc16 are also described in U.S. patents US RE 47194 (Genentech 11D10); 11,453,721, 10,759,869, 10,738,130, and 7,202,346. The CDRs of any of these antibodies can be used in the bi-specific antibodies of this disclosure.

[000148] "Sodium-dependent Phosphate Transport Protein 2B", also referred to as NaPi-2b, SLC34A2, NaPiIb, and Npt2, is a member of the sodium/phosphate co-transporter family. It is a cell surface sodium-dependent phosphate transporter that regulates phosphate homeostasis. NaPi-2b is primarily expressed in the lung alveolar type II cells and the small intestine, where it facilitates the active transport of phosphate ions across cell membranes in conjunction with sodium ions.

[000149] NaPi-2b is a lineage marker that is expressed in 80-90% of epithelial ovarian cancers. It has been used as a target for therapeutic antibodies.

[000150] NaPi-2b has the UniProt accession number O95436. The protein is encoded by the SLC34A2 gene, which is located on chromosome 4p15.2.

[000151] Antibodies known to specifically bind NaPi-2b include, for example, lifastuzumab and Upifitamab (see, e.g., [url.drugs.ncats.io/substance/15OY7NA275](http://url.drugs.ncats.io/substance/15OY7NA275)). Antibodies that specifically bind NaPi-2b are also described in U.S. patent 11,407,825. The CDRs of any of these antibodies can be used in the bi-specific antibodies of this disclosure.

[000152] In another embodiment, a tetravalent antibody comprises first and second paratopes directed to the same epitope of HER2, and third and fourth paratopes directed to the same epitope of Trop2. The paratopes that bind the same epitope of HER2 can be positioned in the NW/NE positions, SW/SE positions, or the NW/SW positions.

[000153] In another embodiment, a tetravalent antibody comprises a first paratope directed to a first epitope of Her2, a second paratope directed to a second epitope of Her2 and third and fourth paratopes directed to the same epitope of Trop2. The two paratopes that bind the same epitope of Trop2 can be positioned in the NE/SE positions.

## 5. Her2/Her2/PD-L1

[000154] A tri-specific, tetravalent antibody of this disclosure comprises a first paratope against a first epitope of Her2, a second paratope against a second epitope of Her2, a third paratope against an epitope of PD-L1, and a fourth paratope against the same epitope of PD-L1.

[000155] The antibody can have any of the four platform architectures disclosed herein, particularly, Platform 2 and Platform 4.

[000156] In one embodiment, the paratopes against the first epitope of Her2 is located in the NE position, the paratope against a second epitope of Her2 is located in the NW position, and the two paratopes against PD-L1 are located in the SW and SE positions. This is an asymmetric antibody, and it is understood that the knob-in-hole structures can be oriented east-west or west-east.

[000157] In certain embodiments, there is no spacer or substantially no spacer between the Fab regions and the diabody, and between the diabody and the Fc region. In another embodiment, there is a spacer of about 15 amino acids between the Fab regions and the diabody and a spacer of about 10 amino acids between the diabody and the Fc region.

- 5 [000158] Antibodies of this embodiment include, for example, AB113, AB114, AB115, AB116, AB117, AB118, AB119, AB120, AB121, AB122, AB123.

#### 6. PD-L1/PD-L1/CD30

[000159] A tri-specific, tetravalent antibody of this disclosure comprises a first paratope against a first epitope of PD-L1, a second paratope against a second epitope of PD-L1, a third  
10 paratope against an epitope of CD30, and a fourth paratope against the same epitope of CD30.

[000160] The antibody can have any of the four platform architectures disclosed herein, particularly, Platform 2 and Platform 4.

[000161] In one embodiment, the paratopes against the same CD30 epitope are not located in NW/SE or NE/SW positions. This is an asymmetric antibody, and it is understood that the knob-  
15 in-hole structures can be oriented east-west or west-east.

[000162] In certain embodiments, there is no spacer or substantially no spacer between the Fab regions and the diabody, and between the diabody region and the Fc region. In another embodiment, there is a spacer of about 15 amino acids between the Fab regions and the diabody region and a spacer of about 10 amino acids between the diabody region and the Fc  
20 region.

[000163] Antibodies of this embodiment include, for example, AB205-AB216, AB219, AB220, AB221, AB222, AB623.

#### 7. Her2/Her2/Trop2

[000164] A tri-specific, tetravalent antibody of this disclosure comprises a first paratope  
25 against a first epitope of Her2, a second paratope against the first epitope of Her2, a third paratope against a second, different epitope of Her2, and a fourth paratope against Trop2.

[000165] The antibody can have any of the four platform architectures disclosed herein, particularly, Platform 2 and Platform 4.

[000166] In one embodiment, the paratopes against the same Her2 epitope and the paratopes  
30 against the same CD30 epitope are not located in NW/SE or NE/SW positions. This is an asymmetric antibody, and it is understood that the knob-in-hole structures can be oriented east-west or west-east.

[000167] In certain embodiments, there is no spacer or substantially no spacer between the Fab regions and the diabody region, and between the diabody and the Fc region. In another

embodiment, there is a spacer of about 15 amino acids between the Fab regions and the diabody and a spacer of about 10 amino acids between the diabody and the Fc region.

[000168] Antibodies of this embodiment include, for example, AB616, AB617, AB618, AB619, AB620, AB622, AB623, AB624, AB625.

5                                      8.        Her2/Her2/PD-L1/PD-L1

[000169] A tetra-specific, tetravalent antibody of this disclosure comprises a first paratope against a first epitope of Her2, a second paratope against a second epitope of Her2, a third paratope against a first epitope of PD-L1, and a fourth paratope against a second epitope of PD-L1.

10    [000170] The antibody can have any of the four platform architectures disclosed herein, particularly, Platform 2 and Platform 4.

[000171] In one embodiment, the paratope against the first epitope of Her2 is located in the SW position, the paratope against a second epitope of Her2 is located in the SE position, the first paratope against PD-L1 is located in the NW position, and the second paratope against PD-L1 is located in the NE position. In one embodiment, this antibody has a Platform 2 format. This is an asymmetric antibody, and it is understood that the knob-in-hole structures can be oriented east-west or west-east.

[000172] In another embodiment, the paratope against the first epitope of Her2 is located in the NW position, the paratope against a second epitope of Her2 is located in the NE position, the first paratope against PD-L1 is located in the SW position, and the second paratope against PD-L1 is located in the SE position. In one embodiment, this antibody has a Platform 4 format. This is an asymmetric antibody, and it is understood that the knob-in-hole structures can be oriented east-west or west-east.

[000173] In certain embodiments, there is no spacer or substantially no spacer between the diabody regions and the Fc region. In another embodiment, there is a spacer of about 10 amino acids between the diabody regions and the Fc region. In another embodiment, there is no spacer or substantially no spacer between the Fc region and the Fab region. In another embodiment, there is a spacer of about 20 amino acids between the Fc region and the Fab region. In another embodiment, there is no spacer or substantially no spacer between the Fab regions and the diabody regions. In another embodiment, there is a spacer of about 20 amino acids between the Fab regions and the diabody regions.

[000174] Antibodies of this embodiment include, for example, AB124, AB125, AB126 and AB127.

## 9. Her2/Her2/PD-L1/Trop2

[000175] A tetra-specific, tetravalent antibody of this disclosure comprises a first paratope against a first epitope of Her2, a second paratope against a second epitope of Her2, a third paratope against an epitope of PD-L1, and a fourth paratope against an epitope of PD-L1.

- 5 [000176] The antibody can have any of the four platform architectures disclosed herein, particularly, Platform 2 and Platform 4.

- [000177] In one embodiment, the paratope against the first epitope of Her2 is located in the SW position, the paratope against a second epitope of Her2 is located in the SE position, the paratope against PD-L1 is located in the NW position, and the paratope against Trop2 is located  
10 in the NE position. In one embodiment, this antibody has a Platform 2 format. This is an asymmetric antibody, and it is understood that the knob-in-hole structures can be oriented east-west or west-east.

- [000178] In certain embodiments, there is a spacer of about 10 amino acids between the diabody regions and the Fc region. In another embodiment, there is a spacer of about 20  
15 amino acids between the Fc region and the Fab region.

[000179] Antibodies of this embodiment include, for example, AB611 .

## 10. CDR Sequence Sets

[000180] Exemplary CDR sequence sets are provided in the sequences disclosed herein, where they are indicated by underlining.

- 20 [000181] Exemplary CDR sequence sets for anti-her2 antibodies include:

AB101 (Her2 10423)

AB102 (Her2 11053).

[000182] Exemplary CDR sequence sets for anti-CD30 antibodies include:

AB217 (CD30 18436).

- 25 [000183] Exemplary CDR sequence sets for anti-PD-L1 antibodies include:

AB202 (PD-L1 18608)

AB203 (PD-L1 18446)

AB204 (PD-L1 18463)

AB218 (PD-L1 18465-V1)

- 30 AB223 (PD-L1 18446-V1).

[000184] Exemplary CDR sequence sets for anti-Trop2 antibodies include:

AB601 (TROP2 17487)

AB621 (TROP2 17487-H1D3).

[000185] Exemplary CDR sequence sets for anti-muc16 antibodies include:



AB305.

[000186] Exemplary CDR sequence sets for anti-NaPi-2b antibodies include:

AB304.

[000187] It is understood that the antibody platforms disclosed herein can include CDR  
5 sequence sets for targets from any antibody known to bind that target.

### 11. Light Chains, Heavy Chain Regions, Diabody Regions and Fc Regions

[000188] Tetrameric antibodies of this disclosure comprise functional elements including light  
chains, heavy chain regions, diabody regions, and Fc regions. Examples of each of these  
10 functional elements are provided as portions of sequences disclosed in Table 1 and can be  
discerned from these sequences by inspection (for example, as determined by sequence  
termini and spacer sequences). Contemplated here is the incorporation of sequences of these  
elements into antibodies of the subject formats that also contain sequences of functional  
elements not provided herein. For example, an antibody could comprise sequences of a light  
15 chain and a heavy chain region provided herein for binding an epitope of Her2, and additionally  
comprise an Fc portion containing, e.g., cysteine substitutions not provided in the sequences of  
Table 1.

### III. Antibody Conjugates

[000189] An antibody conjugated to a chemical entity (*i.e.*, “payload”) is referred to herein as  
20 an “antibody conjugate” or an “immunoconjugate”. Conjugation can be effected by covalent  
coupling or non-covalent interactions (e.g., ionic, van der Waals, electrostatic, or hydrogen  
bonds). The chemical entity conjugated to the antibody also can be referred to as a moiety.  
Chemical moieties or payloads include, without limitation, a drug, a radionuclide, a biotin, RNA,  
an antibiotic, a protein and a detectable moiety (e.g., a fluorophore).

25 [000190] As used herein the term “antibody-drug conjugate” or “ADC” refers to an  
immunoconjugate wherein an antibody is conjugated to a drug, such as a cytotoxic drug, or an  
immune stimulator. Cytotoxic drugs include, without limitation, maytansinoid, DM-1, DM-4,  
auristatin, monomethyl auristatin E, monomethyl auristatin F, dolastatin, tubulysin, eribulin,  
cryptophycin, benzodiazepine, indolino-benzodiazepine, isoquinolidino-benzodiazepine, pyrrolo-  
30 benzodiazepine, alpha-amanitin, trichothene, camptothecin derivatives (SN-38, exatecan,  
belotecan, DXd, topotecan, samrotectan), duocarmycin, DGN549, CC1065, calicheamicin, N-  
acetyl calicheamicin, an enediyne antibiotic, taxane, doxorubicin derivatives, anthracycline and  
stereoisomers, azanofide, as well as isosteres, analogs, heterodimers, homodimers or  
derivatives of the foregoing. Cytotoxic drugs may also comprise any of the drug “payloads” in  
35 Colombo et al. Cancer Discov (2024) 14 (11): 2089–2108.

[000191] As used herein, the term “labeled antibody” refers to an antibody bound to a detectable label such that the presence of a target (e.g., a molecule) can be detected by detecting the presence of the detectable label bound to the target. As used herein, the term “detectable label” refers to a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, chemical, or other physical means. Examples of detectable labels are described herein and include, without limitation, colorimetric, fluorescent, chemiluminescent, enzymatic, and radioactive labels. For the purposes of the present disclosure, a detectable label can also be a moiety that does not itself produce a signal (e.g., biotin), but that binds to a second moiety that is able to produce a signal (e.g., labeled avidin or streptavidin).

[000192] The term “small molecule” refers to an organic or inorganic molecule having a size up to about 5000 Da, up to about 2000 Da, or up to about 1000 Da.

[000193] “Potency” refers to  $IC_{50}$  of a compound for killing cells, e.g., in culture.

[000194] Many conjugation methods are known in the art. In some embodiments, the payload is attached to the antibody through a spacer. These include, without limitation, conjugation through cysteine residues, and conjugation through lysine, arginine or tyrosine residues. In some embodiments, conjugation involves covalent binding through a linker.

#### A. Cysteine Residue Conjugation

[000195] Cysteine residue conjugation involves targeting the thiol (-SH) group of cysteine residues in an antibody. This can be achieved, for example, by reducing existing disulfide bonds to expose free thiols or by engineering additional cysteine residues into the antibody. The exposed thiol groups are reactive and can be conjugated with, for example, maleimide-functionalized drugs or labels, forming stable thioether bonds.

#### B. Lysine Residue Conjugation

[000196] Lysine residue conjugation involves targeting the amine groups (-NH<sub>2</sub>) on the side chains of lysine residues. This can be done, for example, by using N-hydroxysuccinimide (NHS) esters, which react with the amine groups to form stable amide bonds.

#### C. Site-specific Conjugation Method

[000197] Linker-payloads can be conjugated to a given antibody using any of these site-selective conjugation methods that fall broadly into eight categories: cysteine engineering, non-natural amino acid engineering, conjugation to native cysteines, peptide tags, glycan modification, enzymatic modification, disulfide rebridging, and conjugation to native lysines (see, e.g., Walsh SJ, et al. “Site-selective modification strategies in antibody-drug conjugates,” Chem Soc Rev. 2021;50:1305–53. doi:10.1039/d0cs00310g. PMID: 33290462 for additional details).

**D. Linker Chemistries**

[000198] Payloads are coupled to antibodies typically through linkers. Linkers include cleavable linkers and non-cleavable linkers.

[000199] Linkers also can be conjugated through a non-natural amino acid, disulfide re-bridging, a peptide tag, glycan modification, or an enzymatic modification method used to generate site-specific immunoconjugates.

**E. Drug-Antibody Ratio**

[000200] The drug-antibody ratio, or DAR, refers to the average number of payload moieties attached to antibodies in a composition. DAR is a function of the number of conjugatable sites on an antibody. When disulfide bonds of an antibody are reduced, producing reactive thiols, this may allow a DAR between 1 and 12. However, the introduction of cysteine residues into an immunoglobulin chain can significantly increase the possible DAR. The DAR of an antibody composition can be, for example, at least any of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 or 12 or more.

**F. Cysteine-substituted Antibodies**

[000201] A cysteine-substituted antibody is an antibody comprising at least one light chain or heavy chain constant region immunoglobulin amino acid residue that has been substituted with a cysteine residue that is not present in the naturally occurring antibody. These are sometimes referred to as "THIOMABS" (Junutula et al. Nature Biotechnology, 2008:26(8):925-32, doi: 10.1038/nbt.1480). A non-naturally occurring substitution is one that is not isotypic. In certain embodiments, the substituted residues in the heavy chain constant regions can include residues A118C, T155C, S157C, S239C, V266C, H285C, R301C, V303C, T307C, G316C, Y436C and L441C. These sites are based on EU numbering, as known in the art and described at [www.imgt.org/IMGTScientificChart/Numbering/Hu\\_IgHGnber.html](http://www.imgt.org/IMGTScientificChart/Numbering/Hu_IgHGnber.html) and Edelman, G.M. et al., Proc. Natl. Acad. USA, 63, 78-85 (1969). PMID: 5257969. The substituted residues in the light chain constant region can include residue V205C (Kabat numbering Kabat, E.A. et al., Sequences of proteins of immunological interest. 5th Edition - US Department of Health and Human Services, NIH publication no. 91-3242, pp 662,680,689 (1991)). In some embodiments, the constant region is of isotype IgG1, IgG2, IgG3 or IgG4.

**IV. Nucleic Acids, Recombinant Cells In Methods Of Making**

[000202] Provided herein are nucleic acid molecules encoding immunoglobulin chains of the antibodies of this disclosure. The antibodies of this disclosure can comprise a plurality of different polypeptides assembled into an antibody. For example, an antibody can comprise two identical heavy chains and two identical light chains. Alternatively, an antibody can comprise two different heavy chains. Further combinations of different polypeptides are possible, such as, for example, two different heavy chains and one or two different light chains. Therefore, further provided herein are nucleic acid molecules or collections of nucleic acid molecules that, as an

ensemble, encode polypeptides which, when assembled, produce the antibodies of this disclosure.

#### A. Nucleic Acid Molecules

- 5 [000203] Antibodies of this disclosure can be made by expressing polypeptides from nucleic acid molecules that encode them. Nucleic acids comprising nucleotide sequences that encode heavy chain and light chain molecules can be incorporated into recombinant DNA molecules (such as expression vectors), transfected into cells, expressed by the cells in culture, harvested and purified. Such methods are well known in the fields of molecular biology, cell biology and biopharmaceutical manufacturing.
- 10 [000204] A nucleic acid molecule encodes a polypeptide if it comprises a nucleotide sequence that, upon transcription and/or translation, produce the polypeptide. This includes, without limitation, contiguous nucleotide sequences that encode a polypeptide and noncontiguous nucleotide sequences that encode a polypeptide. Noncontiguous nucleotide sequences encoding a polypeptide include, for example, nucleotide sequences that include both introns
- 15 and exons. Such non-coding sequences are spliced out of messenger RNAs.

#### B. Expression Constructs and Vectors

- [000205] The nucleic acid molecules encoding immunoglobulin molecules can be incorporated into an expression construct for expression. An expression construct is a polynucleotide comprising an expression control sequence operatively linked with a heterologous nucleotide
- 20 sequence (i.e., a sequence to which the expression control sequence is not normally connected to in nature) that is to be expressed.

- [000206] An expression control sequence is a nucleotide sequence that regulates transcription and/or translation of a nucleotide sequence operatively linked thereto. Expression control sequences include promoters, enhancers, repressors (transcription regulatory
- 25 sequences) and ribosome binding sites (translation regulatory sequences). Suitable regulatory sequences may be derived from a variety of sources, including bacterial, fungal, viral, mammalian, or insect genes.

- [000207] A nucleotide sequence is "operatively linked" with an expression control sequence when the expression control sequence functions in a cell to regulate transcription of the
- 30 nucleotide sequence. This includes initiating transcription of the nucleotide sequence through an interaction between a polymerase and a transcriptional regulatory sequence such as, for example, a promoter.

- [000208] Promoters typically used in eukaryotic expression systems include, without limitation, the following. CMV (Cytomegalovirus) promoter, EF-1 $\alpha$  (Elongation Factor-1 alpha) promoter,
- 35 SV40 (Simian Virus 40) promoter, PGK (Phosphoglycerate kinase) promoter, CAG promoter, AOX1 (Alcohol oxidase 1) promoter, GAP (Glyceraldehyde-3-phosphate dehydrogenase)

promoter. Some promoters used in yeast, such as *Saccharomyces cerevisiae*, are ADH (Alcohol dehydrogenase) promoter, GAL1 and GAL10.

[000209] An expression vector is a polynucleotide comprising an expression construct and sequences sufficient for replication in a host cell or insertion into a host chromosome. A vector  
5 can comprise any intermediary vehicle for a nucleic acid molecule which enables said nucleic acid molecule, for example, to be introduced into prokaryotic and/or eukaryotic cells and/or integrated into a genome. Exemplary vectors for transfection of cells include, for example, a plasmid, a viral vector (e.g., a retrovirus, a lentivirus, an adenovirus, a papovavirus (e.g., SV40, polyoma) a parvovirus (e.g., adeno-associated virus), or a herpes simplex virus), a bacterial  
10 artificial chromosome, and a yeast artificial chromosome. The term "plasmid" as used herein generally refers to a construct of extrachromosomal genetic material, usually a circular DNA duplex, which can replicate independently of chromosomal DNA. The vector should be compatible with the host cell used. Other sequences, such as an origin of replication, DNA restriction sites, enhancers, and sequences conferring inducibility of transcription may be  
15 incorporated into the expression vector.

[000210] The recombinant expression vectors may also contain a marker gene which facilitates the selection of host cells transformed, infected or transfected with a vector for expressing an antibody described herein.

[000211] The recombinant expression vectors may also contain expression cassettes which  
20 encode a fusion moiety which provides increased expression or stability of the recombinant peptide; increased solubility of the recombinant peptide; or that aids in the purification of the target recombinant peptide by acting as a ligand in affinity purification, including for example, tags and labels described herein (e.g., a (His)<sub>6</sub> tag) (SEQ ID NO: 179). A recombinant peptide and its fusion moiety are collectively termed a "fusion protein." Further, a proteolytic cleavage  
25 site may be added to the fusion protein to allow separation of the recombinant peptide from the fusion moiety subsequent to purification of the fusion protein. Typical fusion expression vectors include pGEX (Amrad Corp., Melbourne, Australia), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the recombinant protein.

### 30 C. Recombinant Cells

[000212] Antibodies as disclosed herein can be made by culturing cells engineered to express nucleic acid constructs encoding immunoglobulin polypeptides.

[000213] The recombinant host cell can be generated using any cell suitable for producing a polypeptide, for example, suitable for producing an antibody. For example, to introduce a  
35 nucleic acid (e.g., a vector) into a cell, the cell may be transfected, transformed or infected, depending upon the vector employed.

[000214] Methods for transfecting cells with recombinant DNA molecules are known in the art and include, for example, electroporation, liposomes and exosomes, and transfection via viral vectors.

[000215] Suitable host cells include a wide variety of prokaryotic and eukaryotic host cells.

- 5 For example, the proteins described herein may be expressed in a mammalian cell (e.g., CHO, 293); an insect cell (e.g., in Sf9 cell or a high five (BTI-Tn-5B1-4) cell); a yeast cell (e.g., *Pichia pastoris* or and *Saccharomyces cerevisiae*); a bacterial cell (e.g., *E. coli*); or a plant cell (e.g., *Arabidopsis*).

- [000216] Mammalian cells that may be suitable include, among others: a Chinese hamster  
10 ovary (CHO) cell, an NS0 cell, an SP2/0 cell, a human embryonic kidney HEK 293 cell, or a Per.C6 cell). Suitable expression vectors for directing expression in mammalian cells generally include a promoter (e.g., derived from viral genomes such as polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40), as well as other transcriptional and translational control sequences. Examples of mammalian expression vectors include pCDM8 and pMT2PC.

- 15 [000217] Yeast and fungal host cells suitable for expressing an antibody include, but are not limited to *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, the genera *Pichia* or *Kluyveromyces* and various species of the genus *Aspergillus*. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1, pMFa, pJRY88, and pYES2 (Invitrogen Corporation, San Diego, CA). Protocols for the transformation of yeast and fungi are well  
20 known to those of ordinary skill in the art.

#### D. Antibody Production

[000218] Transformed/transfected cells are grown under suitable conditions that allow them to express the recombinant antibody.

- [000219] The number of different immunoglobulin chains that must be expressed in a cell to  
25 produce an antibody depends on the configuration of the antibody. Generally, fewer different chains results in more effective antibody assembly.

- [000220] Antibodies described herein may contain one or two different heavy chains, depending on architecture. Antibodies with the same heavy chain require only production of only one heavy chain in a cell, and they will associate naturally. If the antibody comprises  
30 different heavy chains, two polypeptides are produced, and knob-into-hole arrangements can facilitate proper assembly of antibodies, discouraging association of two "knob" chains or two "hole" chains.

- [000221] Light chains also will associate with their respective heavy chains. Where the antibody comprises two of the same heavy chains, then only one light chain need also be  
35 expressed. However, in certain asymmetric antibodies, two different light chains may be needed to associate with the asymmetric heavy chains. However, in certain situations, it may

be possible to produce two different paratopes directed to different epitopes that comprise different heavy chain regions and the same light chain.

[000222] For cells that secrete the recombinant antibody chains, culture medium comprising the immunoglobulin molecules is harvested, and antibodies are purified from the medium using protein A or protein G chromatography, which binds specifically to the Fc region of antibodies. In certain embodiments, recombinant cells containing light chains and/or heavy chains are lysed, and the immunoglobulin chains are purified from the lysate using standard biochemical procedures.

[000223] If desired, purified antibodies are then conjugated with payloads of the kind and by the methods of which are described herein.

## V. Pharmaceutical Compositions

[000224] Further provided herein is a composition comprising an antibody, immunoconjugate, nucleic acid molecule, vector or recombinant cell described herein, optionally with a suitable diluent, e.g., a pharmaceutically acceptable carrier. The composition can for example, comprise one or more antibodies or immunoconjugates.

[000225] In one embodiment, a pharmaceutical composition comprises an antibody or immunoconjugate as described herein formulated in a pharmaceutically acceptable carrier. The composition is typically formulated for intravenous injection. Accordingly, the carrier can be an aqueous carrier, such as sterilized water or saline solution. The composition can further comprise ingredients to stabilize the antibody molecules. These can include, for example, sugars and polyols, which assist in freeze-drying. Mannitol also can be used as a tonicity adjuster and bulking agent in freeze-dried formulations. Surfactants, such as polysorbate 20 or polysorbate 80 are also commonly used in monoclonal antibody formulations. Buffers, such as phosphate, histidine and citrate, are frequently used in such formulations.

[000226] The compositions described herein can be prepared by per se known methods for the preparation of pharmaceutically acceptable compositions that can be administered to subjects, such that an effective quantity of the active substance is combined in a mixture with a pharmaceutically acceptable vehicle.

[000227] The term "pharmaceutically acceptable" refers to a carrier that is compatible with the other ingredients of a pharmaceutical composition and can be safely administered to a subject. The term is used synonymously with "physiologically acceptable" and "pharmacologically acceptable". Pharmaceutical compositions and techniques for their preparation and use are known to those of skill in the art in light of the present disclosure. For a detailed listing of suitable pharmacological compositions and techniques for their administration one may refer to texts such as Remington's Pharmaceutical Sciences, 17th ed. 1985; Brunton et al., "Goodman and Gilman's The Pharmacological Basis of Therapeutics," McGraw-Hill, 2005; University of the

Sciences in Philadelphia (eds.), "Remington: The Science and Practice of Pharmacy," Lippincott Williams & Wilkins, 2005; and University of the Sciences in Philadelphia (eds.), "Remington: The Principles of Pharmacy Practice," Lippincott Williams & Wilkins, 2008.

**[000228]** Pharmaceutically acceptable carriers will generally be sterile, at least for human use.

- 5 A pharmaceutical composition will generally comprise agents for buffering and preservation in storage, and can include buffers and carriers for appropriate delivery, depending on the route of administration. Examples of pharmaceutically acceptable carriers include, without limitation, normal (0.9%) saline, phosphate-buffered saline (PBS) Hank's balanced salt solution (HBSS) and multiple electrolyte solutions such as PlasmaLyte ATM (Baxter).

- 10 **[000229]** Suitable diluents for polypeptides, including antibodies and/or cells include but are not limited to saline solutions, pH buffered solutions and glycerol solutions or other solutions suitable for freezing polypeptides and/or cells.

**[000230]** Suitable diluents for nucleic acids include but are not limited to water and saline solutions.

- 15 **[000231]** Pharmaceutical compositions include, without limitation, lyophilized powders or aqueous or non-aqueous sterile injectable solutions or suspensions, which may further contain antioxidants, buffers, bacteriostats and solutes that render the compositions substantially compatible with the tissues or the blood of an intended recipient. Other components that may be present in such compositions include water, surfactants (such as Tween), alcohols, polyols, glycerin and vegetable oils, for example. Exemplary injection solutions and suspensions may be prepared from sterile powders, granules, tablets, or concentrated solutions or suspensions. The composition may be supplied, for example, but not by way of limitation, as a lyophilized powder which is reconstituted with sterile water or saline prior to administration to the patient.

