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(54) **Titre : PROTEINES MULTISPECIFIQUES DE LIAISON A L'ANTIGENE**
(54) **Title: MULTISPECIFIC ANTIGEN-BINDING PROTEINS**

(57) **Abrégé/Abstract:**

Provided are, inter alia, multispecific antigen binding proteins, or antigen-binding fragments thereof, comprising one or more mutations in the VH/VL domains and/or CH1/CL domains, pharmaceutical compositions comprising same, isolated nucleic acids, vectors, and host cells encoding/expressing same, method of making the multispecific antigen binding proteins, computer readable media for evaluating multispecific antigen binding proteins, and libraries.



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(57) Abstract: Provided are, inter alia, multispecific antigen binding proteins, or antigen-binding fragments thereof, comprising one or more mutations in the VH/VL domains and/or CH1/CL domains, pharmaceutical compositions comprising same, isolated nucleic acids, vectors, and host cells encoding/expressing same, method of making the multispecific antigen binding proteins, computer readable media for evaluating multispecific antigen binding proteins, and libraries.



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JUMBO APPLICATIONS/PATENTS

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MULTISPECIFIC ANTIGEN-BINDING PROTEINS

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of priority to U.S. Provisional Application Nos. 62/152,735 filed April 24, 2015, 62/264,291 filed December 7, 2015, and 62/310,555 filed March 18, 2016, all of which are hereby incorporated by reference in their entirety.

SEQUENCE LISTING

[0002] The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on April 22, 2016, is named P05841WO_PCTSequenceListing.txt and is 131,134 bytes in size.

BACKGROUND OF THE INVENTION

[0003] The development of bispecific antibodies as therapeutic agents for human diseases has great clinical potential. However, production of bispecific antibodies in IgG format has been challenging, as antibody heavy chains have evolved to bind antibody light chains in a relatively promiscuous manner. As a result of this promiscuous pairing, concomitant expression of, *e.g.*, two antibody heavy chains and two antibody light chains naturally leads to heavy chain homodimerization and scrambling of heavy chain/light chain pairings.

[0004] One approach to circumvent the problem of heavy chain homodimerization, known as ‘knobs-into-holes’, aims at forcing the pairing of two different antibody heavy chains by introducing mutations into the CH3 domains to modify the contact interface. On one heavy chain original amino acids were replaced by amino acids with short side chains to create a ‘hole’. Conversely, amino acids with large side chains were introduced into the other CH3 domain, to create a ‘knob’. By coexpressing these two heavy chains (and two identical light chains, which have to be appropriate for both heavy chains), high yields of heterodimer formation (‘knob-hole’) versus homodimer formation (‘hole-hole’ or ‘knob-knob’) was observed (Ridgway, J. B., Protein Eng. 9 (1996) 617-621; and WO 96/027011).

[0005] Minimizing the scrambling of heavy chain/light chain has been more difficult due to the complex multidomain heterodimeric interactions within antibody Fabs. Bispecific antibodies formats aimed at addressing heavy chain/light scrambling include: DVD-Ig (Dual Variable Domain Ig) (Nature Biotechnology 25, 1290-1297 (2007)); Cross-over Ig (Schaefer W *et al* (2011) PNAS 108(27): 11187-11192); Two-in-One Ig (Science 2009, 323, 1610); BiTE® antibodies (PNAS 92(15):7021-7025; 1995) and strategies described in Lewis *et al.* (2014) “Generation of bispecific IgG antibodies by structure-based design of an orthogonal Fab interface.” *Nat Biotechnol* 32, 191-8; Liu *et al.* (2015) “A Novel

Antibody Engineering Strategy for Making Monovalent Bispecific Heterodimeric IgG Antibodies by Electrostatic Steering Mechanism.” *J Biol Chem*. Published online January 12, 2015, doi:10.1074/jbc.M114.620260; Mazor *et al.* 2015. “Improving target cell specificity using a novel monovalent bispecific IgG design.” *Mabs*. Published online January 26, 2015, doi: 10.1080/19420862.2015.1007816; WO 2014/081955, WO 2014/082179, and WO 2014/150973.

[0006] There continues to be a need to reduce mispaired heavy chain/light chain by-products and increase bispecific antibody yield.

BRIEF SUMMARY OF THE INVENTION

[0007] As described in more detail below, multispecific antigen-binding proteins (such as bispecific antibodies) that have been modified to include such asymmetrical mutations are produced in a single cell with, *inter alia*, improved correct heavy chain/light chain pairing and/or improved yields of multispecific antigen-binding proteins as compared with multispecific antigen-binding proteins with sequences without modifications. In certain embodiments, the multispecific antigen-binding proteins comprise modification(s) in the VH/VL and/or CH1/CL regions to facilitate correct heavy/light chain pairing. In certain other embodiments, the multispecific antigen-binding proteins further comprise modification(s) in the Fc region to facilitate heterodimerization of the two arms of the multispecific antigen-binding protein.

[0008] Provided herein is a multispecific antigen binding protein, or an antigen-binding fragment thereof, comprising: a) a first heavy chain/light chain pair binding to a first antigen which comprises a first heavy chain polypeptide (H1) and a first light chain polypeptide (L1), and b) a second heavy chain/light chain pair binding to a second antigen which comprises a second heavy chain polypeptide (H2) and a second light chain polypeptide (L2), wherein each H1 and H2 comprises a heavy chain variable domain (VH) and a heavy chain constant domain (CH1), and each L1 and L2 comprises a light chain variable domain (VL) and a light chain constant domain (CL); wherein the CH1 domain of H1 comprises an amino acid substitution at S183 (EU numbering), and wherein the CL domain of L1 comprises an amino acid substitution at V133 (EU numbering). In certain embodiments according to (or as applied to) any of the embodiments above, L1 is a kappa chain. In certain embodiments according to (or as applied to) any of the embodiments above, L2 is a kappa chain. In certain embodiments according to (or as applied to) any of the embodiments above, L1 and L2 are each a kappa chain.

[0009] In some embodiments according to (or as applied to) any of the embodiments above, the S183 substitution is selected from the group consisting of S183A, S183T, S183V, S183Y, S183F, S183H, S183N, S183D, S183E, S183R, and S183K, and the V133 substitution is selected from the group consisting of V133E, V133S, V133L, V133W, V133K, V133R, and V133D. In some embodiments according to (or as applied to) any of the embodiments above the amino acid at EU position S183 on the

CH1 domain of H1 is replaced with a positively charged residue, and the amino acid at V133 on the CL domain of L1 is replaced with a negatively charged residue. In some embodiments according to (or as applied to) any of the embodiments above the amino acid at EU position S183 on the CH1 domain of H1 is replaced with a negatively charged residue, and the amino acid at V133 on the CL domain of L1 is replaced with a positively charged residue. In some embodiments according to (or as applied to) any of the embodiments above the positively charged residue is selected from the group consisting of R and K. In some embodiments according to (or as applied to) any of the embodiments above the negatively charged residue is selected from the group consisting of D and E.

[0010] In certain embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H1 consists of an amino acid substitution at S183 (EU numbering), and the CL domain of L1 consists of an amino acid substitution at V133 (EU numbering).

[0011] In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H1 comprises the S183D mutation, and the CL domain of L1 comprises the V133K mutation; the CH1 domain of H1 comprises the S183E mutation, and the CL domain of L1 comprises the V133K mutation; the CH1 domain of H1 comprises the S183A mutation, and the CL domain of L1 comprises the V133E mutation; the CH1 domain of H1 comprises the S183A mutation, and the CL domain of L1 comprises the V133S mutation; the CH1 domain of H1 comprises the S183A mutation, and the CL domain of L1 comprises the V133L mutation; the CH1 domain of H1 comprises the S183A mutation, and the CL domain of L1 comprises the V133W mutation; the CH1 domain of H1 comprises the S183A mutation, and the CL domain of L1 comprises the V133K mutation; the CH1 domain of H1 comprises the S183A mutation, and the CL domain of L1 comprises the V133R mutation; the CH1 domain of H1 comprises the S183A mutation, and the CL domain of L1 comprises the V133D mutation; the CH1 domain of H1 comprises the S183T mutation, and the CL domain of L1 comprises the V133E mutation; the CH1 domain of H1 comprises the S183T mutation, and the CL domain of L1 comprises the V133S mutation; the CH1 domain of H1 comprises the S183T mutation, and the CL domain of L1 comprises the V133L mutation; the CH1 domain of H1 comprises the S183T mutation, and the CL domain of L1 comprises the V133W mutation; the CH1 domain of H1 comprises the S183T mutation, and the CL domain of L1 comprises the V133K mutation; the CH1 domain of H1 comprises the S183T mutation, and the CL domain of L1 comprises the V133R mutation; the CH1 domain of H1 comprises the S183T mutation, and the CL domain of L1 comprises the V133D mutation; the CH1 domain of H1 comprises the S183V mutation, and the CL domain of L1 comprises the V133E mutation; the CH1 domain of H1 comprises the S183V mutation, and the CL domain of L1 comprises the V133S mutation; the CH1 domain of H1 comprises the S183V mutation, and the CL domain of L1 comprises the V133L mutation; the CH1 domain of H1 comprises the S183V mutation, and the CL domain of L1 comprises the V133W mutation; the CH1 domain of H1 comprises the S183V mutation, and the CL domain of L1 comprises the

V133K mutation; the CH1 domain of H1 comprises the S183V mutation, and the CL domain of L1 comprises the V133R mutation; the CH1 domain of H1 comprises the S183V mutation, and the CL domain of L1 comprises the V133D mutation; the CH1 domain of H1 comprises the S183Y mutation, and the CL domain of L1 comprises the V133E mutation; the CH1 domain of H1 comprises the S183Y mutation, and the CL domain of L1 comprises the V133S mutation; the CH1 domain of H1 comprises the S183Y mutation, and the CL domain of L1 comprises the V133L mutation; the CH1 domain of H1 comprises the S183Y mutation, and the CL of L1 domain comprises the V133W mutation; the CH1 domain of H1 comprises the S183Y mutation, and the CL of L1 domain comprises the V133K mutation; the CH1 domain of H1 comprises the S183Y mutation, and the CL domain of L1 comprises the V133R mutation; the CH1 domain of H1 comprises the S183Y mutation, and the CL domain of L1 comprises the V133D mutation; the CH1 domain of H1 comprises the S183F mutation, and the CL domain of L1 comprises the V133E mutation; the CH1 domain of H1 comprises the S183F mutation, and the CL domain of L1 comprises the V133S mutation; the CH1 domain of H1 comprises the S183F mutation, and the CL domain of L1 comprises the V133L mutation; the CH1 domain of H1 comprises the S183F mutation, and the CL domain of L1 comprises the V133W mutation; the CH1 domain of H1 comprises the S183F mutation, and the CL domain of L1 comprises the V133K mutation; the CH1 domain of H1 comprises the S183F mutation, and the CL domain of L1 comprises the V133R mutation; the CH1 domain of H1 comprises the S183F mutation, and the CL of L1 domain comprises the V133D mutation; the CH1 domain of H1 comprises the S183H mutation, and the CL domain of L1 comprises the V133S mutation; the CH1 domain of H1 comprises the S183H mutation, and the CL domain of L1 comprises the V133L mutation; the CH1 domain of H1 comprises the S183H mutation, and the CL domain of L1 comprises the V133W mutation; the CH1 domain of H1 comprises the S183N mutation, and the CL domain of L1 comprises the V133L mutation; or the CH1 domain of H1 comprises the S183E mutation, and the CL domain of L1 comprises the V133L mutation.

[0012] In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H1 comprises the S183D mutation, and the CL domain of L1 comprises the V133K mutation; the CH1 domain of H1 comprises the S183E mutation, and the CL domain of L1 comprises the V133K mutation; the CH1 domain of H1 comprises the S183T mutation, and the CL domain of L1 comprises the V133K mutation; or the CH1 domain of H1 comprises the S183V mutation, and the CL domain of L1 comprises the V133E mutation.

[0013] In certain embodiments, the CH1 domain of H1 comprises the S183K mutation, and the CL domain of L1 comprises the V133E mutation.

[0014] In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H1 consists of the S183D mutation, and the CL domain of L1 consists of the V133K mutation; the CH1 domain of H1 consists of the S183E mutation, and the CL domain of L1 consists of the V133K

mutation; the CH1 domain of H1 consists of the S183T mutation, and the CL domain of L1 consists of the V133K mutation; or the CH1 domain of H1 consists of the S183V mutation, and the CL domain of L1 consists of the V133E mutation. In certain embodiments, the CH1 domain of H1 consists of the S183K mutation, and the CL domain of L1 consists of the V133E mutation.

[0015] In some embodiments according to (or as applied to) any of the embodiments above the CH1 domain of H2 and/or the CL domain of L2 does not comprise an amino acid substitution. In some embodiments according to (or as applied to) any of the embodiments above the CH1 domain of H2 does not comprise a substitution at S183 and the CL domain of L2 do not comprise substitution at V133.

[0016] In some embodiments according to (or as applied to) any of the embodiments above the VH domain of H1 and/or H2 comprises an amino acid substitution at position Q39 (Kabat numbering), and the VL domain of L1 and/or L2 comprises an amino acid substitution at position Q38 (Kabat numbering). In some embodiments according to (or as applied to) any of the embodiments above the amino acid at Q39 in the VH domain is replaced with a positively charged residue, and the amino acid at Q38 in the VL domain is replaced with a negatively charged residue. In some embodiments according to (or as applied to) any of the embodiments above the amino acid at Q39 in the VH domain is replaced with a negatively charged residue, and the amino acid at Q38 in the VL domain is replaced with a positively charged residue. In some embodiments according to (or as applied to) any of the embodiments above the positively charged residue is selected from the group consisting of R and K. In some embodiments according to (or as applied to) any of the embodiments above the negatively charged residue is selected from the group consisting of D and E.

[0017] In some embodiments according to (or as applied to) any of the embodiments above the amino acid at EU position S183 on the CH1 domain of H1 is replaced with a negatively charged residue, the amino acid at Q39 in the VH domain is replaced with a positively charged residue, the amino acid at V133 on the CL domain of L1 is replaced with a positively charged residue, and the amino acid at Q38 in the VL domain is replaced with a negatively charged residue (Kabat numbering).

[0018] In some embodiments according to (or as applied to) any of the embodiments above the amino acid at EU position S183 on the CH1 domain of H1 is replaced with a positively charged residue, the amino acid at Q39 in the VH domain is replaced with a negatively charged residue, the amino acid at V133 on the CL domain of L1 is replaced with a negatively charged residue, and the amino acid at Q38 in the VL domain is replaced with a positively charged residue (Kabat numbering). In some embodiments according to (or as applied to) any of the embodiments above the amino acid at EU position S183 on the CH1 domain of H1 is replaced with a positively charged residue, the amino acid at Q39 in the VH domain is replaced with a negatively charged residue, the amino acid at V133 on the CL domain of L1 is replaced with a negatively charged residue, and the amino acid at Q38 in the VL domain of L1 is

replaced with a positively charged residue (Kabat numbering). In further embodiments, the amino acid at EU position S183 on the CH1 domain of H2 is replaced with a negative charged residue, the amino acid at Q39 in the VH domain of H2 is replaced with a positively charged residue, the amino acid at V133 on the CL domain of L2 is replaced with a positively charged residue, and the amino acid at Q38 in the VL domain is replaced with a negatively charged residue (Kabat numbering).