- [000232]** Pharmaceutical compositions may comprise a pharmaceutically acceptable carrier.
- 25 Suitable pharmaceutically acceptable carriers include essentially chemically inert and nontoxic compositions that do not interfere with the effectiveness of the biological activity of the pharmaceutical composition. Examples of suitable pharmaceutical carriers include, but are not limited to, water, saline solutions, glycerol solutions, ethanol, N-(1(2,3-dioleoyloxy)propyl)N,N,N-trimethylammonium chloride (DOTMA), dioleoylphosphatidyl-ethanolamine (DOPE), and liposomes. Such compositions should contain a therapeutically effective amount of the compound, optionally with a suitable amount of carrier so as to provide the form for direct administration to the patient.

- [000233]** The composition may be in the form of a pharmaceutically acceptable salt which includes, without limitation, those formed by hydrochloric, phosphoric, acetic, oxalic, and tartaric acids, etc. with free amino groups, and those formed by sodium, potassium, ammonium,
- 35



calcium, ferric hydroxides, isopropylamine, triethylamine, and 2-ethylamino ethanol, etc. with free carboxyl groups.

[000234] The terms “dose” and “dosage” are used interchangeably herein. A dose refers to the amount of active ingredient given to an individual at each administration. For the present invention, the dose can refer to the concentration of the antibody or associated components, e.g., the amount of therapeutic agent or dosage of radiolabel. The dose will vary depending on a number of factors, including frequency of administration; size and tolerance of the individual; severity of the condition; risk of side effects; the route of administration; and the imaging modality of the detectable label (if present). One of skill in the art will recognize that the dose can be modified depending on the above factors and/or based on therapeutic progress. The term “dosage form” refers to the particular format of the pharmaceutical, and depends on the route of administration. For example, a dosage form can be in a liquid, e.g., a saline solution for injection.

## VI. Methods of Use

### A. Methods of Treatment

#### 1. Diseases

[000235] Provided herein are methods of treating a disease in a subject that comprises administering to the subject an effective amount of a nucleic acid, an antibody or an immunoconjugate of this disclosure. An “effective amount” is an amount sufficient for an antibody or immunoconjugate to accomplish a stated purpose relative to the absence of the compound. The stated purpose may be, for example, killing pathological cells, either in vitro or in vivo, or producing a therapeutic benefit to a subject. An example of an “effective amount” is an amount sufficient to contribute to the treatment, prevention, or reduction of a symptom or symptoms of a disease, which could also be referred to as a “therapeutically effective amount.” A “reduction” of, or “reducing” a symptom means elimination of, or decreasing of the severity or frequency of, the symptom. A “prophylactically effective amount” of a substance (e.g., an antibody) is an amount of that substance which, when administered to a subject, will prevent or delay the onset or reoccurrence of a disease, pathology or condition, or its symptoms, or reduce the likelihood of such. An effective amount does not necessarily occur by administration of one dose, and may occur only after administration of a series of doses. Thus, an effective amount may be administered in one or more administrations. The exact amounts will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques (see, e.g., Lieberman, *Pharmaceutical Dosage Forms* (vols. 1-3, 1992); Lloyd, *The Art, Science and Technology of Pharmaceutical Compounding* (1999); Pickar, *Dosage Calculations* (1999); and Remington: *The Science and Practice of Pharmacy*, 20th Edition, 2003, Gennaro, Ed., Lippincott, Williams & Wilkins).

[000236] For any antibody or ADC described herein, the therapeutically effective amount can be initially estimated or determined using cell culture assays. Target concentrations will be those concentrations of antibody or ADC that are capable of achieving a desired result (e.g., slowing cell growth), as measured using the methods described herein or known in the art. As is well known in the art, therapeutically effective amounts for use in humans can also be determined from animal models. For example, a dose for humans can be formulated to achieve a concentration that has been found to be effective in animals. The dosage in humans can be adjusted by monitoring effectiveness and adjusting the dosage upwards or downwards, as described above. Adjusting the dose to achieve maximal efficacy in humans based on the methods described above and other methods is well within the capabilities of the ordinarily skilled artisan.

[000237] Cancers that can be treated include, without limitation, solid tumors such as, for example, carcinomas, sarcomas, and adenocarcinomas, and lymphoid cancers such as, for example, leukemias and lymphomas. Examples of different types of cancer include, but are not limited to, lung cancer (e.g., non-small cell lung cancer or NSCLC), breast cancer, ovarian cancer, prostate cancer, colorectal cancer, bladder cancer, leukemia, liver cancer (i.e., hepatocarcinoma), renal cancer (i.e., renal cell carcinoma), thyroid cancer, pancreatic cancer, uterine cancer, cervical cancer, testicular cancer, esophageal cancer, stomach (gastric) cancer, kidney cancer, cancer of the central nervous system, skin cancer, glioblastoma and melanoma.

[000238] Cancer cells that express two epitopes targeted by the ADCs of this disclosure are expected to be present in mixed populations in which different cells express each of these biomarkers to a different degree. Without wishing to be limited by theory, bi-specific, ADC antibodies are expected to be more effective against such populations than ADC antibodies directed to only a single target.

## 2. Routes of Administration

[000239] Pharmaceutical compositions comprising antibodies of this disclosure can be administered to a subject by any suitable route of administration.

[000240] Intravenous administration involves delivering the pharmaceutical composition directly into the bloodstream which facilitates rapid systemic distribution and enables immediate therapeutic action. Intravenous administration can comprise administration of a bolus, or can comprise a slow infusion, depending on the desired pharmacokinetic profile in the therapeutic indication.

[000241] Intraperitoneal administration involves introducing the pharmaceutical composition into the peritoneal cavity. This mode of administration is especially useful for diseases localized within the abdominal region, as it offers direct access to the site of pathology.

[000242] The pharmaceutical composition can be administered subcutaneously, that is into the fatty tissue underneath the skin.

[000243] In intramuscular administration, a pharmaceutical composition is injected into muscle tissue. In certain cancers, the pharmaceutical composition can be administered directly into the tumor.

[000244] For diseases of the central nervous system the composition can be administered intrathecally or intraventricularly, e.g., into the spinal canal or the brain ventricles.

### 3. Treatment Regimen

[000245] The treatment regimen for cancers using the antibodies or ADCs of this disclosure is customized to the cancer in the patient. However, exemplary regimens for existing treatments include the following. Between 1 mg and 12 mg of antibody or ADC per kilogram of body weight is administered as a dose. After an initial dose, the drug can be administered about every week for about every three weeks for five or more cycles, e.g., until remission, sufficient reduction of symptoms, complete reduction of symptoms, or until side effects or toxicity become unmanageable or the drug ceases to have therapeutic benefit.

#### B. Methods of Killing Cells

[000246] The antibodies and immunoconjugates of this disclosure are useful for killing cells or labeling cells, either in vitro or in vivo. The methods involve contacting the cells with an antibody or immunoconjugate of this disclosure (e.g., by introducing said antibody or immunoconjugate into a subject in need thereof) and allowing the antibodies to bind to the target cells. Effectiveness of killing cells can be a function of ability to kill target cells, but not non-target cells, in a mixed population of cells. Ability to kill cells also can be compared with that of a control, e.g., a control antibody, wherein greater ability of the test antibody compared with the control antibody to kill cells indicates that the test antibody is effective in killing those cells.

[000247] Contacting cells from cancer cell lines with the compositions disclosed herein, in vitro, is useful for determining toxicity of the composition on the cells.

[000248] Contacting cells in vivo with immunoconjugates labeled with a radioisotope is useful in imaging the location of binding and, therefore, the location of a malignant cell. Detection methods include gamma camera imaging, single photon emission coupled tomography (SPECT), and positron emission tomography (PET).

#### C. Methods of Detection

[000249] Antibodies of this disclosure are also useful to detect the presence of cells expressing epitopes targeted by the antibodies of this disclosure in a sample or in a subject. The methods involve contacting the sample or providing the subject with an antibody of this disclosure and detecting binding between the antibody and a cell.

[000250] Binding can be detected by providing antibodies bearing detectable labels, and detecting the label.

[000251] Methods of detection include, without limitation, enzyme-linked immunosorbent assay (ELISA), immunofluorescence (including fluorescent-activated cell sorting (FACS),  
5 surface plasmon resonance, microscopy and immunoprecipitation.

[000252] In vivo methods of detection include, for example, positron emission tomography (PET), in which antibodies are conjugated with a radioactive isotope; and magnetic resonance imaging (MRI), in which antibodies are conjugated with MRI contrast agents.

[000253] Such methods are also useful in the diagnosis of malignancies. The detection of  
10 cells epitopes targeted by the antibodies of this disclosure in amounts above control amounts indicates the presence of malignant cells.

### EXEMPLARY EMBODIMENTS

[000254] Exemplary embodiments of the disclosure include, without limitation:

[000255] 1. An antibody, e.g., an immunoconjugate, comprising a tetravalent antibody  
15 comprising one or more payloads conjugated thereto, wherein the antibody comprises first, second, third, and fourth light chains, and first and second heavy chains, and comprises, from N-terminus to C-terminus:

- a) a first pair of paratopes comprised in Fab regions;
- b) an Fc region; and
- 20 c) a second pair of paratopes, comprised in Fab regions.

[000256] 2. An antibody, e.g., an immunoconjugate, comprising a payload conjugated to an antibody that comprises first, second, third and fourth light chains, and first and second heavy chains, wherein:

- a) the first light chain comprises, from N-terminus to C-terminus, a first light chain  
25 variable (VL) region and a first light chain constant (CL) region;
- b) the second light chain comprises, from N-terminus to C-terminus, a second VL region and a second CL region;
- c) the third light chain comprises, from N-terminus to C-terminus, a third light chain variable (VL) region and a third light chain constant (CL) region;
- 30 d) the fourth light chain comprises, from N-terminus to C-terminus, a fourth VL region and a fourth CL region;
- e) the first heavy chain comprises, from N-terminus to C-terminus:
  - (i) a first heavy chain portion comprising a first heavy chain variable (VH) region and a first heavy chain constant 1 (CH1) region;
  - 35 (ii) a first Fc region comprising a first heavy chain constant 2 (CH2) region and a first heavy chain constant 3 (CH3) region;

(iii) a second heavy chain portion comprising a second heavy chain variable (VH) region and a second heavy chain constant 1 (CH1) region; and

f) the second heavy chain comprises, from N-terminus to C-terminus:

(i) a third heavy chain portion comprising a third heavy chain variable (VH) region and a third heavy chain constant 1 (CH1) region;

(ii) a second Fc region comprising a second heavy chain constant 2 (CH2) region and a second heavy chain constant 3 (CH3) region;

(iii) a fourth heavy chain portion comprising a fourth heavy chain variable (VH) region and a fourth heavy chain constant 1 (CH1) region; and

wherein:

the first light chain and the first heavy chain portion form a first Fab portion comprising a first paratope; and

the second light chain and the second heavy chain portion form a second Fab portion comprising a second paratope;

the third light chain and the third heavy chain portion form a third Fab portion comprising a third paratope; and

the fourth light chain and the fourth heavy chain portion form a fourth Fab portion comprising a fourth paratope.

**[000257]** 3. An antibody, e.g., an immunoconjugate, comprising a tetravalent antibody comprising one or more payloads conjugated thereto, wherein the antibody comprises first and second light chains, and first and second heavy chains, and comprises, from N-terminus to C-terminus:

a) a first pair of paratopes, comprised in a diabody;

b) an Fc region; and

c) a second pair of paratopes comprised in Fab regions.

**[000258]** 4. An antibody, e.g., an immunoconjugate, comprising a payload conjugated to an antibody that comprises first and second light chains and first and second heavy chains, wherein:

a) the first light chain comprises, from N-terminus to C-terminus, a first light chain variable (VL) region and a first light chain constant (CL) region;

b) the second light chain comprises, from N-terminus to C-terminus, a second VL region and a second CL region;

c) the first heavy chain comprises, from N-terminus to C-terminus:

(i) a first diabody region comprising a first VH region and a third VL region, in either order; and

(ii) a first Fc region comprising a first heavy chain constant 2 (CH2) region and a first heavy chain constant 3 (CH3) region; and

- (iii) a first heavy chain portion comprising a second heavy chain variable (VH) region and a first heavy chain constant 1 (CH1) region;
- d) the second heavy chain comprises, from N-terminus to C-terminus:
- (i) a second diabody region comprising a third VH region and a fourth VL region, in either order; and
- (ii) a second Fc region comprising a second heavy chain constant 2 (CH2) region and a second heavy chain constant 3 (CH3) region; and
- (iii) a second heavy chain portion comprising a fourth heavy chain variable (VH) region and a second heavy chain constant 1 (CH1) region;
- wherein:
- the first light chain and the first heavy chain portion form a first Fab portion comprising a first paratope; and
- the second light chain and the second heavy chain portion form a second Fab portion comprising a second paratope; and
- the first and second diabody regions form a diabody forming a third paratope comprising the third VL region and the third VH region, and a fourth paratope comprising the fourth VL region and the first VH region.

**[000259]** 5. An antibody, e.g., an immunoconjugate, comprising a tetravalent antibody comprising one or more payloads conjugated thereto, wherein the antibody comprises first, second, third, and fourth light chains, and first and second heavy chains, and comprises, from N-terminus to C-terminus:

- a) a first pair of paratopes comprised in Fab regions;
- b) a second pair of paratopes, comprised in Fab regions; and
- c) an Fc region.

**[000260]** 6. An antibody, e.g., an immunoconjugate, comprising a payload conjugated to an antibody that comprises first, second, third and fourth light chains, and first and second heavy chains, wherein:

- a) the first light chain comprises, from N-terminus to C-terminus, a first light chain variable (VL) region and a first light chain constant (CL) region;
- b) the second light chain comprises, from N-terminus to C-terminus, a second VL region and a second CL region;
- c) the third light chain comprises, from N-terminus to C-terminus, a third light chain variable (VL) region and a third light chain constant (CL) region;
- d) the fourth light chain comprises, from N-terminus to C-terminus, a fourth VL region and a fourth CL region;
- e) the first heavy chain comprises, from N-terminus to C-terminus:

- (i) a first heavy chain portion comprising a first heavy chain variable (VH) region and a first heavy chain constant 1 (CH1) region;
- (ii) a second heavy chain portion comprising a second heavy chain variable (VH) region and a second heavy chain constant 1 (CH1) region; and
- 5 (iii) a first Fc region comprising a first heavy chain constant 2 (CH2) region and a first heavy chain constant 3 (CH3) region;
- f) the second heavy chain comprises, from N-terminus to C-terminus:
- (i) a third heavy chain portion comprising a third heavy chain variable (VH) region and a third heavy chain constant 1 (CH1) region;
- 10 (ii) a fourth heavy chain portion comprising a fourth heavy chain variable (VH) region and a fourth heavy chain constant 1 (CH1) region; and
- (iii) a second Fc region comprising a second heavy chain constant 2 (CH2) region and a second heavy chain constant 3 (CH3) region;
- wherein:
- 15 the first light chain and the first heavy chain portion form a first Fab portion comprising a first paratope; and
- the second light chain and the second heavy chain portion form a second Fab portion comprising a second paratope;
- the third light chain and the third heavy chain portion form a third Fab portion
- 20 comprising a third paratope; and
- the fourth light chain and the fourth heavy chain portion form a fourth Fab portion comprising a fourth paratope.

**[000261]** 7. An antibody, e.g., an immunoconjugate, comprising a tetravalent antibody comprising one or more payloads conjugated thereto, wherein the antibody comprises first and

25 second light chains, and first and second heavy chains, and comprises, from N-terminus to C-terminus:

- a) a first pair of paratopes comprised in Fab regions;
- b) a second pair of paratopes, comprised in a diabody; and
- c) an Fc region.
- 30 **[000262]** 8. An antibody, e.g., an immunoconjugate, comprising a payload conjugated to an antibody that comprises first and second light chains and first and second heavy chains, wherein:
- a) the first light chain comprises, from N-terminus to C-terminus, a first light chain variable (VL) region and a first light chain constant (CL) region;
- 35 b) the second light chain comprises, from N-terminus to C-terminus, a second VL region and a second CL region;
- c) the first heavy chain comprises, from N-terminus to C-terminus:

- (i) a first heavy chain portion comprising a first heavy chain variable (VH) region and a first heavy chain constant 1 (CH1) region;
- (ii) a first diabody region comprising a second VH region and a third VL region, in either order; and
- 5 (iii) a first Fc region comprising a first heavy chain constant 2 (CH2) region and a first heavy chain constant 3 (CH3) region; and
- d) the second heavy chain comprises, from N-terminus to C-terminus:
- (i) a second heavy chain portion comprising a third VH region and a second CH1 region;
- 10 (ii) a second diabody region comprising a fourth VH region and a fourth VL region, in either order; and
- (iii) a second Fc region comprising a second CH2 region and a second CH3 region;
- wherein:
- 15 the first light chain and the first heavy chain portion form a first Fab portion comprising a first paratope; and
- the second light chain and the second heavy chain portion form a second Fab portion comprising a second paratope;
- the first and second diabody regions form a diabody forming a third paratope
- 20 comprising the fourth VL region and the second VH region, and a fourth paratope comprising the third VL region and the fourth VH region.
- [000263]** 9. The antibody or immunoconjugate of any of embodiments 1 to 8, comprising at least one paratope that binds to a first epitope of Her2, and at least one paratope that binds to a second epitope of Her2.
- 25 **[000264]** 10. The antibody or immunoconjugate of any of embodiments 1 to 8, comprising at least one paratope that binds to CD30, and at least one paratope that binds to an epitope of PD-L1.
- [000265]** 11. The antibody or immunoconjugate of any of embodiments 1 to 8, comprising at least one paratope that binds to a first epitope of Her2, at least one paratope that binds to PD-
- 30 L1, and, optionally, at least one paratope that binds to a second epitope of Her2.
- [000266]** 12. The antibody or immunoconjugate of any of embodiments 1 to 8, comprising at least one paratope that binds to CD30, at least one paratope that binds to a first epitope of PD-L1, and at least one paratope that binds to a second epitope of PD-L1.
- [000267]** 13. The antibody or immunoconjugate of any of embodiments 1 to 8, comprising at
- 35 least one paratope that binds to Trop2, and at least one paratope that binds to a first epitope of



Her2, at least one paratope that binds to a second epitope of Her2 and a paratope that binds to PD-L1.

5 [000268] 14. The antibody or immunoconjugate of any of embodiments 1 to 8, comprising at least one paratope that binds to Trop2, at least one paratope that binds to a first epitope of Her2, and, optionally, at least one paratope that binds to a second epitope of Her2.

[000269] 14bis. The antibody or immunoconjugate of any of embodiments 1 to 8, comprising at least one paratope that binds to Muc16, at least one paratope that binds to an epitope of NaPi-2b.

10 [000270] 15. The antibody or immunoconjugate of any of embodiments 1 to 8, which is a mono-specific antibody, wherein all the paratopes specifically bind to the same epitope.

[000271] 16. The antibody or immunoconjugate of any of embodiments 1 to 8, which is a bi-specific antibody, wherein at least one of the paratopes specifically binds a first epitope, and at least another of the paratopes bind a second, different epitope.

15 [000272] 17. The antibody or immunoconjugate of embodiment 15, wherein, wherein two of the paratopes specifically bind to a first epitope and two of the paratopes specifically bind to a second, different epitope; or three of the paratopes bind to the same first epitope, and one of the paratopes specifically binds to a second, different epitope.

20 [000273] 18. The antibody or immunoconjugate of embodiment 15, wherein the first and second paratopes bind the same first epitope, and the third and fourth paratopes bind the same second epitope; or the first and third paratopes bind the same first epitope, and the second and fourth paratopes bind the same second epitope.

25 [000274] 19. The antibody or immunoconjugate of embodiment 15, wherein two of the paratopes bind the same first epitope of Her2, and two of the paratopes bind the same second epitope of Her2, e.g., the first and second paratopes bind the same first epitope and the third and fourth paratopes bind the same second epitope; or, the first and third paratopes bind the same first epitope and the second and fourth paratopes bind the same second epitope.

[000275] 20. The antibody or immunoconjugate of embodiment 18, wherein the first epitope is an epitope bound by trastuzumab and the second epitope is an epitope bound by pertuzumab.

30 [000276] 21. The antibody or immunoconjugate of embodiment 15, wherein one of the paratopes binds CD30, one of the paratopes bind a first epitope of Her2, and two of the paratopes bind the same second epitope of Her2.

35 [000277] 22. The antibody or immunoconjugate of any of embodiments 1 to 8, which is a tri-specific antibody, wherein at least one of the paratopes binds to a first epitope, at least one of the paratopes binds to a second, different epitope, and at least one of the paratopes binds to a third, different epitope, e.g., two of the paratopes bind to the same first epitope, one of the

paratopes binds to a second, different epitope, and one of the paratopes binds to a third epitope that is different from the first and second epitopes.

5 [000278] 23. The antibody or immunoconjugate of embodiment 21, wherein the first and second paratopes bind the same epitope; the first and third paratopes bind the same epitope; or the second and third paratopes bind the same epitope.

[000279] 24. The antibody or immunoconjugate of any of embodiments 1-21, wherein at least two paratopes bind to different epitopes of the same antigen.

10 [000280] 25. The antibody or immunoconjugate of any of embodiments 1-23, wherein two of the paratopes bind to different epitopes of the same first antigen, and two of the paratopes bind to different epitopes of the same second antigen.

[000281] 26. The antibody or immunoconjugate of embodiment 21, wherein:  
a first paratope and a second paratope each bind an epitope of CD30;  
a third paratope binds a first epitope of PD-L1; and  
a fourth paratope binds a second epitope of PD-L1.

15 [000282] 27. The antibody or immunoconjugate of embodiment 21, wherein:  
a first paratope and a second paratope each bind an epitope of Trop2;  
a third paratope binds a first epitope of Her2; and  
a fourth paratope binds a second epitope of Her2.

20 [000283] 28. The antibody or immunoconjugate of embodiment 1 or 3, which is a tetra-specific antibody, wherein each of the paratopes binds to a different epitope.

[000284] 29. The antibody or immunoconjugate of any of embodiments 1-27, wherein the first and second heavy chains have different amino acid sequences, and are associated through a knob-into-hole structure.

25 [000285] 30. The antibody or immunoconjugate of embodiment 28, wherein the Fc region comprises two non-identical heavy chains, wherein at least one of the two non-identical heavy chains comprises an amino acid modification so as to form complementation between the two non-identical heavy chains thereby increasing the probability of forming heterodimers of the non-identical heavy chains and decreasing the probability of forming homodimers of identical heavy chains.

30 [000286] 31. The antibody or immunoconjugate of any of embodiments 1-30, wherein the heavy and light chains are produced from a cell genetically engineered to produce two heavy chains and one light chain.

[000287] 32. The antibody or immunoconjugate of any of embodiments 1-30, wherein all of the light chain variable regions have the same amino acid sequence.

**[000288]** 33. The antibody or immunoconjugate of any of embodiments 1-30, wherein both light chains comprise light chain variable regions having the same amino acid sequence.

**[000289]** 34. The antibody or immunoconjugate of any of embodiments 1-30, wherein the first and second light chains have the same amino acid sequences.

5 **[000290]** 35. The antibody or immunoconjugate of any of embodiments 1-30, wherein the first and second heavy chains have identical amino acid sequences.

**[000291]** 36. The antibody or immunoconjugate of any of embodiments 1-35, wherein the antibody comprises:

- 10 a) a diabody region optionally attached to an Fc region through Spacer 1, and the Fc region attached to the heavy chain portion through a Spacer 2;
- b) a heavy chain portion optionally attached through Spacer 3 to a diabody region, and the diabody region optionally attached through a Spacer 4 to an Fc region;
- c) an Fc region attached to a heavy chain portion through a Spacer 5; or
- d) a heavy chain attached to another heavy chain portion through a Spacer 6.

15 **[000292]** 37. The antibody or immunoconjugate of embodiment 36, wherein Spacers 1-6 independently comprise between 0 and 50 amino acids.

**[000293]** 38. The antibody or immunoconjugate of embodiment 37, wherein Spacers 1-6 are independently selected from a monomer or polymer of the sequence (GGGGS)<sub>n</sub> (SEQ ID NO: 170), (GGGGA)<sub>n</sub> (SEQ ID NO: 171) or (GGGGG) (SEQ ID NO: 172), wherein n is any of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

**[000294]** 39. The antibody or immunoconjugate of embodiment 38, wherein Spacers 1-6 are independently selected from GGGGSGGGGSEPKSSDKTHT (SEQ ID NO: 173), GGGSGGGSGGGSGGGSGSTG (SEQ ID NO: 174), LEDKHTKVEPKSS (SEQ ID NO: 175), SGSETPGTSESATPESGGG (SEQ ID NO: 176), and GTTAASGSSGGSSSGA (SEQ ID NO: 177).

**[000295]** 40. The antibody or immunoconjugate of embodiment 38, comprising a diabody region optionally attached to an Fc region through Spacer 1, and the Fc region attached to the heavy chain portion through Spacer 2; wherein Spacer 1 and Spacer 2, if present, are selected from the following pairs:

| Spacer 1 – Diabody-Fc                | Spacer 2 – Fc-Fab                    |
|--------------------------------------|--------------------------------------|
| No spacer or substantially no spacer | No spacer or substantially no spacer |
| About 10 amino acids                 | About 20 amino acids                 |
| About 10 amino acids                 | About 10 amino acids                 |
| About 10 amino acids                 | About 5 amino acids                  |
| About 10 amino acids                 | No spacer or substantially no spacer |

|                                      |                                      |
|--------------------------------------|--------------------------------------|
| About 5 amino acids                  | About 20 amino acids                 |
| About 5 amino acids                  | No spacer or substantially no spacer |
| No spacer or substantially no spacer | About 20 amino acids                 |
| No spacer or substantially no spacer | No spacer or substantially no spacer |
| About 10 amino acids                 | About 20 amino acids                 |

**[000296]** 41. The antibody or immunoconjugate of embodiment 40, wherein Spacer 1 and Spacer 2, if present, are selected from the following pairs:

| Spacer 1 – Diabody-Fc | Spacer 2 – Fc-Fab |
|-----------------------|-------------------|
| (G4S)0                | (G4S)0            |
| (G4S)2                | (G4S)4            |
| (G4S)2                | (G4S)2            |
| (G4S)2                | (G4S)1            |
| (G4S)2                | (G4S)0            |
| (G4S)1                | (G4S)4            |
| (G4S)1                | (G4S)0            |
| (G4S)0                | (G4S)4            |
| (G4S)0                | (G4S)0            |
| (G4S)2                | (G4S)4            |

- 5 **[000297]** 42. The antibody or immunoconjugate of embodiment 36, comprising (i) a heavy chain portion optionally attached through Spacer 3 to a diabody region, and the diabody region optionally attached through Spacer 4 to an Fc region, wherein Spacer 3 and Spacer 4, if present, are selected from the following pairs:

| Spacer 3 – Fab-Diabody               | Spacer 4 – Diabody-Fc                |
|--------------------------------------|--------------------------------------|
| No spacer or substantially no spacer | No spacer or substantially no spacer |
| About 20 amino acids                 | About 10 amino acids                 |
| About 5 amino acids                  | About 10 amino acids                 |
| About 20 amino acids                 | No spacer or substantially no spacer |
| About 15 amino acids                 | About 10 amino acids                 |
| About 10 amino acids                 | About 10 amino acids                 |
| About 5 amino acids                  | About 10 amino acids                 |
| No spacer or substantially no spacer | About 10 amino acids                 |
| No spacer or substantially no spacer | About 5 amino acids                  |

**[000298]** 43. The antibody or immunoconjugate of embodiment 42, wherein Spacer 3 and Spacer 4, if present, are selected from the following pairs:

| Spacer 3 – Fab-Diabody | Spacer 4 – Diabody-Fc |
|------------------------|-----------------------|
| (G4S)0                 | (G4S)0                |
| (G4S)4                 | (G4S)2                |
| (G4S)4                 | (G4S)1                |
| (G4S)4                 | (G4S)0                |
| (G4S)3                 | (G4S)2                |
| (G4S)2                 | (G4S)2                |
| (G4S)1                 | (G4S)2                |
| (G4S)0                 | (G4S)2                |
| (G4S)0                 | (G4S)1                |

5 **[000299]** 44. The antibody or immunoconjugate of any of embodiments 1-43, wherein the payload is conjugated through a reduced disulfide bond.

**[000300]** 45. The antibody or immunoconjugate of any of embodiments 1-43, comprising a plurality of payload molecules conjugated to the antibody.

10 **[000301]** 46. The antibody or immunoconjugate of any of embodiments 1-43, wherein the antibody is a thiomab comprising at least one cysteine residue substitution in a heavy chain or a light chain, wherein the payload is conjugated through the substituted cysteine residue.

**[000302]** 47. The antibody or immunoconjugate of embodiment 46, wherein the thiomab comprises amino acid substitutions:

- 15 (a) HC-A118C and LC-V205C; and/or  
 (b) HC-S157C, HC-S239C, and HC-V266C (EU numbering)  
 (c) T155C, H285C, R301C, V303C, T307C, G316C, Y436C and L441C (EU numbering)

**[000303]** 48. The antibody or immunoconjugate of any of embodiments 1-47, wherein the payload comprises a cytotoxic agent, radioactive isotope, fluorescent moiety, or an enzyme.

20 **[000304]** 49. The antibody or immunoconjugate of embodiment 48, wherein the payload comprises a cytotoxic agent selected from maytansinoid, DM-1, DM-4, auristatin, monomethyl auristatin E, monomethyl auristatin F, dolastatin, tubulysin, eribulin, cryptophycin, benzodiazepine, indolino-benzodiazepine, isoquinolidino-benzodiazepine, pyrrolo-benzodiazepine, alpha-amanitin, trichothene, camptothecin derivatives (SN-38, exatecan, 25 belotecan, DXd, topotecan, samrotercan), duocarmycin, DGN549, CC1065, calicheamicin, N-

acetyl calicheamicin, an enediyne antibiotic, taxane, doxorubicin derivatives, anthracycline and stereoisomers, azanofide, as well as isosteres, analogs, heterodimers, homodimers or derivatives of the foregoing.

5 **[000305]** 50. The antibody or immunoconjugate of any of embodiments 1-49 wherein the antibodies comprise at least one light chain, heavy chain or full CDR sequence set of an antibody chain of Appendix 1.

**[000306]** 51. The antibody or immunoconjugate of embodiment 50, wherein:

a) a CDR sequence set for Her2 binding, if present, is selected from the light chain, heavy chain or full CDR sequence set of AB101 or the CDR sequence set of AB102;

10 b) a CDR sequence set for CD30 binding, if present, is selected from the light chain, heavy chain or full CDR sequence set of AB217;

c) a CDR sequence set for PD-L1 binding, if present, is selected from the light chain, heavy chain or full CDR sequence sets of AB202, AB203, AB204, AB218 or AB223;

d) a CDR sequence set for Trop2 binding, if present, is selected from the light chain, heavy chain or full CDR sequence sets of AB601 or AB621.

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**[000307]** 52. The antibody or immunoconjugate of any of embodiments 50-51, wherein:

a) a light chain for Her2 binding, if present, is selected from AB101, AB102, AB103, AB105, AB106, AB107, AB108, AB113, AB114, AB115, AB116, AB117, AB118, AB119, AB120, AB121, AB122, AB123, AB124, AB125, AB126, AB127, AB128, AB129, AB130, AB131, AB132, AB133, AB134, AB135, AB136, AB137, AB138, AB139, AB140, AB141, AB142, AB143, AB144, AB607, AB608, AB609, AB610, AB611, AB612, AB613, AB614, AB616, AB617, AB618, AB619, AB620, AB622, AB623, AB624, AB625;

b) a light chain for Trop2 binding, if present, is selected from AB601, AB605, AB606, AB608, AB610, AB613, AB614, AB626;

25 c) a light chain for PD-L1 binding, if present, is selected from AB205, AB206, AB207, AB208, AB210, AB211, AB212, AB213, AB216, AB220, AB222; or

d) a light chain for CD30 binding, if present, is selected from AB205, AB206, AB207, AB208, AB209, AB211, AB212, AB213, AB214, AB215, AB216, AB217, AB219, AB220, AB221, AB222.

30 **[000308]** 53. The antibody or immunoconjugate of any of embodiments 50-52, wherein:

a) a heavy chain for Her2 binding, if present, is selected from AB101, AB102, AB103, AB105, AB106, AB107, AB108, AB113, AB114, AB115, AB116, AB117, AB118, AB119, AB120, AB121, AB122, AB123, AB124, AB125, AB126, AB127, AB128, AB129, AB130, AB131, AB132, AB133, AB134, AB135, AB136, AB137, AB138, AB139, AB140, AB141, AB142, AB143, AB144, AB607, AB608, AB609, AB610, AB611, AB612, AB613, AB614, AB616, AB617, AB618, AB619, AB620, AB622, AB623, AB624, AB625;

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b) a heavy chain for Trop2 binding, if present, is selected from AB601, AB605, AB606, AB608, AB610, AB613, AB614, AB626;

c) a heavy chain for PD-L1 binding, if present, is selected from AB205, AB206, AB207, AB208, AB210, AB211, AB212, AB213, AB216, AB220, AB222; or

5 d) a heavy chain for CD30 binding, if present, is selected from AB205, AB206, AB207, AB208, AB209, AB211, AB212, AB213, AB214, AB215, AB216, AB217, AB219, AB220, AB221, AB222.

**[000309]** 54. The antibody or immunoconjugate of any of embodiments 50-53, wherein:

10 a) a diabody region for binding different Her2 epitopes, if present, is selected from the diabody region of AB106, AB128, AB129, AB130, AB131, AB132, AB133, AB134, AB135, AB136, AB137, AB138, AB139, AB140, AB141, AB142, AB143, AB144 or AB606;

b) a diabody region for binding the same Her2 epitopes, if present, is selected from the diabody region of AB107, AB108, AB608, AB613;

15 c) a diabody region for binding different PD-L1 epitopes, if present, is selected from the diabody region of AB209, AB214, AB215, AB124, AB125, AB126, AB127, AB219, AB221;

d) a diabody region for binding the same CD30 epitope, if present, is selected from the diabody region of AB210;

20 e) a diabody region for binding PD-L1 and CD30, if present, is selected from the diabody region of AB216, AB220, AB222; or

f) a diabody region for binding the same Trop2 epitope, if present, is selected from the diabody region of AB607, AB609, or AB612

25 g) a diabody region for binding Her2 and Trop2, if present, is selected from the diabody region of AB610, AB614, AB616, AB617, AB618, AB619, AB620, AB622, AB623, AB624, AB625.

h) a diabody region for binding PD-L1 and Trop2, if present, is selected from the diabody region of AB611.

**[000310]** 55. The antibody or immunoconjugate of any of embodiments 50-54, comprising an Fc region selected from Table 1.

30 **[000311]** 56. The antibody or immunoconjugate of any of embodiments 1-55, comprising one or more antibody chains of Table 1.

**[000312]** 57. A method of making an immunoconjugate comprising:

a) providing an antibody of any of embodiments 1-56; and

b) conjugating one or more payloads to the antibody.

35 **[000313]** 58. The method of embodiment 57, wherein at least one of the payloads is conjugated to the antibody through a linker.

**[000314]** 59. The method of embodiment 57, wherein at least one of the payloads is conjugated to the antibody through a reduced disulfide bond.

**[000315]** 60. The method of embodiment 57, wherein the antibody is a cysteine-substituted antibody ("thiomab"), and at least one cytotoxic payload is coupled to the antibody through a substituted cysteine.

**[000316]** 61. The method of embodiment 57, wherein the immunoconjugate has a drug-antibody ratio ("DAR") of at least any of 1, 2, 3, 4, 6, 7, 8, 9, 10, 11, and 12.

**[000317]** 62. One or more nucleic acid molecules that encode a heavy chain and/or a light chain of an antibody of any of embodiments 1-61.

**[000318]** 63. The one or more nucleic acid molecules of embodiment 62, encoding one or more antibodies of any of embodiments 1-56.

**[000319]** 64. The one or more nucleic acid molecules of embodiment 61, encoding both a light chain and a heavy chain of the antibody any of embodiments 1-- 56.

**[000320]** 65. The one or more nucleic acid molecules of any of embodiments 62-64, further comprising one or more expression control sequences operatively linked to one or more nucleotide sequences encoding the one or more light chain variable regions and/or one or more heavy chain variable regions.

**[000321]** 66. The one or more nucleic acid molecules of any of embodiments 61-64, comprised within one or more vectors, e.g., selected from a plasmid, a viral vector (e.g., a retrovirus, a lentivirus, and adenovirus, and adeno-associated virus, or a herpes simplex virus), a bacterial artificial chromosome, and a yeast artificial chromosome.

**[000322]** 67. A cell comprising the one or more nucleic acid molecules of any of embodiments 61-65.

**[000323]** 68. The cell of embodiment 56, selected from a mammalian cell (e.g., a Chinese hamster ovary (CHO) cell, in an NS0 cell, an SP2/0 cell, and human embryonic kidney HEK 293 cell, or a Per.C6 cell); an insect cell (e.g., in Sf9 cell or a high five (BTI-Tn-5B1-4) cell); a yeast cell (e.g., Pichia pastoris or and Saccharomyces cerevisiae); a bacterial cell (e.g., E. coli); and a plant cell.

**[000324]** 69. A method of making an antibody comprising:  
 a) providing a cell or cells of any of embodiments 67-68;  
 b) expressing immunoglobulin molecules encoded by the nucleotide sequences in the cell or cells; and  
 c) recovering the expressed immunoglobulin molecules.



**[000325]** 70. The method of embodiment 69, wherein the antibody is an asymmetric antibody and the cell comprises one or more nucleic acid molecules encoding a heavy chain comprising a knob, a heavy chain comprising a hole, and at least one light chain.

5 **[000326]** 71. The method of embodiment 70, wherein the cell comprises nucleotide sequences encoding only one light chain, wherein the light chain is configured to associate with different heavy chain regions to produce two paratopes.

10 **[000327]** 72. The method of embodiment 70, wherein the cell comprises nucleic acids encoding two different light chains, wherein a first light chain is configured to associate with a first heavy chain region to produce a first paratope that binds to a first epitope, and a second light chain is configured to associate with a second heavy chain region to produce a second paratope that binds to a second, different epitope.

**[000328]** 73. The method of embodiment 70, comprising producing different immunoglobulin chains in different cells, recovering the immunoglobulin chains, and contacting the immunoglobulin chains, wherein the immunoglobulin chains assemble into an antibody.

15 **[000329]** 74. The method of embodiment 70, further comprising purifying the recovered antibody, e.g. using protein A or protein G.

**[000330]** 75. A pharmaceutical composition comprising an antibody or immunoconjugate of any one of embodiments 1-45, and a pharmaceutically acceptable carrier, diluent, or excipient.

20 **[000331]** 76. The pharmaceutical composition of embodiment 75, formulated for intravenous injection.

**[000332]** 77. A method for treating cancer in a subject, comprising administering to the subject a therapeutically effective amount of the pharmaceutical composition of any of embodiments 64-65.

25 **[000333]** 78. The method of embodiment 77, wherein the cancer is selected from ovarian, breast, lung, stomach, endometrial and pancreatic.

**[000334]** 79. A method for detecting a cell that expresses an antigen comprising an epitope, comprising: a) contacting the cell with an antibody or immunoconjugate of any of embodiments 1-45 to allow binding between the antibody or immunoconjugate and the cell; and b) detecting the binding of the antibody or immunoconjugate to the cell.

30 **[000335]** 80. The method of embodiment 79, comprising a) contacting the cell with an immunoconjugate comprising an antibody conjugated to a detectable moiety; and b) detecting the detectable moiety bound to the cell.

35 **[000336]** 81. A method of killing a cell comprising contacting a cell with an antibody or immunoconjugate of any of embodiments 1-56, wherein one or more paratopes of the antibody specifically bind to an epitope of the cell.

[000337] 82. The method of embodiment 81, wherein two different paratopes of the antibody bind to two different epitopes of the cell.

[000338] 83. The method of embodiment 82, wherein the epitope is comprised in a cell surface antigen.

5 [000339] 84. Use of an antibody or immunoconjugate of any of embodiments 1-56 in the manufacture of a medicament.

[000340] 85. Use of an antibody of any of embodiments 1-56 to produce an immunoconjugate.

## EXAMPLES

### 10 I. Example 1: Her2/Her2 Bi-paratopic Antibodies

[000341] Figure 9 shows production and activity of bi-specific, tetravalent antibodies against first and second different epitopes of HER2. Mono-specific (AB108) or Bi-specific (AB106 and AB107), tetravalent antibodies were produced in the Fab-Diabody-Fc format (AB106) and Diabody-Fc-Fab (AB107, AB108) format in which a first pair of paratopes (10423) bound Her2 domain 4, and a second pair of paratopes (11053) bound Her2 domain 2 and both paratopes share a common light chain. All of them were resulted in similar yields to that of a Trastuzumab (AB103), an industry standard and exhibited single peak on HPLC. All the antibodies have engineered cysteine residues at HC-A118C (EU numbering) and LC-V205C (Kabat numbering) to enable site-specific conjugation to a linker-payload, which allows conjugation of the cytotoxic moiety without the need to break naturally occurring disulfide bonds.

[000342] Antibody-drug conjugates (ADCs) in standard IgG or tetravalent Fab-Diabody-Fc / Diabody-Fc-Fab format configuration derivatized with monomethyl auristatin E (MMAE) using the following conjugation method: Antibodies are reduced with 40x molar equivalent of 10mM Tris(2carboxyethyl)phosphine (TCEP) by incubating overnight at room temperature. Reduced samples were then dialyzed using 10kDa dialysis tubing using 1x PBS buffer, pH 7.4 for 3.5h at room temperature. After dialysis, samples were re-oxidized with 30x molar equivalent of 10mM dehydro ascorbic acid (DHAA) for 3.5h at room temperature to enable formation of inter-chain disulfide bonds. After re-oxidation, antibodies were conjugated with 10x molar equivalents of MC-vc-PAB-MMAE linker-payload (See, e.g., Doronina SO, et al., "Development of potent monoclonal antibody auristatin conjugates for cancer therapy," Nat Biotechnol. 2003 Jul;21(7):778-84. doi: 10.1038/nbt832. Epub 2003 Jun 1. PMID: 12778055.) by incubating at room temperature for overnight and excess linker-payload is then dialyzed against ADC formulation buffer. Number of drugs per antibody (DAR) were quantitated by analyzing ADC samples on LC/MS.

[000343] Both Bi-specific tetravalent ADCs (AB106 and AB107) showed superior in vitro potency over mono-specific tetravalent ADC (AB108) and a standard bivalent trastuzumab (AB103) ADC. **Figures 9C, 9D and 9E** show the inhibitory concentration 50% (IC<sub>50</sub>) of the antibodies depicted against Her2 antigen expressing hi-copy (SKBr3) and low-copy (JIMT1) cell lines. To determine inhibitory concentration 50% (IC<sub>50</sub>) values of the ADCs, SKBr3/JIMT1 cells were seeded in 96 well tissue culture clear bottom plate at 5000 cells/well in 100uL cell culture medium and incubated overnight at 37°C under 5% CO<sub>2</sub>. Serially diluted ADC samples (50uL) were added to each well in duplicates after overnight incubation, resulting in final ADC concentrations ranging from 1000ng/mL to 0.05ng/mL. Plates were incubated at 37°C for an additional 60-72h. To measure cell viability, plates were equilibrated at room temperature for 30min. 100ul of CellTiter-Glo Luminescent Solution (Promega, Cat# G7570) was added to each well and incubated a plate shaker (300rpm) for 20min. Luminescence was measured using BioTek Synergy plate reader. IC<sub>50</sub> values were calculated using GraphPad software.

## II. Example 2: CD30-PD-L1 Tri-specific Antibodies

[000344] **Figure 10** shows characterization of individual CD30 and PD-L1 binders (IgGs). Biochemical affinities for all IgGs were characterized by testing their binding to respective antigens through Bio-Layer Interferometry (BLI) analysis using OCTET system.

[000345] CD30L blockade assay: Binding of recombinant CD30 to CD30L was measured using ELISA. Briefly, 1 µg/ml of CD30-Fc fusion protein (813-CD, R&D Biosystems) diluted in PBS was coated onto 384-well maxisorp plates overnight at 4 degrees. Remaining binding sites were blocked with 0.5% Bovine Serum Albumin diluted in PBS for 1 hour at ambient temperature. Wells were washed 6x 80 µl in PBS+0.05% Tween-20. Twenty five microliters of test antibodies diluted to a concentration of 1 µM in PBS+0.05% Tween-20 were added to the wells for thirty minutes at ambient temperature and then 5 µl of His-tagged CD30L (1028-CL-050, R&D Biosystems) was added to a final assay concentration of 0.2 µg/ml (~EC75 concentration) for 20 minutes. Unbound protein was removed by washing as before and Immobilized protein was detected using an HRP-conjugated anti-his secondary antibody (A7058, Sigma) in PBS+0.5% BSA for 20 minutes. Unbound protein was removed by washing as before, and HRP was detected using TMB reagent. Absorbance measurements at 450 nm were determined using an Epoch plate reader (Biotek, inc). Assays were performed in triplicate and data were analyzed using GraphPad Prism.

[000346] PD1/PD-L1 function blocking assay: Inhibition of PD-L1 was measured using the PD1-PD-L1 Blockade Bioassay (J1255, Promega). This thaw-and-use cellular assay is based upon the coculture of PD1 expressing Jurkat T-cells engineered to contain a luciferase gene under control of an NFAT response element with a CHO-K1 cell line engineered to express human PD-L1 and an additional cell-surface protein that can activate T-cell receptors in an antigen-independent manner. When co-cultured, the PD1/PD-L1 interaction inhibits activation of

the TCR response leading to low levels of luciferase expression. Upon inhibition of the PD1/PD-L1 interaction by test antibodies, this control is released to allow TCR activation, resulting in luciferase expression. Assays were performed per the manufacturer's protocols to test antibodies for inhibition of PD-L1 at final assay concentrations of 50, 12.5 and 0.5 nM.

- 5 Luminescence was measured using a Biotek Synergy Multimode Plate Reader (Biotek, Inc). Assays were performed in triplicate and data were analyzed in GraphPad Prism.

[000347] All IgGs were conjugated with MC-vc-PAB-MMAE linker-payload as described in the paragraph 000259 and tested the in vitro cellular potency to determine their IC50 values (described in the paragraph 000260) in the Karpas299 cell line.

- 10 [000348] Figures 11-13 describe various schematics that were designed and generated for various tri-specific, tetravalent antibodies against CD30, and first and second different epitopes of PD-L1.

[000349] Figure 14: Production and characterization of various tri-specific, tetravalent CD30/PD-L1 antibodies.

- 15 [000350] Figure 15: Cellular binding analyses were done using FACS for various tri-specific, tetravalent CD30/PD-L1 antibodies.

- [000351] Figure 16: Mono-specific CD30 (AB201) or PD-L1 (AB204) and CD30/PD-L1 tri-specific, tetravalent CD30/PD-L1 antibodies were conjugated with MC-vc-PAB-MMAE at four drugs per antibody (4DAR) and their cellular potency was determined as described in the paragraph 000260 with either CD30+ve (CD30-expressing) or PD-L1+ ve (PD-L1-expressing) cell lines. Unlike mono-specific ADCs, only CD30/PD-L1 tri-specific, tetravalent ADCs showed cellular potency in both cell lines.
- 20

- [000352] Figure 17: All CD30/PD-L1 tri-specific, tetravalent CD30/PD-L1 antibodies showed comparable PD1/PD-L1 function blocking activity (as described in the paragraph 000263) to that of Avelumab or Atezolizumab or BMS936559.
- 25

### III. Example 3: Her2/Trop2 Tri-specific Antibodies

- [000353] Figures 18-19 show activity of tri-specific, tetravalent ADC against Trop2, and first and second different epitopes of HER2. AB606 (Tri-specific, tetravalent Her2/Trop2 antibody) and AB103 (Mono-specific, bivalent Her2 antibody) were conjugated with MC-vc-PAB-MMAE linker-payload via engineered cysteine residues (HC-A118C and LC-V205C) as described above to produce 4DAR ADCs. These ADCs are tested in various cell lines (A431, HCC1569 and MCF7). Her2/Trop2 tri-specific, tetravalent ADC showed consistently improved cellular potency compared to Her2 mono-specific ADC.
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- Figures 20-26: Several bi-specific or tri-specific tetravalent Her2/Trop2 antibodies (AB607-AB610 and AB612-AB614) were designed, produced, and conjugated to MC-vc-PAB-MMAE
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linker-payload at DAR4 and tested their cellular potency in various cell lines (SKOV3, JIMT1 and OVCAR3) expressing both Her2 and Trop2 antigens. Some showed superior cellular potency over AB103 and some over AB601 (mono-specific ADCsz), but they consistently displayed target-dependent cellular potency across all cell lines tested.

5 **IV. Example 4: Muc16/NaPi2b Bi-specific Tetravalent Antibodies**

[000354] **Figures 27-32 and 42** show activity of bi-specific, tetravalent antibodies against Muc16 and NaPi2b.

[000355] **Figs. 27A-27C** show production of three bi-specific, tetravalent ADCs, derivatized with monomethyl auristatin E (MMAE) and analyzed as described above, comprising binding  
10 sites for NaPi-2b and Muc16. The ADC of **Fig. 27A** (AB304-ADC; SEQ ID NO:69 and SEQ ID NO:70) is in the Fab-diabody-Fc format. It comprises paratopes that bind NaPi-2b in the NW/NE positions and paratopes that bind Muc16 in the SW/SE positions. The ADC of **Fig. 27B** (AB305-ADC; SEQ ID NO:71 and SEQ ID NO:72) also is in the Fab-diabody-Fc format. It comprises paratopes that bind Muc16 in the NW/NE positions and paratopes that bind NaPi-2b in the  
15 SW/SE positions. The ADC of **Fig. 27C** (AB309-ADC) is in the diabody-Fc-Fab format. It comprises paratopes that bind NaPi-2b in the NW/NE positions and paratopes that bind Muc16 in the SW/SE positions. These ADCs comprise cysteine-substituted antibodies and have a DAR of 4.

[000356] **Fig. 28** shows the inhibitory concentration 50% (IC<sub>50</sub>) of the ADCs depicted in **Fig. 27** against OVCAR3 cells, an ovarian cancer cell line. Cells used in assays: NIH:OVCAR-3 (OVCAR3, ATCC# HTB-161™). To determine inhibitory concentration 50% (IC<sub>50</sub>) values of the ADCs, OVCAR3 cells were seeded in 96 well tissue culture clear bottom plate at 5000 cells/well in 100uL cell culture medium and incubated overnight at 37°C under 5% CO<sub>2</sub>. Serially diluted (1:3 dilution) ADC samples (50uL) were added to each well in duplicates after overnight  
20 incubation, resulting in final ADC concentrations ranging from 1000ng/mL to 0.05ng/mL. Plates were incubated at 37°C for an additional 60-72h under 5% CO<sub>2</sub>. To measure cell viability, plates were equilibrated at room temperature for 30min. 100ul of CellTiter-Glo Luminescent Solution (Promega, Cat# G7570) was added to each well and incubated a plate shaker (300rpm) for 20min. Luminescence was measured using BioTek Synergy plate reader. IC<sub>50</sub> values were  
25 calculated using GraphPad software. AB304-ADC demonstrated best cellular potency of any of the five ADCs, because the IC<sub>50</sub> value is 0.03, compared to 0.6 for either AB305-ADC or AB309-ADC, and 0.53 for the control monoclonal antibody lifastuzumab. The error bars are derived from a duplicate data set of a single experiment.

[000357] **Fig. 29** shows that a bi-specific ADC, AB304-ADC (Fab-diabody-Fc ADC; NaPi-2b NW/NE, Muc16 SW/SE), retained toxic potency against a partial Muc16-KO OVCAR3 cell line, compared with ADC AB301-ADC (anti-Muc16 IgG ADC). Here, engineered OVCAR3-AV cells  
35

were used to measure cellular potency of ADCs. OVCAR3 cells with MUC-16 knockout (KO) were generated by CRISPR. To enrich for the MUC-16 KO, cell sorting was performed based on the fluorescence intensity of MUC-16. Initial two rounds of enrichment were performed for MUC-16 to generate OVCAR3-AV cells that consists of both original OVCAR3 cells and MUC-16 KO cells. The dependency of cytotoxicity of the mono-specific and bi-specific ADCs on the presence of MUC-16 protein on the cell surface was tested by using these mixed pool of OVCAR3 and MUC-16 KO cells. As expected, the potency of the mono-specific MUC-16-targeting ADC, AB302-ADC, was significantly reduced in the mixed pool of MUC-16 KO cells, while the potency of the mono-specific ADC targeting NaPi-2b, AB301-ADC, as well as bi-specific ADCs remained essentially unaffected.

**[000358]** Fig. 30 shows that mono-specific ADCs lose potency against OVCAR3 cells in which their targets are knocked out. Bi-specific tetravalent ADCs, AB304-ADC and AB309-ADC, retain potency against such cells. OVCAR3 cells with MUC-16 knockout (KO) and OVCAR3 cells with NaPi-2b KO were generated by CRISPR. The phenotypic KO status (impaired expression of either MUC-16 or NaPi-2b proteins on the cell surface) of KO cells was validated by FACS analysis using anti- MUC-16 and anti-NaPi-2b antibodies (2000 ng/mL) followed by secondary antibody (1:1000). To enrich for the MUC-16 KO and the NaPi-2b KO population, cell sorting was performed based on the fluorescence intensity of MUC-16 and NaPi2b expression, respectively. Three rounds of enrichment were performed for MUC-16 to generate "MUC-16 KO" cells. Wild type (WT) and MUC-16 KO cells were incubated with various concentrations of ADCs to assess cytotoxic potency. As expected, the cytotoxic potency of AB302-ADC (binds MUC-16) and AB301-ADC (binds NaPi-2b) was greatly reduced (by over 100-fold) when incubated with MUC-16 KO and NaPi-2b KO cells respectively. As a result, cytotoxic potency of all bi-specific ADCs is now comparable to mono-specific ADCs when incubated with their corresponding KO cells. These data demonstrate that bi-specific ADCs can kill MUC-16 expressing cells (with low/no NaPi-2b expression), NaPi-2b expressing (with low/no MUC-16 expression) and dual positive (expressing both MUC-16 and NaPi-2b) cells. Co-expression of both targets further boosts the potency of bi-specific ADCs. IC50 values for the ADCs in various cell types is shown.

**[000359]** Fig. 31 shows that a bi-specific, tetravalent ADC, AB304-ADC, demonstrated greater potency against cell populations that are mixtures of cells with constant levels of NaPi-2b and varying levels of Muc16 expression, compared with monovalent ADCs, AB301-ADC (NaPi-2b) and AB302-ADC (MUC-16). To assess the potency of AB304-ADC towards cells expressing normal or reduced amounts of MUC-16, the ADC was incubated with mixtures of WT and MUC-16 KO OVCAR3 cells in various proportions. These conditions simulate the compositions of patient tumors where cells may have the tissues have varying levels of MUC-16 expression but a constant level of NaPi-2b expression. However, the experiment does not necessarily address

the effects on tumors with the varying antigen density levels on the cell surface. As expected, cytotoxic potency, as measured by IC<sub>50</sub>, of ADC AB301-ADC (binds NaPi-2b) and AB304-ADC (binds NaPi-2b and MUC16) remain similar under all the 4 conditions tested, whereas the potency of AB302-ADC (binds MUC-16) reduces as the proportion of MUC16-expressing WT cells decreases in the cell mixture. A-D show normalized cell viability (%) at various concentrations of ADCs in various mixtures of WT and KO cells. E. IC<sub>50</sub> values for AB301-ADC, AB302-ADC, and AB304-ADC under the four test conditions. IC<sub>50</sub> values are derived from a duplicate set of experiments.