[0019] In some embodiments according to (or as applied to) any of the embodiments above, the VH domain of H1 comprises a Q39E substitution mutation (Kabat numbering), and the VL domain of L1 comprises a Q38K substitution mutation (Kabat numbering). In some embodiments according to (or as applied to) any of the embodiments above the VH domain of H1 comprises a Q39E substitution mutation, the VL domain of L1 comprises a Q38K substitution mutation, and the VH domain of H2 comprises a Q39K substitution mutation. In some embodiments according to (or as applied to) any of the embodiments above, the VH domain of H1 comprises the Q39E substitution mutation, the VL domain of L1 comprises the Q38K substitution mutation, the VH domain of H2 comprises a Q39K substitution mutation, and the VL domain of L2 comprises a Q38E substitution mutation.

[0020] In some embodiments according to (or as applied to) any of the embodiments above, the VH domain of H1 comprises a Q39K substitution mutation (Kabat numbering), and the VL domain of L1 comprises a Q38E substitution mutation (Kabat numbering). In some embodiments according to (or as applied to) any of the embodiments above, the VH domain of H1 comprises a Q39K substitution mutation, the VL domain of L1 comprises a Q38E substitution mutation, and the VH domain of H2 comprises a Q39E substitution mutation (all Kabat numbering). In some embodiments according to (or as applied to) any of the embodiments above, the VH domain of H1 comprises a Q39K substitution mutation, the VH domain of H2 comprises a Q39E substitution mutation, and the VL domain of L2 comprises a Q38K substitution mutation (all Kabat numbering). In some embodiments according to (or as applied to) any of the embodiments above, the VH domain of H1 comprises the Q39K substitution mutation, the VL domain of L1 comprises the Q38E substitution mutation, the VH domain of H2 comprises a Q39E substitution mutation, and the VL domain of L2 comprises a Q38K substitution mutation (all Kabat numbering).

[0021] In some embodiments according to (or as applied to) any of the embodiments above, the interaction between the two substituted amino acids is via hydrogen bonds. In some embodiments according to (or as applied to) any of the embodiments above, the interaction between the two substituted amino acids is via electrostatic interaction.

[0022] In some embodiments according to (or as applied to) any of the embodiments above, the VH domain of H1 comprises a Q39K substitution mutation and the CH1 domain of H1 comprises the S183E substitution mutation, the VL domain of L1 comprises a Q38E substitution mutation and the CL domain

of L1 comprises the V133K mutation, the VH domain of H2 comprises the Q39E substitution mutation, and the VL domain of L2 comprises the Q38K substitution mutation.

[0023] In some embodiments according to (or as applied to) any of the embodiments above, the VH domain of H1 comprises a Q39K substitution mutation and the CH1 domain of H1 comprises the S183T substitution mutation, the VL domain of L1 comprises a Q38E substitution mutation and the CL domain of L1 comprises the V133K mutation, the VH domain of H2 comprises the Q39E substitution mutation, and the VL domain of L2 comprises the Q38K substitution mutation.

[0024] In some embodiments according to (or as applied to) any of the embodiments above, the VH domain of H1 comprises a Q39K substitution mutation and the CH1 domain of H1 comprises the S183Y substitution mutation, the VL domain of L1 comprises a Q38E substitution mutation and the CL domain of L1 comprises the V133K mutation, the VH domain of H2 comprises the Q39E substitution mutation, and the VL domain of L2 comprises the Q38K substitution mutation.

[0025] In some embodiments according to (or as applied to) any of the embodiments above, the VH domain of H1 comprises a Q39K substitution mutation and the CH1 domain of H1 comprises the S183F substitution mutation, the VL domain of L1 comprises a Q38E substitution mutation and the CL domain of L1 comprises the V133K mutation, the VH domain of H2 comprises the Q39E substitution mutation, and the VL domain of L2 comprises the Q38K substitution mutation.

[0026] In some embodiments according to (or as applied to) any of the embodiments above, the VH domain of H1 comprises a Q39E substitution mutation and the CH1 domain of H1 comprises the S183E substitution mutation, the VL domain of L1 comprises a Q38K substitution mutation and the CL domain of L1 comprises the V133K mutation, the VH domain of H2 comprises the Q39K substitution mutation, and the VL domain of L2 comprises the Q38E substitution mutation.

[0027] In some embodiments according to (or as applied to) any of the embodiments above, the VH domain of H1 comprises a Q39K substitution mutation, the VL domain of L1 comprises a Q38E substitution mutation, the VH domain of H2 comprises the Q39E substitution mutation and the CH1 domain of H2 comprises the S183E substitution mutation, and the VL domain of L2 comprises the Q38K substitution mutation and the CL domain of L1 comprises the V133K mutation.

[0028] In some embodiments according to (or as applied to) any of the embodiments above, the VH domain of H1 comprises the Q39E substitution mutation and the CH1 domain of H1 comprises the S183K substitution mutation, the VL domain of L1 comprises the Q38K substitution mutation and the CL domain of L1 comprises the V133E substitution mutation, the VH domain of H2 comprises a Q39K substitution mutation and the CH1 domain of H2 comprises the S183E substitution mutation, and the VL

domain of L2 comprises a Q38E substitution mutation and the CL domain of L2 comprises the V133K mutation.

[0029] In some embodiments according to (or as applied to) any of the embodiments above, the VH domain of H1 comprises the Q39E substitution mutation and the CH1 domain of H1 comprises the S183E substitution mutation, the VL domain of L1 comprises the Q38K substitution mutation and the CL domain of L1 comprises the V133K substitution mutation, the VH domain of H2 comprises a Q39K substitution mutation and the CH1 domain of H2 comprises the S183K substitution mutation, and the VL domain of L2 comprises a Q38E substitution mutation and the CL domain of L2 comprises the V133E mutation.

[0030] In some embodiments according to (or as applied to) any of the embodiments above, the VH domain of H1 comprises the Q39E substitution mutation and the CH1 domain of H1 comprises the S183E substitution mutation, the VL domain of L1 comprises the Q38K substitution mutation and the CL domain of L1 comprises the V133K substitution mutation, the VH domain of H2 comprises a Q39K substitution mutation and the CH1 domain of H2 comprises the S183K substitution mutation, and the VL domain of L2 comprises a Q38E substitution mutation and the CL domain of L2 comprises the V133E mutation.

[0031] In some embodiments according to (or as applied to) any of the embodiments above, the VH domain of H1 comprises the Q39K substitution mutation and the CH1 domain of H1 comprises the S183E substitution mutation, the VL domain of L1 comprises the Q38K substitution mutation and the CL domain of L1 comprises the V133E substitution mutation, the VH domain of H2 comprises a Q39E substitution mutation and the CH1 domain of H2 comprises the S183E substitution mutation, and the VL domain of L2 comprises a Q38K substitution mutation and the CL domain of L2 comprises the V133K mutation.

[0032] In some embodiments according to (or as applied to) any of the embodiments above, the VH domain of H1 comprises the Q39K substitution mutation and the CH1 domain of H1 comprises the S183E substitution mutation, the VL domain of L1 comprises the Q38E substitution mutation and the CL domain of L1 comprises the V133K substitution mutation, the VH domain of H2 comprises a Q39E substitution mutation and the CH1 domain of H2 comprises the S183K substitution mutation, and the VL domain of L2 comprises a Q38K substitution mutation and the CL domain of L2 comprises the V133E mutation.

[0033] In some embodiments according to (or as applied to) any of the embodiments above, the VH domain of H1 comprises the Q39K substitution mutation, the CH1 domain of H1 comprises the S183K substitution mutation, the VL domain of L1 comprises the Q38E substitution mutation, the CL domain of

L1 comprises the V133E substitution mutation, the VH domain of H2 comprises a Q39E substitution mutation, the CH1 domain of H2 comprises the S183E substitution mutation, the VL domain of L2 comprises a Q38K substitution mutation, and the CL domain of L2 comprises the V133K mutation.

[0034] In some embodiments according to (or as applied to) any of the embodiments above, each of H1 and/or H2 comprises an Fc region comprising a CH2 and a CH3 domain. In some embodiments according to (or as applied to) any of the embodiments above, the Fc region of H1 and/or H2 is human IgG1, human IgG2 or human IgG4 Fc. In some embodiments according to (or as applied to) any of the embodiments above, the Fc region of H1 and/or H2 is mouse IgG1, mouse IgG2 or mouse IgG4 Fc. In some embodiments according to (or as applied to) any of the embodiments above, the CH3 domains of H1 and H2 each meet at an interface, and each of the CH3 domains comprises an amino acid substitution such that the Fc region of H1 preferentially pairs with that of H2 as compared to H1. In some embodiments according to (or as applied to) any of the embodiments above, the amino acid substitutions in the CH3 domains result in greater electrostatic complementarity. In some embodiments according to (or as applied to) any of the embodiments above, the amino acid substitutions in the CH3 domains result in greater steric complementarity. In some embodiments according to (or as applied to) any of the embodiments above, the CH3 domain of H1 is altered, so that within the CH3/CH3 interface, one or more amino acid residues are replaced with one or more amino acid residues having a larger side chain volume, thereby generating a protuberance on the surface of the CH3 domain of H1 that interacts with the CH3 domain of H2 and the CH3 domain of H2 is altered so that within the CH3/CH3 interface one or more amino acid residues are replaced with amino acid residues having a smaller side chain volume, thereby generating a cavity on the surface of the CH3 domain of H2 that interacts with the CH3 domain of H1. In some embodiments according to (or as applied to) any of the embodiments above, the CH3 domain of H2 is altered, so that within the CH3/CH3 interface, one or more amino acid residues are replaced with one or more amino acid residues having a larger side chain volume, thereby generating a protuberance on the surface of the CH3 domain of H2 that interacts with the CH3 domain of H1 and the CH3 domain of H1 is altered so that within the CH3/CH3 interface, one or more amino acid residues are replaced with amino acid residues having a smaller side chain volume, thereby generating a cavity on the surface of the CH3 domain of H1 that interacts with the CH3 domain of H2. In some embodiments according to (or as applied to) any of the embodiments above, the protuberance is a knob mutation. In some embodiments according to (or as applied to) any of the embodiments above, the alteration to generate the knob is T366W (EU numbering). In some embodiments according to (or as applied to) any of the embodiments above, the cavity is a hole mutation (EU numbering). In some embodiments according to (or as applied to) any of the embodiments above, the alterations to generate the hole are at least one of T366S, L368A, and Y407V.

[0035] In some embodiments according to (or as applied to) any of the embodiments above, the knob comprises T366W (EU numbering). In some embodiments according to (or as applied to) any of the embodiments above, the hole mutation comprises at least one, at least two, or all three of T366S, L368A, and Y407V.

[0036] In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H1 is further altered so that within the CH1/CL interface, two or more amino acid residues are replaced with an equivalent number of amino acid residues having a larger side chain volume, thereby generating a protuberance on the surface of the CH1 domain of H1 that interacts with the CL domain of L1, and the CL domain of L1 is further altered so that within the CH1/CL interface, two or more amino acid residues are replaced with an equivalent number of amino acid residues having a smaller side chain volume, thereby generating a cavity on the surface of the CL domain of L1 that interacts with the CH1 domain of H1.

[0037] In some embodiments according to (or as applied to) any of the embodiments above, the CL domain is further altered so that within the CH1/CL interface, two or more amino acid residues are replaced with an equivalent number of amino acid residues having a larger side chain volume, thereby generating a protuberance on the surface of the CL domain that interacts with the CH1 domain of H1, and the CH1 domain of H1 is further altered so that within the CH1/CL interface, two or more amino acid residues are replaced with an equivalent number of amino acid residues having a smaller side chain volume, thereby generating a cavity on the surface of the CH1 domain of H1 that interacts with the CL domain.

[0038] Also provided herein is a multispecific antigen binding protein, or an antigen-binding fragment thereof, comprising: a) a first heavy chain/light chain pair comprising a first heavy chain polypeptide (H1) and a first light chain polypeptide (L1), and b) a second heavy chain/light chain pair comprising a second heavy chain polypeptide (H2) and a second light chain polypeptide (L2), each H1 and H2 comprises a heavy chain variable domain (VH) and a heavy chain constant domain (CH1), and each L1 and L2 comprises a light chain variable domain (VL) and a light chain constant domain (CL); the CH1 domain of H1 comprises an amino acid substitution at F170 (EU numbering), and the CL domain of L1 comprises an amino acid substitution at S176 (EU numbering). In certain embodiments according to (or as applied to) any of the embodiments above, L1 is a kappa chain. In certain embodiments according to (or as applied to) any of the embodiments above, L2 is a kappa chain. In certain embodiments according to (or as applied to) any of the embodiments above, L1 and L2 are each a kappa chain.

[0039] In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H1 further comprises one or more amino acid substitutions at a position selected from the group consisting of: A141, S181, S183, and V185 (EU numbering). In some embodiments according to

(or as applied to) any of the embodiments above, the CL domain of L1 further comprises one or more amino acid substitutions at a position selected from the group consisting of F116, S131, V133, L135, S162, S174, and T178 (EU numbering). In some embodiments according to (or as applied to) any of the embodiments above, the amino acid substitutions result in steric complementarity.

[0040] In some embodiments according to (or as applied to) any of the embodiments above, the one or more amino acid substitutions at a position selected from the group consisting of A141, F170, S181, S183, and V185 (EU numbering) of CH1 and/or the one or more amino acid substitutions at a position selected from the group consisting of F116, S131, V133, L135, S162, S174, S176, and T178 (EU numbering) of CL are not substituted with charged amino acid residues.

[0041] In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H1 comprises an amino acid substitution selected from the group consisting of F170S and F170A, and the CL domain of L1 comprises an amino acid substitution of S176F. In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H1 comprises the F170S mutation, and the CL domain of L1 comprises the S176F mutation; or the CH1 domain of H1 comprises the F170A mutation, and the CL domain of L1 comprises the S176F mutation. In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H1 comprises the F170S mutation, and the CL domain of L1 comprises the S176F mutation.

[0042] In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H1 comprises the A141I, F170S, S181M, S183V, and V185A mutations, and the CL domain of L1 comprises the F116A, V133I, L135V, S162M, S174A, S176F, and T178V mutations; the CH1 domain of H1 comprises the A141I, F170S, S181M, S183A, and V185A mutations and the CL domain of L1 comprises the F116A, S131D, L135V, S162A, S174A, S176F, and T178I mutations; the CH1 domain of H1 comprises the A141I, F170S, S181M, S183A, and V185A mutations and the CL domain of L1 comprises the F116A, L135V, S174A, S176F, and T178V mutations; or the CH1 domain of H1 comprises the A141I, F170A, S181M, S183V, and V185A mutations and the CL domain of L1 comprises the F116A, L135V, S162M, S174A, S176F, and T178V mutations. In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H1 comprises A141I, F170S, S181M, S183A, and V185A mutations and the CL domain of L1 comprises F116A, L135V, S174A, S176F, and T178V mutations.

[0043] In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H1 comprises A141I, F170S, S181M, S183A, and V185A mutations and the CL domain of L1 comprises F116A, L135V, S174A, S176F, and T178V mutations.

In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H1 comprises A141I, F170S, S181M, S183A, and V185A mutations, the CL domain of L1 comprises F116A, L135V, S174A, S176F, and T178V mutations, the CH1 domain of H2 comprises an amino acid substitution mutation at S183 (EU numbering) and the CL domain of L2 comprises an amino acid substitution mutation V133K (EU numbering). In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H1 comprises A141I, F170S, S181M, S183A, and V185A mutations, the CL domain of L1 comprises F116A, L135V, S174A, S176F, and T178V mutations, the CH1 domain of H2 comprises an amino acid substitution mutation at S183 (EU numbering) and the CL domain of L2 comprises an amino acid substitution mutation V133 (EU numbering). In certain embodiments according to (or as applied to) any of the embodiments above, the amino acid at position S183 in the CH1 domain of H2 is replaced with a positively charged amino acid, and the amino acid at position V133 in the CL domain of L2 is replaced with a negatively charged amino acid. In certain embodiments according to (or as applied to) any of the embodiments above, the amino acid at position S183 in the CH1 domain of H2 is replaced with a negatively charged amino acid, and wherein the amino acid at position V133 in the CL domain of L2 is replaced with a positively charged amino acid.

[0044] In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H1 comprises A141I, F170S, S181M, S183A, and V185A mutations (EU numbering), the VH domain of H1 comprises a Q39E mutation (Kabat numbering) and the CL domain of L1 comprises F116A, L135V, S174A, S176F, and T178V mutations (EU numbering), the VL domain of L1 comprises a Q38K mutation (Kabat numbering), the VH domain of H2 comprises a Q39K mutation (Kabat numbering), and the VL domain of L2 comprises a Q38E mutation (Kabat numbering).

[0045] In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H1 comprises A141I, F170S, S181M, S183A, and V185A mutations (EU numbering) and the CL domain of L1 comprises F116A, L135V, S174A, S176F, and T178V mutations (EU numbering), the CH1 domain of H2 comprises an S183E mutation (EU numbering) and the CL domain of L2 comprises a V133K mutation (EU numbering).

[0046] In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H1 comprises A141I, F170S, S181M, S183A, and V185A mutations (EU numbering), the VH domain of H1 comprises a Q39E mutation (Kabat numbering) and the CL domain of L1 comprises F116A, L135V, S174A, S176F, and T178V mutations (EU numbering), the VL domain of L1 comprises a Q38K mutation (Kabat numbering), the CH1 domain of H2 comprises an S183E mutation (EU numbering), the VH domain of H2 comprises a Q39K mutation (Kabat numbering), the CL domain of L2 comprises a V133K mutation (EU numbering), and the VL domain of L2 comprises a Q38E mutation (Kabat numbering).

[0047] In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H1 comprises A141I, F170S, S181M, S183A, and V185A mutations (EU numbering), the VH domain of H1 comprises a Q39K mutation (Kabat numbering), the CL domain of L1 comprises F116A, L135V, S174A, S176F, and T178V mutations, the VL domain of L1 comprises a Q38E mutation (Kabat numbering), the VH domain of H2 comprises a Q39E mutation (Kabat numbering), and the VL domain of L2 comprises a Q38K mutation (Kabat numbering).

[0048] In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H1 comprises A141I, F170S, S181M, S183A, and V185A mutations, the CL domain of L1 comprises F116A, L135V, S174A, S176F, and T178V mutations, the CH1 domain of H2 comprises an S183K mutation (EU numbering), and the CL domain of L2 comprises a V133K mutation (EU numbering).

[0049] In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H1 comprises A141I, F170S, S181M, S183A, and V185A mutations (EU numbering), the VH domain of H1 comprises a Q39K mutation (Kabat numbering), the CL domain of L1 comprises F116A, L135V, S174A, S176F, and T178V mutations, the VL domain of L1 comprises a Q38E mutation (Kabat numbering), the CH1 domain of H2 comprises an S183K mutation (EU numbering), the VH domain of H2 comprises a Q39E mutation (Kabat numbering), the CL domain of L2 comprises a V133K mutation (EU numbering), and the VL domain of L2 comprises a Q38K mutation (Kabat numbering).

[0050] In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H1 comprises F170S, S181M, S183A, and V185A mutations and the CL domain of L1 comprises L135V, S174A, S176F, and T178V mutations; the CH1 domain of H1 comprises A141I, F170S, S183A, and V185A mutations and the CL domain of L1 comprises F116A, S174A, S176F, and T178V mutations; the CH1 domain of H1 comprises A141I, F170S, S181M, and V185A mutations and the CL domain of L1 comprises F116A, L135V, S176F, and T178V mutations; the CH1 domain of H1 comprises A141I, F170S, S181M, and S183A mutations and the CL domain of L1 comprises F116A, L135V, S174A, S176F, and T178V mutations; the CH1 domain of H1 comprises F170S, S183A, and V185A mutations and the CL domain of L1 comprises F116A, S176F, and T178V mutations; the CH1 domain of H1 comprises F170S, S181M, and V185A mutations and the CL domain of L1 comprises F116A, L135V, and S176F mutations; the CH1 domain of H1 comprises F170S, S181M, and S183A mutations and the CL domain of L1 comprises F116A, L135V, and S176F mutations; the CH1 domain of H1 comprises A141I, F170S, and V185A mutations and the CL domain of L1 comprises F116A and S176F mutations; the CH1 domain of H1 comprises A141I, F170S, and S183A mutations and the CL domain of L1 comprises F116A and S176F mutations; the CH1 domain of H1 comprises A141I, F170S, and S181M mutations and the CL domain of L1 comprises F116A, L135V, S174A, S176F, and T178V mutations; the CH1 domain of H1 comprises F170S and V185A mutations and the CL domain of L1

comprises F116A and S176F mutations; the CH1 domain of H1 comprises A141I and F170S mutations and the CL domain of L1 comprises F116A, L135V, S174A, S176F, and T178V mutations; the CH1 domain of H1 comprises A141I and F170S mutations and the CL domain of L1 comprises F116A, L135V, S176F, and T178V mutations; the CH1 domain of H1 comprises A141I and F170S mutations and the CL domain of L1 comprises F116A, L135V, S174A, S176F, and T178V mutations; the CH1 domain of H1 comprises A141I and F170S mutations and the CL domain of L1 comprises F116A, L135V, and S176F mutations; the CH1 domain of H1 comprises A141I and F170S mutations and the CL domain of L1 comprises F116A, L135V, and S176F mutations; the CH1 domain of H1 comprises the F170S mutation and the CL domain of L1 comprises F116A, L135V, S174A, S176F, and T178V mutations; the CH1 domain of H1 comprises the F170S mutation and the CL domain of L1 comprises F116A, L135V, S176F, and T178V mutations; the CH1 domain of H1 comprises the F170S mutation and the CL domain of L1 comprises F116A, L135V, S174A, S176F, and T178V mutations; the CH1 domain of H1 comprises the F170S mutation and the CL domain of L1 comprises F116A, L135V, and S176F mutations; or the CH1 domain of H1 comprises the F170S mutation and the CL domain of L1 comprises F116A, L135V, and S176F mutations.

[0051] In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H1 comprises the CH1 domain of H1 comprises A141I, F170S, S181M, and S183A mutations and the CL domain of L1 comprises F116A, L135V, S174A, and S176F mutations; the CH1 domain of H1 comprises F170S, S181M, and S183A mutations and the CL domain of L1 comprises F116A, and S176F mutations; the CH1 domain of H1 comprises A141I and F170S mutations and the CL domain of L1 comprises F116A, L135V, S174A, and S176F mutations; the CH1 domain of H1 comprises A141I and F170S mutations and the CL domain of L1 comprises F116A, and S176F mutations; the CH1 domain of H1 comprises the F170S mutation and the CL domain of L1 comprises F116A, L135V, S174A, and S176F mutations; or the CH1 domain of H1 comprises the F170S mutation and the CL domain of L1 comprises F116A, and S176F mutations.

[0052] In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H1 comprises A141I, F170S, and S181M mutations and the CL domain of L1 comprises F116A, L135V, S174A, S176F, and T178V mutations. In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H1 comprises A141I and F170S mutations and the CL domain of L1 comprises F116A, L135V, S174A, S176F, and T178V mutations. In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H1 comprises the F170S mutation and the CL domain of L1 comprises F116A, L135V, S174A, S176F, and T178V mutations.

[0053] In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H1 comprises A141I and F170S mutations and the CL domain of L1 comprises F116A, L135V, S174A, and S176F mutations.

[0054] Provided herein is an antigen binding protein, or an antigen-binding fragment thereof, comprising: a) a first heavy chain/light chain pair comprising a first heavy chain sequence (H1) and a first light chain sequence (L1), and b) a second heavy chain/light chain pair comprising a second heavy chain sequence (H2) and a second light chain sequence (L2), each H1 and H2 comprises a heavy chain variable domain (VH) and a heavy chain constant domain (CH1), and each L1 and L2 comprises a light chain variable domain (VL) and a light chain constant domain (CL); the CH1 domain of H1 comprises amino acid substitutions at L128 and V185, (EU numbering) and the CL domain of C1 comprises a amino acid substitutions at F118 and L135 (EU numbering). In certain embodiments according to (or as applied to) any of the embodiments above, L1 is a kappa chain. In certain embodiments according to (or as applied to) any of the embodiments above, L2 is a kappa chain. In certain embodiments according to (or as applied to) any of the embodiments above, L1 and L2 are each a kappa chain.

[0055] Also provided herein is an antigen binding protein, or an antigen-binding fragment thereof, comprising: a) a first heavy chain/light chain pair comprising a first heavy chain sequence (H1) and a first light chain sequence (L1), and b) a second heavy chain/light chain pair comprising a second heavy chain sequence (H2) and a second light chain sequence (L2), each H1 and H2 comprises a heavy chain variable domain (VH) and a heavy chain constant domain (CH1), and each L1 and L2 comprises a light chain variable domain (VL) and a light chain constant domain (CL); the CH1 domain of H1 comprises an amino acid substitutions at L128, (EU numbering) and the CL domain of C1 comprises a amino acid substitutions at F118 and L135 (EU numbering). In certain embodiments according to (or as applied to) any of the embodiments above, L1 is a kappa chain. In certain embodiments according to (or as applied to) any of the embodiments above, L2 is a kappa chain. In certain embodiments according to (or as applied to) any of the embodiments above, L1 and L2 are each a kappa chain. In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H1 further comprises an amino acid substitution at V185 (EU numbering).

[0056] In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H1 further comprises one or more amino acid substitutions at a position selected from the group consisting of: A141, F170, S181, and S183 (EU numbering). In some embodiments according to (or as applied to) any of the embodiments above, the CL domain of L1 further comprises one or more amino acid substitutions at a position selected from the group consisting of S131, V133, S162, T164, S176 and T178 (EU numbering). In some embodiments according to (or as applied to) any of the embodiments above, the amino acid substitutions result in greater steric complementarity.

[0057] In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H1 comprises an amino acid substitution at a position selected from the group consisting of A141, F170, S181, and S183, and the CL domain comprises an amino acid substitution at a position selected from the group consisting of S131, V133, S162, T164, S176 and T178.

[0058] In some embodiments according to (or as applied to) any of the embodiments above, the one or more amino acid substitutions at a position selected from the group consisting of L128 A141, F170, S181, S183, V185 (EU numbering) of CH1 and/or the one or more amino acid substitutions at a position selected from the group consisting of F118, S131, V133, and L135 S162, T164, S176 and T178 (EU numbering) of CL are not substituted with charged amino acid residues.

[0059] In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H1 comprises L128F, A141M, F170M, S181I and S183A mutations and the CL domain comprises F118V, S131T, V133A, L135Y, S162A, T164S, S176M, and T178L mutations; the CH1 domain of H1 comprises L128F, A141M, F170Y, S181I, S183A, and V185A mutations and the CL domain comprises F118V, S131T, V133A, L135F, S162A, S176A, and T178L mutations; the CH1 domain of H1 comprises L128F, A141T, F170M, S181T, S183A, and V185L mutations and the CL domain comprises F118V, S131T, V133A, L135F, S162A, T164S, S176T, and T178L mutations; or the CH1 domain of H1 comprises L128F, A141M, F170M, S181T, and S183A, mutations and the CL domain comprises F118V, S131T, V133A, L135F, S162M, T164S, S176M, and T178L mutations. In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H1 comprises the L128F, A141M, F170Y, S181I, S183A, and V185A mutations, and the CL domain comprises the F118V, S131T, V133A, L135F, S162A, S176A, and T178L mutations.

[0060] In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H2 comprises S183E mutation, and the CL domain of L2 comprises V133K mutation. In some embodiments according to (or as applied to) any of the embodiments above, the VH domain of H1 comprises a Q39E mutation, the VL domain of L1 comprises a Q38K mutation, the VH domain of H2 comprises a Q39K mutation and the VL domain of L2 comprises a Q38E mutation.

[0061] In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H2 comprises S183K mutation, and the CL domain of L2 comprises V133E mutation. In some embodiments according to (or as applied to) any of the embodiments above, the VH domain of H1 comprises a Q39K mutation, the VL domain of L1 comprises a Q38E mutation, the VH domain of H2 comprises a Q39E mutation and the VL domain of L2 comprises a Q38K mutation.

[0062] In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H2 comprises an amino acid substitution at EU position S183, and the CL domain of L2

comprises an amino acid substitution at EU position V133. In some embodiments according to (or as applied to) any of the embodiments above, the interaction between the amino acid substitution at EU position S183 on the CH1 domain of H2 and the amino acid substitution at EU position V133 on the CL domain of L2 is via electrostatic interaction. In some embodiments according to (or as applied to) any of the embodiments above, the amino acid at EU position S183 on the CH1 domain of H2 is replaced with a positively charged residue, and the amino acid at EU position V133 on the CL domain of L2 is replaced with a negatively charged residue. In some embodiments according to (or as applied to) any of the embodiments above, the amino acid at EU position S183 on the CH1 domain of H2 is replaced with a negatively charged residue, and the amino acid at EU position V133 on the CL domain of L2 is replaced with a positively charged residue. In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H2 comprises an amino acid substitution at a position selected from the group consisting of EU position S183A, S183T, S183V, S183Y, S183F, S183H, S183N, S183D, S183E, S183R, and S183K, and the CL domain of L2 comprises an amino acid substitution at a position selected from the group consisting of EU position V133E, V133S, V133L, V133W, V133K, V133R, and V133D.

[0063] In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H2 comprises the EU position S183D mutation, and the CL domain of L2 comprises the EU position V133K mutation; the CH1 domain of H2 comprises the EU position S183E mutation, and the CL domain of L2 comprises the EU position V133K mutation; the CH1 domain of H2 comprises the EU position S183A mutation, and the CL domain of L2 comprises the EU position V133E mutation; the CH1 domain of H2 comprises the EU position S183A mutation, and the CL domain of L2 comprises the EU position V133S mutation; the CH1 domain of H2 comprises the EU position S183A mutation, and the CL domain of L2 comprises the EU position V133L mutation; the CH1 domain of H2 comprises the EU position S183A mutation, and the CL domain of L2 comprises the EU position V133W mutation; the CH1 domain of H2 comprises the EU position S183A mutation, and the CL domain of L2 comprises the EU position V133K mutation; the CH1 domain of H2 comprises the EU position S183A mutation, and the CL domain of L2 comprises the EU position V133R mutation; the CH1 domain of H2 comprises the EU position S183A mutation, and the CL domain of L2 comprises the EU position V133D mutation; the CH1 domain of H2 comprises the EU position S183T mutation, and the CL domain of L2 comprises the EU position V133E mutation; the CH1 domain of H2 comprises the EU position S183T mutation, and the CL domain of L2 comprises the EU position V133S mutation; the CH1 domain of H2 comprises the EU position S183T mutation, and the CL domain of L2 comprises the EU position V133L mutation; the CH1 domain of H2 comprises the EU position S183T mutation, and the CL domain of L2 comprises the EU position V133W mutation; the CH1 domain of H2 comprises the EU position S183T mutation, and the CL domain of L2 comprises the EU position V133K mutation; the CH1 domain of H2 comprises the EU position S183T mutation, and the CL domain of L2 comprises the EU position V133R mutation; the CH1

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comprises the EU position S183D substitution, and the CL domain of L2 comprises EU position V133K substitution. In some embodiments according to (or as applied to) any of the embodiments above, the CH1 domain of H2 and the VL domain of L2 do not comprise an amino acid substitution.