[000360] Fig. 32 shows that a bi-specific, tetravalent ADC, AB304-ADC, demonstrated greater potency compared to either individual mono specific ADCs (AB301-ADC or AB302-ADC) or their combination (AB301-ADC+AB302-ADC). AB001-ADC is non-binding ADC that had no detectable activity. To investigate if the cytotoxic potency of the bi-specific ADCs AB304-ADC and AB309-ADC towards OVCAR3 cells expressing normal or reduced amounts of MUC16 was due to additive or synergistic action of binding of these ADCs to their target antigens, the potency of these individual ADCs was compared to that of a mixture the two reference mono-specific ADCs binding only NaPi-2b (AB301-ADC) or only MUC-16 (AB302-ADC). In the cell mixture, 20% of the cells were expression positive for both target antigens while 60% were expression positive for only NaPi-2b, and 20% were expression positive for only MUC-16. This mixture was a model for a heterogenous tumor expressing variable levels of the two target antigens. Both bi-specific ADCs showed superior potency (lower IC<sub>50</sub> values) compared to the mixture of the two control mono-specific ADCs or their combination.

[000361] Figs. 33A-33B shows manufacturability of various antibody formats. Fab-Diabody-Fc format and Diabody-Fc-Fab format demonstrate highest yields. Antibodies identified by hashtag have lowest manufacture yields. All antibody molecules were expressed in Expi293 cells and purified from clarified culture supernatant using Protein A chromatography. Protein yield after Protein A purification was assessed and used to calculate expression titers (shown in Fig. 33 as milligrams of protein per liter of cell culture). Purified proteins were analyzed by size exclusion chromatography (SEC) to assess homogeneity. A non-specific IgG was used as an internal control in the assay.

[000362] Figs. 34A-34C show the efficacy of various ADCs in the OVCAR3 ovarian xenograft model using female CB.17 SCID Mice. Tumor xenografts were initiated with OVCAR3 human ovarian carcinomas maintained by serial subcutaneous transplantation in athymic nude mice. On the day of tumor implant, each test mouse received a 4 mm<sup>3</sup> OVCAR3 fragment implanted subcutaneously in the right flank, and tumor growth was monitored as the average size approached the target range of 100 to 150 mm<sup>3</sup>. Tumors were measured in two dimensions using calipers, and volume was calculated. Tumor weight may be estimated with the assumption that 1 mg is equivalent to 1 mm<sup>3</sup> of tumor volume. When palpable tumors were

established, mice were randomized to a mean tumor volume of 150 mm<sup>3</sup> in each group (8 mice/group; range = 100–150 mm<sup>3</sup> and then treated intravenously once (day 1) with AB301-ADC, AB302-ADC, AB304-ADC and AB309-ADC at the 15nmole doses (**Fig. 34A**). Mean tumor volumes ( $\pm$  s.e.m.) are plotted over time (**Fig. 34B**). Both bi-specific ADCs (AB304-ADC and AB309-ADC) displayed superior efficacy compared to mono-specific ADCs (AB301-ADC and AB302-ADC). There were no body weight changes observed during the study duration (**Fig. 34C**), indicating that all ADCs are safe at this dose. All ADCs have same drug-to antibody (DAR) of 4.

**[000363]** **Fig. 35** shows *in vitro* validation of different ADCs in the OVCAR3 cell line that are intended for *in vivo* tumor model testing in OVCAR3 xenograft model. The percent normalized viability of OVCAR3 cells exposed to different ADCs: AB001-ADC (non-binding ADC control), AB301-ADC, AB302-ADC, AB301-ADC+AB302-ADC (combination), AB304-ADC and AB309-ADC or AB312-ADC (DMUC4064A(Genentech®) made and analyzed as described in **Figs. 27-28** above. Both bi-specific ADCs (AB304-ADC and AB309-ADC) performed better than the mono-specific ADCs (AB301-ADC, AB302-ADC) or their combination (AB301-ADC+AB302-ADC) or a clinical comparator (AB312-ADC). All ADCs have same drug-to antibody (DAR) of 4.

**[000364]** **Figs. 36A-36D** show the efficacy of various ADCs at 40 nmole dose in the OVCAR3 ovarian xenograft model using female CB.17 SCID Mice. The study was conducted as described in **Fig. 34**. All ADCs were injected intravenously on day1 with a single 40 nmole dose (**Fig. 36A**) and mean tumor volumes ( $\pm$  s.e.m.) are plotted over time (**Fig. 36B**). Tumor growth differences observed on day 32 among various treatment groups is shown in **Fig. 36C** and p-values between different dose groups are shown in **Fig. 36D**. Both bi-specific ADCs (AB304-ADC and AB309-ADC) displayed superior efficacy compared to mono-specific ADCs (AB301-ADC and AB302-ADC) or their combination (AB301-ADC+AB302-ADC) or the clinical comparator (AB312-ADC). All ADCs have same drug-to antibody (DAR) of 4.

**[000365]** **Figs. 37A-37D** show the efficacy of AB309-ADC at different doses in comparison to AB301-ADC. The study was conducted as described in the **Fig. 34**. AB309-ADC was injected intravenously on day 1 with a single dose of 10 nmole or 20 nmole or 40 nmole dose (**Fig. 37A**) and mean tumor volumes ( $\pm$  s.e.m.) are plotted over time (**Fig. 37B**) and compared to a single 40 nmole dose of AB301-ADC. AB309-ADC at 10 nmole dose showed similar efficacy to that of 40 nmole dose of AB301-ADC indicating an approximately 4-fold improvement in the efficacy for AB309-ADC. Both 20 nmole and 40 nmole doses of AB309-ADC showed statistically significant improvement in the efficacy compared to 40 nmole of AB301-ADC. All ADCs have same drug-to antibody (DAR) of 4.

**[000366]** **Figs. 38A-38D** show comparison of AB309-ADC efficacy to AB312-ADC at different doses. The study was conducted as described in **Fig. 34**. AB309-ADC (10 nmole or 20 nmole or 40 nmole dose) or AB312-ADC (20 nmole or 40 nmole or 80 nmole dose) were injected



intravenously on day1 with a single dose of (Fig. 38A) and mean tumor volumes ( $\pm$  s.e.m.) are plotted over time (Fig. 38B) AB309-ADC at 10 nmole dose or 20 nmole showed similar efficacy to that of 40 nmole dose or 80 nmole dose, respectively of AB312-ADC indicating an approximately 4-fold improvement in the efficacy for AB309-ADC. Both 20 nmole and 40 nmole doses of AB309-ADC showed statistically significant improvement in the efficacy compared to 40 nmole or 80 nmole doses of AB312-ADC. All ADCs have same drug-to antibody (DAR) of 4.

[000367] Fig. 39 shows there were no body weight changes observed during the study duration indicating that all ADCs are safe at the dose ranges (10 nmole-80 nmole) tested.

[000368] Fig. 40 depicts the characterization of pharmacokinetic (PK) properties of AB304 and AB309 antibodies when given via a single intravenous (IV) (slow bolus) injection, to cynomolgus monkeys. Non-human primates (NHP) were dosed at 3mg/kg and blood was drawn for serum chemistry at the indicated intervals. Serum concentrations of AB304 antibody and AB309 antibody determined using standard ELISA based bioanalytical methods and plotted against time intervals. There were no AB304 antibody or AB309 antibody -related changes in body weights. All animals survived to end of study. There were no AB304 antibody or AB309 antibody-related clinical observations. In conclusion, administration of AB304 antibody or AB309 antibody by intravenous (slow bolus) injection was tolerated at 3 mg/kg. The mean clearance (Cl) for AB304 antibody and AB309 antibody were 19.84 mL/day/kg and 13.37 mL/day/kg, respectively. These clearance rates were in the same range of reported clearance values for anti-NaPi-2b antibody (13.8 mL/day/kg) as described in Clin Cancer Res. 2015;21(22):5139-5150.

[000369] Fig. 41 shows validation of different ADCs in the OVCAR3 cell line. The percent normalized viability of OVCAR3 cells exposed to different ADCs: AB304 (Tetravalent bi-specific ADC) or AB306 (bivalent bi-specific ADC) made and analyzed as described in Fig 37 above except with following changes. Cells are incubated with ADCs for a short time (4hrs instead of continuous exposure). After 4hrs, cells were washed and added to growth medium not containing ADCs. Tetravalent bi-specific ADC (AB304) shows 4-fold improvement in the potency compared to mono-specific ADC. Both ADCs have the same drug-to-antibody ratio (DAR) of 4.

[000370] Fig. 42 shows the percent normalized viability of OVCAR3 cells exposed to each of three different antibodies in ADC format, AB301-ADC, AB303-ADC and AB306-ADC made and analyzed as described in Figs. 27-28 above. Both bi-specific ADCs (AB303-ADC and AB306-ADC) performed better than the mono-specific ADC (AB301-ADC).

#### V. Example 5: Her2/Her2/PD-L1 Bi-specific Tetravalent Antibodies

[000371] Fig.43. describes that Her2 biparatopic AB105-ADC had superior potency compared to mono-specific AB103-ADC. The high copy number Her2 expressing (SKBr) cell line and low copying Her2 expressing cell line (JIMT1) were incubated with ADCs short time (4hr) and

growth media consisting of ADCs were removed and replaced with fresh growth medium and cell viability was measured after 96hr. Her2 Biparatopic ADC showed more profound improvement in the potency with the low copy number cell line.

#### VI. Example 6: PD-L1/PD-L1/CD30 Tri-specific Tetravalent Antibodies

5 [000372] Fig. 49. shows that mono-specific ADCs lose potency against Karpus 299 cells in which their targets are knocked out. CD30-PD-L1 tetravalent ADC, AB209-ADC retain potency against such cells. Karpus 299 cells with CD30 knockout (KO) and Karpus 299 cells with PD-L1 KO were generated by CRISPR. The phenotypic KO status (impaired expression of either CD30 or PD-L1 proteins on the cell surface) of KO cells was validated by FACS analysis using anti-  
10 CD30 and anti-PD-L1 antibodies. CD30 KO cells or PD-L1 KO cells or mixed cell population (CD30-KO:PD-L1-KO/75:25 ratios) were incubated with various concentrations of ADCs to assess cytotoxic potency. As expected, the cytotoxic potency of AB201-ADC (binds CD30) and AB204-ADC (binds PD-L1) was greatly reduced when incubated with CD30 KO (100-fold) and PD-L1 cells (7-fold) respectively. As a result, cytotoxic potency of CD30-PD-L1 multi-specific  
15 ADC is now comparable to mono-specific ADCs when incubated with their corresponding KO cells. In the mixed cell population, the multi-specific ADC out-performed both mono-specific ADCs.

#### VII. Example 7: Her2/Her2/Trop2 Tri-specific Tetravalent Antibodies

[000373] Fig.51. describes in vitro cell potency of Her2-Trop2 bi-specific tetravalent (AB612-  
20 ADC) or multi-specific tetravalent ADCs (AB616-618 ADCs) in the JIMT1 and SKOV3 cells.

[000374] Fig.52. describes that Her2-Trop2 multi-specific tetravalent (AB616-ADC and AB618-ADC) showed superior potency compared to both mono-specific ADCs (Her2 binding AB103-ADC or Trop2 binding AB601-ADC) and bivalent bi-specific ADC (AB605-ADC) in the SKOV3 cells. The activity of individual paratope in the multi-specific ADCs was demonstrated by  
25 adding excess unconjugated antibodies. Trop2-17487 paratope ADC activity was tested in the presence of excess Her2-10423 + Her2-11053 antibodies. Her-10423 paratope ADC activity was tested in the presence of excess Trop2-17487 + Her2-11053 antibodies. Her-11053 paratope ADC activity was tested in the presence of excess Trop2-17487 + Her2-10423 antibodies.

30 Fig.53. describes that Her2-Trop2 multi-specific tetravalent (AB616-ADC and AB618-ADC) showed either similar or slightly superior potency compared to mono-specific ADCs (Her2 binding AB103-ADC or Trop2 binding AB601-ADC) and bivalent bi-specific ADC (AB605-ADC) in the NCI-N87 cells. The activity of individual paratope in the multi-specific ADCs was demonstrated by adding excess unconjugated antibodies as described in the Fig. 52.

35 [000375] As used herein, the following meanings apply unless otherwise specified. The words “can” and “may” are used in a permissive sense (i.e., meaning having the potential to), rather

than the mandatory sense (i.e., meaning must). The words "include", "including", and "includes" and the like mean including, but not limited to. The singular forms "a," "an," and "the" include plural referents. Thus, for example, reference to "an element" includes a combination of two or more elements, notwithstanding use of other terms and phrases for one or more elements, such as "one or more." The phrase "at least one" includes "one", "one or more", "one or a plurality", and, therefore, contemplates the use of the term "a plurality". The term "or" is, unless indicated otherwise, non-exclusive, i.e., encompassing both "and" and "or." The term "any of" between a modifier and a sequence means that the modifier modifies each member of the sequence. So, for example, the phrase "at least any of 1, 2 or 3" means "at least 1, at least 2, or at least 3".

10 The term "about" refers to a range that is 5% plus or minus from a stated numerical value within the context of the particular usage. The term "consisting essentially of" refers to the inclusion of recited elements and other elements that do not materially affect the basic and novel characteristics of a claimed combination.

**[000376]** It should be understood that the description and the drawings are not intended to  
15 limit the invention to the particular form disclosed, but to the contrary, the intention is to cover all modifications, equivalents, and alternatives falling within the spirit and scope of the present invention as defined by the appended claims. Further modifications and alternative embodiments of various aspects of the invention will be apparent to those skilled in the art in view of this description. Accordingly, this description and the drawings are to be construed as  
20 illustrative only and are for the purpose of teaching those skilled in the art the general manner of carrying out the invention. It is to be understood that the forms of the invention shown and described herein are to be taken as examples of embodiments. Elements and materials may be substituted for those illustrated and described herein, parts and processes may be reversed or omitted, and certain features of the invention may be utilized independently, all as would be  
25 apparent to one skilled in the art after having the benefit of this description of the invention. Changes may be made in the elements described herein without departing from the spirit and scope of the invention as described in the following claims.

**[000377]** All publications, patents, and patent applications mentioned in this specification are  
herein incorporated by reference to the same extent as if each individual publication, patent, or  
30 patent application was specifically and individually indicated to be incorporated by reference.

Table 1: Engineered Antibodies

| Project Name       | Antibody Type | Antibody Name | Target                             |
|--------------------|---------------|---------------|------------------------------------|
| Control            | IgG           | AB001         | Isotype non-binding<br>ADC control |
|                    |               |               |                                    |
| Target Her2/Her2   | IgG           | AB101         | Her2-1                             |
|                    | IgG           | AB102         | Her2-2                             |
|                    | IgG           | AB103         |                                    |
|                    | IgG           | AB104         |                                    |
|                    | Bis-IgG       | AB105         |                                    |
|                    | Platform4     | AB106         |                                    |
|                    | Platform2     | AB107         |                                    |
|                    | Platform2     | AB108         |                                    |
|                    | Platform4     | AB128         |                                    |
|                    | Platform4     | AB129         |                                    |
|                    | Platform4     | AB130         |                                    |
|                    | Platform4     | AB131         |                                    |
|                    | Platform4     | AB132         |                                    |
|                    | Platform4     | AB133         |                                    |
|                    | Platform4     | AB134         |                                    |
|                    | Platform4     | AB135         |                                    |
|                    | Platform2     | AB136         |                                    |
|                    | Platform2     | AB137         |                                    |
|                    | Platform2     | AB138         |                                    |
|                    | Platform2     | AB139         |                                    |
|                    | Platform2     | AB140         |                                    |
|                    | Platform2     | AB141         |                                    |
|                    | Platform2     | AB142         |                                    |
|                    | Platform2     | AB143         |                                    |
|                    | Platform2     | AB144         |                                    |
| Target: Her2/PD-L1 | Platform2     | AB109         |                                    |
|                    | Platform2     | AB110         |                                    |
|                    | Platform4     | AB111         |                                    |
|                    | Platform4     | AB112         |                                    |
|                    | Platform4     | AB113         |                                    |

|                    |           |       |               |
|--------------------|-----------|-------|---------------|
|                    | Platform4 | AB114 |               |
|                    | Platform4 | AB115 |               |
|                    | Platform4 | AB116 |               |
|                    | Platform4 | AB117 |               |
|                    | Platform4 | AB118 |               |
|                    | Platform4 | AB119 |               |
|                    | Platform4 | AB120 |               |
|                    | Platform4 | AB121 |               |
|                    | Platform2 | AB122 |               |
|                    | Platform2 | AB123 |               |
| Target: CD30/PD-L1 | IgG       | AB201 | CD30          |
|                    | IgG       | AB217 | CD30          |
|                    | IgG       | AB202 | PD-L1-1       |
|                    | IgG       | AB203 | PDL2-2        |
|                    | IgG       | AB204 | PD-L1-3       |
|                    | IgG       | AB218 | AB204 variant |
|                    | IgG       | AB223 | AB203 variant |
|                    | Platform1 | AB205 |               |
|                    | Platform1 | AB206 |               |
|                    | Platform1 | AB207 |               |
|                    | Platform1 | AB208 |               |
|                    |           |       |               |
|                    | Platform2 | AB209 |               |
|                    | Platform2 | AB210 |               |
|                    | Platform2 | AB219 |               |
|                    | Platform2 | AB220 |               |
|                    |           |       |               |
|                    | Platform3 | AB211 |               |
|                    | Platform3 | AB212 |               |
|                    | Platform3 | AB213 |               |
|                    |           |       |               |
|                    | Platform4 | AB214 |               |
|                    | Platform4 | AB215 |               |
|                    | Platform4 | AB216 |               |
|                    | Platform4 | AB221 |               |

|                          |            |       |               |
|--------------------------|------------|-------|---------------|
|                          | Platform4  | AB222 |               |
|                          |            |       |               |
| Target Her2/Trop2        | IgG        | AB601 | Trop2         |
|                          | IgG        | AB621 | AB601 variant |
|                          | Bis-IgG    | AB602 |               |
|                          | Bis-IgG    | AB603 |               |
|                          | Bis-IgG    | AB604 |               |
|                          | Bis-IgG    | AB605 |               |
|                          | Bis-IgG    | AB626 |               |
|                          |            |       |               |
|                          | Platform2  | AB606 |               |
|                          | Platform2  | AB607 |               |
|                          | Platform2  | AB608 |               |
|                          | Platform2  | AB609 |               |
|                          | Platform2  | AB610 |               |
| Target: Her2/PD-L1/Trop2 |            | AB611 |               |
|                          | Platform2  |       |               |
|                          | Platform2  | AB619 |               |
|                          | Platform2  | AB620 |               |
|                          | Platform2  | AB624 |               |
|                          | Platform2  | AB625 |               |
|                          |            |       |               |
|                          | Platform4  | AB612 |               |
|                          | Platform4  | AB613 |               |
|                          | Platform4  | AB614 |               |
|                          | Platform 4 | AB615 |               |
|                          | Platform 4 | AB616 |               |
|                          | Platform 4 | AB617 |               |
|                          | Platform 4 | AB618 |               |
|                          | Platform 4 | AB622 |               |
|                          | Platform 4 | AB623 |               |

The table shows bi-specific antibodies used for binding to dual targets (CD30 and PD-L1, HER2 and TROP2) and antibodies that bind to different epitopes on the same target (HER2). Amino acid sequences of the molecules listed in the “Antibody Name” column (AB101, AB102, *etc.*) are provided elsewhere herein in Table 2 entitled “Antibody Sequences.”

Table 2: Antibody Sequences:

CDRs: underlined or overlined with asterisks  
Cysteine residues for thiomabs: underlined or overlined with hashtag  
Constant Domains in AB101 and AB102: *Italicized*

5

AB101

Heavy Chain:

10 EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW  
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ  
15 VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRW  
QQGNVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID NO:1)

Light Chain: AB101LC

DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTD  
20 FTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNIFY  
PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFN  
RGEC (SEQ ID NO:2)

AB102

Heavy Chain:

25 EVQLVESGGGLVQPGGSLRLSCAASGFTFIDYTMDWVRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGG  
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY  
30 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGDSFFLYSKLTVDKSRWQ  
QQGNVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID NO:3)

Light Chain: AB101LC (SEQ ID NO:2)

35

AB103

Heavy Chain:

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW  
5 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ  
VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRW  
QQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:4)

**Light Chain: AB103LC**

10 DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGRSGTD  
FTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY  
PREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPCTKSFN  
RGEK (SEQ ID NO:5)

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**15 AB104****Heavy Chain:**

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSGG  
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
20 TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY  
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQ  
QQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:6)

25 **Light Chain: AB103LC (SEQ ID NO:5)**

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**AB105****Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
30 SADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW  
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPM  
VFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRW  
35 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:7)

**Heavy Chain 2:**



EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTEMDWVRQAPGKGLEWVADVNPNSSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGTLLTVSSCSSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW  
5 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ  
VYTLPPPIRELMTSNQVSLSCAVKGFPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRW  
QQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:8)

Light Chain: AB103LC (SEQ ID NO:5)

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AB106

Heavy Chain 1:

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGTLLTVSSCSSTKGPSVFPLAPSSKSTSG  
15 GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTGGGGSGGGSGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFNIKDT  
YIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARWGGD  
GFYAMDYWGQGTLLTVSSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLL  
IYSASFLYSGVPSRFSGRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKEIKGGGGSGGGGS  
20 EPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH  
NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSR  
EEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC  
SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:9)

25 Heavy Chain 2:

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTEMDWVRQAPGKGLEWVADVNPNSSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGTLLTVSSCSSTKGPSVFPLAPSSKSTSGG  
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
TKVDKKVEPKSCDKTHTGGGGSGGGSGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTFTDYT  
30 MDWVRQAPGKGLEWVADVNPNSSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPS  
FYFDYWGQGTLLTVSSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIY  
SASFLYSGVPSRFSGRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKEIKGGGGSGGGGSEP  
KSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNA  
KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPIREL  
35 MTSNQVSLSCAVKGFPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSV  
MHEALHNHYTQKSLSLSPGK (SEQ ID NO:10)

Light Chain: AB103LC (SEQ ID NO:5)

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**AB107****Heavy chain:**

5 EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASV  
GDRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGRSGTDFTLTISLQPEDFAT  
YYCQQHYTTPPTFGQGTKVEIKGGGGSGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI  
SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV  
10 SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT  
TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGTGE  
VQLVESGGGLVQPGGSLRLSCAASGFTFTDYTEMDWVRQAPGKGLEWVADVPNSGGSIYNQRFKGRFTLS  
VDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSGGT  
AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT  
15 KVDKKVEPKSCDKTHT (SEQ ID NO:11)

Light Chain: AB103LC (SEQ ID NO:5)

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**AB108****20 Heavy Chain:**

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASV  
GDRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGRSGTDFTLTISLQPEDFAT  
YYCQQHYTTPPTFGQGTKVEIKGGGGSGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI  
25 SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV  
SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT  
TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGTGE  
VQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTIS  
ADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSGG  
30 TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
TKVDKKVEPKSCDKTHT (SEQ ID NO:12)

Light Chain: AB103LC (SEQ ID NO:5)

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**35 AB109****Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFTLENYDIHWVRQAPGKGLEWVAWIYPRNGFTAYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARLLWYDIHAMDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASV  
GDRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGRSGTDFTLTISLQPEDFAT  
YYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI  
5 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV  
SNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKT  
TPPVLDSGSEFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSG  
GGGSEVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADVPNSGGSIYNQRFKG  
RFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGLTVTVSSASTKGPSVFPLAPSSKS  
10 TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNH  
KPSNTKVDKKVEPKSCDKTHT (SEQ ID NO:13)

**Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFTLVDAIMHWVRQAPGKGLEWVASSWNSLSIYADSVKGRFTISA  
15 DTSKNTAYLQMNSLRAEDTAVYYCARSEVYAFYGFYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASVGD  
RVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGRSGTDFTLTISLQPEDFATYY  
CQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR  
TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN  
KALPAPIEKTISKAKGQPREPQVYTLPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTP  
20 PVLDSGSEFFLVSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGG  
GSEVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRF  
TISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGLTVTVSSASTKGPSVFPLAPSSKST  
SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHK  
PSNTKVDKKVEPKSCDKTHT (SEQ ID NO: 14)

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**Light Chain: AB101LC (SEQ ID NO: 2)****AB110****Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFTLVDAIMHWVRQAPGKGLEWVASSWNSLSIYADSVKGRFTISA  
30 DTSKNTAYLQMNSLRAEDTAVYYCARSEVYAFYGFYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASVGD  
RVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGRSGTDFTLTISLQPEDFATYY  
CQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR  
TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN  
35 KALPAPIEKTISKAKGQPREPQVYTLPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTP  
PVLDSGSEFFLVSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGG  
GSEVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRF  
TISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKST

SGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHK  
PSNTKVDKKVEPKSCDKTHT (SEQ ID NO: 15)

**Heavy Chain 2:**

5 EVQLVESGGGLVQPGGSLRLSCAASGFTLENYDIHWVRQAPGKGLEWVAWIYPRNGFTAYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARLLWYDIHAMDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASV  
GDRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSRSGTDFTLTISLQPEDFAT  
YYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI  
SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV  
10 SNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKT  
TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSG  
GGGSEVQLVESGGGLVQPGGSLRLSCAASGFTFTDYMWDWRQAPGKGLEWVADNPNSGGSIYNQRFK  
RFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGLTVTVSSCSTKGPSVFPLAPSSKS  
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNH  
15 KPSNTKVDKKVEPKSCDKTHT (SEQ ID NO: 16)

**Light Chain: AB103LC (SEQ ID NO:5)**

**AB111**

**Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYMWDWRQAPGKGLEWVADNPNSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGG  
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
TKVDKKVEPKSCDKTHTGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLENYD  
25 IHWVRQAPGKGLEWVAWIYPRNGFTAYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARLLWYD  
IHAMDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASVGDRTITCRASQDVNTAVAWYQQKPGKAPKLLI  
YSASFYSGVPSRFSRSGTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSE  
PKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN  
AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSRE  
30 EMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFS  
VMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 17)

**Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
35 SADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLVDA  
YMHVWRQAPGKGLEWVASSWNSLSIYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARSEVYAF

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YGF<sub>1</sub>FDYWGQGT<sub>2</sub>LVTVSSGGGGSDIQMTQSPSSLSASVGDRV<sub>3</sub>ITCRASQDVNTAVAWYQQKPGKAPKLLIY  
SASFLYSGVPSR<sub>4</sub>FSGRSGTDFTLT<sub>5</sub>ISSLQPEDFATYYCQQHYTTPPTFGQGT<sub>6</sub>KVEIKGGGSGGGGSEP  
KSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNA  
KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPIREL  
5 MTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSV  
MHEALHNHYTQKSLSLSPGK (SEQ ID NO: 18)

**Light Chain: AB101LC (SEQ ID NO:2)**

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**10 AB112**

**Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGT<sub>1</sub>LVTVSSC<sub>2</sub>STKGPSVFPLAPSSKSTSGG  
TAALGCLVKDYFPEPVT<sub>3</sub>SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
15 TKVDKKVEPKSCDKTHTGGGGSGGGSGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLENYD  
IHWVRQAPGKGLEWVAWIYPRNGFTAYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARLLWYD  
IHAMDYWGQGT<sub>4</sub>LVTVSSGGGGSDIQMTQSPSSLSASVGDRV<sub>5</sub>ITCRASQDVNTAVAWYQQKPGKAPKLLI  
YSASFLYSGVPSR<sub>6</sub>FSGRSGTDFTLT<sub>7</sub>ISSLQPEDFATYYCQQHYTTPPTFGQGT<sub>8</sub>KVEIKGGGSGGGGSE  
PKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNA  
20 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSRE  
EMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS  
VMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 19)

**Heavy Chain 2:**

25 EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGT<sub>1</sub>LVTVSSC<sub>2</sub>STKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVT<sub>3</sub>SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTGGGGSGGGSGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLVDA  
YMHWVRQAPGKGLEWVASSWNSLSIYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARSEVYAF  
30 YGF<sub>1</sub>FDYWGQGT<sub>2</sub>LVTVSSGGGGSDIQMTQSPSSLSASVGDRV<sub>3</sub>ITCRASQDVNTAVAWYQQKPGKAPKLLIY  
SASFLYSGVPSR<sub>4</sub>FSGRSGTDFTLT<sub>5</sub>ISSLQPEDFATYYCQQHYTTPPTFGQGT<sub>6</sub>KVEIKGGGSGGGGSEP  
KSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNA  
KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPIREL  
MTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSV  
35 MHEALHNHYTQKSLSLSPGK (SEQ ID NO: 20)