[0064] In some embodiments according to (or as applied to) any of the embodiments above, the VH domain of H1 comprises an amino acid substitution at Kabat position Q39, and the VL domain of V1 comprises an amino acid substitution at Kabat position Q38. In some embodiments according to (or as applied to) any of the embodiments above, the amino acid at Kabat position Q39 on the VH domain of H1 is replaced with a positively charged residue, and the amino acid at Kabat position Q38 on the VL domain of L1 is replaced with a negatively charged residue. In some embodiments according to (or as applied to) any of the embodiments above, the amino acid at Kabat position Q39 on the VH domain of H1 is replaced with a negatively charged residue, and the amino acid at Kabat position Q38 on the VL domain of L1 is replaced with a positively charged residue. In some embodiments according to (or as applied to) any of the embodiments above, the positively charged residue is selected from the group consisting of R and K. In some embodiments according to (or as applied to) any of the embodiments above, the negatively charged residue is selected from the group consisting of D and E. In some embodiments according to (or as applied to) any of the embodiments above, the VH domain of H1 comprises a Kabat position Q39E substitution mutation, the VL domain of L1 comprises a Kabat position Q38K substitution, the VH domain of H2 comprises a Kabat position Q39K substitution mutation, and the VL domain of L2 comprises a Kabat position Q38E substitution mutation.

[0065] In some embodiments according to (or as applied to) any of the embodiments above, the VH domain of H1 comprises a Kabat position Q39E substitution mutation, the VL domain of L1 comprises a Kabat position Q38K substitution. In some embodiments according to (or as applied to) any of the embodiments above, the VH domain of H1 comprises a Kabat position Q39E substitution mutation, the VL domain of L1 comprises a Kabat position Q38K substitution, and the VH domain of H2 comprises a Kabat position Q39K substitution mutation. In some embodiments according to (or as applied to) any of the embodiments above, the VH domain of H1 comprises a Kabat position Q39E substitution mutation, the VL domain of L1 comprises a Kabat position Q38K substitution, the VH domain of H2 comprises a Kabat position Q39K substitution mutation, and the VL domain of L2 comprises a Kabat position Q38E substitution mutation.

[0066] In some embodiments according to (or as applied to) any of the embodiments above, the VH domain of H1 comprises a Kabat position Q39K substitution mutation, the VL domain of L1 comprises a Kabat position Q38E substitution. In some embodiments according to (or as applied to) any of the embodiments above, the VH domain of H1 comprises a Kabat position Q39K substitution mutation, the VL domain of L1 comprises a Kabat position Q38E substitution, and the VH domain of H2 comprises a Kabat position Q39E substitution mutation. In some embodiments according to (or as applied to) any of

the embodiments above, the VH domain of H1 comprises a Kabat position Q39K substitution mutation, the VL domain of L1 comprises a Kabat position Q38E substitution, the VH domain of H2 comprises a Kabat position Q39E substitution mutation, and the VL domain of L2 comprises a Kabat position Q38K substitution mutation.

[0067] In some embodiments according to (or as applied to) any of the embodiments above, H1 preferentially pairs with L1 as compared to L2, and H2 preferentially pairs with L2 as compared to L1.

[0068] In some embodiments according to (or as applied to) any of the embodiments above, H1 comprises an Fc region comprising a CH2 and a CH3 domain. In some embodiments according to (or as applied to) any of the embodiments above, the Fc region of H1 and/or H2 is IgG1, IgG2 or IgG4 Fc.

[0069] In some embodiments according to (or as applied to) any of the embodiments above, the Fc region of H1 and/or H2 is mouse IgG1, mouse IgG2 or mouse IgG4 Fc.

[0070] In some embodiments according to (or as applied to) any of the embodiments above, the CH3 domains of H1 and H2 each meet at an interface, and each of the CH3 domains comprises an amino acid substitution such that the Fc region of H1 preferentially pairs with that of H2 as compared to H1. In some embodiments according to (or as applied to) any of the embodiments above, the amino acid substitutions in the CH3 domains result in greater electrostatic complementarity. In some embodiments according to (or as applied to) any of the embodiments above, the amino acid substitutions in the CH3 domains result in greater steric complementarity.

[0071] In some embodiments according to (or as applied to) any of the embodiments above, the CH3 domain of H1 is altered, so that within the CH3/CH3 interface, one or more amino acid residues are replaced with one or more amino acid residues having a larger side chain volume, thereby generating a protuberance on the surface of the CH3 domain of H1 that interacts with the CH3 domain of H2; and the CH3 domain of H2 is altered so that within the CH3/CH3 interface one or more amino acid residues are replaced with amino acid residues having a smaller side chain volume, thereby generating a cavity within on the surface of the CH3 domain of H2 that interacts with the CH3 domain of H1.

[0072] In some embodiments according to (or as applied to) any of the embodiments above, the CH3 domain of H2 is altered, so that within the CH3/CH3 interface, one or more amino acid residues are replaced with one or more amino acid residues having a larger side chain volume, thereby generating a protuberance on the surface of the CH3 domain of H2 that interacts with the CH3 domain of H1; and the CH3 domain of H1 is altered so that within the CH3/CH3 interface, one or more amino acid residues are replaced with amino acid residues having a smaller side chain volume, thereby generating a cavity on the surface of the CH3 domain of H1 that interacts with the CH3 domain of H2.

[0073] In some embodiments according to (or as applied to) any of the embodiments above, the protuberance is a knob. In some embodiments according to (or as applied to) any of the embodiments above, the alteration to generate the knob is T366W. In some embodiments according to (or as applied to) any of the embodiments above, the cavity is a hole. In some embodiments according to (or as applied to) any of the embodiments above, the alterations to generate the hole are at least one of T366S, L368A, and Y407V.

[0074] In some embodiments according to (or as applied to) any of the embodiments above, the knob comprises T366W (EU numbering). In some embodiments according to (or as applied to) any of the embodiments above, the hole mutation comprises at least one, at least two, or all three of T366S, L368A, and Y407V.

[0075] In some embodiments according to (or as applied to) any of the embodiments above, H1 preferentially pairs with L1 as compared to L2, and wherein H2 preferentially pairs with L2 as compared to L1.

[0076] In some embodiments according to (or as applied to) any of the embodiments above, the first antigen and the second antigen are the same. In some embodiments according to (or as applied to) any of the embodiments above, the first heavy chain/light chain pair and the second heavy chain/light chain pair each bind to a different epitope on the same antigen. In some embodiments according to (or as applied to) any of the embodiments above, the first antigen and the second antigen are different.

[0077] Also provided herein is a pharmaceutical composition comprising the multispecific antigen binding protein of any of the embodiments above, and a pharmaceutically acceptable carrier. Further provided herein is a method of treating a disease in an individual, comprising administering to the individual an effective amount of the pharmaceutical composition according to (or as applied to) any of the embodiments above.

[0078] Isolated nucleic acids(s) encoding at least one polypeptide sequence of the multispecific antigen binding protein of any one of the embodiments above are provided. Also provided is a vector comprising the nucleic acid(s) according to (or as applied to) any of the embodiments above. Also provided is an isolated host cell comprising the nucleic acid(s) according to (or as applied to) any of the embodiments above, or the vector according to (or as applied to) any of the embodiments above.

[0079] In some embodiments according to (or as applied to) any of the embodiments above, the host cell is a prokaryotic host cell, and E. coli cell, a eukaryotic host cell, a yeast cell, a mammalian cell, or a CHO cell.

[0080] Provided herein is a method of producing the multispecific antigen binding protein according to (or as applied to) any of the embodiments above, comprising: (a) obtaining the H1, H2, L1, and L2 polypeptides; (b) allowing H1 to pair preferentially with L1 as compared to L2, and H2 to pair preferentially with L2 as compared to L1 so as to form the multispecific antigen binding protein.

[0081] Also provided is a method of producing the multispecific antigen binding protein according to (or as applied to) any of the embodiments above, comprising: (a) introducing a set of polynucleotides encoding H1, L1, H2, and L2 into a host cell; and (b) culturing the host cell to produce the multispecific antigen binding protein. In some embodiments according to (or as applied to) any of the embodiments above, the set of polynucleotides encoding H1, L1, H2, and L2 is introduced into the same host cell. In some embodiments according to (or as applied to) any of the embodiments above, the set of polynucleotides encoding H1, L1, H2, and L2 is introduced into a cell line. In some embodiments according to (or as applied to) any of the embodiments above, the cell line is a stable cell line stably coexpressing H1, L1, H2, and L2. In some embodiments according to (or as applied to) any of the embodiments above, the cell line is a stable cell line stably expressing the multispecific antigen binding protein. In some embodiments according to (or as applied to) any of the embodiments above, the set of polynucleotides encoding H1, L1, H2, and L2 are introduced into the host cell at a predetermined ratio. In some embodiments according to (or as applied to) any of the embodiments above, the method further comprises determining an optimal ratio of the polynucleotides for introduction into the host cell. In some embodiments according to (or as applied to) any of the embodiments above, the multispecific antigen binding protein is produced with a relative yield of 60% or higher. In certain embodiments according to (or as applied to) any of the embodiments above, the multispecific antigen binding protein is produced with a relative yield of at least about 70%, at least about 71%, at least about 71%, at least about 72%, at least about 73%, at least about 74%, at least about 75%, at least about 76%, at least about 77%, at least about 78%, at least about 79%, at least about 80%, at least about 81%, at least about 82%, at least about 83%, at least about 84%, at least about 85%, at least about 86%, at least about 87%, at least about 88%, at least about 89%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 99%, or more than about 99%. In certain embodiments according to (or as applied to) any of the embodiments above, the multispecific antigen binding protein is produced with a relative yield of at least about 85%, at least about 86%, at least about 87%, at least about 88%, at least about 89%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 99%, or more than about 99%. In certain embodiments according to (or as applied to) any of the embodiments above, the multispecific antigen binding protein is produced with a relative yield of at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 99%, or more than about 99%. In certain embodiments according to (or as applied to) any of the embodiments above, the

multispecific antigen binding protein is produced with a relative yield of at least about 95%, at least about 96%, at least about 97%, at least about 99%, or more than about 99%.

[0082] Also provided is a method of producing a multispecific antigen binding protein comprising culturing the host cell according to (or as applied to) any of the embodiments above, and producing the multispecific antigen binding protein. In some embodiments according to (or as applied to) any of the embodiments above, the method further comprises recovering the multispecific antigen binding protein. Also provided is a multispecific antigen binding protein produced by the methods according to (or as applied to) any of the embodiments above.

[0083] Provided herein is a library comprising a plurality of polynucleotides encoding a plurality of multispecific antigen binding proteins according to (or as applied to) any of the embodiments above. Also provided is a method of screening for a multispecific antigen binding protein that binds to a first antigen and a second antigen, comprising: (a) obtaining a plurality of multispecific antigen binding proteins from the library according to (or as applied to) any of the embodiments above; (b) assaying for binding of the plurality of multispecific antigen binding proteins to the first and second antigen; and (c) identifying the multispecific antigen binding protein that binds to the first and second antigen.

[0084] Also provided is a computer readable medium for evaluating a multispecific antigen binding protein comprising 1) a first heavy chain/light chain pair binding to a first antigen which comprises a first heavy chain sequence (H1) and a first light chain sequence (L1), and 2) a second heavy chain/light chain pair binding to a second antigen which comprises a second heavy chain sequence (H2) and a second light chain sequence (L2), wherein each H1 and H2 comprises a heavy chain variable domain (VH) and a heavy chain constant domain (CH1), and each L1 and L2 comprises a light chain variable domain (VL) and a light chain constant domain (CL); comprising: a) a dataset comprising data representing amino acid substitutions in H1, L1, H2, and L2, wherein at least one of the amino acid substitutions in the CH1 domain of H1 comprises an amino acid substitution at EU position F170 or L128 and V185, and wherein the CL domain comprises an amino acid substitution at EU position S176 or F118 and L135; and/or a dataset comprising data representing amino acid substitutions in H1, L1, H2, and L2, wherein at least one of the amino acid substitutions in the CH1 domain of H1 comprises an amino acid substitution at EU position S183, and wherein the of C1 comprises an amino acid substitution at EU position V133; and (b) computer executable code for determining the likelihood that H1 will preferentially pair with L1 as compared to L2 and/or H2 will preferentially pair with L2 as compared to L1.

[0085] Also provided is a computer readable medium for evaluating a multispecific antigen binding protein comprising 1) a first heavy chain/light chain pair binding to a first antigen which comprises a first heavy chain sequence (H1) and a first light chain sequence (L1), and 2) a second heavy chain/light chain pair binding to a second antigen which comprises a second heavy chain sequence (H2) and a second light

chain sequence (L2), wherein each H1 and H2 comprises a heavy chain variable domain (VH) and a heavy chain constant domain (CH1), and each L1 and L2 comprises a light chain variable domain (VL) and a light chain constant domain (CL); comprising: a) a dataset comprising data representing amino acid substitutions in H1, L1, H2, and L2, wherein at least one of the amino acid substitutions in the CH1 domain of H1 comprises an amino acid substitution at EU position F170 or L128, and wherein the CL domain comprises an amino acid substitution at EU position S176 or F118 and L135; and/or a dataset comprising data representing amino acid substitutions in H1, L1, H2, and L2, wherein at least one of the amino acid substitutions in the CH1 domain of H1 comprises an amino acid substitution at EU position S183, and wherein the of C1 comprises an amino acid substitution at EU position V133; and (b) computer executable code for determining the likelihood that H1 will preferentially pair with L1 as compared to L2 and/or H2 will preferentially pair with L2 as compared to L1. In certain embodiments, in the dataset comprising data representing amino acid substitutions in H1, L1, H2, and L2, the at least one of the amino acid substitutions in the CH1 domain of H1 comprises an amino acid substitution at EU position F170 or L128 and V185.

BRIEF DESCRIPTION OF THE DRAWINGS

[0086] FIG. 1 (FIG. A and FIG. 1B) shows protein A recovery from 1 ml 293T cultures of antibodies containing a heavy chain bearing a substitution mutation at position L128, G143, L145, S183, or V185 and a light chain bearing a substitution at F118, V133, or L135.

[0087] FIG. 2 provides the results of mammalian culture expression assays that were performed to identify amino acid mutations in CH1 that restore antibody expression when co-expressed with CL having a F118, V133, or L135 substitution mutation.

[0088] FIG. 3 provides a schematic of the interior of the interface of the light chain constant region (CL) and the heavy chain CH1 domain.