**Light Chain: AB103LC (SEQ ID NO:5)**

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## AB201

## Heavy Chain:

QIQQLQQSGPEVVKPGASVKISCKASGYTFTDYYITWVKQKPGQGLEWIGWIYPGSGNTKYNEKFKGKATL  
TVDTSSSTAFLMQLSSLTSEDVAVYFCANYIGNYWFAYWGQGTQVTVSACSTKGPSVFPLAPSSKSTSGGTA  
5 ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTK  
VDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD  
GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY  
LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG  
NVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID NO: 21)

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## Light Chain:

DIVLTQSPASLAIVSLGQRATISCKKASQSVDFDGDSYMNWYQQKPGQPPKVLIIAASNLESGIPARFSGSG  
SGTDFTLNIHPVEEEDAATYYCQQSNEDPWTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL  
NNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSPCT  
15 KSFNRGEC (SEQ ID NO:22)

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## AB202

## Heavy Chain:

EVQLVESGGGLVQPGGSLRLSCAASGFTLKDIDMHWVRQAPGKLEWVARIFPRIGYTQYADSVKGRFTI  
20 SADTSKNTAYLQMNSLRAEDTAVYYCARWGGYDHFADYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW  
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ  
VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW  
25 QQGNVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID NO:23)

Light Chain: AB101LC (SEQ ID NO:2)

## AB203

## 30 Heavy Chain:

EVQLVESGGGLVQPGGSLRLSCAASGFTLENYDIHWVRQAPGKLEWVAWIYPRNGFTAYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARLLWYDIHAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW  
35 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ  
VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW  
QQGNVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID NO:24)

Light Chain: AB101LC (SEQ ID NO:2)

**AB204****Heavy Chain:**

5 EVQLVESGGGLVQPGGSLRLSCAASGFTLVDAYMHWVRQAPGKGLEWVASSWNSLSIYADSVKGRFTISA  
DTSKNTAYLQMNSLRAEDTAVYYCARSEVYAFYGFFDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGT  
AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT  
KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV  
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY  
10 TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQ  
GNVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID NO:25)

Light Chain: AB101LC (SEQ ID NO:2)

**15 AB205****Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFTLKDNSLHWVRQAPGKGLEWVAEIIYSLSHYIGYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARLGRDAFYAMDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
20 NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW  
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPM  
VFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW  
QQGNVFSCSVMEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRL  
SCAASGFTLKDIDMHWRQAPGKGLEWVARI FPRIGYTQYADSVKGRFTISADTSKNTAYLQMNSLRAED  
25 TAVYYCARWGGYDHFAFDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS  
WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT  
(SEQ ID NO:26)

**Heavy Chain 2:**

30 EVQLVESGGGLVQPGGSLRLSCAASGFTLKDNSLHWVRQAPGKGLEWVAEIIYSLSHYIGYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARLGRDAFYAMDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW  
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ  
35 VYTLPPPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLVSKLTVDKSRW  
QQGNVFSCSVMEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRL  
SCAASGFTLVDAYMHWRQAPGKGLEWVASSWNSLSIYADSVKGRFTISADTSKNTAYLQMNSLRAEDTA  
VYYCARSEVYAFYGFYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN

SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT

(SEQ ID NO:27)

Light Chain: AB103LC (SEQ ID NO:5)

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**AB206****Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFTLKDNSLHWVRQAPGKGLEWVAEIIYSLSHYIGYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARLGRDAFYAMDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSG  
10 GTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW  
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPM  
VFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW  
QQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRL  
15 SCAASGFTLENYDIHWVRQAPGKGLEWVAWIYPRNGFTAYADSVKGRFTISADTSKNTAYLQMNSLRAED  
TAVYYCARLLWYDIHAMDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS  
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT  
(SEQ ID NO:28)

20 Heavy Chain 2: Heavy chain 2 of AB205 (SEQ ID NO:27)

Light Chain: AB103LC (SEQ ID NO:5)

**AB207**25 **Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFTLKDNSLHWVRQAPGKGLEWVAEIIYSLSHYIGYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARLGRDAFYAMDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSG  
GTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW  
30 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ  
VYTLPPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRW  
QQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRL  
SCAASGFTLKDNSLHWVRQAPGKGLEWVAEIIYSLSHYIGYADSVKGRFTISADTSKNTAYLQMNSLRAED  
TAVYYCARLGRDAFYAMDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS  
35 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT  
(SEQ ID NO:29)

**Heavy Chain 2:**



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**PCT/US2024/059071**

EVQLVESGGGLVQPGGSLRLSCAASGFTLKDIDMHWRQAPGKGLEWVARIFPRIGYTQYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARWGGYDHFADYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW  
5 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPM  
VFDLPPSREEMTKNQVSLWCMVKGFYPDSIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW  
QQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRL  
SCAASGFTLVDAYMHWRQAPGKGLEWVASSWNSLSIYADSVKGRFTISADTSKNTAYLQMNSLRAEDTA  
VYYCARSEVYAFYGFYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN  
10 SGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT  
(SEQ ID NO:30)

Light Chain: AB103LC (SEQ ID NO:5)

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15 **AB208**

Heavy Chain 1: Heavy chain 1 of AB207 (SEQ ID NO:29)

Heavy Chain 2:

EVQLVESGGGLVQPGGSLRLSCAASGFTLENYDIHWVRQAPGKGLEWVAWIYPRNGFTAYADSVKGRFTI  
20 SADTSKNTAYLQMNSLRAEDTAVYYCARLLWYDIHAMDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW  
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPM  
VFDLPPSREEMTKNQVSLWCMVKGFYPDSIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW  
25 QQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRL  
SCAASGFTLVDAYMHWRQAPGKGLEWVASSWNSLSIYADSVKGRFTISADTSKNTAYLQMNSLRAEDTA  
VYYCARSEVYAFYGFYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN  
SGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT  
(SEQ ID NO:31)

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Light Chain: AB103LC (SEQ ID NO:5)

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**AB209**

Heavy Chain 1:

35 EVQLVESGGGLVQPGGSLRLSCAASGFTLKDIDMHWRQAPGKGLEWVARIFPRIGYTQYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARWGGYDHFADYWGQGLTVTVSSGGGSDIQMTQSPSSLSASV  
GDRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGRSGTDFTLTISLQPEDFAT  
YYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI

SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDNLGKEYKCKV  
SNKALPAPIEKTISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKT  
TPPVLDSDGSFFLVSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGG  
GGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLKDNSLHWVRQAPGKGLEWVAEIIYSLSHYIGYADSVKG  
5 RFTISADTSKNTAYLQMNSLRAEDTAVYYCARLGRDAFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSK  
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVN  
HKPSNTKVDKKVEPKSCDKTHT (SEQ ID NO:32)

**Heavy Chain 2:**

10 EVQLVESGGGLVQPGGSLRLSCAASGFTLVDAIMHWVRQAPGKGLEWVASSWNSLSIYADSVKGRFTISA  
DTSKNTAYLQMNSLRAEDTAVYYCARSEVYAFYGFYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASVGD  
RVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSRSGTDFTLTISLQPEDFATYY  
CQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR  
TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDNLGKEYKCKVSN  
15 KALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKTTP  
PVLDSDGSFFLYSLKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGGG  
GSEVQLVESGGGLVQPGGSLRLSCAASGFTLKDNSLHWVRQAPGKGLEWVAEIIYSLSHYIGYADSVKGRF  
TISADTSKNTAYLQMNSLRAEDTAVYYCARLGRDAFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKST  
SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHK  
20 PSNTKVDKKVEPKSCDKTHT (SEQ ID NO:33)

**Light Chain: AB103LC (SEQ ID NO:5)**

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**AB210**

25 **Heavy Chain 1:**  
EVQLVESGGGLVQPGGSLRLSCAASGFTLKDNSLHWVRQAPGKGLEWVAEIIYSLSHYIGYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARLGRDAFYAMDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASV  
GDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSRSGTDFTLTISLQPEDFAT  
YYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI  
30 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDNLGKEYKCKV  
SNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKT  
TPPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSGG  
GGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLKDIDMHWRQAPGKGLEWVARIFPRIGYTQYADSVKG  
RFTISADTSKNTAYLQMNSLRAEDTAVYYCARWGGYDHFADYWGQGLTVTVSSCSTKGPSVFPLAPSSK  
35 STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVN  
HKPSNTKVDKKVEPKSCDKTHT (SEQ ID NO:34)

**Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFTLKDNSLHWVRQAPGKGLEWVAEIIYSLSHYIGYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARLGRDAFYAMDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASV  
GDRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGSRSGTDFTLTISLQPEDFAT  
YYCQQHYTTPPTFGQGTKVEIKGGGGSGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI  
5 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV  
SNKALPAPIEKTISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKT  
TPPVLDSGSEFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSG  
GGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLVDAYMHWVRQAPGKGLEWVASSWNSLSIYADSVKGRF  
TISADTSKNTAYLQMNSLRAEDTAVYYCARSEVYAFYGFYWGQGLTVTVSSCSTKGPSVFPLAPSSKST  
10 SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHK  
PSNTKVDKKVEPKSCDKTHT (SEQ ID NO:35)

Light Chain: AB103LC (SEQ ID NO:5)

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## 15 AB211

### Heavy Chain 1:

EVQLVESGGGLVQPGGSLRLSCAASGFTLKDNSLHWVRQAPGKGLEWVAEIIYSLSHYIGYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARLGRDAFYAMDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
20 NTKVDKKVEPKSCDKTHTSGGGSGGGSGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLKDIDMHW  
VRQAPGKGLEWVARIFPRIGYTQYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARWGGYDHF  
FDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV  
LQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLF  
PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW  
25 LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWES  
NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ  
ID NO:36)

### Heavy Chain 2:

EVQLVESGGGLVQPGGSLRLSCAASGFTLKDNSLHWVRQAPGKGLEWVAEIIYSLSHYIGYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARLGRDAFYAMDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTSGGGSGGGSGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLVDAYMHW  
VRQAPGKGLEWVASSWNSLSIYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARSEVYAFYGF  
35 YWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ  
SSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPP  
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN  
GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNG

QPENNYKTTPPVLDSGFFLVSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID NO:37)

Light Chain: AB103LC (SEQ ID NO:5)

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**AB212****Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFTLKDNSLHWVRQAPGKLEWVAEIIYSLSHYIGYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARLGRDAFYAMDYWGQGTTLTVSSASTKGPSVFPLAPSSKSTSG  
10 GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLENYDIHW  
VRQAPGKLEWVAWIYPRNGFTAYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARLLWYDIHA  
MDYWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV  
LQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLF  
15 PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW  
LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWES  
NGQPENNYKTTPPVLDSGFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK (SEQ  
ID NO:38)

20 Heavy Chain 2: Heavy chain 2 of AB211 (SEQ ID NO:37)

Light Chain: AB103LC (SEQ ID NO:5)

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**AB213****25 Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFTLKDNSLHWVRQAPGKLEWVAEIIYSLSHYIGYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARLGRDAFYAMDYWGQGTTLTVSSASTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLKDNSLHW  
30 VRQAPGKLEWVAEIIYSLSHYIGYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARLGRDAFYA  
MDYWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV  
LQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLF  
PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW  
LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPIRELMTSNQVSLSCAVKGFYPSDIAVEWES  
35 NGQPENNYKTTPPVLDSGFFLVSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK (SEQ  
ID NO:39)

**Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFTLENYDIHWVRQAPGKGLEWVAWIYPRNGFTAYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARLLWYDIHAMDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTSGGGSGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLVDAVMHW  
5 VRQAPGKGLEWVASSWNSLSIYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARSEVYAFYGF  
YWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ  
SSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPP  
KPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN  
GKEYCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNG  
10 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID  
NO:40)

Light Chain: AB103LC (SEQ ID NO:5)

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## 15 AB214

### Heavy Chain 1:

EVQLVESGGGLVQPGGSLRLSCAASGFTLKDNSLHWVRQAPGKGLEWVAEIIYSLSHYIGYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARLGRDAFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPS  
20 NTKVDKKVEPKSCDKTHTGGGGSGGGSGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLVDA  
YMHVVRQAPGKGLEWVASSWNSLSIYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARSEVYAF  
YGFYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASVGDRTITCRASQDVNTAVAWYQQKPGKAPKLLIY  
SASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKEIKGGGGSGGGGSEP  
KSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNA  
25 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSREE  
MTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV  
MEALHNHYTQKSLSLSPGK (SEQ ID NO:41)

### Heavy Chain 2:

30 EVQLVESGGGLVQPGGSLRLSCAASGFTLKDNSLHWVRQAPGKGLEWVAEIIYSLSHYIGYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARLGRDAFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTGGGGSGGGSGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLKDI  
DMHWVRQAPGKGLEWVARIFPRIGYTQYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARWGGY  
35 DHFAFDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASVGDRTITCRASQDVNTAVAWYQQKPGKAPKLL  
IYSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKEIKGGGGSGGGGS  
EPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH  
NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPIR

ELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTPPVLSDSGSFFLVSKLTVDKSRWQQGNVFSC  
SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:42)

Light Chain: AB103LC (SEQ ID NO:5)

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**AB215**

Heavy Chain 1: Heavy chain 1 of AB214 (SEQ ID NO:41)

Heavy Chain 2:

10 EVQLVESGGGLVQPGGSLRLSCAASGFTLKDNSLHWVRQAPGKGLEWVAEIIYSLSHYIGYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARLGRDAFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTGGGGSGGGSGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLENY  
DIHWVRQAPGKGLEWVAWIYPRNGFTAYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARLLWY  
15 DIHAMDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASVGDRTITCRASQDVNTAVAWYQQKPGKAPKLL  
IYSASFLYSGVPSRFSGRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGS  
EPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH  
NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPIR  
ELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTPPVLSDSGSFFLVSKLTVDKSRWQQGNVFSC  
20 SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:43)

Light Chain: AB103LC (SEQ ID NO:5)

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**AB216**

25 Heavy Chain 1:

EVQLVESGGGLVQPGGSLRLSCAASGFTLENYDIHWVRQAPGKGLEWVAWIYPRNGFTAYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARLLWYDIHAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTGGGGSGGGSGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLVDA  
30 YMHWVRQAPGKGLEWVASSWNSLSIYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARSEVYAF  
YGFYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASVGDRTITCRASQDVNTAVAWYQQKPGKAPKLLIY  
SASFLYSGVPSRFSGRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEP  
KSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNA  
KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPIREL  
35 MTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTPPVLSDSGSFFLVSKLTVDKSRWQQGNVFSCSV  
MHEALHNHYTQKSLSLSPGK (SEQ ID NO:44)

**Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFTLKDNSLHWVRQAPGKGLEWVAEIIYSLSHYIGYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARLGRDAFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
5 NTKVDKKVEPKSCDKTHTGGGGSGGGSGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLKDN  
SLHWVRQAPGKGLEWVAEIIYSLSHYIGYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARLGRD  
AFYAMDYWGQGLTVTVSSGGGSDIQMTQSPSSLSASVGRVTITCRASQDVNTAVAWYQQKPKAPKLL  
IYSASFYSGVPSRFSGRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGS  
EPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH  
10 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSR  
EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFC  
SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:45)

**Light Chain: AB103LC (SEQ ID NO:5)**

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**AB217****Heavy Chain:**

EVQLVESGGGLVQPGGSLRLSCAASGFTLKDNSLHWVRQAPGKGLEWVAEIIYSLSHYIGYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARLGRDAFYAMDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSG  
20 GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW  
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ  
VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW  
QQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:46)

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**Light Chain: AB101LC (SEQ ID NO:2)****AB601****Heavy Chain:**

EVQLVESGGGLVQPGGSLRLSCAASGFTIHYSSMHWVRQAPGKGLEWVASISPSYVYTAYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARVHYATSYSGMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTS  
GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKP  
SNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN  
WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP  
35 QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR  
WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:47)

Light Chain: AB103LC (SEQ ID NO:5)

**AB602****Heavy Chain 1:**

5 EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLLTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVCWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW  
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ  
10 VYTLPPPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRW  
QQGNVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID NO:48)

**Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFTIHYSSMHWRQAPGKGLEWVASISPSYVYTAYADSVKGRFTI  
15 SADTSKNTAYLQMNSLRAEDTAVYYCARVHYATSYSGMDYWGQGTLLTVSSCSTKGPSVFPLAPSSKSTS  
GGTAALGCLVKDYFPEPVTVCWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKP  
SNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN  
WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP  
MVFDPSPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSR  
20 WQQGNVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID NO:49)

Light Chain: AB101LC (SEQ ID NO:2)

**AB603****Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGTLLTVSSCSTKGPSVFPLAPSSKSTSGG  
TAALGCLVKDYFPEPVTVCWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY  
30 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
YTLPPPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQ  
QGNVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID NO:50)

Heavy Chain 2: Heavy chain 2 of AB602 (SEQ ID NO:49)

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Light Chain: AB101LC (SEQ ID NO:2)



**AB604****Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTEMDWVRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGTLLTVSSCSTKGPSVFPLAPSSKSTSGG  
5 TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
TKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY  
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV  
YTLPPIRELMTSNQVLSLCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQ  
QGNVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID NO:51)

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**Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFTIHYSSMHWVRQAPGKGLEWVASISPSYVYTAYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARVHYATSYSGMDYWGQGTLLTVSSCSTKGPSVFPLAPSSKSTS  
GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
15 SNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFN  
WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP  
MVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR  
WQQGNVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID NO:52)

20 **Light Chain: AB103LC (SEQ ID NO:5)****AB605****Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
25 SADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLLTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW  
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ  
VYTLPPIRELMTSNQVLSLCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRW  
30 QQGNVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID NO:53)

**Heavy Chain 2: heavy chain 2 of AB604 (SEQ ID NO:52)****Light Chain: AB103LC (SEQ ID NO:5)**

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**AB606****Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTEMDWVRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGTLLTVTVSSGGGGSDIQMTQSPSSLSASVG  
DRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGRSGTDFTLTITSSLPEDFATY  
YCQQHYHTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS  
5 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS  
NKALPAPIEKTISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTT  
PPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGG  
GGSEVQLVESGGGLVQPGGSLRLSCAASGFTIHYSSMHWVRQAPGKGLEWVASISPSYVYTAYADSVKGR  
FTISADTSKNTAYLQMNSLRAEDTAVYYCARVHYATSYSGMDYWGQGTLLTVTVSSCSTKGPSVFPLAPSSK  
10 STSGGTAALGCLVKDYFPEPVTVCWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVN  
HKPSNTKVDKKVEPKSCDKTHT (SEQ ID NO:54)

**Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
15 SADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLLTVTVSSGGGGSDIQMTQSPSSLSASV  
GDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGRSGTDFTLTITSSLPEDFAT  
YYCQQHYHTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI  
SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV  
SNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKT  
20 TPPVLDSGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGG  
GGGSEVQLVESGGGLVQPGGSLRLSCAASGFTIHYSSMHWVRQAPGKGLEWVASISPSYVYTAYADSVKG  
RFTISADTSKNTAYLQMNSLRAEDTAVYYCARVHYATSYSGMDYWGQGTLLTVTVSSCSTKGPSVFPLAPSS  
KSTSGGTAALGCLVKDYFPEPVTVCWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNV  
NHKPSNTKVDKKVEPKSCDKTHT (SEQ ID NO:55)

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**Light Chain: AB101LC (SEQ ID NO:2)****AB607****Heavy Chain 1:**

30 EVQLVESGGGLVQPGGSLRLSCAASGFTIHYSSMHWVRQAPGKGLEWVASISPSYVYTAYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARVHYATSYSGMDYWGQGTLLTVTVSSGGGGSDIQMTQSPSSLSAS  
VGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGRSGTDFTLTITSSLPEDFA  
TYYCQQHYHTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM  
ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK  
35 VSNKALPAPIEKTISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYK  
TTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGS  
GGGGSEVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVK  
GRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLLTVTVSSCSTKGPSVFPLAPSS

KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV  
NHKPSNTKVDKKVEPKSCDKTHT (SEQ ID NO:56)

**Heavy Chain 2:**

5 EVQLVESGGGLVQPGGSLRLSCAASGFTIHYSMHWVRQAPGKGLEWVASISPSYVYTAYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARVHYATSYSGMDYWGQGTLLTVTVSSGGGGSDIQMTQSPSSLSAS  
VGDRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGRSGTDFTLTISLQPEDFA  
TYYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLM  
ISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK  
10 VSNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYK  
TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGS  
GGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADVPNPSSGGSIYNQRFK  
GRFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGTLLTVTVSSCSTKGPSVFPLAPSSK  
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN  
15 HKPSNTKVDKKVEPKSCDKTHT (SEQ ID NO:57)

**Light Chain: AB103LC (SEQ ID NO:5)**

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**AB608****20 Heavy Chain:**

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLLTVTVSSGGGGSDIQMTQSPSSLSASV  
GDRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGRSGTDFTLTISLQPEDFAT  
YYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMI  
25 SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV  
SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT  
TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGS  
GGGSEVQLVESGGGLVQPGGSLRLSCAASGFTIHYSMHWVRQAPGKGLEWVASISPSYVYTAYADSVKG  
RFTISADTSKNTAYLQMNSLRAEDTAVYYCARVHYATSYSGMDYWGQGTLLTVTVSSCSTKGPSVFPLAPSS  
30 KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV  
NHKPSNTKVDKKVEPKSCDKTHT (SEQ ID NO:58)

**Light Chain: AB103LC (SEQ ID NO:5)**

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**35 AB609****Heavy Chain:**

EVQLVESGGGLVQPGGSLRLSCAASGFTIHYSMHWVRQAPGKGLEWVASISPSYVYTAYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARVHYATSYSGMDYWGQGTLLTVTVSSGGGGSDIQMTQSPSSLSAS

VGDRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGRSGTDFTLTISLQPEDFA  
TYYCQQHYTTPPTFGQGTKVEIKGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM  
ISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK  
VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK  
5 TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGS  
GGGGSEVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVK  
GRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSS  
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV  
NHKPSNTKVDKKVEPKSCDKTHT (SEQ ID NO:59)

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Light Chain: AB103LC (SEQ ID NO:5)

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## AB610

### Heavy Chain 1:

15 EVQLVESGGGLVQPGGSLRLSCAASGFTIHYSSMHWRQAPGKGLEWVASISPSYVYTAYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARVHYATSYSGMDYWGQGLTVTVSSGGGSDIQMTQSPSSLSAS  
VGDRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGRSGTDFTLTISLQPEDFA  
TYYCQQHYTTPPTFGQGTKVEIKGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM  
ISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK  
20 VSNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYK  
TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGS  
GGGGSEVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVK  
GRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSS  
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV  
25 NHKPSNTKVDKKVEPKSCDKTHT (SEQ ID NO:60)

### Heavy Chain 2:

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGLTVTVSSGGGSDIQMTQSPSSLSASV  
30 GDRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGRSGTDFTLTISLQPEDFAT  
YYCQQHYTTPPTFGQGTKVEIKGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI  
SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV  
SNKALPAPIEKTISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKT  
TPPVLDSDGSFFLVSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKGGGSGGGGSGGGGSG  
35 GGGSEVQLVESGGGLVQPGGSLRLSCAASGFTIHYSSMHWRQAPGKGLEWVASISPSYVYTAYADSVKG  
RFTISADTSKNTAYLQMNSLRAEDTAVYYCARVHYATSYSGMDYWGQGLTVTVSSCSTKGPSVFPLAPSS  
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV  
NHKPSNTKVDKKVEPKSCDKTHT (SEQ ID NO:61)

Light Chain: AB103LC (SEQ ID NO:5)

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## AB611

### 5 Heavy Chain 1:

EVQLVESGGGLVQPGGSLRLSCAASGFTIHYSMHWVRQAPGKGLEWVASISPSYVYTAYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARVHYATSYSGMDYWGQGTILVTVSSGGGGSDIQMTQSPSSLSAS  
VGDRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGRSGTDFTLTISLQPEDFA  
TYYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLM  
10 ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK  
VSNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYK  
TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSQSVSMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGG  
GGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADVPNSGGSIYNQRFK  
GRFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGTILVTVSSCSTKGPSVFPLAPSSK  
15 STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVN  
HKPSNTKVDKKVEPKSCDKTHT (SEQ ID NO:62)

Heavy Chain 2: Heavy chain 1 of AB110 (SEQ ID NO:15)

20 Light Chain: AB103LC (SEQ ID NO:5)

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## AB612

### Heavy Chain:

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
25 SADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTILVTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTIHYS  
SMHWVRQAPGKGLEWVASISPSYVYTAYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARVHYA  
TSYSGMDYWGQGTILVTVSSGGGGSDIQMTQSPSSLSASVGDRVITITCRASQDVNTAVAWYQQKPGKAPKL  
30 LIYSASFYSGVPSRFSGRSGTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGGSGGGG  
SEPKSSDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV  
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS  
REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS  
CSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:63)

35

Light Chain: AB103LC (SEQ ID NO:5)

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## AB613

## Heavy Chain:

EVQLVESGGGLVQPGGSLRLSCAASGFTIHYSMMHWVRQAPGKGLEWVASISPSYVYTAYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARVHYATSYSGMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTS  
5 GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKP  
SNTKVDKKVEPKSCDKTHTGGGSGGGSGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFNIKD  
TYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGG  
DGFYAMDYWGQGLTVTVSSGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKL  
LIYSASFYLSGVPSRFSRSGTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGSGGGG  
10 SEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV  
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS  
REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS  
CSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 64)

15 Light Chain: AB103LC (SEQ ID NO: 5)

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## AB614

## Heavy Chain 1:

EVQLVESGGGLVQPGGSLRLSCAASGFTIHYSMMHWVRQAPGKGLEWVASISPSYVYTAYADSVKGRFTI  
20 SADTSKNTAYLQMNSLRAEDTAVYYCARVHYATSYSGMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTS  
GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKP  
SNTKVDKKVEPKSCDKTHTGGGSGGGSGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTIHYS  
SSMMHWVRQAPGKGLEWVASISPSYVYTAYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARVHY  
ATSYSGMDYWGQGLTVTVSSGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPK  
25 LLIYSASFYLSGVPSRFSRSGTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGSGGGG  
GSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVE  
VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPP  
SREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF  
SCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 65)

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## Heavy Chain 2:

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
35 NTKVDKKVEPKSCDKTHTGGGSGGGSGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFNIKDT  
YIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGD  
GFYAMDYWGQGLTVTVSSGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLL  
IYSASFYLSGVPSRFSRSGTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGSGGGGS

EPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH  
NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPIR  
ELMTSNQVSLSCAVKGFPYSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFC  
SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 66)

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Light Chain: AB103LC (SEQ ID NO: 5)

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## AB615

### Heavy Chain 1:

10 EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTGGGGSGGGSGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLVDA  
YMHVVRQAPGKGLEWVASSWNSLSIYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARSEVYAF  
15 YGFDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASVGDRVITTCRASQDVNTAVAWYQQKPGKAPKLLIY  
SASFLYSGVPSRFSGRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEP  
KSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNA  
KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPIREL  
MTSNQVSLSCAVKGFPYSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFC  
20 MHEALHNHYTQKSLSLSPGK (SEQ ID NO: 67)

### Heavy Chain 2:

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSGG  
25 TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
TKVDKKVEPKSCDKTHTGGGGSGGGSGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTIHYSS  
MHVVRQAPGKGLEWVASISPSYVYTAYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARVHYAT  
SYSGMDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASVGDRVITTCRASQDVNTAVAWYQQKPGKAPKLL  
IYSASFLYSGVPSRFSGRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGS  
30 EPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH  
NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSR  
EEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLTVDKSRWQQGNVFC  
SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 68)

35 Light Chain: AB103LC (SEQ ID NO: 5)

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## AB304

WO 2025/122988

PCT/US2024/059071

Heavy Chain:

\*\*HCDR1\*\*

\*\*HCDR2\*\*\*\*

EVQLVESGGGLVQPGGSLRLSCAASGFSFSDFAMSWVRQAPGKGLEWVATIGRVAFHITYYPD SMKGRFTI

\*\*HCDR3\*\*\*\*

5 SRDNSKNTLYLQMNSLRAEDTAVYYCARHRGFDVGHFDFWGQGLTVTVSS

#

CSTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT

VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTGGGSGGGGSGGGGSGGGGSEVQLVESGGGLV

QPGGSLRLSCAASGYSTNDYAWNVRQAPGKGLEWVGYSISGYTTYNPSLKSRTISRDTSKNTLYLQ

10 MNSLRAEDTAVYYCARWTSGLDYWGQGLTVTVSSGGGSDIQMTQSPSSLSASVGDRVITITCKASDLIHN

WLAWYQQKPGKAPKLLIYGATSLETGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYWTTPTFTFGQG

TKVEIKGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH

DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA

KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK

15 LTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID NO:69)

Light Chain:

\*\*\*LCDR1\*\*\*\*\*

\*LCDR2

DIQMTQSPSSLSASVGDRVITITCRSSETLVHSSGNTYLEWYQQKPGKAPKLLIYRVSNRF

20 \*

\*\*LCDR3\*\*

SGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCFQGSFNPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQL

KSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL

#

SSTLTLSKADYEKKHKVYACEVTHQGLSSPCTKSFNRGEC (SEQ ID NO:70)

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## AB305

## Heavy Chain:

\*\*\*HCDR1\*\*\* \*\*HCDR2\*\*  
EVQLVESGGGLVQPGGSLRLSCAASGYSITNDYAWNWVRQAPGKGLEWVGYISYSGYTTY  
5 \*HCDR3\* #  
NPSLKSRFTISRDTSKNTLYLQMNSLRAEDTAVYYCARWTSGLDYWGQGTLLTVVSSCSTKGPSVFPLAPS  
SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICN  
VNHKPSNTKVDKKVEPKSCDKTHTGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASG  
FSFSDFAMSWVRQAPGKGLEWVATIGRVAFTHTYYPDSMKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYC  
10 ARHRGFDVGHFDWVGQGTLLTVVSSGGGSDIQMTQSPSSLSASVGDRVTITCRSSETLVHSSGNTYLEWY  
QQKPGKAPKLLIYRVSNRFSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCFQGSFNPLTFGQGTKVEI  
KGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVK  
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR  
EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK  
15 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 71)

## Light Chain:

\*\*LCDR1\*\*\*\* \*LCDR2\*  
DIQMTQSPSSLSASVGDRVTITCKASDLIHNWLAWYQQKPGKAPKLLIYGATSLETGVPS  
20 \*\*LCDR3\*\*  
RFSGSGSGTDFTLTISLQPEDFATYYCQQYWTTPFTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTA  
SVVCLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLT  
#  
LSKADYEKHKVYACEVTHQGLSSPCTKSFNRGEC (SEQ ID NO: 72)

25

## AB309

## Heavy Chain:

EVQLVESGGGLVQPGGSLRLSCAASGFSFSDFAMSWVRQAPGKGLEWVATIGRVAFTHTYYPDSMKGRFTI  
SRDN SKNTLYLQMNSLRAEDTAVYYCARHRGFDVGHFDWVGQGTLLTVVSSGGGSDIQMTQSPSSLSASV  
30 GDRVTITCRSSETLVHSSGNTYLEWYQQKPGKAPKLLIYRVSNRFSGVPSRFSGSGSGTDFTLTISLQ  
EDFATYYCFQGSFNPLTFGQGTKVEIKGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPK  
DTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE  
YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE  
NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGSGGGGSG  
35 GGTGEVQLVESGGGLVQPGGSLRLSCAASGYSITNDYAWNWVRQAPGKGLEWVGYISYSGYTTYNPSLKS  
RFTISRDTSKNTLYLQMNSLRAEDTAVYYCARWTSGLDYW  
#

**PCT/US2024/059071**

Light Chain:

AB113:

Heavy Chain2:

94

LMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGSEFFLVSKLTVDKSRWQQGNVFSCS  
VMHEALHNHYTQKSLSLSPGK (SEQ ID NO:76)

Light Chain: AB103 LC (SEQ ID NO:5)

5

AB114:

Heavy Chain 1:

10 EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTGGGGSGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLENYDIHWV  
RQAPGKGLEWVAWIYPRNGFTAYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARLLWYDIHAM  
15 DYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSAS  
FLYSGVPSRFSGRSGTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSS  
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTK  
PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTK  
NQVSLWCMVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGSEFFLVSKLTVDKSRWQQGNVFSCSVMHE  
20 ALHNHYTQKSLSLSPGK (SEQ ID NO:77)

Heavy Chain 2:

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKLEWVADVNPNSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSGG  
25 TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
TKVDKKVEPKSCDKTHTGGGGSGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLENYDIHWVR  
QAPGKLEWVAWIYPRNGFTAYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARLLWYDIHAMD  
YWGQGLTVTVSSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASF  
LYSGVPSRFSGRSGTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSD  
30 KTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKP  
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPIRELMTSN  
QVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPVLDSGSEFFLVSKLTVDKSRWQQGNVFSCSVMHEA  
LHNHYTQKSLSLSPGK (SEQ ID NO:78)

35 Light Chain: AB103 LC (SEQ ID NO:5)

AB115:

## Heavy Chain 1:

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
5 SADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLENYDIHWVRQAPG  
KGLEWVAWIYPRNGFTAYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARLLWYDIHAMDYWGQ  
GTLTVTVSSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSG  
10 VPSRFGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHT  
CPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ  
YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSL  
WCMVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH  
YTQKSLSLSPGK (SEQ ID NO: 79)

15

## Heavy Chain 2:

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADVNPNSSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSGG  
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
20 TKVDKKVEPKSCDKTHTGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLENYDIHWVRQAPGK  
GLEWVAWIYPRNGFTAYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARLLWYDIHAMDYWGQG  
TLTVTVSSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGV  
PSRFGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTC  
PPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY  
25 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPIRELMTSNQVSL  
CAVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHY  
TQKSLSLSPGK (SEQ ID NO: 80)

Light Chain: AB103 LC (SEQ ID NO: 5)

30

AB116:

## Heavy Chain 1:

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
35 SADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLENYDIHWVRQAPGKGLEW  
VAWIYPRNGFTAYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARLLWYDIHAMDYWGQGLTVT

VSSGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRF  
SGSRSGTDFTLTISSSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGSGGGGSEPKSSDKTHTCPPCP  
APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY  
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVK  
5 GFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS  
LSLSPGK (SEQ ID NO:81)

**Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTEMDWVRQAPGKLEWVADVNPNSGGSIYNQRFKGRFTL  
10 SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSGG  
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
TKVDKKVEPKSCDKTHTGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLENYDIHWVRQAPGKLEWV  
AWIYPRNGFTAYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARLLWYDIHAMDYWGQGLTVTV  
SSGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFS  
15 GSRSGTDFTLTISSSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGSGGGGSEPKSSDKTHTCPPCPA  
PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR  
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKG  
FYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL  
SLSPGK (SEQ ID NO:82)

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**Light Chain:** AB103 LC (SEQ ID NO:5)

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**AB117:**

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**Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
30 NTKVDKKVEPKSCDKTHTTEVQLVESGGGLVQPGGSLRLSCAASGFTLENYDIHWVRQAPGKLEWVAVIY  
PRNGFTAYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARLLWYDIHAMDYWGQGLTVTVSSGG  
GGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSR  
GTDFTLTISSSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGSGGGGSEPKSSDKTHTCPPCPAPELL  
GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV  
35 LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPS  
DIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP  
GK (SEQ ID NO:83)

**Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTEMDWVRQAPGKGLEWVADVNPNSSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGTTLTVSSCSTKGPSVFPLAPSSKSTSGG  
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
TKVDKKVEPKSCDKTHTEVQLVESGGGLVQPGGSLRLSCAASGFTLENYDIHWVRQAPGKGLEWVAWIYP  
5 RNGFTAYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARLLWYDIHAMDYWGQGTTLTVSSGGG  
GSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFVLYSGVPSRFSGSRSG  
TDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCPAPELLG  
GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL  
TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKGFPYPSD  
10 IAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG  
K (SEQ ID NO:84)

Light Chain: AB103 LC (SEQ ID NO:5)

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AB118:

Heavy Chain 1:

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
20 SADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGTTLTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTEVQLVESGGGLVQPGGSLRLSCAASGFTLENYDIHWVRQAPGKGLEWVAWIY  
PRNGFTAYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARLLWYDIHAMDYWGQGTTLTVSSGG  
GGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFVLYSGVPSRFSGSRSG  
25 GTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGGSEPKSSDKTHTCPPCPAPELLGGPSV  
FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH  
QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVE  
WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  
(SEQ ID NO:85)

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Heavy Chain 2:

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTEMDWVRQAPGKGLEWVADVNPNSSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGTTLTVSSCSTKGPSVFPLAPSSKSTSGG  
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
35 TKVDKKVEPKSCDKTHTEVQLVESGGGLVQPGGSLRLSCAASGFTLENYDIHWVRQAPGKGLEWVAWIYP  
RNGFTAYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARLLWYDIHAMDYWGQGTTLTVSSGGG  
GSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFVLYSGVPSRFSGSRSG  
TDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFL  
FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ

DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKGFYPSDIAVEW  
ESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  
(SEQ ID NO:86)

5 Light Chain: AB103 LC (SEQ ID NO:5)

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AB119:

10 Heavy Chain 1:

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTEVQLVESGGGLVQPGGSLRLSCAASGFTLENYDIHWVRQAPGKGLEWVAWIY  
15 PRNGFTAYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARLLWYDIHAMDYWGQGLTVTVSSGG  
GGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGRS  
GTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKEPKSSDKTHTCPPCPAPELLGGPSVFLFPP  
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN  
GKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNG  
20 QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID  
NO:87)

Heavy Chain 2:

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTL  
25 SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSTFYFDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSGG  
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
TKVDKKVEPKSCDKTHTEVQLVESGGGLVQPGGSLRLSCAASGFTLENYDIHWVRQAPGKGLEWVAWIYP  
RNGFTAYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARLLWYDIHAMDYWGQGLTVTVSSGGG  
GSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGRSG  
30 TDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKEPKSSDKTHTCPPCPAPELLGGPSVFLFPPK  
PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG  
KEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQ  
PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID  
NO:88)

35 Light Chain: AB103 LC (SEQ ID NO:5)

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AB120:

**Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
5 SADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTGGGSGGGSGGGSGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLENYD  
IHWVRQAPGKGLEWVAWIYPRNGFTAYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARLLWYD  
DHAMDYWGQGLTVTVSSGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLI  
10 YSASFLYSGVPSRFSRSGTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGSGGGGSE  
PKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN  
AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPSSRE  
EMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS  
VMHEALHNHYTQKSLSLSPGK (SEQ ID NO:89)

15

**Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADVNPNSSGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSGG  
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
20 TKVDKKVEPKSCDKTHTGGGSGGGSGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLENYD  
IHWVRQAPGKGLEWVAWIYPRNGFTAYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARLLWYD  
DHAMDYWGQGLTVTVSSGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLI  
YSASFLYSGVPSRFSRSGTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGSGGGGSE  
PKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN  
25 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPVYTLPPIRE  
LMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCS  
VMHEALHNHYTQKSLSLSPGK (SEQ ID NO:90)

**Light Chain:** AB103 LC (SEQ ID NO:5)

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AB121:

**Heavy Chain 1:**

35 EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTTEVQLVESGGGLVQPGGSLRLSCAASGFTLENYDIHWVRQAPGKGLEWVAWIY



PRNGFTAYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARLLWYDDHAMDYWGQGLTVTVSSGG  
GGSDIQMTQSPSSLSASVGDRTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGRS  
GTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKEPKSSDKTHTCPPCPAPELLGGPSVFLFPP  
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN  
5 GKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNG  
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID  
NO: 91)

**Heavy Chain 2:**

10 EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADVPNSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSTFDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSGG  
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTQTYICNVNHKPSN  
TKVDKKVEPKSCDKTHTEVQLVESGGGLVQPGGSLRLSCAASGFTLENYDIHWVRQAPGKGLEWVAWIYP  
RNGFTAYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARLLWYDDHAMDYWGQGLTVTVSSGGG  
15 GSDIQMTQSPSSLSASVGDRTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGRSG  
TDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKEPKSSDKTHTCPPCPAPELLGGPSVFLFPPK  
PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG  
KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQ  
PENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID  
20 NO: 92)

**Light Chain:** AB103 LC (SEQ ID NO:5)

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**AB122:**

**Heavy Chain 1:**

30 EVQLVESGGGLVQPGGSLRLSCAASGFTLENYDIHWVRQAPGKGLEWVAWIYPNGFTAYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARLLWYDDHAMDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASV  
GDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGRSGTDFTLTISLQPEDFAT  
YYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI  
SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV  
SNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKT  
35 TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGSG  
GGGSEVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKG  
RFTISADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSK

STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN  
HKPSNTKVDKKVEPKSCDKTHT (SEQ ID NO:93)

**Heavy Chain 2:**

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EVQLVESGGGLVQPGGSLRLSCAASGFTLENYDIHWVRQAPGKGLEWVAWIYPRNGFTAYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARLLWYDDHAMDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASV  
GDRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGRSGTDFTLTISLQPEDFAT  
YYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI  
10 SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV  
SNKALPAPIEKTISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKT  
TPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSG  
GGGSEVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADVPNSGGSIYNQRFKG  
RFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGLTVTVSSCSTKGPSVFPLAPSSKS  
15 TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN  
HKPSNTKVDKKVEPKSCDKTHT (SEQ ID NO:94)

**Light Chain: AB103 LC (SEQ ID NO:5)**

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**AB123:****Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFTLENYDIHWVRQAPGKGLEWVAWIYPRNGFTAYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARLLWYDDHAMDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASV  
25 GDRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGRSGTDFTLTISLQPEDFAT  
YYCQQHYTTPPTFGQGTKVEIKEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV  
VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE  
KTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS  
FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKEVQLVESGGGLVQPGGSLRLSCAASG  
30 FNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYC  
ARWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL  
TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT (SEQ ID  
NO:95)

35

**Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFTLENYDIHWVRQAPGKGLEWVAWIYPRNGFTAYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARLLWYDDHAMDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASV  
GDRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGRSGTDFTLTISLQPEDFAT

YYCQQHYTTPPTFGQGTKVEIKEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV  
VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE  
KTISKAKGQPREPQVYITLPPIRELMTSNQVLSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS  
FFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKEVQLVESGGGLVQPGGSLRLSCAASG  
5 FTFTDYTMDWVRQAPGKGLEWVADVNPNSSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYYC  
ARNLGPSFYFDYWGQGTLLTVSSCSTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT  
SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT (SEQ ID  
NO:96)

10 Light Chain: AB103 LC (SEQ ID NO:5)

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AB124:

15 Heavy Chain 1:

EVQLVESGGGLVQPGGSLRLSCAASGFTLKDIDMHWVRQAPGKGLEWVARIFPRIGYTQYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARWGGYDHFADYWGQGTLLTVSSGGGGSDIQMTQSPSSLSASV  
GDRVITICRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGRSGTDFTLTISLQPEDFAT  
YYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI  
20 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV  
SNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKT  
TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSG  
GGGSEVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKG  
RFTISADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGTLLTVSSCSTKGPSVFPLAPSSK  
25 STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN  
HKPSNTKVDKKVEPKSCDKTHT (SEQ ID NO:97)

Heavy Chain 2:

30 EVQLVESGGGLVQPGGSLRLSCAASGFTIRDSFMHWVRQAPGKGLEWVASSWNSLSIYADSVKGRFTISA  
DTSKNTAYLQMNSLRAEDTAVYYCARSKGDAFYAMDYWGQGTLLTVSSGGGGSDIQMTQSPSSLSASVGD  
RVTITICRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGRSGTDFTLTISLQPEDFATYY  
CQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR  
TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN  
35 KALPAPIEKTISKAKGQPREPQVYITLPPIRELMTSNQVLSLSCAVKGFYPSDIAVEWESNGQPENNYKTTP  
PVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGG  
GSEVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADVNPNSSGGSIYNQRFKGRF  
TLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGTLLTVSSCSTKGPSVFPLAPSSKSTS

GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT (SEQ ID NO:98)

Light Chain: AB103 LC (SEQ ID NO:5)

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AB125:

Heavy Chain 1:

10 EVQLVESGGGLVQPGGSLRLSCAASGFTLKDIDMHWVRQAPGKGLEWVARIFPRIGYTQYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARWGGYDHFADYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASV  
GDRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGRSGTDFTLTISLQPEDFAT  
YYCQQHYTTPPTFGQGTKVEIKEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV  
VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE  
15 KTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGS  
FFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGKEVQLVESGGGLVQPGGSLRLSCAASG  
FNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYC  
ARWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL  
TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT (SEQ ID  
20 NO:99)

Heavy Chain 2:

EVQLVESGGGLVQPGGSLRLSCAASGFTIRDSFMHWVRQAPGKGLEWVASSWNSLSIYADSVKGRFTISA  
DTSKNTAYLQMNSLRAEDTAVYYCARSKGDAFYAMDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASVGD  
25 RVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGRSGTDFTLTISLQPEDFATYY  
CQQHYTTPPTFGQGTKVEIKEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD  
VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT  
ISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFF  
LVSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGKEVQLVESGGGLVQPGGSLRLSCAASGFT  
30 FTDYTMDWVRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYYCAR  
NLGPSFYFDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG  
VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT (SEQ ID  
NO:100)

35 Light Chain: AB103 LC (SEQ ID NO:5)

AB126:

## Heavy Chain 1:

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
5 SADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTGGGGSGGGSGGGSGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTIRDSF  
MHWVRQAPGKGLEWVASSWNSLSIYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARSKGDAFY  
AMDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYS  
10 ASFLYSGVPSRFSRSGTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPK  
SSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAK  
TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPSSREEM  
TKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVM  
HEALHNHYTQKSLSLSPGK (SEQ ID NO:101)

15

## Heavy Chain 2:

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADVPNPSSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSGG  
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
20 TKVDKKVEPKSCDKTHTGGGGSGGGSGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLKDID  
MHWVRQAPGKGLEWVARIFPRIGYTQYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARWGGYD  
HFAFDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLI  
YSASFLYSGVPSRFSRSGTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSE  
PKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHN  
25 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPIRE  
LMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFCFS  
VMHEALHNHYTQKSLSLSPGK (SEQ ID NO:102)

Light Chain: AB103 LC (SEQ ID NO:5)

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AB127:

## Heavy Chain 1:

35 EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTTEVQLVESGGGLVQPGGSLRLSCAASGFTIRDSFMHWVRQAPGKGLEWVASSW

NSLSIYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARSKGDAFYAMDYWGQGLTVTVSSGGGG  
SDIQMTQSPSSLSASVGDRTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGT  
DFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKEPKSSDKTHTCPPCPAPELLGGPSVFLFPPK  
KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK  
5 EYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQP  
ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID  
NO:103)

**Heavy Chain 2:**

10 EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADVPNSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSGG  
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
TKVDKKVEPKSCDKTHTTEVQLVESGGGLVQPGGSLRLSCAASGFTLKDIDMHWRQAPGKGLEWVARIFP  
RIGYTQYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARWGGYDHFAFDYWGQGLTVTVSSGGG  
15 GSIDIQMTQSPSSLSASVGDRTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSG  
TDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKEPKSSDKTHTCPPCPAPELLGGPSVFLFPPK  
PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG  
KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQ  
PENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID  
20 NO:104)

**Light Chain:** AB103 LC (SEQ ID NO:5)

25 **AB128:**

**Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSG  
30 GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTTEVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIY  
PTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGLTVTVSSGG  
GGSDIQMTQSPSSLSASVGDRTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSR  
GTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKEPKSSDKTHTCPPCPAPELLGGPSVFLFPP  
35 KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN  
GKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNG  
QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID  
NO:105)

**Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTEMDWVRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGTLLTVVSSCSTKGPSVFPLAPSSKSTSGG  
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
5 TKVDKKVEPKSCDKHTHTEVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTEMDWVRQAPGKGLEWVADVNP  
NSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGTLLTVVSSGGGG  
SDIQMTQSPSSLSASVGRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYLYSGVPSRFSGRSGT  
DFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKEPKSSDKHTHTCPPCPAPELLGGPSVFLFPPKP  
KDTLMISRTPPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK  
10 EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQP  
ENNYKTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID  
NO:106)

**Light Chain: AB103 LC (SEQ ID NO:5)**

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**AB129:****Heavy Chain 1:**

20 EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGTLLTVVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKHTHTEVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIY  
PTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGTLLTVVSSGG  
25 GGSDIQMTQSPSSLSASVGRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYLYSGVPSRFSGRS  
GTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGGSEPKSSDKHTHTCPPCPAPELLGGPSV  
FLFPPKPKDTLMISRTPPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH  
QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVE  
WESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  
30 (SEQ ID NO:107)

**Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTEMDWVRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGTLLTVVSSCSTKGPSVFPLAPSSKSTSGG  
35 TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
TKVDKKVEPKSCDKHTHTEVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTEMDWVRQAPGKGLEWVADVNP  
NSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGTLLTVVSSGGGG  
SDIQMTQSPSSLSASVGRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYLYSGVPSRFSGRSGT  
DFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGGSEPKSSDKHTHTCPPCPAPELLGGPSVFL

FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD  
WLNQKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKGFYPSDIAVEWE  
SNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ  
ID NO:108)

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Light Chain: AB103 LC (SEQ ID NO:5)

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10 AB130:

**Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSG  
15 GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTEVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIY  
PTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGLTVTVSSGG  
GGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGRS  
GTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGSGGGGSEPKSSDKTHTCPPCPAPELL  
20 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV  
LTVLHQDWLNQKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPS  
DIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP  
GK (SEQ ID NO:109)

25 **Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTEMDWVRQAPGKGLEWVADVNPNSSGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSGG  
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
30 TKVDKKVEPKSCDKTHTEVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTEMDWVRQAPGKGLEWVADVNP  
NSGGSIIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGLTVTVSSGGGG  
SDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGRSGT  
DFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGSGGGGSEPKSSDKTHTCPPCPAPELLGG  
PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT  
35 VLHQDWLNQKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKGFYPSDI  
AVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK  
(SEQ ID NO:110)

Light Chain: AB103 LC (SEQ ID NO:5)



AB131:

5 Heavy Chain 1:

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEW  
10 VARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGLTVT  
VSSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRF  
SGSRSGTDFTLTITSSSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCP  
APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY  
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVK  
15 GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS  
LSLSPGK (SEQ ID NO:111)

Heavy Chain 2:

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYMWDVRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTL  
20 SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSGG  
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
TKVDKKVEPKSCDKTHTGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTFTDYMWDVRQAPGKGLEWV  
ADVNPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGLTVTVS  
SGGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSG  
25 SRSGTDFTLTITSSSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCPAP  
ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV  
VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKGF  
YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS  
LSPGK (SEQ ID NO:112)

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Light Chain: AB103 LC (SEQ ID NO:5)

AB132:

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Heavy Chain 1:

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS

NTKVDKKVEPKSCDKTHTGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPG  
KGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQ  
GTLVTVSSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSG  
VPSRFSGRSGTDFTLTISLQPEDFATYYCQQHYYTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHT  
5 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ  
YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSL  
WCMVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNH  
YTQKSLSLSPGK (SEQ ID NO:113)

10 **Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKLEWVADVNPNSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGTTLVTVSSCSTKGPSVFPLAPSSKSTSGG  
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
TKVDKKVEPKSCDKTHTGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGK  
15 GLEWVADVNPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGT  
LTVTVSSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVP  
SRFSGSRSGTDFTLTISLQPEDFATYYCQQHYYTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCP  
PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN  
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPPIRELMTSNQVSLSC  
20 AVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFCFSVMHEALHNHYT  
QKSLSLSPGK (SEQ ID NO:114)

**Light Chain:** AB103 LC (SEQ ID NO:5)

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**AB133:**

**Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKLEWVARIYPTNGYTRYADSVKGRFTI  
30 SADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGTTLVTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWV  
RQAPGKLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAM  
DYWGQGTTLVTVSSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSAS  
35 FLYSGVPSRFSGRSGTDFTLTISLQPEDFATYYCQQHYYTPPTFGQGTKVEIKGGGGSGGGGSEPKSS  
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK  
PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTK  
NQVSLWCMVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHE  
ALHNHYTQKSLSLSPGK (SEQ ID NO:115)

**Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTEMDWVRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSGG  
5 TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
TKVDKKVEPKSCDKTHTGGGGSGGGSGGGSGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTEMDWVR  
QAPGKGLEWVADVNPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDY  
WGQGLTVTVSSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFL  
YSGVPSRFSGRSGTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDK  
10 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR  
EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPIRELMTSNQ  
VSLSCAVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEAL  
HNHYTQKSLSLSPGK (SEQ ID NO:116)

15 **Light Chain:** AB103 LC (SEQ ID NO:5)

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**AB134:**

20 **Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTGGGGSGGGSGGGSGGGSEVQLVESGGGLVQPGGSLRLSCAASGFNIKDT  
25 YIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARWGGD  
GYAMDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLL  
IYSASFLYSGVPSRFSGRSGTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKEPKSSDKTHT  
CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ  
YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSL  
30 WCMVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNH  
YTQKSLSLSPGK (SEQ ID NO:117)

**Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTEMDWVRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTL  
35 SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSGG  
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
TKVDKKVEPKSCDKTHTGGGGSGGGSGGGSGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTE  
MDWVRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPS  
FYFDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIY

SASFLYSGVPSRFSGRSGTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKEIKEPKSSDKTHTCP  
PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN  
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPIRELMTSNQVSLSC  
AVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYT  
5 QKSLSLSPGK (SEQ ID NO:118)

Light Chain: AB103 LC (SEQ ID NO:5)

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10 AB135:

**Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSG  
15 GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTGGGGSGGGSGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFNIKDT  
YIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARWGGD  
GFYAMDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLL  
IYSASFLYSGVPSRFSGRSGTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKEIKGGGGSEPKSS  
20 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK  
PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTK  
NQVSLWCMVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE  
ALHNHYTQKSLSLSPGK (SEQ ID NO:119)

**Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKLEWVADVNPNSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSGG  
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
TKVDKKVEPKSCDKTHTGGGGSGGGSGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTFTDYT  
30 MDWVRQAPGKLEWVADVNPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPS  
FYFDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIY  
SASFLYSGVPSRFSGRSGTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKEIKGGGGSEPKSSDK  
THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR  
EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPIRELMTSNQ  
35 VSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEAL  
HNHYTQKSLSLSPGK (SEQ ID NO:120)

Light Chain: AB103 LC (SEQ ID NO:5)

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AB136:

## Heavy Chain 1:

5 EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASV  
GDRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGRSGTDFTLTISLQPEDFAT  
YYCQQHYTTPPTFGQGTKVEIKEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV  
VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE  
10 KTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGS  
FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKEVQLVESGGGLVQPGGSLRLSCAASG  
FNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYC  
ARWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL  
TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT (SEQ ID  
15 NO:121)

## Heavy Chain 2:

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTL  
20 SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASVG  
DRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGRSGTDFTLTISLQPEDFATY  
YCQQHYTTPPTFGQGTKVEIKEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV  
DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK  
TISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSF  
25 FLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKEVQLVESGGGLVQPGGSLRLSCAASGF  
TFTDYTMDWVRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYYCA  
RNLGPSFYFDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS  
GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT (SEQ ID  
NO:122)

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Light Chain: AB103 LC (SEQ ID NO:5)

AB137:

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## Heavy Chain 1:

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASV  
GDRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGRSGTDFTLTISLQPEDFAT

YYCQQHYTTPPTFGQGTKVEIKEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV  
VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE  
KTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS  
FFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSEVQLVE  
5 SGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSK  
NTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGTSLTVTVSSCSTKGPSVFPLAPSSKSTSGGTAALG  
CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDK  
KVEPKSCDKTHT (SEQ ID NO:123)

10 **Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGTSLTVTVSSGGGGSDIQMTQSPSSLSASVG  
DRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGRSGTDFTLTISLQPEDFATY  
YCQQHYTTPPTFGQGTKVEIKEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV  
15 DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK  
TISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF  
FLVSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSEVQLVES  
GGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTLSVDRSKN  
TLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGTSLTVTVSSCSTKGPSVFPLAPSSKSTSGGTAALGCL  
20 VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKV  
EPKSCDKTHT (SEQ ID NO:124)