[0089] FIG. 4 provides the results of mammalian culture expression assays that were performed to analyze antibody expression in cultures expressing a light chains/heavy chain pair having V133X/S183X substitution mutations.

[0090] FIG. 5 shows the results of FACS analyses of binding to the antigen IL-13 of various mutant antibodies with amino acid substitutions either in VH Q39 or VL Q38 or both.

[0091] FIG. 6 the results of additional FACS analyses that were performed to identify Q39X-VH/Q38X-VL mutant pairs that favor VH/VL pairing.

[0092] FIG. 7 shows the results of mammalian culture expression assays that were performed to identify Q39X-VH/Q38X-VL mutant pairs that favor VH/VL pairing.

[0093] FIG. 8 shows exemplary results for the % presence of bispecific antibody variants with correct heavy chain-light chain pairing, measured by Orbitrap mass spectrometry from mammalian co-expressed antibodies. The mutants tested are shown on the X-axis. The four letters in each set of mutations refers to the amino acid substitutions at Q39X_{HCI}/Q38X_{LCI} knob/Q39X_{HCI2}/Q38X_{LC2} hole, respectively.

[0094] FIG. 9A shows the results of QTOF assays performed to assess heavy chain/light chain pairing in a 4D5/UCHT1 bispecific antibody. FIG. 9B shows the results of QTOF assays performed to assess heavy chain/light chain pairing in a 4D5/UCHT1 bispecific antibody that was modified so that the 4D5 arm contained a VL having the Q38K mutation and a VH having a Q39E mutation and the UCHT1 arm contained a VL having the Q38E mutation and a VH having a Q39K mutation (“EKKE”).

[0095] FIG. 10A shows an enlargement of FIG. 10B. FIG. 10B shows the results of high resolution mass spectrometry performed to assess heavy chain/light chain pairing in a bispecific 4D5/UCHT1 antibody in which the UCHT1 arm was modified to contain VL-Q38E, CL-V133K, VH-Q39K, and CH1-S183E mutations, and in which the 4D5 arm of the 4D5/UCHT1 antibody was modified to contain VL-Q38K and VH-Q39E mutations. FIG. 10C shows an enlargement of FIG. 10D. FIG. 10D shows the results of high resolution mass spectrometry performed to assess heavy chain/light chain pairing in a bispecific 4D5/UCHT1 antibody in which the UCHT1 arm was modified to contain CL-V133K and CH1-S183E mutations. FIG. 10E shows the results of high resolution mass spectrometry performed to assess heavy chain/light chain pairing in a WT bispecific 4D5/UCHT1 antibody.

[0096] FIG 11A shows the overlapping crystal structures of the wild type 4D5 Fab and the 4D5 Fab modified to have VL-Q38K, CL-V133E, VH-Q39E, and CH1-S183K mutations. FIG. 11B shows the bonds (*e.g.*, salt bridges and hydrogen bonds) formed by VL-Q38K and VH-Q39E in the modified 4D5 Fab. FIG. 11C shows the bonds (*e.g.*, salt bridges and hydrogen bonds) formed by CL-V133E and CH1-S183K in the modified 4D5 Fab.

[0097] FIG 12A shows the overlapping crystal structures of the wild type 4D5 Fab and the 4D5 Fab modified to have VL-Q38E, CL-V133K, VH-Q39K, and CH1-S183E mutations. FIG. 12B shows the bonds formed by VL-Q38E and VH-Q39K in the modified 4D5 Fab. FIG. 12C shows the bonds formed by CL-V133K and CH1-S183E in the modified 4D5 Fab.

[0098] FIG. 13A depicts one design approach (*i.e.*, “Approach A”) for generating a mutant CH1/CL pair. FIG. 13B depicts a second design approach (*i.e.*, “Approach B”) for generating a mutant CH1/CL pair for 4D5/UCHT1 bispecific antibody (anti-HER2/anti-CD3).

[0099] FIG. 14 shows a schematic diagram of the sandwich ELISA experiment used to determine bispecific IgG content from single cell co-expression.

[0100] FIG. 15 shows the results of sandwich ELISAs performed on the JS20, JS78, YS18, and YT65 variants.

[0101] FIG. 16A provides the amino acid sequences of portion of the heavy chains of JS20 (SEQ ID NO: 49), JS78 (SEQ ID NO: 50), JT20 (SEQ ID NO: 51), JT25 (SEQ ID NO: 52), YS08 (SEQ ID NO: 28), YS18 (SEQ ID NO: 29), YT65 (SEQ ID NO: 29), and YT34 variants (SEQ ID NO: 44). FIG 16A also provides the amino acid sequence of portion of the 4D5 wild type heavy chain "4D5wt-Hc" (SEQ ID NO: 67). FIG. 16B provides the amino acid sequences of portion of the light chains of JS20 (SEQ ID NO: 69), JS78 (SEQ ID NO: 70), JT20 (SEQ ID NO: 71), JT25 (SEQ ID NO: 72), YS08 (SEQ ID NO: 73), YS18 (SEQ ID NO: 74), YT65 (SEQ ID NO: 75), and YT34 variants (SEQ ID NO: 76). FIG 16B also provides the amino acid sequence of portion of the 4D5 WT light chain "4D5wt-Lc" (SEQ ID NO: 68).

[0102] FIG. 17A shows the results of mass spectrometry performed on a wild-type 4D5/UCHT1 coexpressed bispecific antibody. FIG. 17B shows the results of mass spectrometry performed on a 4D5/UCHT1 coexpressed antibody comprising YT65 CH1/CL mutations and VH-Q39E and VL-Q38K mutations on the 4D5 arm, and VL-Q38E and VH-Q39K mutations on the UCHT1 arm.

[0103] FIG. 18A shows the results of mass spectrometry performed on a wild-type 4D5/UCHT1 bispecific antibody. FIG. 18B shows the results of mass spectrometry performed on a 4D5/UCHT1 antibody comprising YT65 CH1/CL mutations and VH-Q39E and VL-Q38K mutations on the 4D5 arm, and VL-Q38E and VH-Q39K mutations on the UCHT1 arm.

[0104] FIG. 19A provides the amino acid sequences of portion of the heavy chains of the YT65 (SEQ ID NO: 78), YT65.1 (SEQ ID NO: 79), YT65.2 (SEQ ID NO: 80), YT65.3 (SEQ ID NO: 81), YT65.4 (SEQ ID NO: 82), YT65.5 (SEQ ID NO: 83), YT65.6 (SEQ ID NO: 84), YT65.7 (SEQ ID NO: 85), YT65.8 (SEQ ID NO: 86), YT65.9 (SEQ ID NO: 87), YT65.10 (SEQ ID NO: 88), YT65.11 (SEQ ID NO: 89), YT65.12 (SEQ ID NO: 90), and YT65.13 variants (SEQ ID NO: 91). FIG 19B discloses portion of the 4D5 wt heavy chain sequence "4D5wt-Hc" as SEQ ID NO: 77. FIG. 19B provides the amino acid sequences of portin of the light chains of the YT65 (SEQ ID NO: 93), YT65.1 (SEQ ID NO: 94), YT65.2 (SEQ ID NO: 95), YT65.3 (SEQ ID NO: 96), YT65.4 (SEQ ID NO: 97), YT65.5 (SEQ ID NO: 98), YT65.6 (SEQ ID NO: 99), and YT65.7 variants (SEQ ID NO: 100). FIG 19B discloses portion of the 4D5 wt light chain sequence "4D5wt-Lc" as SEQ ID NO: 92.

[0105] FIG. 20A shows the results of pH neutral native mass spectrometry performed on a 4D5/UCHT1 antibody comprising YT65 CH1/CL mutations and VH-Q39E and VL-Q38K mutations on the 4D5 arm, and VH-Q39K and VL-Q38E mutations on the UCHT1 arm. FIG. 20B shows the results

of experiments that were performed to confirm the detection sensitivity of the analysis used to obtain the data in Figure 20A.

[0106] FIG. 21 shows the quantitative results of high resolution mass spectrometry experiments performed to assess the effects of YT65, EKKE, and both YT65 and EKKE on heavy chain/light chain pairing in anti-IL4/IL13, anti-EGFR/MET, anti-VEGFA/ANG2 anti-VEGFA /VEGFC, and anti-HER2/CD3 (*i.e.*, 4D5/UCHT1) bispecific antibodies.

[0107] FIG. 22A shows the crystal structure of the 4D5 Fab modified to have VL-Q38K, VH-Q39E, and the YT65 mutations. FIG. 22B shows overlapping crystal structures of a CH1 domain of the wild type 4D5 Fab and the CH1 domain of the 4D5 Fab modified to have the YT65 mutations.

[0108] FIG 23 shows the biological activities of anti-HER2/CD3 + EKKE + V133K/S183E_{hole}, anti-HER2/CD3 + EKKE + YT65_{knob}, and unmodified anti-HER2/CD3 in an *in vitro* T-cell mediated B-cell cytotoxicity assay.

[0109] FIG 24 shows the mean serum levels of (i) anti-HER2, (ii) anti-gD/CD3, (iii) anti-HER2/CD3, (iv) anti-HER2/CD3 + EKKE + YT65_{knob}, and (iv) anti-HER2/CD3 + EKKE + V133E/S183K_{knob} + V133K/S183E_{hole} at various time points following 5 mg/kg intravenous administration of the antibody in C.B-17 SCID mice.

DETAILED DESCRIPTION OF THE INVENTION

[0110] Unless defined otherwise herein, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Singleton, *et al.*, DICTIONARY OF MICROBIOLOGY AND MOLECULAR BIOLOGY, 2D Ed., John Wiley and Sons, New York (1994), and Hale & Margham, THE HARPER COLLINS DICTIONARY OF BIOLOGY, Harper Perennial, NY (1991) provide one of skill with a general dictionary of many of the terms used in this invention. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, the preferred methods and materials are described. Numeric ranges are inclusive of the numbers defining the range. Unless otherwise indicated, nucleic acids are written left to right in 5' to 3' orientation; amino acid sequences are written left to right in amino to carboxy orientation, respectively. Practitioners are particularly directed to Sambrook *et al.*, 1989, and Ausubel FM *et al.*, 1993, for definitions and terms of the art. It is to be understood that this invention is not limited to the particular methodology, protocols, and reagents described, as these may vary.

[0111] Numeric ranges are inclusive of the numbers defining the range.

[0112] Unless otherwise indicated, nucleic acids are written left to right in 5' to 3' orientation; amino acid sequences are written left to right in amino to carboxy orientation, respectively.

[0113] The headings provided herein are not limitations of the various aspects or embodiments which can be had by reference to the specification as a whole. Accordingly, the terms defined immediately below are more fully defined by reference to the specification as a whole.

Definitions

[0114] The term “multispecific antigen-binding protein” herein is used in the broadest sense refers to a binding protein capable of binding two or more antigens. In certain aspects the multispecific binding protein refers to a bispecific antibody, *e.g.*, a human bispecific antibody, a humanized bispecific antibody, a chimeric bispecific antibody, or a mouse bispecific antibody. In certain embodiments, a multispecific antigen-binding protein provided herein, such as a bispecific antibody, binds to two different antigens. In certain embodiments, the multispecific antigen-binding protein, such as a bispecific antibody, binds to different epitopes on one antigen.

[0115] The term “antibody” herein is used in the broadest sense and refers to any immunoglobulin (Ig) molecule comprising two heavy chains and two light chains, and any fragment, mutant, variant or derivation thereof so long as they exhibit the desired biological activity (*e.g.*, epitope binding activity). Examples of antibodies include monoclonal antibodies, polyclonal antibodies, multispecific antibodies (*e.g.*, bispecific antibodies) and antibody fragments as described herein. An antibody can be mouse, chimeric, human, humanized and/or affinity matured.

[0116] As a frame of reference, as used herein an antibody will refer to the structure of an immunoglobulin G (IgG). However, one skilled in the art would understand/recognize that an antibody of any immunoglobulin class may be utilized in the inventive method described herein. For clarity, an IgG molecule contains a pair of heavy chains (HCs) and a pair of light chains (LCs). Each LC has one variable domain (VL) and one constant domain (CL), while each HC has one variable (VH) and three constant domains (CH1, CH2, and CH3). The CH1 and CH2 domains are connected by a hinge region. This structure is well known in the art.

[0117] Briefly, the basic 4-chain antibody unit is a heterotetrameric glycoprotein composed of two light (L) chains and two heavy (H) chains (an IgM antibody consists of 5 of the basic heterotetramer unit along with an additional polypeptide called J chain, and therefore contain 10 antigen binding sites, while secreted IgA antibodies can polymerize to form polyvalent assemblages comprising 2-5 of the basic 4-chain units along with J chain). In the case of IgGs, the 4-chain unit is generally about 150,000 daltons. Each L chain is linked to an H chain by one covalent disulfide bond, while the two H chains are linked to each other by one or more disulfide bonds depending on the H chain isotype. Each H and L chain also

has regularly spaced intrachain disulfide bridges. Each H chain has at the N-terminus, a variable domain (V_H) followed by three constant domains (C_H) for each of the α and γ chains and four C_H domains for μ and ϵ isotypes. Each L chain has at the N-terminus, a variable domain (V_L) followed by a constant domain (C_L) at its other end. The V_L is aligned with the V_H and the C_L is aligned with the first constant domain of the heavy chain (C_{H1}). Particular amino acid residues are believed to form an interface between the light chain and heavy chain variable domains. The pairing of a V_H and V_L together forms a single antigen-binding site. For the structure and properties of the different classes of antibodies, *see, e.g.,* Basic and Clinical Immunology, 8th edition, Daniel P. Stites, Abba I. Terr and Tristram G. Parslow (eds.), Appleton & Lange, Norwalk, CT, 1994, page 71 and Chapter 6.

[0118] The L chain from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains. Depending on the amino acid sequence of the constant domain of their heavy chains (C_H), immunoglobulins can be assigned to different classes or isotypes. There are five classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, having heavy chains designated α , δ , γ , ϵ , and μ , respectively. The γ and α classes are further divided into subclasses on the basis of relatively minor differences in C_H sequence and function, *e.g.,* humans express the following subclasses: IgG1, IgG2, IgG3, IgG4, IgA1, and IgA2.

[0119] The term “VL” domain comprises the amino terminal variable domain of an immunoglobulin light chain.

[0120] The term “VH domain” comprises the amino terminal variable domain of an immunoglobulin heavy chain.

[0121] The term “CL domain” comprises the constant region domain of an immunoglobulin light chain that extends, *e.g.* from about Kabat position 107A-216 (EU positions 108-214 (kappa)). The Eu/Kabat conversion table for the Kappa C domain is provided below. The CL domain is adjacent to the VL domain and includes the carboxy terminal of an immunoglobulin light chain. An exemplary amino acid sequence for CL domain of human kappa light chain is shown below in SEQ ID NO: 30, including the R residue at the N-terminus that is present in the mature CL domain as the result of gene splicing.