**Light Chain:** AB103 LC (SEQ ID NO:5)

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**AB138:**

**Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
30 SADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGTSLTVTVSSGGGGSDIQMTQSPSSLSASV  
GDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGRSGTDFTLTISLQPEDFAT  
YYCQQHYTTPPTFGQGTKVEIKGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE  
VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL  
PAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKTTPPVLD  
35 SDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKEVQLVESGGGLVQPGGSLRLS  
CAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDT  
AVYYCARWGGDGFYAMDYWGQGTSLTVTVSSCSTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW  
NSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT  
(SEQ ID NO:125)

**Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTEMDWVRQAPGKGLEWVADVNPNSSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGTLLTVSSGGGGSDIQMTQSPSSLSASVG  
5 DRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGRSGTDFTLTITSSLPEDFATY  
YCQQHYTTPPTFGQGTKVEIKGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV  
TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP  
APIEKTISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLD  
SDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKEVQLVESGGGLVQPGGSLRLSC  
10 AASGFTFTDYTEMDWVRQAPGKGLEWVADVNPNSSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTA  
VYYCARNLGPSFYFDYWGQGTLLTVSSCSTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS  
GALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT (SEQ  
ID NO:126)

15 **Light Chain:** AB103 LC (SEQ ID NO:5)

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**AB139:**

20 **Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGTLLTVSSGGGGSDIQMTQSPSSLSASV  
GDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGRSGTDFTLTITSSLPEDFAT  
YYCQQHYTTPPTFGQGTKVEIKGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE  
25 VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL  
PAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKTTPPVLD  
DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGGGSE  
VQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTIS  
ADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGTLLTVSSCSTKGPSVFPLAPSSKSTSGG  
30 TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
TKVDKKVEPKSCDKTHT (SEQ ID NO:127)

**Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTEMDWVRQAPGKGLEWVADVNPNSSGGSIYNQRFKGRFTL  
35 SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGTLLTVSSGGGGSDIQMTQSPSSLSASVG  
DRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGRSGTDFTLTITSSLPEDFATY  
YCQQHYTTPPTFGQGTKVEIKGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV  
TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP  
APIEKTISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLD

SDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGSGGGSGGGSGGGGSEV  
QLVESGGGLVQPGGSLRLSCAASGFTFTDYMWDWRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTLSV  
DRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGTTLTVSSCSTKGPSVFPLAPSSKSTSGGTA  
ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTK  
5 VDKKVEPKSCDKTHT (SEQ ID NO:128)

Light Chain: AB103 LC (SEQ ID NO:5)

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10 AB140:

Heavy Chain 1:

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGTTLTVSSGGGGSDIQMTQSPSSLSASV  
15 GDRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGRSGTDFTLTISLQPEDFAT  
YYCQQHYTTPPTFGQGTKVEIKGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI  
SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV  
SNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKT  
TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKEVQLVESGGGLVQPGG  
20 SLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSL  
RAEDTAVYYCARWGGDGFYAMDYWGQGTTLTVSSCSTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP  
VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDDKKVEPKSCDKT  
HT (SEQ ID NO:129)

25 Heavy Chain 2:

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYMWDWRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGTTLTVSSGGGGSDIQMTQSPSSLSASVG  
DRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGRSGTDFTLTISLQPEDFATY  
YCQQHYTTPPTFGQGTKVEIKGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS  
30 RTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS  
NKALPAPIEKTISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTT  
PPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKEVQLVESGGGLVQPGGS  
LRLSCAASGFTFTDYMWDWRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLR  
AEDTAVYYCARNLGPSFYFDYWGQGTTLTVSSCSTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT  
35 VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDDKKVEPKSCDKTHT  
(SEQ ID NO:130)

Light Chain: AB103 LC (SEQ ID NO:5)

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AB141:

**Heavy Chain 1:**

5 EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASV  
GDRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSRSGTDFTLTISLQPEDFAT  
YYCQQHYTTPPTFGQGTKVEIKGGGGSGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI  
SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV  
10 SNKALPAPIEKTISKAKGQPREPMVFDLPSSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKT  
TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKGGGGSEVQLVESGGGL  
VQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYL  
QMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSGGTAALGCLVKD  
YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPK  
15 SCDKTHT (SEQ ID NO:131)

**Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTEMDWVRQAPGKGLEWVADVNPNSSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASVG  
20 DRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSRSGTDFTLTISLQPEDFATY  
YCQQHYTTPPTFGQGTKVEIKGGGGSGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS  
RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS  
NKALPAPIEKTISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTT  
PPVLDSDGSFFLVSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKGGGGSEVQLVESGGGLV  
25 QPGGSLRLSCAASGFTFTDYTEMDWVRQAPGKGLEWVADVNPNSSGGSIYNQRFKGRFTLSVDRSKNTLYLQ  
MNSLRAEDTAVYYCARNLGPSFYFDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF  
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC  
DKTHT (SEQ ID NO:132)

30 **Light Chain:** AB103 LC (SEQ ID NO:5)

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AB142:

**Heavy Chain 1:**

35 EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASV  
GDRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSRSGTDFTLTISLQPEDFAT  
YYCQQHYTTPPTFGQGTKVEIKGGGGSGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI  
SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV

SNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKT  
 TPPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSEVQLVE  
 SGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSK  
 NTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGTTLTVSSCSTKGPSVFPLAPSSKSTSGGTAALG  
 5 CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDK  
 KVEPKSCDKTHT (SEQ ID NO:133)

**Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTL  
 10 SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGTTLTVSSGGGGSDIQMTQSPSSLSASVG  
 DRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGRSGTDFTLTISLQPEDFATY  
 YCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS  
 RTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS  
 NKALPAPIEKTISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTT  
 15 PPVLDSGDSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSEVQLVES  
 GGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTLSVDRSKN  
 TLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGTTLTVSSCSTKGPSVFPLAPSSKSTSGGTAALGCL  
 VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKV  
 EPKSCDKTHT (SEQ ID NO:134)

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**Light Chain:** AB103 LC (SEQ ID NO:5)

**AB143:**

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**Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
 SADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGTTLTVSSGGGGSDIQMTQSPSSLSASV  
 GDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGRSGTDFTLTISLQPEDFAT  
 30 YYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI  
 SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV  
 SNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKT  
 TPPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSE  
 VQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTIS  
 35 ADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGTTLTVSSCSTKGPSVFPLAPSSKSTSGG  
 TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
 TKVDKKVEPKSCDKTHT (SEQ ID NO:135)

**Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTEMDWVRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGTLLTVSSGGGGSDIQMTQSPSSLSASVG  
DRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGRSGTDFTLTISLQPEDFATY  
YCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS  
5 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS  
NKALPAPIEKTISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTT  
PPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSEV  
QLVESGGGLVQPGGSLRLSCAASGFTFTDYTEMDWVRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTLSV  
DRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGTLLTVSSCSTKGPSVFPLAPSSKSTSGGTA  
10 ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK  
VDKKVEPKSCDKTHT (SEQ ID NO:136)

Light Chain: AB103 LC (SEQ ID NO:5)

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AB144:

Heavy Chain 1:

20 EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGTLLTVSSGGGGSDIQMTQSPSSLSASV  
GDRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGRSGTDFTLTISLQPEDFAT  
YYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI  
SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV  
25 SNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKT  
TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSG  
GGGSEVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKG  
RFTISADTSKNTAYLQMNSLRAEDTAVYYCARWGGDGFYAMDYWGQGTLLTVSSCSTKGPSVFPLAPSSK  
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN  
30 HKPSNTKVDKKVEPKSCDKTHT (SEQ ID NO:137)

Heavy Chain 2:

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTEMDWVRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGTLLTVSSGGGGSDIQMTQSPSSLSASVG  
35 DRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGRSGTDFTLTISLQPEDFATY  
YCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS  
RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS  
NKALPAPIEKTISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTT  
PPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGG

GGSEVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADVPNSGGSIYNQRFKGR  
FTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGLTVTVSSCSTKGPSVFPLAPSSKST  
SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHK  
PSNTKVDKKVEPKSCDKTHT (SEQ ID NO:138)

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Light Chain: AB103 LC (SEQ ID NO:5)

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AB218:

Heavy Chain:

EVQLVESGGGLVQPGGSLRLSCAASGFTIRDSFMHWVRQAPGKGLEWVASSWNSLSIYADSVKGRFTISA  
15 DTSKNTAYLQMNSLRAEDTAVYYCARSKGDAFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSGGT  
AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT  
KVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV  
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY  
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQ  
20 GNVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID NO:139)

Light Chain: AB103LC

DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTD  
FTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY  
25 PREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPCTKSFN  
RGEC (SEQ ID NO:5)

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AB223:

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Heavy Chain:

EVQLVESGGGLVQPGGSLRLSCAASGFTLENYDIHWVRQAPGKGLEWVAWIYPRNGFTAYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARLLWYDDHAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
35 NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW  
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ  
VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW  
QQGNVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID NO:140)

Light Chain: AB103LC (SEQ ID NO:5)

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AB219:

Heavy Chain 1:

EVQLVESGGGLVQPGGSLRLSCAASGFTIRDSFMHWVRQAPGKGLEWVASSWNSLSIYADSVKGRFTISA  
10 DTSKNTAYLQMNSLRAEDTAVYYCARSKGDAFYAMDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASVGD  
RVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGRSGTDFTLTISLQPEDFATYY  
CQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISR  
TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN  
KALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKTFP  
15 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSGGG  
GSEVQLVESGGGLVQPGGSLRLSCAASGFTLKDNSLHWVRQAPGKGLEWVAEIIYSLSHYIGYADSVKGRF  
TISADTSKNTAYLQMNSLRAEDTAVYYCARLGRDAFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKST  
SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHK  
PSNTKVDKKVEPKSCDKTHT (SEQ ID NO:141)

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Heavy Chain 2:

EVQLVESGGGLVQPGGSLRLSCAASGFTLKDIDMHWRQAPGKGLEWVARIFPRIGYTQYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARWGGYDHFAFDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASV  
GDRVITICRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGRSGTDFTLTISLQPEDFAT  
25 YYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI  
SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV  
SNKALPAPIEKTISKAKGQPREPQVYTLPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKT  
TPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSG  
GGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLKDNSLHWVRQAPGKGLEWVAEIIYSLSHYIGYADSVKG  
30 RFTISADTSKNTAYLQMNSLRAEDTAVYYCARLGRDAFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSK  
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVN  
HKPSNTKVDKKVEPKSCDKTHT (SEQ ID NO:142)

Light Chain: AB103LC (SEQ ID NO:5)

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AB220:

**Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFTLKDNSLHWVRQAPGKGLEWVAEIIYSLSHYIGYADSVKGRFTI  
5 SADTSKNTAYLQMNSLRAEDTAVYYCARLGRDAFYAMDYWGQGTTLTVSSGGGGSDIQMTQSPSSLSASV  
GDRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGRSGTDFTLTISLQPEDFAT  
YYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI  
SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV  
SNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKT  
10 TPPVLDSGSEFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSG  
GGGSEVQLVESGGGLVQPGGSLRLSCAASGFTIRDSFMHWVRQAPGKGLEWVASSWNSLSIYADSVKGRF  
TISADTSKNTAYLQMNSLRAEDTAVYYCARSKGDAFYAMDYWGQGTTLTVSSCSTKGPSVFPLAPSSKST  
SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHK  
PSNTKVDKKVEPKSCDKTHT (SEQ ID NO:143)

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**Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFTLKDIDMHWRQAPGKGLEWVARIFPRIGYTQYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARWGGYDHFAFDYWGQGTTLTVSSGGGGSDIQMTQSPSSLSASV  
GDRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGRSGTDFTLTISLQPEDFAT  
20 YYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI  
SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV  
SNKALPAPIEKTISKAKGQPREPQVYTLPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKT  
TPPVLDSGSEFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGSG  
GGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLKDNSLHWVRQAPGKGLEWVAEIIYSLSHYIGYADSVKG  
25 RFTISADTSKNTAYLQMNSLRAEDTAVYYCARLGRDAFYAMDYWGQGTTLTVSSCSTKGPSVFPLAPSSK  
STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVN  
HKPSNTKVDKKVEPKSCDKTHT (SEQ ID NO:144)

**Light Chain:** AB103LC (SEQ ID NO:5)

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AB221: AV-P379:

**Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFTLKDNSLHWVRQAPGKGLEWVAEIIYSLSHYIGYADSVKGRFTI  
35 SADTSKNTAYLQMNSLRAEDTAVYYCARLGRDAFYAMDYWGQGTTLTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLKDI  
DMHWVRQAPGKGLEWVARIFPRIGYTQYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARWGGY

DHFAFDYWGQGLVTVSSGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLL  
IYSASFLYSGVPSRFSGRSGTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKEIKGGGSGGGGS  
EPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH  
NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPIR  
5 ELMTSNQVSLSCAVKGFYPDSIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSC  
SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:145)

**Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFTLKDNSLHWVRQAPGKGLEWVAEIIYSLSHYIGYADSVKGRFTI  
10 SADTSKNTAYLQMNSLRAEDTAVYYCARLGRDAFYAMDYWGQGLVTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTIRDS  
FMHWVRQAPGKGLEWVASSWNSLSIYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARSKGDAF  
YAMDYWGQGLVTVTVSSGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIY  
15 SASFLYSGVPSRFSGRSGTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKEIKGGGSGGGGSEP  
KSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA  
KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSREE  
MTKNQVSLWCMVKGFPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV  
MHEALHNHYTQKSLSLSPGK (SEQ ID NO:146)

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**Light Chain:** AB103LC (SEQ ID NO:5)

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**AB222:**

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**Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFTIRDSFMHWVRQAPGKGLEWVASSWNSLSIYADSVKGRFTISA  
DTSKNTAYLQMNSLRAEDTAVYYCARSKGDAFYAMDYWGQGLVTVSSCSTKGPSVFPLAPSSKSTSGGT  
AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT  
30 KVDKKVEPKSCDKTHTGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLKDIDM  
HWVRQAPGKGLEWVARIFPRIGYTQYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARWGGYDH  
FAFDYWGQGLVTVTVSSGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIY  
SASFLYSGVPSRFSGRSGTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKEIKGGGSGGGGSEP  
KSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA  
35 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPIREL  
MTSNQVSLSCAVKGFYPDSIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSV  
MHEALHNHYTQKSLSLSPGK (SEQ ID NO:147)

**Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFTLKDNSLHWVRQAPGKGLEWVAEIIYSLSHYIGYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARLGRDAFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
5 NTKVDKKVEPKSCDKTHTGGGGSGGGSGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLKDN  
SLHWVRQAPGKGLEWVAEIIYSLSHYIGYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARLGRD  
AFYAMDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLL  
IYSASFYSGVPSRFSGSRSGTDFTLTISSLPEDFATYYCQQHYTTPPTFGQGTKEIKGGGGSGGGGS  
EPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH  
10 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSR  
EEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC  
SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:148)

Light Chain: AB103LC (SEQ ID NO:5)

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AB621:

Heavy Chain:

20 EVQLVESGGGLVQPGGSLRLSCAASGFTIHDSSMHHWVRQAPGKGLEWVASISPSYVYTAYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARVHYATSYSGMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTS  
GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
SNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFN  
WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP  
25 QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSR  
WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:149)

Light Chain: AB103LC (SEQ ID NO:5)

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AB626:

Heavy Chain 1:

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSG  
35 GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW  
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ  
VYTLPPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLVSKLTVDKSRW  
QQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:150)



**Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFTIHDSMHWVRQAPGKGLEWVASISPSYVYTAYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARVHYATSYSGMDYWGQGT<sup>1</sup>LVTVSSCSTKGPSVFPLAPSSKSTS  
5 GGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP  
SNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFN  
WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP  
MVF<sup>2</sup>DLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR  
WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:151)

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**Light Chain:** AB103LC (SEQ ID NO:5)**AB616:**

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**Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGT<sup>1</sup>LVTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS  
20 NTKVDKKVEPKSCDKTHTGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFNIKDT  
YIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGD  
GFYAMDYWGQGT<sup>2</sup>LVTVSSGGGGSDIQMTQSPSSLSASVGD<sup>3</sup>RVTITCRASQDVNTAVAWYQQKPGKAPKLL  
IYSASFLYSGVPSRFSGSRSGTDF<sup>4</sup>TLTISSLQPEDFATYYCQQHYTTPPTFGQGTKEIKGGGGSGGGGS  
EPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH  
25 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPIR  
ELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSC  
SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:152)

**Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGT<sup>1</sup>LVTVSSCSTKGPSVFPLAPSSKSTSGG  
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN  
TKVDKKVEPKSCDKTHTGGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTIHYSS  
MHWVRQAPGKGLEWVASISPSYVYTAYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARVHYAT  
35 SYSGMDYWGQGT<sup>2</sup>LVTVSSGGGGSDIQMTQSPSSLSASVGD<sup>3</sup>RVTITCRASQDVNTAVAWYQQKPGKAPKLL  
IYSASFLYSGVPSRFSGSRSGTDF<sup>4</sup>TLTISSLQPEDFATYYCQQHYTTPPTFGQGTKEIKGGGGSGGGGS  
EPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH  
NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSR

EEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC  
SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:153)

Light Chain: AB103LC (SEQ ID NO:5)

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AB617:

Heavy Chain 1:

10 EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEW  
VARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGLTVT  
15 VSSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRF  
SGSRSGTDFTLTITSSLPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCP  
APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY  
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVK  
GFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS  
20 LSLSPGK\* (SEQ ID NO:154)

Heavy Chain 2:

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSGG  
25 TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
TKVDKKVEPKSCDKTHTGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTIHYSSMHWRQAPGKGLEWV  
ASISPSYVYTAYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARVHYATSYSGMDYWGQGLTVT  
VSSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRF  
SGSRSGTDFTLTITSSLPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCP  
30 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY  
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVK  
GFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS  
LSLSPGK\* (SEQ ID NO:155)

35 Light Chain: AB103LC (SEQ ID NO:5)

AB618:

**Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
5 SADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKHTHTEVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIY  
PTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGLTVTVSSGG  
GGSDIQMTQSPSSLSASVGDRTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRS  
10 GTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKEPKSSDKHTHTCPPCPAPELLGGPSVFLFPP  
KPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDNLN  
GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNG  
QPENNYKTTPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK\* (SEQ  
ID NO:156)

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**Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTEMDWVRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSGG  
20 TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
TKVDKKVEPKSCDKHTHTEVQLVESGGGLVQPGGSLRLSCAASGFTIHYSSMHWVRQAPGKGLEWVASISP  
SYVYTAYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARVHYATSYSGMDYWGQGLTVTVSSGG  
GGSDIQMTQSPSSLSASVGDRTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRS  
GTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKEPKSSDKHTHTCPPCPAPELLGGPSVFLFPP  
25 KPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDNLN  
GKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNG  
QPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID  
NO:157)

30 **Light Chain:** AB103LC (SEQ ID NO:5)

AB619: AV-P309:

35 **Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFTIHYSSMHWVRQAPGKGLEWVASISPSYVYTAYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARVHYATSYSGMDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSAS  
VGDRTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRS GTDFTLTISSLQPEDFA  
TYYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLM

ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK  
VSNKALPAPIEKTISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYK  
TTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGGS  
GGGGSEVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVK  
5 GRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLLTVVSSCSTKGPSVFPLAPSS  
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV  
NHKPSNTKVDKKVEPKSCDKTHT\* (SEQ ID NO:158)

**Heavy Chain 2:**

10 EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLLTVVSSGGGGSDIQMTQSPSSLSASV  
GDRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGRSGTDFTLTISLQPEDFAT  
YYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI  
SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV  
15 SNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKT  
TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKGGGGSGGGSGGGSG  
GGGSEVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKLEWVADVNPNSSGGSIYNQRFKG  
RFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGTLLTVVSSCSTKGPSVFPLAPSSKS  
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNH  
20 KPSNTKVDKKVEPKSCDKTHT\* (SEQ ID NO:159)

**Light Chain:** AB103LC (SEQ ID NO:5)

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25 **AB620:**

**Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFTIHYSSMHVVRQAPGKLEWVASISPSYVYTAYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCARVHYATSYSGMDYWGQGTLLTVVSSGGGGSDIQMTQSPSSLSAS  
30 VGDRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGRSGTDFTLTISLQPEDFA  
TYYCQQHYTTPPTFGQGTKVEIKEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV  
VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI  
EKTISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG  
SFFLVSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGKEVQLVESGGGLVQPGGSLRLSCAAS  
35 GFNIKDTYIHWVRQAPGKLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYY  
CSRWGGDGFYAMDYWGQGTLLTVVSSCSTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA  
LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT\* (SEQ  
ID NO:160)

**Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASV  
GDRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFVSGVPSRFSGRSGTDFTLTISLQPEDFAT  
5 YYCQQHYTTPPTFGQGTKVEIKEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV  
VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE  
KTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGS  
FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKEVQLVESGGGLVQPGGSLRLSCAASG  
FTFTDYMWDVVRQAPGKGLEWVADVNPNSSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYYC  
10 ARNLGPSFYFDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT  
SGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT\* (SEQ ID  
NO:161)

**Light Chain: AB103LC (SEQ ID NO:5)**

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**AB622:****Heavy Chain 1:**

20 EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYMWDVVRQAPGKGLEWVADVNPNSSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSGG  
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
TKVDKKVEPKSCDKTHTGGGGSGGGSGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTIHDSS  
MHWVRQAPGKGLEWVASISPSYVYTAYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARVHYAT  
25 SYSGMDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASVGDVITITCRASQDVNTAVAWYQQKPGKAPKLL  
IYSASFVSGVPSRFSGRSGTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGS  
EPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH  
NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSR  
EEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC  
30 SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:162)

**Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSG  
35 GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTGGGGSGGGSGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFNIKDT  
YIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGD  
GFYAMDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASVGDVITITCRASQDVNTAVAWYQQKPGKAPKLL  
IYSASFVSGVPSRFSGRSGTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGS

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EPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH  
NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPIR  
ELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSC  
SVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:163)

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Light Chain: AB103LC (SEQ ID NO:5)

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AB623:

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Heavy Chain 1:

EVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTEMDWVRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTL  
SVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGTTLVTVSSCSTKGPSVFPLAPSSKSTSGG  
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSN  
TKVDKKVEPKSCDKTHTEVQLVESGGGLVQPGGSLRLSCAASGFTIHDSSMHWVRQAPGKGLEWVASISP  
SYVYTAYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCARVHYATSYSGMWYWGQGTTLVTVSSGG  
GGSDIQTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRS  
GTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKEPKSSDKTHTCPPCPAPELLGGPSVFLFPP  
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN  
GKEYKCKVSNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNG  
QPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID  
NO:164)

Heavy Chain 2:

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTTLVTVSSCSTKGPSVFPLAPSSKSTSG  
GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPS  
NTKVDKKVEPKSCDKTHTEVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIY  
PTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTTLVTVSSGG  
GGSDIQTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRS  
GTDFTLTISLQPEDFATYYCQQHYTTPPTFGQGTKVEIKEPKSSDKTHTCPPCPAPELLGGPSVFLFPP  
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN  
GKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNG  
QPENNYKTTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID  
NO:165)

Light Chain: AB103LC (SEQ ID NO:5)

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AB624:

**Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFTIHDSMHWVRQAPGKGLEWVASISPSYVYTAYADSVKGRFTI  
5 SADTSKNTAYLQMNSLRAEDTAVYYCARVHYATSYSGMDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSAS  
VGDRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGRSGTDFTLTISLQPEDFA  
TYYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM  
ISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK  
VSNKALPAPIEKTISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYK  
10 TTPPVLDSDGSFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGS  
GGGGSEVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVK  
GRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSS  
KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNV  
NHKPSNTKVDKKVEPKSCDKTHT (SEQ ID NO:166)

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**Heavy Chain 2:**

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
SADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASV  
GDRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGRSGTDFTLTISLQPEDFAT  
20 YYCQQHYTTPPTFGQGTKVEIKGGGGSGGGGSEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI  
SRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV  
SNKALPAPIEKTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKT  
TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKGGGGSGGGGSGGGGS  
GGGSEVQLVESGGGLVQPGGSLRLSCAASGFTFTDYTMDWVRQAPGKGLEWVADVNPNSSGGSIYNQRFKG  
25 RFTLSVDRSKNTLYLQMNSLRAEDTAVYYCARNLGPSFYFDYWGQGLTVTVSSCSTKGPSVFPLAPSSKS  
TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNH  
KPSNTKVDKKVEPKSCDKTHT (SEQ ID NO:167)

**Light Chain:** AB103LC (SEQ ID NO:5)

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AB625:

**Heavy Chain 1:**

EVQLVESGGGLVQPGGSLRLSCAASGFTIHDSMHWVRQAPGKGLEWVASISPSYVYTAYADSVKGRFTI  
35 SADTSKNTAYLQMNSLRAEDTAVYYCARVHYATSYSGMDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSAS  
VGDRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGRSGTDFTLTISLQPEDFA  
TYYCQQHYTTPPTFGQGTKVEIKEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV  
VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI

EKTISKAKGQPREPQVYTLPPIRELMTSNQVSLSCAVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG  
SFFLVSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKEVQLVESGGGLVQPGGSLRLSCAAS  
GFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYY  
CSRWGGDGFYAMDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA  
5 LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT (SEQ  
ID NO:168)

Heavy Chain 2:

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTI  
10 SADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGLTVTVSSGGGGSDIQMTQSPSSLSASV  
GDRVITITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFYSGVPSRFSGRSGTDFTLTISLQPEDFAT  
YYCQQHYTPPTFGQGTKVEIKPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV  
VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE  
KTISKAKGQPREPMVFDLPPSREEMTKNQVSLWCMVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGS  
15 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGKEVQLVESGGGLVQPGGSLRLSCAASG  
FTFTDYTMDWVRQAPGKGLEWVADVNPNSGGSIYNQRFKGRFTLSVDRSKNTLYLQMNSLRAEDTAVYYC  
ARNLGPSFYFDYWGQGLTVTVSSCSTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT  
SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHT (SEQ ID  
NO:169)

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Light Chain: AB103LC (SEQ ID NO:5)

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## CLAIMS

## WHAT IS CLAIMED IS:

1. An antibody, e.g., an immunoconjugate, comprising a tetravalent antibody comprising one or more payloads conjugated thereto, wherein the antibody comprises first, second, third, and fourth light chains, and first and second heavy chains, and comprises, from N-terminus to C-terminus:
  - a) a first pair of paratopes comprised in Fab regions;
  - b) an Fc region; and
  - c) a second pair of paratopes, comprised in Fab regions.
2. An antibody, e.g., an immunoconjugate, comprising a payload conjugated to an antibody that comprises first, second, third and fourth light chains, and first and second heavy chains, wherein:
  - a) the first light chain comprises, from N-terminus to C-terminus, a first light chain variable (VL) region and a first light chain constant (CL) region;
  - b) the second light chain comprises, from N-terminus to C-terminus, a second VL region and a second CL region;
  - c) the third light chain comprises, from N-terminus to C-terminus, a third light chain variable (VL) region and a third light chain constant (CL) region;
  - d) the fourth light chain comprises, from N-terminus to C-terminus, a fourth VL region and a fourth CL region;
  - e) the first heavy chain comprises, from N-terminus to C-terminus:
    - (i) a first heavy chain portion comprising a first heavy chain variable (VH) region and a first heavy chain constant 1 (CH1) region;
    - (ii) a first Fc region comprising a first heavy chain constant 2 (CH2) region and a first heavy chain constant 3 (CH3) region;
    - (iii) a second heavy chain portion comprising a second heavy chain variable (VH) region and a second heavy chain constant 1 (CH1) region; and
  - f) the second heavy chain comprises, from N-terminus to C-terminus:
    - (i) a third heavy chain portion comprising a third heavy chain variable (VH) region and a third heavy chain constant 1 (CH1) region;
    - (ii) a second Fc region comprising a second heavy chain constant 2 (CH2) region and a second heavy chain constant 3 (CH3) region;
    - (iii) a fourth heavy chain portion comprising a fourth heavy chain variable (VH) region and a fourth heavy chain constant 1 (CH1) region; and
 wherein:

the first light chain and the first heavy chain portion form a first Fab portion comprising a first paratope; and

the second light chain and the second heavy chain portion form a second Fab portion comprising a second paratope;

5 the third light chain and the third heavy chain portion form a third Fab portion comprising a third paratope; and

the fourth light chain and the fourth heavy chain portion form a fourth Fab portion comprising a fourth paratope.

3. An antibody, e.g., an immunoconjugate, comprising a tetravalent antibody  
10 comprising one or more payloads conjugated thereto, wherein the antibody comprises first and second light chains, and first and second heavy chains, and comprises, from N-terminus to C-terminus:

- a) a first pair of paratopes, comprised in a diabody;
- b) an Fc region; and
- 15 c) a second pair of paratopes comprised in Fab regions.

4. An antibody, e.g., an immunoconjugate, comprising a payload conjugated to an antibody that comprises first and second light chains and first and second heavy chains, wherein:

- a) the first light chain comprises, from N-terminus to C-terminus, a first light chain  
20 variable (VL) region and a first light chain constant (CL) region;
  - b) the second light chain comprises, from N-terminus to C-terminus, a second VL region and a second CL region;
  - c) the first heavy chain comprises, from N-terminus to C-terminus:
    - (i) a first diabody region comprising a first VH region and a third VL  
25 region, in either order; and
    - (ii) a first Fc region comprising a first heavy chain constant 2 (CH2) region and a first heavy chain constant 3 (CH3) region; and
    - (iii) a first heavy chain portion comprising a second heavy chain variable (VH) region and a first heavy chain constant 1 (CH1) region;
  - 30 d) the second heavy chain comprises, from N-terminus to C-terminus:
    - (i) a second diabody region comprising a third VH region and a fourth VL region, in either order; and
    - (ii) a second Fc region comprising a second heavy chain constant 2 (CH2) region and a second heavy chain constant 3 (CH3) region; and
    - 35 (iii) a second heavy chain portion comprising a fourth heavy chain variable (VH) region and a second heavy chain constant 1 (CH1) region;
- wherein:

the first light chain and the first heavy chain portion form a first Fab portion comprising a first paratope; and

the second light chain and the second heavy chain portion form a second Fab portion comprising a second paratope; and

- 5           the first and second diabody regions form a diabody forming a third paratope comprising the third VL region and the third VH region, and a fourth paratope comprising the fourth VL region and the first VH region.

5.       An antibody, e.g., an immunoconjugate, comprising a tetravalent antibody comprising one or more payloads conjugated thereto, wherein the antibody comprises first, 10 second, third, and fourth light chains, and first and second heavy chains, and comprises, from N-terminus to C-terminus:

- a) a first pair of paratopes comprised in Fab regions;
- b) a second pair of paratopes, comprised in Fab regions; and
- c) an Fc region.

15       6.       An antibody, e.g., an immunoconjugate, comprising a payload conjugated to an antibody that comprises first, second, third and fourth light chains, and first and second heavy chains, wherein:

- a) the first light chain comprises, from N-terminus to C-terminus, a first light chain variable (VL) region and a first light chain constant (CL) region;
- 20       b) the second light chain comprises, from N-terminus to C-terminus, a second VL region and a second CL region;
- c) the third light chain comprises, from N-terminus to C-terminus, a third light chain variable (VL) region and a third light chain constant (CL) region;
- d) the fourth light chain comprises, from N-terminus to C-terminus, a fourth VL 25 region and a fourth CL region;
- e) the first heavy chain comprises, from N-terminus to C-terminus:
  - (i) a first heavy chain portion comprising a first heavy chain variable (VH) region and a first heavy chain constant 1 (CH1) region;
  - (ii) a second heavy chain portion comprising a second heavy chain 30 variable (VH) region and a second heavy chain constant 1 (CH1) region; and
  - (iii) a first Fc region comprising a first heavy chain constant 2 (CH2) region and a first heavy chain constant 3 (CH3) region;
- f) the second heavy chain comprises, from N-terminus to C-terminus:
  - (i) a third heavy chain portion comprising a third heavy chain variable 35 (VH) region and a third heavy chain constant 1 (CH1) region;
  - (ii) a fourth heavy chain portion comprising a fourth heavy chain variable (VH) region and a fourth heavy chain constant 1 (CH1) region; and

(iii) a second Fc region comprising a second heavy chain constant 2 (CH2) region and a second heavy chain constant 3 (CH3) region;

wherein:

- the first light chain and the first heavy chain portion form a first Fab portion comprising a first paratope; and
- the second light chain and the second heavy chain portion form a second Fab portion comprising a second paratope;
- the third light chain and the third heavy chain portion form a third Fab portion comprising a third paratope; and
- the fourth light chain and the fourth heavy chain portion form a fourth Fab portion comprising a fourth paratope.

7. An antibody, e.g., an immunoconjugate, comprising a tetravalent antibody comprising one or more payloads conjugated thereto, wherein the antibody comprises first and second light chains, and first and second heavy chains, and comprises, from N-terminus to C-

- a) a first pair of paratopes comprised in Fab regions;
- b) a second pair of paratopes, comprised in a diabody; and
- c) an Fc region.

8. An antibody, e.g., an immunoconjugate, comprising a payload conjugated to an antibody that comprises first and second light chains and first and second heavy chains, wherein:

- a) the first light chain comprises, from N-terminus to C-terminus, a first light chain variable (VL) region and a first light chain constant (CL) region;
- b) the second light chain comprises, from N-terminus to C-terminus, a second VL region and a second CL region;
- c) the first heavy chain comprises, from N-terminus to C-terminus:
  - (i) a first heavy chain portion comprising a first heavy chain variable (VH) region and a first heavy chain constant 1 (CH1) region;
  - (ii) a first diabody region comprising a second VH region and a third VL region, in either order; and
  - (iii) a first Fc region comprising a first heavy chain constant 2 (CH2) region and a first heavy chain constant 3 (CH3) region; and
- d) the second heavy chain comprises, from N-terminus to C-terminus:
  - (i) a second heavy chain portion comprising a third VH region and a second CH1 region;
  - (ii) a second diabody region comprising a fourth VH region and a fourth VL region, in either order; and

(iii) a second Fc region comprising a second CH2 region and a second CH3 region;

wherein:

- the first light chain and the first heavy chain portion form a first Fab portion  
5 comprising a first paratope; and  
the second light chain and the second heavy chain portion form a second Fab portion comprising a second paratope;  
the first and second diabody regions form a diabody forming a third paratope comprising the fourth VL region and the second VH region, and a fourth paratope comprising  
10 the third VL region and the fourth VH region.

9. The antibody or immunoconjugate of any of claims 1 to 8, comprising at least one paratope that binds to a first epitope of Her2, and at least one paratope that binds to a second epitope of Her2.

10. The antibody or immunoconjugate of any of claims 1 to 8, comprising at  
15 least one paratope that binds to CD30, and at least one paratope that binds to an epitope of PD-L1.

11. The antibody or immunoconjugate of any of claims 1 to 8, comprising at least one paratope that binds to a first epitope of Her2, at least one paratope that binds to PD-L1, and, optionally, at least one paratope that binds to a second epitope of Her2.

20 12. The antibody or immunoconjugate of any of claims 1 to 8, comprising at least one paratope that binds to CD30, at least one paratope that binds to a first epitope of PD-L1, and at least one paratope that binds to a second epitope of PD-L1.

13. The antibody or immunoconjugate of any of claims 1 to 8, comprising at least one paratope that binds to Trop2, and at least one paratope that binds to a first epitope of  
25 Her2, at least one paratope that binds to a second epitope of Her2 and a paratope that binds to PD-L1.

14. The antibody or immunoconjugate of any of claims 1 to 8, comprising at least one paratope that binds to Trop2, at least one paratope that binds to a first epitope of Her2, and, optionally, at least one paratope that binds to a second epitope of Her2.

30 15. The antibody or immunoconjugate of any of claims 1 to 8, which is a mono-specific antibody, wherein all the paratopes specifically bind to the same epitope.

16. The antibody or immunoconjugate of any of claims 1 to 8, which is a bi-specific antibody, wherein at least one of the paratopes specifically binds a first epitope, and at least another of the paratopes bind a second, different epitope.

5 17. The antibody or immunoconjugate of claim 15, wherein, wherein two of the paratopes specifically bind to a first epitope and two of the paratopes specifically bind to a second, different epitope; or three of the paratopes bind to the same first epitope, and one of the paratopes specifically binds to a second, different epitope.

10 18. The antibody or immunoconjugate of claim 15, wherein the first and second paratopes bind the same first epitope, and the third and fourth paratopes bind the same second epitope; or the first and third paratopes bind the same first epitope, and the second and fourth paratopes bind the same second epitope.

15 19. The antibody or immunoconjugate of claim 15, wherein two of the paratopes bind the same first epitope of Her2, and two of the paratopes bind the same second epitope of Her2, e.g., the first and second paratopes bind the same first epitope and the third and fourth paratopes bind the same second epitope; or, the first and third paratopes bind the same first epitope and the second and fourth paratopes bind the same second epitope.

20. The antibody or immunoconjugate of claim 18, wherein the first epitope is an epitope bound by trastuzumab and the second epitope is an epitope bound by pertuzumab.

20 21. The antibody or immunoconjugate of claim 15, wherein one of the paratopes binds CD30, one of the paratopes bind a first epitope of Her2, and two of the paratopes bind the same second epitope of Her2.

25 22. The antibody or immunoconjugate of any of claims 1 to 8, which is a tri-specific antibody, wherein at least one of the paratopes binds to a first epitope, at least one of the paratopes binds to a second, different epitope, and at least one of the paratopes binds to a third, different epitope, e.g., two of the paratopes bind to the same first epitope, one of the paratopes binds to a second, different epitope, and one of the paratopes binds to a third epitope that is different from the first and second epitopes.

30 23. The antibody or immunoconjugate of claim 21, wherein the first and second paratopes bind the same epitope; the first and third paratopes bind the same epitope; or the second and third paratopes bind the same epitope.

24. The antibody or immunoconjugate of any of claims 1-21, wherein at least two paratopes bind to different epitopes of the same antigen.

25. The antibody or immunoconjugate of any of claims 1-23, wherein two of the paratopes bind to different epitopes of the same first antigen, and two of the paratopes bind to different epitopes of the same second antigen.

5 26. The antibody or immunoconjugate of claim 21, wherein:  
a first paratope and a second paratope each bind an epitope of CD30;  
a third paratope binds a first epitope of PD-L1; and  
a fourth paratope binds a second epitope of PD-L1.

10 27. The antibody or immunoconjugate of claim 21, wherein:  
a first paratope and a second paratope each bind an epitope of Trop2;  
a third paratope binds a first epitope of Her2; and  
a fourth paratope binds a second epitope of Her2.

28. The antibody or immunoconjugate of claim 1 or 3, which is a tetra-specific antibody, wherein each of the paratopes binds to a different epitope.

15 29. The antibody or immunoconjugate of any of claims 1-27, wherein the first and second heavy chains have different amino acid sequences, and are associated through a knob-into-hole structure.

20 30. The antibody or immunoconjugate of claim 28, wherein the Fc region comprises two non-identical heavy chains, wherein at least one of the two non-identical heavy chains comprises an amino acid modification so as to form complementation between the two non-identical heavy chains thereby increasing the probability of forming heterodimers of the non-identical heavy chains and decreasing the probability of forming homodimers of identical heavy chains.

25 31. The antibody or immunoconjugate of any of claims 1-30, wherein the heavy and light chains are produced from a cell genetically engineered to produce two heavy chains and one light chain.

32. The antibody or immunoconjugate of any of claims 1-30, wherein all of the light chain variable regions have the same amino acid sequence.

33. The antibody or immunoconjugate of any of claims 1-30, wherein both light chains comprise light chain variable regions having the same amino acid sequence.

30 34. The antibody or immunoconjugate of any of claims 1-30, wherein the first and second light chains have the same amino acid sequences.

35. The antibody or immunoconjugate of any of claims 1-30, wherein the first and second heavy chains have identical amino acid sequences.

36. The antibody or immunoconjugate of any of claims 1-35, wherein the antibody comprises:

- 5 a) a diabody region optionally attached to an Fc region through Spacer 1, and the Fc region attached to the heavy chain portion through a Spacer 2;
- b) a heavy chain portion optionally attached through Spacer 3 to a diabody region, and the diabody region optionally attached through a Spacer 4 to an Fc region;
- c) an Fc region attached to a heavy chain portion through a Spacer 5; or
- 10 d) a heavy chain attached to another heavy chain portion through a Spacer 6.

37. The antibody or immunoconjugate of claim 36, wherein Spacers 1-6 independently comprise between 0 and 50 amino acids.

38. The antibody or immunoconjugate of claim 37, wherein Spacers 1-6 are independently selected from a monomer or polymer of the sequence (GGGGS)<sub>n</sub> (SEQ ID NO: 170), (GGGGA)<sub>n</sub> (SEQ ID NO: 171) or (GGGGG) (SEQ ID NO: 172), wherein n is any of 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10.

15

39. The antibody or immunoconjugate of claim 38, wherein Spacers 1-6 are independently selected from GGGGSGGGGSEPKSSDKTHT (SEQ ID NO: 173), GGGSGGGSGGGSGGGSGSTG (SEQ ID NO: 174), LEDKTHTKVEPKSS (SEQ ID NO: 175), SGSETPGTSESATPESGGG (SEQ ID NO: 176), and GTTAASGSSGGSSSGA (SEQ ID NO: 177).

20

40. The antibody or immunoconjugate of claim 38, comprising a diabody region optionally attached to an Fc region through Spacer 1, and the Fc region attached to the heavy chain portion through Spacer 2; wherein Spacer 1 and Spacer 2, if present, are selected from the following pairs:

25

| Spacer 1 – Diabody-Fc                | Spacer 2 – Fc-Fab                    |
|--------------------------------------|--------------------------------------|
| No spacer or substantially no spacer | No spacer or substantially no spacer |
| About 10 amino acids                 | About 20 amino acids                 |
| About 10 amino acids                 | About 10 amino acids                 |
| About 10 amino acids                 | About 5 amino acids                  |
| About 10 amino acids                 | No spacer or substantially no spacer |
| About 5 amino acids                  | About 20 amino acids                 |
| About 5 amino acids                  | No spacer or substantially no spacer |
| No spacer or substantially no spacer | About 20 amino acids                 |



|                                      |                                      |
|--------------------------------------|--------------------------------------|
| No spacer or substantially no spacer | No spacer or substantially no spacer |
| About 10 amino acids                 | About 20 amino acids                 |

**41.** The antibody or immunoconjugate of claim **40**, wherein Spacer 1 and Spacer 2, if present, are selected from the following pairs:

| Spacer 1 – Diabody-Fc | Spacer 2 – Fc-Fab |
|-----------------------|-------------------|
| (G4S)0                | (G4S)0            |
| (G4S)2                | (G4S)4            |
| (G4S)2                | (G4S)2            |
| (G4S)2                | (G4S)1            |
| (G4S)2                | (G4S)0            |
| (G4S)1                | (G4S)4            |
| (G4S)1                | (G4S)0            |
| (G4S)0                | (G4S)4            |
| (G4S)0                | (G4S)0            |
| (G4S)2                | (G4S)4            |

**42.** The antibody or immunoconjugate of claim **36**, comprising (i) a heavy chain portion optionally attached through Spacer 3 to a diabody region, and the diabody region optionally attached through Spacer 4 to an Fc region, wherein Spacer 3 and Spacer 4, if present, are selected from the following pairs:

| Spacer 3 – Fab-Diabody               | Spacer 4 – Diabody-Fc                |
|--------------------------------------|--------------------------------------|
| No spacer or substantially no spacer | No spacer or substantially no spacer |
| About 20 amino acids                 | About 10 amino acids                 |
| About 5 amino acids                  | About 10 amino acids                 |
| About 20 amino acids                 | No spacer or substantially no spacer |
| About 15 amino acids                 | About 10 amino acids                 |
| About 10 amino acids                 | About 10 amino acids                 |
| About 5 amino acids                  | About 10 amino acids                 |
| No spacer or substantially no spacer | About 10 amino acids                 |
| No spacer or substantially no spacer | About 5 amino acids                  |

**43.** The antibody or immunoconjugate of claim **42**, wherein Spacer 3 and Spacer 4, if present, are selected from the following pairs:

| Spacer 3 – Fab-Diabody | Spacer 4 – Diabody-Fc |
|------------------------|-----------------------|
|------------------------|-----------------------|

|        |        |
|--------|--------|
| (G4S)0 | (G4S)0 |
| (G4S)4 | (G4S)2 |
| (G4S)4 | (G4S)1 |
| (G4S)4 | (G4S)0 |
| (G4S)3 | (G4S)2 |
| (G4S)2 | (G4S)2 |
| (G4S)1 | (G4S)2 |
| (G4S)0 | (G4S)2 |
| (G4S)0 | (G4S)1 |

**44.** The antibody or immunoconjugate of any of claims **1-43**, wherein the payload is conjugated through a reduced disulfide bond.

**45.** The antibody or immunoconjugate of any of claims **1-43**, comprising a plurality of payload molecules conjugated to the antibody.

**46.** The antibody or immunoconjugate of any of claims **1-43**, wherein the antibody is a thiomab comprising at least one cysteine residue substitution in a heavy chain or a light chain, wherein the payload is conjugated through the substituted cysteine residue.

**47.** The antibody or immunoconjugate of claim **46**, wherein the thiomab comprises amino acid substitutions:

- (a) HC-A118C and LC-V205C; and/or
- (b) HC-S157C, HC-S239C, and HC-V266C (EU numbering)
- (c) T155C, H285C, R301C, V303C, T307C, G316C, Y436C and L441C (EU numbering).

**48.** The antibody or immunoconjugate of any of claims **1-47**, wherein the payload comprises a cytotoxic agent, radioactive isotope, fluorescent moiety, or an enzyme.

**49.** The antibody or immunoconjugate of claim **48**, wherein the payload comprises a cytotoxic agent selected from maytansinoid, DM-1, DM-4, auristatin, monomethyl auristatin E, monomethyl auristatin F, dolastatin, tubulysin, eribulin, cryptophycin, benzodiazepine, indolino-benzodiazepine, isoquinolidino-benzodiazepine, pyrrolo-benzodiazepine, alpha-amanitin, trichothene, camptothecin derivatives (SN-38, exatecan, belotecan, DXd, topotecan, samrofecan), duocarmycin, DGN549, CC1065, calicheamicin, N-acetyl calicheamicin, an enediyne antibiotic, taxane, doxorubicin derivatives, anthracycline and

stereoisomers, azanofide, as well as isosteres, analogs, heterodimers, homodimers or derivatives of the foregoing.

50. The antibody or immunoconjugate of any of claims 1-49 wherein the antibodies comprise at least one light chain, heavy chain or full CDR sequence set of an antibody chain of Appendix 1.

51. The antibody or immunoconjugate of claim 50, wherein:

- a) a CDR sequence set for Her2 binding, if present, is selected from the light chain, heavy chain or full CDR sequence set of AB101 or the CDR sequence set of AB102;
- b) a CDR sequence set for CD30 binding, if present, is selected from the light chain, heavy chain or full CDR sequence set of AB217;
- c) a CDR sequence set for PD-L1 binding, if present, is selected from the light chain, heavy chain or full CDR sequence sets of AB202, AB203, AB204, AB218 or AB223;
- d) a CDR sequence set for Trop2 binding, if present, is selected from the light chain, heavy chain or full CDR sequence sets of AB601 or AB621.

52. The antibody or immunoconjugate of any of claims 50-51, wherein:

- a) a light chain for Her2 binding, if present, is selected from AB101, AB102, AB103, AB105, AB106, AB107, AB108, AB113, AB114, AB115, AB116, AB117, AB118, AB119, AB120, AB121, AB122, AB123, AB124, AB125, AB126, AB127, AB128, AB129, AB130, AB131, AB132, AB133, AB134, AB135, AB136, AB137, AB138, AB139, AB140, AB141, AB142, AB143, AB144, AB607, AB608, AB609, AB610, AB611, AB612, AB613, AB614, AB616, AB617, AB618, AB619, AB620, AB622, AB623, AB624, AB625;
- b) a light chain for Trop2 binding, if present, is selected from AB601, AB605, AB606, AB608, AB610, AB613, AB614, AB626;
- c) a light chain for PD-L1 binding, if present, is selected from AB205, AB206, AB207, AB208, AB210, AB211, AB212, AB213, AB216, AB220, AB222; or
- d) a light chain for CD30 binding, if present, is selected from AB205, AB206, AB207, AB208, AB209, AB211, AB212, AB213, AB214, AB215, AB216, AB217, AB219, AB220, AB221, AB222.

53. The antibody or immunoconjugate of any of claims 50-52, wherein:

- a) a heavy chain for Her2 binding, if present, is selected from AB101, AB102, AB103, AB105, AB106, AB107, AB108, AB113, AB114, AB115, AB116, AB117, AB118, AB119, AB120, AB121, AB122, AB123, AB124, AB125, AB126, AB127, AB128, AB129, AB130, AB131, AB132, AB133, AB134, AB135, AB136, AB137, AB138, AB139, AB140, AB141, AB142, AB143, AB144, AB607, AB608, AB609, AB610, AB611, AB612, AB613, AB614, AB616, AB617, AB618, AB619, AB620, AB622, AB623, AB624, AB625;

b) a heavy chain for Trop2 binding, if present, is selected from AB601, AB605, AB606, AB608, AB610, AB613, AB614, AB626;

c) a heavy chain for PD-L1 binding, if present, is selected from AB205, AB206, AB207, AB208, AB210, AB211, AB212, AB213, AB216, AB220, AB222; or

5 d) a heavy chain for CD30 binding, if present, is selected from AB205, AB206, AB207, AB208, AB209, AB211, AB212, AB213, AB214, AB215, AB216, AB217, AB219, AB220, AB221, AB222.

**54.** The antibody or immunoconjugate of any of claims **50-53**, wherein:

10 a) a diabody region for binding different Her2 epitopes, if present, is selected from the diabody region of AB106, AB128, AB129, AB130, AB131, AB132, AB133, AB134, AB135, AB136, AB137, AB138, AB139, AB140, AB141, AB142, AB143, AB144 or AB606;

b) a diabody region for binding the same Her2 epitopes, if present, is selected from the diabody region of AB107, AB108, AB608, AB613;

15 c) a diabody region for binding different PD-L1 epitopes, if present, is selected from the diabody region of AB209, AB214, AB215, AB124, AB125, AB126, AB127, AB219, AB221;

d) a diabody region for binding the same CD30 epitope, if present, is selected from the diabody region of AB210;

20 e) a diabody region for binding PD-L1 and CD30, if present, is selected from the diabody region of AB216, AB220, AB222; or

f) a diabody region for binding the same Trop2 epitope, if present, is selected from the diabody region of AB607, AB609, or AB612

25 g) a diabody region for binding Her2 and Trop2, if present, is selected from the diabody region of AB610, AB614, AB616, AB617, AB618, AB619, AB620, AB622, AB623, AB624, AB625.

h) a diabody region for binding PD-L1 and Trop2, if present, is selected from the diabody region of AB611.

**55.** The antibody or immunoconjugate of any of claims **50-54**, comprising an Fc region selected from Table 1.

30 **56.** The antibody or immunoconjugate of any of claims **1-55**, comprising one or more antibody chains of Table 1.

**57.** A method of making an immunoconjugate comprising:

a) providing an antibody of any of claims **1-56**; and

b) conjugating one or more payloads to the antibody.

58. The method of claim 57, wherein at least one of the payloads is conjugated to the antibody through a linker.

59. The method of claim 57, wherein at least one of the payloads is conjugated to the antibody through a reduced disulfide bond.

5 60. The method of claim 57, wherein the antibody is a cysteine-substituted antibody ("thiomab"), and at least one cytotoxic payload is coupled to the antibody through a substituted cysteine.

61. The method of claim 57, wherein the immunoconjugate has a drug-antibody ratio ("DAR") of at least any of 1, 2, 3, 4, 6, 7, 8, 9, 10, 11, and 12.

10 62. One or more nucleic acid molecules that encode a heavy chain and/or a light chain of an antibody of any of claims 1-61.

63. The one or more nucleic acid molecules of claim 62, encoding one or more antibodies of any of claims 1-56.

15 64. The one or more nucleic acid molecules of claim 61, encoding both a light chain and a heavy chain of the antibody of any of claims 1-- 56.

65. The one or more nucleic acid molecules of any of claims 62-64, further comprising one or more expression control sequences operatively linked to one or more nucleotide sequences encoding the one or more light chain variable regions and/or one or more heavy chain variable regions.

20 66. The one or more nucleic acid molecules of any of claims 61-64, comprised within one or more vectors, e.g., selected from a plasmid, a viral vector (e.g., a retrovirus, a lentivirus, and adenovirus, and adeno-associated virus, or a herpes simplex virus), a bacterial artificial chromosome, and a yeast artificial chromosome.

25 67. A cell comprising the one or more nucleic acid molecules of any of claims 61-65.

30 68. The cell of claim 56, selected from a mammalian cell (e.g., a Chinese hamster ovary (CHO) cell, in an NS0cell, an SP2/0 cell, and human embryonic kidney HEK 293 cell, or a Per.C6 cell); an insect cell (e.g., in Sf9 cell or a high five (BTI-Tn-5B1-4) cell); a yeast cell (e.g., Pichia pastoris or and Saccharomyces cerevisiae); a bacterial cell (e.g., E. coli); and a plant cell.

69. A method of making an antibody comprising:

- a) providing a cell or cells of any of claims **67-68**;
- b) expressing immunoglobulin molecules encoded by the nucleotide sequences in the cell or cells; and
- c) recovering the expressed immunoglobulin molecules.

5                   **70.**     The method of claim **69**, wherein the antibody is an asymmetric antibody and the cell comprises one or more nucleic acid molecules encoding a heavy chain comprising a knob, a heavy chain comprising a hole, and at least one light chain.

**71.**     The method of claim **70**, wherein the cell comprises nucleotide sequences encoding only one light chain, wherein the light chain is configured to associate with  
10 different heavy chain regions to produce two paratopes.

**72.**     The method of claim **70**, wherein the cell comprises nucleic acids encoding two different light chains, wherein a first light chain is configured to associate with a first heavy chain region to produce a first paratope that binds to a first epitope, and a second light chain is configured to associate with a second heavy chain region to produce a second  
15 paratope that binds to a second, different epitope.

**73.**     The method of claim **70**, comprising producing different immunoglobulin chains in different cells, recovering the immunoglobulin chains, and contacting the immunoglobulin chains, wherein the immunoglobulin chains assemble into an antibody.

**74.**     The method of claim **70**, further comprising purifying the recovered  
20 antibody, e.g. using protein A or protein G.

**75.**     A pharmaceutical composition comprising an antibody or immunoconjugate of any one of claims **1-45**, and a pharmaceutically acceptable carrier, diluent, or excipient.

**76.**     The pharmaceutical composition of claim **75**, formulated for intravenous  
25 injection.

**77.**     A method for treating cancer in a subject, comprising administering to the subject a therapeutically effective amount of the pharmaceutical composition of any of claims **64-65**.

**78.**     The method of claim **77**, wherein the cancer is selected from ovarian,  
30 breast, lung, stomach, endometrial and pancreatic.

**79.**     A method for detecting a cell that expresses an antigen comprising an epitope, comprising: a) contacting the cell with an antibody or immunoconjugate of any of claims

**1-45** to allow binding between the antibody or immunoconjugate and the cell; and b) detecting the binding of the antibody or immunoconjugate to the cell.

5           **80.**     The method of claim **79**, comprising a) contacting the cell with an immunoconjugate comprising an antibody conjugated to a detectable moiety; and b) detecting the detectable moiety bound to the cell.

**81.**     A method of killing a cell comprising contacting a cell with an antibody or immunoconjugate of any of claims **1-56**, wherein one or more paratopes of the antibody specifically bind to an epitope of the cell.

10           **82.**     The method of claim **81**, wherein two different paratopes of the antibody bind to two different epitopes of the cell.

**83.**     The method of claim **82**, wherein the epitope is comprised in a cell surface antigen.

**84.**     Use of an antibody or immunoconjugate of any of claims **1-56** in the manufacture of a medicament.

15           **85.**     Use of an antibody of any of claims **1-56** to produce an immunoconjugate.