Table A

Human IG Kappa Chain amino acid translation (SEQ ID NO: 30)	EU numbering	Kabat numbering
(R)	108	108
T	109	109
V	110	110

Human IG Kappa Chain amino acid translation (SEQ ID NO: 30)	EU numbering	Kabat numbering
A	111	111
A	112	112
P	113	113
S	114	114
V	115	115
F	116	116
I	117	117
F	118	118
P	119	119
P	120	120
S	121	121
D	122	122
E	123	123
Q	124	124
L	125	125
K	126	126
-	-	-
-	-	-
-	-	-
S	127	127
G	128	128
T	129	129
A	130	130
S	131	131
V	132	132
V	133	133
C	134	134
L	135	135
L	136	136
N	137	137
N	138	138
F	139	139

Human IG Kappa Chain amino acid translation (SEQ ID NO: 30)	EU numbering	Kabat numbering
Y	140	140
P	141	141
-	-	-
-	-	-
R	142	142
E	143	143
A	144	144
K	145	145
V	146	146
Q	147	147
W	148	148
K	149	149
V	150	150
D	151	151
N	152	152
A	153	153
L	154	154
Q	155	155
S	156	156
G	157	157
-	-	-
-	-	-
N	158	158
S	159	159
Q	160	160
E	161	161
S	162	162
V	163	163
T	164	164
E	165	165
Q	166	166
D	167	167

Human IG Kappa Chain amino acid translation (SEQ ID NO: 30)	EU numbering	Kabat numbering
S	168	168
K	169	169
D	170	170
-	-	-
-	-	-
-	-	-
-	-	-
-	-	-
S	171	171
T	172	172
Y	173	173
S	174	174
L	175	175
S	176	176
S	177	177
T	178	178
L	179	179
T	180	180
L	181	181
S	182	182
K	183	183
A	184	184
D	185	185
Y	186	186
-	-	-
-	-	-
E	187	187
K	188	188
H	189	189
K	190	190
V	191	191
Y	192	192

Human IG Kappa Chain amino acid translation (SEQ ID NO: 30)	EU numbering	Kabat numbering
A	193	193
C	194	194
E	195	195
V	196	196
T	197	197
H	198	198
Q	199	199
G	200	200
-	-	-
-	-	-
L	201	201
S	202	202
S	203	203
P	204	204
V	205	205
T	206	206
K	207	207
S	208	208
F	209	209
N	210	210
R	211	211
G	212	212
E	213	213
C	214	214
-	-	215
-	-	216

[0122] As used herein, the term “CH1 domain” of a human IgG comprises the first (most amino terminal) constant region domain of an immunoglobulin heavy chain that extends, *e.g.*, from about positions 114-223 in the Kabat numbering system (EU positions 118-215). The CH1 domain is adjacent to the VH domain and amino terminal to the hinge region of an immunoglobulin heavy chain molecule,

does not form a part of the Fc region of an immunoglobulin heavy chain, and is capable of dimerizing with an immunoglobulin light chain constant domain (*i.e.*, “CL”).

[0123] The EU/Kabat conversion tables for the IgG1 heavy chain (SEQ ID NO: 65) are provided below. The exemplary CH1 sequence is shown in SEQ ID NO:53, hinge sequence is shown in SEQ ID NO: 129, CH2 sequence is shown in SEQ ID NO: 130, and CH3 sequence is shown in SEQ ID NO: 131.

Table B

CH1 (SEQ ID NO: 53)		
	EU numbering	Kabat numbering
(A)	118	114
S	119	115
T	120	116
K	121	117
G	122	118
P	123	119
S	124	120
V	125	121
F	126	122
P	127	123
L	128	124
A	129	125
P	130	126
S	131	127
S	132	128
K	133	129
S	134	130
T	135	133
S	136	134
G	137	135
G	138	136
T	139	137
A	140	138
A	141	139

Table C

HINGE (SEQ ID NO:129)		
	EU numbering	Kabat numbering
(E)	216	226
P	217	227
K	218	228
S	219	232
C	220	233
D	221	234
K	222	235
T	223	236
H	224	237
T	225	238
C	226	239
P	227	240
P	228	241
C	229	242
P	230	243

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L	142	140
G	143	141
C	144	142
L	145	143
V	146	144
K	147	145
D	148	146
Y	149	147
F	150	148
P	151	149
E	152	150
P	153	151
V	154	152
T	155	153
V	156	154
S	157	156
W	158	157
N	159	162
S	160	163
G	161	164
A	162	165
L	163	166
T	164	167
S	165	168
G	166	169
V	167	171
H	168	172
T	169	173
F	170	174
P	171	175
A	172	176
V	173	177
L	174	178

Q	175	179
S	176	180
S	177	182
G	178	183
L	179	184
Y	180	185
S	181	186
L	182	187
S	183	188
S	184	189
V	185	190
V	186	191
T	187	192
V	188	193
P	189	194
S	190	195
S	191	196
S	192	197
L	193	198
G	194	199
T	195	200
Q	196	203
T	197	205
Y	198	206
I	199	207
C	200	208
N	201	209
V	202	210
N	203	211
H	204	212
K	205	213
P	206	214
S	207	215

N	208	216
T	209	217
K	210	218
V	211	219
D	212	220
K	213	221
K	214	222
V	215	223
-	-	-

Table D

CH2 (SEQ ID NO: 130)		
	EU numbering	Kabat numbering
(A)	231	244
P	232	245
E	233	246
L	234	247
L	235	248
G	236	249
G	237	250
P	238	251
S	239	252
V	240	253
F	241	254
L	242	255
F	243	256
P	244	257
P	245	258
K	246	259
P	247	260
K	248	261
D	249	262
T	250	263
L	251	264

Table E

CH3 (SEQ ID NO:131)		
	EU numbering	Kabat numbering
(G)	341	361
Q	342	363
P	343	364
R	344	365
E	345	366
P	346	367
Q	347	368
V	348	369
Y	349	370
T	350	371
L	351	372
P	352	373
P	353	374
S	354	375
R	355	376
D	356	377
E	357	378
L	358	381
T	359	382
K	360	383
N	361	384

CH2 (SEQ ID NO: 130)		
	EU numbering	Kabat numbering
M	252	265
I	253	266
S	254	267
R	255	268
T	256	269
P	257	270
E	258	271
V	259	272
T	260	273
C	261	274
V	262	275
V	263	276
V	264	277
D	265	278
V	266	279
S	267	280
H	268	281
E	269	282
D	270	283
P	271	284
E	272	285
V	273	286
K	274	287
F	275	288
N	276	289
W	277	290
Y	278	291
V	279	292
D	280	295
G	281	296
V	282	299

CH3 (SEQ ID NO:131)		
	EU numbering	Kabat numbering
Q	362	385
V	363	386
S	364	387
L	365	388
T	366	389
C	367	390
L	368	391
V	369	392
K	370	393
G	371	394
F	372	395
Y	373	396
P	374	397
S	375	398
D	376	399
I	377	400
A	378	401
V	379	402
E	380	405
W	381	406
E	382	407
S	383	408
N	384	410
G	385	411
Q	386	414
P	387	415
E	388	416
N	389	417
N	390	418
Y	391	419
K	392	420

CH2 (SEQ ID NO: 130)		
	EU numbering	Kabat numbering
E	283	300
V	284	301
H	285	302
N	286	303
A	287	304
K	288	305
T	289	306
K	290	307
P	291	308
R	292	309
E	293	310
E	294	311
Q	295	312
Y	296	313
N	297	314
S	298	317
T	299	318
Y	300	319
R	301	320
V	302	321
V	303	322
S	304	323
V	305	324
L	306	325
T	307	326
V	308	327
L	309	328
H	310	329
Q	311	330
D	312	331
W	313	332

CH3 (SEQ ID NO:131)		
	EU numbering	Kabat numbering
T	393	421
T	394	422
P	395	423
P	396	424
V	397	425
L	398	426
D	399	427
S	400	428
D	401	430
G	402	433
S	403	434
F	404	435
F	405	436
L	406	437
Y	407	438
S	408	439
K	409	440
L	410	441
T	411	442
V	412	443
D	413	444
K	414	445
S	415	446
R	416	447
W	417	448
Q	418	449
Q	419	450
G	420	451
N	421	452
V	422	453
F	423	454

CH2 (SEQ ID NO: 130)		
	EU numbering	Kabat numbering
L	314	333
N	315	334
G	316	335
K	317	336
E	318	337
Y	319	338
K	320	339
C	321	340
K	322	341
V	323	342
S	324	343
N	325	344
K	326	345
A	327	346
L	328	347
P	329	348
A	330	349
P	331	350
I	332	351
E	333	352
K	334	353
T	335	354
I	336	355
S	337	357
K	338	358
A	339	359
K	340	360
-	-	-
-	-	-

CH3 (SEQ ID NO:131)		
	EU numbering	Kabat numbering
S	424	455
C	425	456
S	426	457
V	427	458
M	428	459
H	429	460
E	430	461
A	431	462
L	432	463
H	433	464
N	434	465
H	435	466
Y	436	467
T	437	468
Q	438	469
K	439	470
S	440	471
L	441	472
S	442	473
L	443	474
S	444	475
P	445	476
G	446	477
K	447	478

[0124] As used herein, the term “complementarity” refers to the combination of interactions at the interface of, *e.g.*, the CH1 of a heavy chain and the CL of a light chain of a multispecific antigen-binding protein described herein, that influence heavy chain/light chain pairing. “Steric complementarity” or “conformational complementarity” refers to the compatibility of the three dimensional structures at the interacting surfaces of, *e.g.*, a CH1 domain of a heavy chain and a CL domain of a light chain. “Electrostatic complementarity” refers to the compatibility of the placement of negatively- and/or positively-charged atoms at the interacting surfaces of, *e.g.*, a CH1 domain of a heavy chain and a CL domain of a light chain and/or a VH domain of a heavy chain and a VL domain of a light chain.

[0125] The term “CH2 domain” of a human IgG Fc region usually comprises about residues 231 to about 340 of the IgG according to the EU numbering system. The CH2 domain is unique in that it is not closely paired with another domain. Rather, two N-linked branched carbohydrate chains are interposed between the two CH2 domains of an intact native IgG molecule. It has been speculated that the carbohydrate may provide a substitute for the domain-domain pairing and help stabilize the CH2 domain. Burton, *Mol. Immunol.* 22:161-206 (1985).

[0126] The term “CH3 domain” comprises residues C-terminal to a CH2 domain in an Fc region (*i.e.*, from about amino acid residue 341 to about amino acid residue 447 of an IgG according to the EU numbering system).

[0127] The term “Fc region,” as used herein, generally refers to a dimer complex comprising the C-terminal polypeptide sequences of an immunoglobulin heavy chain, wherein a C-terminal polypeptide sequence is that which is obtainable by papain digestion of an intact antibody. The Fc region may comprise native or variant Fc sequences. Although the boundaries of the Fc sequence of an immunoglobulin heavy chain might vary, the human IgG heavy chain Fc sequence comprises about position Cys226, or from about position Pro230, to the carboxyl terminus of the Fc sequence. Unless otherwise specified herein, numbering of amino acid residues in the Fc region or constant region is according to the EU numbering system, also called the EU index, as described in Kabat *et al.*, *Sequences of Proteins of Immunological Interest*, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD, 1991. The Fc sequence of an immunoglobulin generally comprises two constant domains, a CH2 domain and a CH3 domain, and optionally comprises a CH4 domain. By “Fc polypeptide” herein is meant one of the polypeptides that make up an Fc region, *e.g.*, a monomeric Fc. An Fc polypeptide may be obtained from any suitable immunoglobulin, such as human IgG1, IgG2, IgG3, or IgG4 subtypes, IgA, IgE, IgD or IgM. An Fc polypeptide may be obtained from mouse, *e.g.*, a mouse IgG2a. The Fc region comprises the carboxy-terminal portions of both H chains held together by disulfides. The effector functions of antibodies are determined by sequences in the Fc region; this region is also the part recognized by Fc receptors (FcR) found on certain types of cells. In some embodiments,

an Fc polypeptide comprises part or all of a wild type hinge sequence (generally at its N terminus). In some embodiments, an Fc polypeptide does not comprise a functional or wild type hinge sequence.

[0128] A “functional Fc region” possesses an “effector function” of a native sequence Fc region. Exemplary “effector functions” include C1q binding; CDC; Fc receptor binding; ADCC; phagocytosis; down regulation of cell surface receptors (*e.g.*, B cell receptor; BCR), *etc.* Such effector functions generally require the Fc region to be combined with a binding domain (*e.g.*, an antibody variable domain) and can be assessed using various assays as disclosed, for example, in definitions herein.

[0129] A “native sequence Fc region” comprises an amino acid sequence identical to the amino acid sequence of an Fc region found in nature. Native sequence human Fc regions include a native sequence human IgG1 Fc region (non-A and A allotypes); native sequence human IgG2 Fc region; native sequence human IgG3 Fc region; and native sequence human IgG4 Fc region as well as naturally occurring variants thereof. A native sequence Fc regions also include a native sequence mouse IgG2a.

[0130] A “variant Fc region” comprises an amino acid sequence which differs from that of a native sequence Fc region by virtue of at least one amino acid modification, preferably one or more amino acid substitution(s). Preferably, the variant Fc region has at least one amino acid substitution compared to a native sequence Fc region or to the Fc region of a parent polypeptide, *e.g.*, from about one to about ten amino acid substitutions, and preferably from about one to about five amino acid substitutions in a native sequence Fc region or in the Fc region of the parent polypeptide. The variant Fc region herein will preferably possess at least about 80% homology with a native sequence Fc region and/or with an Fc region of a parent polypeptide, and most preferably at least about 90% homology therewith, more preferably at least about 95%, at least about 96%, at least about 97%, at least about 98% or at least about 99% homology therewith.

[0131] “Fc component” as used herein refers to a hinge region, a CH2 domain or a CH3 domain of an Fc region.

[0132] In certain embodiments, the Fc region comprises an IgG Fc region, preferably derived from a wild-type human IgG Fc region. In certain embodiments, the Fc region is derived from a “wild type” mouse IgG, such as a mouse IgG2a. By “wild-type” human IgG Fc or “wild type” mouse IgG Fc it is meant a sequence of amino acids that occurs naturally within the human population or mouse population, respectively. Of course, just as the Fc sequence may vary slightly between individuals, one or more alterations may be made to a wild type sequence and still remain within the scope of the invention. For example, the Fc region may contain alterations such as a mutation in a glycosylation site or inclusion of an unnatural amino acid.

[0133] The term “variable region” or “variable domain” refers to the domain of an antibody heavy or light chain that is involved in binding the antibody to antigen. The variable domains of the heavy chain and light chain (VH and VL, respectively) of a native antibody generally have similar structures, with each domain comprising four conserved framework regions (FRs) and three hypervariable regions (HVRs). (*See, e.g., Kindt et al. Kuby Immunology*, 61st ed., W.H. Freeman and Co., page 91 (2007).) A single VH or VL domain may be sufficient to confer antigen-binding specificity. Furthermore, antibodies that bind a particular antigen may be isolated using a VH or VL domain from an antibody that binds the antigen to screen a library of complementary VL or VH domains, respectively. *See, e.g., Portolano et al., J. Immunol.* 150:880-887 (1993); Clarkson *et al., Nature* 352:624-628 (1991).

[0134] The phrase “antigen binding arm,” “target molecule binding arm,” “target binding arm” and variations thereof, as used herein, refers to a component part of a multispecific antigen-binding protein provided herein that has an ability to specifically bind a target of interest. Generally and preferably, the antigen binding arm is a complex of immunoglobulin polypeptide sequences, *e.g.*, CDR and/or variable domain sequences of an immunoglobulin light and heavy chain.

[0135] A “target” or “target molecule” refers to a moiety recognized by a binding arm of the multispecific antigen-binding protein. For example, if the multispecific antigen-binding protein is an antibody, then the target may be epitopes on a single molecule or on different molecules, or a pathogen or a tumor cell, depending on the context. Similarly, if the multispecific antigen-binding protein is a receptor-Fc fusion protein the target would be the cognate binding partner for the receptor. One skilled in the art will appreciate that the target is determined by the binding specificity of the target binding arm and that different target binding arms may recognize different targets. A target preferably binds to a multispecific antigen-binding protein provided herein with affinity higher than 1 μ M Kd (according to Scatchard analysis). Examples of target molecules include, but are not limited to, serum soluble proteins and/or their receptors, such as cytokines and/or cytokine receptors, adhesins, growth factors and/or their receptors, hormones, viral particles (*e.g.*, RSV F protein, CMV, Staph A, influenza, hepatitis C virus), microorganisms (*e.g.*, bacterial cell proteins, fungal cells), adhesins, CD proteins and their receptors.

[0136] The term “interface” as used herein refers to the association surface that results from interaction of one or more amino acids in a first antibody domain with one or more amino acids of a second antibody domain. Exemplary interfaces include, *e.g.*, CH1/CL, VH/VL and CH3/CH3. In some embodiments, the interface includes, for example, hydrogen bonds, electrostatic interactions, or salt bridges between the amino acids forming an interface.

[0137] One example of an “intact” or “full-length” antibody is one that comprises an antigen-binding arm as well as a CL and at least heavy chain constant domains, CH1, CH2, and CH3. The constant

domains can be native sequence constant domains (*e.g.*, human native sequence constant domains) or amino acid sequence variants thereof.

[0138] The term “coupling” as used herein refers to the steps necessary to link the first and second heavy chain polypeptides (*i.e.*, H1 and H2) to each other, *e.g.*, formation of a covalent bond. Such steps comprise the reducing, annealing and/or oxidizing of cysteine residues in the first and second heavy chain polypeptides (*i.e.*, H1 and H2) to form an inter-chain disulfide bond. The coupling may be achieved by chemical cross-linking or the use of a redox system. *See, e.g.*, Humphreys *et al.*, J. Immunol. Methods (1998) 217:1-10 and Zhu *et al.*, Cancer Lett., (1994) 86: 127-134.

[0139] “Monospecific” antigen-binding protein refers to the ability of the antigen binding protein, such as an antibody, to bind only one epitope. “Bispecific” antigen-binding protein refers to the ability of the antigen binding protein to bind two different epitopes. “Multispecific” antigen binding protein refers to the ability of the antigen binding protein to bind more than one epitope. In certain embodiments, a multispecific antigen-binding protein, such as a multispecific antibody, encompasses a bispecific antigen-binding protein or a bispecific antibody. For bispecific and multispecific antigen-binding proteins provided herein, the epitopes can be on the same antigen, or each epitope can be on a different antigen. Therefore, in certain embodiments, a multispecific antigen-binding protein provided herein, such as a bispecific antibody, binds to two different antigens. In certain embodiments, the multispecific antigen-binding protein, such as a bispecific antibody, binds to different epitopes on one antigen. In certain embodiments, a multispecific antigen-binding protein provided herein binds to each epitope with a dissociation constant (K_d) of about $\leq 1\mu\text{M}$, about $\leq 100\text{ nM}$, about $\leq 10\text{ nM}$, about $\leq 1\text{ nM}$, about $\leq 0.1\text{ nM}$, about $\leq 0.01\text{ nM}$, or about $\leq 0.001\text{ nM}$ (*e.g.*, about 10^{-8} M or less, *e.g.*, from about 10^{-8} M to about 10^{-13} M , *e.g.*, from about 10^{-9} M to about 10^{-13} M).

[0140] “Antibody fragments” comprise a portion of an intact antibody, preferably the antigen binding or a variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', F(ab')₂, and Fv fragments; diabodies (Db); tandem diabodies (taDb), linear antibodies (*e.g.*, U.S. Patent No. 5,641,870; Zapata *et al.*, Protein Eng. 8(10):1057-1062 (1995)); one-armed antibodies, single variable domain antibodies, minibodies, single-chain antibody molecules; and multispecific antibodies formed from antibody fragments (*e.g.*, including but not limited to, Db-Fc, taDb-Fc, taDb-CH3 and (scFV)₄-Fc).

[0141] Antibodies provided herein can be “chimeric” antibodies in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, provided that they exhibit the desired biological activity (U.S. Patent No. 4,816,567; and Morrison *et al.*,

Proc. Natl. Acad. Sci. USA 81 :6851-6855 (1984)). Chimeric antibodies of interest herein include primatized antibodies comprising variable domain antigen-binding sequences derived from a non-human primate (*e.g.*, Old World Monkey, Ape, *etc.*) and human constant region sequences.

[0142] “Humanized” forms of non-human (*e.g.*, rodent) antibodies are chimeric antibodies that contain minimal sequence derived from the non-human antibody. For the most part, humanized antibodies are human immunoglobulins (recipient antibody) in which residues from a hypervariable region of the recipient are replaced by residues from a hypervariable region of a non-human species (donor antibody) such as mouse, rat, rabbit or non-human primate having the desired antibody specificity, affinity, and capability. In some instances, framework region (FR) residues of the human immunoglobulin are replaced by corresponding non-human residues. Furthermore, humanized antibodies can comprise residues that are not found in the recipient antibody or in the donor antibody. These modifications are made to further refine antibody performance. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the hypervariable loops correspond to those of a nonhuman immunoglobulin and all or substantially all of the FRs are those of a human immunoglobulin sequence. The humanized antibody optionally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. For further details, *see* Jones *et al.*, Nature 321:522-525 (1986); Riechmann *et al.*, Nature 332:323-329 (1988); and Presta, Curr. Op. Struct. Biol. 2:593-596 (1992).

[0143] “Complex” or “complexed” as used herein refers to the association of two or more molecules that interact with each other through bonds and/or forces (*e.g.*, van der Waals, hydrophobic, hydrophilic forces) that are not peptide bonds. In one embodiment, the complex is heteromultimeric. It should be understood that the term “protein complex” or “polypeptide complex” as used herein includes complexes that have a non-protein entity conjugated to a protein in the protein complex (*e.g.*, including, but not limited to, chemical molecules such as a toxin or a detection agent).

[0144] A multispecific antigen-binding protein provided herein “which binds an antigen of interest” is one that binds the antigen, *e.g.*, a protein, with sufficient affinity such that the multispecific antigen-binding protein is useful as a diagnostic and/or therapeutic agent in targeting a protein or a cell or tissue expressing the protein, and does not significantly cross-react with other proteins. In such embodiments, the extent of binding of the antigen-binding protein to a “non-target” protein will be less than about 10% of the binding of the antibody to its particular target protein as determined by fluorescence activated cell sorting (FACS) analysis or radioimmunoprecipitation (RIA) or ELISA. With regard to the binding of a multispecific antigen-binding protein to a target molecule, the term “specific binding” or “specifically binds to” or is “specific for” a particular polypeptide or an epitope on a particular polypeptide target means binding that is measurably different from a nonspecific interaction (*e.g.*, a non-specific interaction may be binding to bovine serum albumin or casein). Specific binding can be measured, for example, by

determining binding of a molecule compared to binding of a control molecule. For example, specific binding can be determined by competition with a control molecule that is similar to the target, for example, an excess of non-labeled target. In this case, specific binding is indicated if the binding of the labeled target to a probe is competitively inhibited by excess unlabeled target. The term “specific binding” or “specifically binds to” or is “specific for” a particular polypeptide or an epitope on a particular polypeptide target as used herein can be exhibited, for example, by a molecule having a K_d for the target of at least about 200 nM, alternatively at least about 150 nM, alternatively at least about 100 nM, alternatively at least about 60 nM, alternatively at least about 50 nM, alternatively at least about 40 nM, alternatively at least about 30 nM, alternatively at least about 20 nM, alternatively at least about 10 nM, alternatively at least about 8 nM, alternatively at least about 6 nM, alternatively at least about 4 nM, alternatively at least about 2 nM, alternatively at least about 1 nM, or greater affinity. In one embodiment, the term “specific binding” refers to binding where a multispecific antigen-binding protein binds to a particular polypeptide or epitope on a particular polypeptide without substantially binding to any other polypeptide or polypeptide epitope.

[0145] “Binding affinity” generally refers to the strength of the sum total of noncovalent interactions between a single binding site of a molecule (*e.g.*, an antibody or a multispecific antigen-binding protein) and its binding partner (*e.g.*, an antigen). Unless indicated otherwise, as used herein, “binding affinity” refers to intrinsic binding affinity which reflects a 1:1 interaction between members of a binding pair (*e.g.*, antibody and antigen). The affinity of a molecule X for its partner Y can generally be represented by the dissociation constant (K_d). For example, the K_d can be about 200 nM or less, about 150 nM or less, about 100 nM or less, about 60 nM or less, about 50 nM or less, about 40 nM or less, about 30 nM or less, about 20 nM or less, about 10 nM or less, about 8 nM or less, about 6 nM or less, about 4 nM or less, about 2 nM or less, or about 1 nM or less. Affinity can be measured by common methods known in the art, including those described herein. Low-affinity antibodies generally bind antigen slowly and tend to dissociate readily, whereas high-affinity antibodies generally bind antigen faster and tend to remain bound longer. A variety of methods of measuring binding affinity are known in the art, any of which can be used for purposes of the present invention.

[0146] In one embodiment, the “ K_d ” or “ K_d value” is measured by using surface plasmon resonance assays using a BIAcore™-2000 or a BIAcore™-3000 (BIAcore, Inc., Piscataway, NJ) at 25°C with immobilized target (*e.g.*, antigen) CM5 chips at -10 response units (RU). Briefly, carboxymethylated dextran biosensor chips (CM5, BIAcore Inc.) are activated with N-ethyl-N'-(3-dimethylaminopropyl)-carbodiimide hydrochloride (EDC) and N-hydroxysuccinimide (NHS) according to the supplier's instructions. Antigen is diluted with 10 mM sodium acetate, pH 4.8, into 5 µg/ml (~0.2 µM) before injection at a flow rate of 5 µl/minute to achieve approximately 10 response units (RU) of coupled protein. Following the injection of antigen, 1M ethanolamine is injected to block unreacted groups. For

kinetics measurements, two-fold serial dilutions of Fab (*e.g.*, 0.78 nM to 500 nM) are injected in PBS with 0.05% Tween 20 (PBST) at 25°C at a flow rate of approximately 25 μ l/min. Association rates (k_{on}) and dissociation rates (k_{off}) are calculated using a simple one-to-one Langmuir binding model (BIAcore Evaluation Software version 3.2) by simultaneous fitting the association and dissociation sensorgram. The equilibrium dissociation constant (K_d) is calculated as the ratio k_{off}/k_{on} . *See, e.g., Chen et al., J. Mol. Biol.* 293:865-881 (1999). If the on-rate exceeds $10^6 \text{ M}^{-1} \text{ s}^{-1}$ by the surface plasmon resonance assay above, then the on-rate can be determined by using a fluorescent quenching technique that measures the increase or decrease in fluorescence emission intensity (excitation = 295 nm; emission = 340 nm, 16 nm band-pass) at 25°C of a 20 nM anti-antigen antibody (Fab form) in PBS, pH 7.2, in the presence of increasing concentrations of antigen as measured in a spectrometer, such as a stop-flow equipped spectrophotometer (Aviv Instruments) or a 8000-series SLM-Aminco spectrophotometer (ThermoSpectronic) with a stirred cuvette.

[0147] “Biologically active” and “biological activity” and “biological characteristics” with respect to a multispecific antigen-binding protein provided herein, such as an antibody (*e.g.*, a bispecific antibody), fragment, or derivative thereof, means having the ability to bind to a biological molecule, except where specified otherwise.

[0148] “Isolated,” when used to describe the various heteromultimer polypeptides means a heteromultimer which has been separated and/or recovered from a cell or cell culture from which it was expressed. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the heteromultimer, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In certain embodiments, the heteromultimer will be purified (1) to greater than 95% by weight of protein as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS PAGE under reducing or nonreducing conditions using Coomassie blue or, preferably, silver stain. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

[0149] The multispecific antigen-binding proteins provided herein are generally purified to substantial homogeneity. The phrases “substantially homogeneous,” “substantially homogeneous form,” and “substantial homogeneity” are used to indicate that the product is substantially devoid of by-products originated from undesired polypeptide combinations (*e.g.*, homomultimers).

[0150] Expressed in terms of purity, substantial homogeneity means that the amount of by-products does not exceed 10%, 9%, 8%, 7%, 6%, 4%, 3%, 2% or 1% by weight or is less than 1% by weight. In one embodiment, the by-product is below 5%.

[0151] “Biological molecule” refers to a nucleic acid, a protein, a carbohydrate, a lipid, and combinations thereof. In one embodiment, the biologic molecule exists in nature.

[0152] Antibody “effector functions” refer to those biological activities attributable to the Fc region (a native sequence Fc region or amino acid sequence variant Fc region) of an antibody, and vary with the antibody isotype. Examples of antibody effector functions include: C1q binding and complement dependent cytotoxicity; Fc receptor binding; antibody-dependent cell-mediated cytotoxicity (ADCC); phagocytosis; down regulation of cell surface receptors (*e.g.*, B cell receptor); and B cell activation.

[0153] “Antibody-dependent cell-mediated cytotoxicity” or “ADCC” refers to a form of cytotoxicity in which secreted Ig bound to Fc receptors (FcRs) present on certain cytotoxic cells (*e.g.*, Natural Killer (NK) cells, neutrophils, and macrophages) enable these cytotoxic effector cells to bind specifically to an antigen-bearing target cell and subsequently kill the target cell with cytotoxic agents. The antibodies “arm” the cytotoxic cells and are absolutely required for such killing. The primary cells for mediating ADCC, NK cells, express FcγRIII only, whereas monocytes express FcγRI, FcγRII, and FcγRIII. FcR expression on hematopoietic cells is summarized in Table 3 on page 464 of Ravetch and Kinet, *Annu. Rev. Immunol.* 9:457-92 (1991). To assess ADCC activity of a molecule of interest, an *in vitro* ADCC assay, such as that described in U.S. Patent No. 5,500,362 or 5,821,337 can be performed. Useful effector cells for such assays include peripheral blood mononuclear cells (PBMC) and Natural Killer (NK) cells. Alternatively, or additionally, ADCC activity of the molecule of interest can be assessed *in vivo*, *e.g.*, in an animal model such as that disclosed in Clynes *et al.*, *Proc. Natl. Acad. Sci. USA* 95:652-656 (1998).

[0154] “Fc receptor” or “FcR” describes a receptor that binds to the Fc region of an antibody. The preferred FcR is a human FcR. Moreover, a preferred FcR is one that binds an IgG antibody (a gamma receptor) and includes receptors of the FcγRI, FcγRII, and FcγRIII subclasses, including allelic variants and alternatively spliced forms of these receptors. FcγRII receptors include FcγRIIA (an “activating receptor”) and FcγRIIB (an “inhibiting receptor”), which have similar amino acid sequences that differ primarily in the cytoplasmic domains thereof. Activating receptor FcγRIIA contains an immunoreceptor tyrosine-based activation motif (ITAM) in its cytoplasmic domain. Inhibiting receptor FcγRIIB contains an immunoreceptor tyrosine-based inhibition motif (ITIM) in its cytoplasmic domain (*see review M. Daeron, Annu. Rev. Immunol.* 15:203-234 (1997)). FcRs are reviewed in Ravetch and Kinet, *Annu. Rev. Immunol.* 9:457-492 (1991); Capel *et al.*, *Immunomethods* 4:25-34 (1994); and de Haas *et al.*, *J. Lab. Clin. Med.* 126:330-41 (1995). Other FcRs, including those to be identified in the future, are encompassed by the term “FcR” herein. The term also includes the neonatal receptor, FcRn, which is responsible for the transfer of maternal IgGs to the fetus (Guyer *et al.*, *J. Immunol.* 117:587 (1976) and Kim *et al.*, *J. Immunol.* 24:249 (1994)).

[0155] “Human effector cells” are leukocytes that express one or more FcRs and perform effector functions. Preferably, the cells express at least FcγRIII and perform ADCC effector function. Examples of human leukocytes that mediate ADCC include peripheral blood mononuclear cells (PBMC), natural killer (NK) cells, monocytes, cytotoxic T cells, and neutrophils; with PBMCs and NK cells being preferred. The effector cells can be isolated from a native source, *e.g.*, from blood.

[0156] “Complement dependent cytotoxicity” or “CDC” refers to the lysis of a target cell in the presence of complement. Activation of the classical complement pathway is initiated by the binding of the first component of the complement system (C1q) to antibodies (of the appropriate subclass) that are bound to their cognate antigen. To assess complement activation, a CDC assay, *e.g.*, as described in Gazzano-Santoro *et al.*, J. Immunol. Methods 202:163 (1996), can be performed.

[0157] The term “therapeutically effective amount” refers to an amount of an antibody (including a multispecific antibody), antigen-binding antibody fragment thereof, or derivative thereof to treat a disease or disorder in a subject. In the case of tumor (*e.g.*, a cancerous tumor), the therapeutically effective amount of the antibody or antibody fragment (*e.g.*, a multispecific antibody or antibody fragment may reduce the number of cancer cells; reduce the primary tumor size; inhibit (*i.e.*, slow to some extent and preferably stop) cancer cell infiltration into peripheral organs; inhibit (*i.e.*, slow to some extent and preferably stop) tumor metastasis; inhibit, to some extent, tumor growth; and/or relieve to some extent one or more of the symptoms associated with the disorder. To the extent the antibody or antibody fragment thereof, or derivative thereof may prevent growth and/or kill existing cancer cells, it may be cytostatic and/or cytotoxic. For cancer therapy, efficacy *in vivo* can, for example, be measured by assessing the duration of survival, time to disease progression (TTP), the response rates (RR), duration of response, and/or quality of life.

[0158] By “reduce or inhibit” is meant the ability to cause an overall decrease preferably of 20% or greater, more preferably of 50% or greater, and most preferably of 75%, 85%, 90%, 95%, or greater. Reduce or inhibit can refer to the symptoms of the disorder being treated, the presence or size of metastases, the size of the primary tumor, or the size or number of the blood vessels in angiogenic disorders.

[0159] The terms “cancer” and “cancerous” refer to or describe the physiological condition in mammals that is typically characterized by unregulated cell growth/proliferation. Included in this definition are benign and malignant cancers. Examples of cancer include but are not limited to, carcinoma, lymphoma, blastoma, sarcoma, and leukemia. More particular examples of such cancers include squamous cell cancer, small-cell lung cancer, non-small cell lung cancer, adenocarcinoma of the lung, squamous carcinoma of the lung, cancer of the peritoneum, hepatocellular cancer, gastric or stomach cancer including gastrointestinal cancer, pancreatic cancer, glioblastoma, glioma, cervical cancer, ovarian

cancer, liver cancer, bladder cancer, hepatoma, breast cancer, colon cancer, colorectal cancer, endometrial or uterine carcinoma, salivary gland carcinoma, kidney cancer (*e.g.*, renal cell carcinoma), liver cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma, anal carcinoma, penile carcinoma, melanoma, and various types of head and neck cancer. By “early stage cancer” is meant a cancer that is not invasive or metastatic or is classified as a Stage 0, I, or II cancer. The term “precancerous” refers to a condition or a growth that typically precedes or develops into a cancer. By “non-metastatic” is meant a cancer that is benign or that remains at the primary site and has not penetrated into the lymphatic or blood vessel system or to tissues other than the primary site. Generally, a nonmetastatic cancer is any cancer that is a Stage 0, I, or II cancer, and occasionally a Stage III cancer.

[0160] An “autoimmune disease” herein is a disease or disorder arising from and directed against an individual’s own tissues or a co-segregate or manifestation thereof or resulting condition therefrom. Examples of autoimmune diseases or disorders include, but are not limited to rheumatoid arthritis, autoimmune hemolytic anemia (*e.g.*, immune pancytopenia, paroxysmal nocturnal hemoglobinuria), autoimmune thrombocytopenia (*e.g.*, idiopathic thrombocytopenic purpura, immune-mediated thrombocytopenia), thyroiditis (*e.g.*, Grave’s disease, Hashimoto’s thyroiditis, juvenile lymphocytic thyroiditis, atrophic thyroiditis), type I diabetes mellitus or insulin-dependent diabetes, demyelinating diseases of the central and peripheral nervous systems (*e.g.*, multiple sclerosis, idiopathic demyelinating polyneuropathy or Guillain-Barré syndrome), chronic inflammatory demyelinating polyneuropathy, bullous skin diseases, erythema multiforme, contact dermatitis, and autoimmune chronic active hepatitis.

[0161] The term “cytotoxic agent” as used herein refers to a substance that inhibits or prevents the function of a cell and/or causes destruction of a cell. The term is intended to include radioactive isotopes (*e.g.*, At²¹¹, I¹³¹, I¹²⁵, Y⁹⁰, Re¹⁸⁶, Re¹⁸⁸, Sm¹⁵³, Bi²¹², Ra²²³, P³², and radioactive isotopes of Lu), chemotherapeutic agents, *e.g.*, methotrexate, adriamycin, vinca alkaloids (vincristine, vinblastine, etoposide), doxorubicin, melphalan, mitomycin C, chlorambucil, daunorubicin or other intercalating agents, enzymes and fragments thereof such as nucleolytic enzymes, antibiotics, and toxins such as small molecule toxins or enzymatically active toxins of bacterial, fungal, plant or animal origin, including fragments and/or variants thereof, and the various antitumor, anticancer, and chemotherapeutic agents disclosed herein. Other cytotoxic agents are described herein. A tumoricidal agent causes destruction of tumor cells.

[0162] As used herein, by “pharmaceutically acceptable” or “pharmacologically compatible” is meant a material that is not biologically or otherwise undesirable, *e.g.*, the material may be incorporated into a pharmaceutical composition administered to a patient without causing any significant undesirable biological effects or interacting in a deleterious manner with any of the other components of the composition in which it is contained. Pharmaceutically acceptable carriers or excipients have preferably

met the required standards of toxicological and manufacturing testing and/or are included on the Inactive Ingredient Guide prepared by the U.S. Food and Drug Administration.

[0163] “Anti-cancer therapy” as used herein refers to a treatment that reduces or inhibits cancer in a subject. Examples of anti-cancer therapy include cytotoxic radiotherapy as well as the administration of a therapeutically effective amount of a cytotoxic agent, a chemotherapeutic agent, a growth inhibitory agent, a cancer vaccine, an angiogenesis inhibitor, a prodrug, a cytokine, a cytokine antagonist, a corticosteroid, an immunosuppressive agent, an anti-emetic, an antibody or antibody fragment, or an analgesic to the subject.

[0164] The term “prodrug” as used in this application refers to a precursor or derivative form of a pharmaceutically active substance that is less cytotoxic to tumor cells compared to the parent drug and is capable of being enzymatically activated or converted into the more active parent form. *See, e.g.,* Wilman, “Prodrugs in Cancer Chemotherapy” *Biochemical Society Transactions*, 14, pp. 375-382, 615th Meeting Belfast (1986) and Stella *et al.*, “Prodrugs: A Chemical Approach to Targeted Drug Delivery,” *Directed Drug Delivery*, Borchardt *et al.*, (ed.), pp. 247-267, Humana Press(1985). Prodrugs include, but are not limited to, phosphate-containing prodrugs, thiophosphate-containing prodrugs, sulfate-containing prodrugs, peptide-containing prodrugs, D-amino acid-modified prodrugs, glycosylated prodrugs, beta-lactam containing prodrugs, optionally substituted phenoxyacetamide-containing prodrugs or optionally substituted phenylacetamide-containing prodrugs, 5-fluorocytosine and other 5-fluorouridine prodrugs which can be converted into the more active cytotoxic free drug. Examples of cytotoxic drugs that can be derivatized into a prodrug form for use in this invention include, but are not limited to, those chemotherapeutic agents described above.

[0165] A “subject” is a vertebrate, such as a mammal, *e.g.,* a human. Mammals include, but are not limited to, farm animals (such as cows), sport animals, pets (such as cats, dogs and horses), primates, mice, and rats.

[0166] Except where indicated otherwise by context, the terms “first” polypeptide (such as a heavy chain (H1) or light chain (L1)) and “second” polypeptide (such as a heavy chain (H2) or light chain (L2)), and variations thereof, are merely generic identifiers, and are not to be taken as identifying a specific or a particular polypeptide or component of multispecific antigen-binding proteins provided herein.

[0167] Commercially available reagents referred to in the Examples were used according to manufacturer’s instructions unless otherwise indicated. The source of those cells identified in the following Examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, Manassas, VA. Unless otherwise noted, the present invention uses standard procedures of recombinant DNA technology, such as those described hereinabove and in the following

textbooks: Sambrook *et al.*, *supra*; Ausubel *et al.*, Current Protocols in Molecular Biology (Green Publishing Associates and Wiley Interscience, NY, 1989); Innis *et al.*, PCR Protocols: A Guide to Methods and Applications (Academic Press, Inc., NY, 1990); Harlow *et al.*, Antibodies: A Laboratory Manual (Cold Spring Harbor Press, Cold Spring Harbor, 1988); Gait, Oligonucleotide Synthesis (IRL Press, Oxford, 1984); Freshney, Animal Cell Culture, 1987; Coligan *et al.*, Current Protocols in Immunology, 1991.

[0168] Reference to “about” a value or parameter herein refers to the usual error range for the respective value readily known to the skilled person in this technical field. Reference to “about” a value or parameter herein includes (and describes) aspects that are directed to that value or parameter *per se*. For example, description referring to “about X” includes description of “X.”

[0169] It is understood that aspects and embodiments of the invention described herein include “comprising,” “consisting of,” and “consisting essentially of” aspects and embodiments.

[0170] All references cited herein, including patent applications and publications, are hereby incorporated by reference in their entirety.

Multispecific Antigen-binding Proteins Comprising Mutant or Modified Heavy/Light Chain Pairs

[0171] The present application is based on the identification of novel mutations in the CH1/CL interface, and/or the VH/VL interface that improve heavy chain/light chain pairing selectivity.

[0172] The multispecific antigen-binding proteins provided herein comprise amino acid modifications at particular residues within the variable and/or constant domains of heavy chain and light chain polypeptides. As one of ordinary skill in the art will appreciate, various numbering conventions may be employed for designating particular amino acid residues within IgG variable region sequences. Commonly used numbering conventions include Kabat and EU index numbering (*see*, Kabat *et al.*, *Sequences of Proteins of Immunological Interest*, 5th Ed, Public Health Service, National Institutes of Health, Bethesda, MD (1991)). Other conventions that include corrections or alternate numbering systems for variable domains include Chothia (Chothia C, Lesk AM (1987), *J Mol Biol* 196: 901-917; Chothia, *et al.* (1989), *Nature* 342: 877-883), IMGT (Lefranc, *et al.* (2003), *Dev Comp Immunol* 27: 55-77), and AHo (Honegger A, Plückthun A (2001) *J Mol Biol* 309: 657-670). These references provide amino acid sequence numbering schemes for immunoglobulin variable regions that define the location of variable region amino acid residues of antibody sequences.

[0173] Unless otherwise expressly stated herein, all references to immunoglobulin heavy chain variable region (*i.e.*, VH) amino acid residues (*i.e.* numbers) appearing in the Examples and Claims are based on the Kabat numbering system, as are all references to VL residues. All references to

immunoglobulin heavy chain constant region CH1 residues (*i.e.*, numbers) appearing in the Examples and Claims are based on the EU system, as are all references to CL residues. With knowledge of the residue number according to Kabat or EU Index numbering, one of ordinary skill can identify amino acid sequence modifications described herein, according to any commonly used numbering convention.

[0174] While the Examples and Claims herein employ Kabat or EU Index to identify particular amino acid residues, it is understood that the SEQ IDs appearing in the Sequence Listing, incorporated herein in its entirety, provide sequential numbering of amino acids within a given polypeptide and, thus, do not conform to the corresponding amino acid numbers as provided by Kabat or EU index. For example, the serine residue number 66 of SEQ ID NO:53 corresponds to S183 of CH1 under the EU numbering system.

[0175] Although items, components, or elements provided herein (such as “multispecific antigen-binding protein”) may be described or claimed in the singular, the plural is contemplated to be within the scope thereof unless limitation to the singular is explicitly stated.

[0176] As described in more detail below, provided herein are modified multispecific antigen-binding proteins that can be produced in a single cell with improved correct heavy chain/light chain pairing and/or improved yields as compared with multispecific antigen-binding proteins with sequences without modifications. In certain embodiments, the multispecific antigen-binding proteins comprise modification(s) in the VH/VL and/or CH1/CL regions to facilitate correct heavy/light chain pairing (*i.e.*, the pairing of a first heavy chain H1 (or fragment thereof) with a first light chain L1 to form a first heavy/light chain pair (*i.e.*, H1/L1) capable of binding a first epitope and the pairing of a second heavy chain H2 (or fragment thereof) with a second light chain L2 to form a second heavy/light chain pair (*i.e.*, H2/L2) capable of binding a second (*e.g.*, different) epitope). It will be apparent to those of ordinary skill in the art that the terms “H1” and “H2” are arbitrary designations, and that “H1” and “H2” in any of the embodiments above can be reversed. That is, any of the mutations above described as being in the CH1 domain of H1 and CL domain of L1 can, alternatively, be in the CH1 domain of H2 and the CL domain of L2.

[0177] In certain other embodiments, the multispecific antigen-binding proteins further comprise modification(s) in the Fc region to facilitate heterodimerization of the two arms of the multispecific antigen-binding protein.

Strategy #1

[0178] In one aspect, it was surprisingly found that a single amino acid modification to position S183 (EU numbering) in the CH1 domain of a heavy chain and a single amino acid modification to position V133 (EU numbering) in the CL domain of a light chain demonstrates preferential pairing between the

modified heavy chain and the modified light chain and reducing pairing between, *e.g.*, the modified heavy chain and a non-modified light chain, or, *e.g.*, a non-modified heavy chain and the modified light chain. These residues were selected by expression data and confirmed by the knowledge and studies of the structure and function of the heavy chain CH1 domain and light chain CL domain. *See Figures 1-3, 11C and 12C.*

[0179] Thus, in certain embodiments, there is provided a multispecific antigen-binding protein comprising: (a) a first heavy chain/light chain pair capable of binding to a first antigen, the first heavy chain/light chain pair comprising a first heavy chain polypeptide (H1) and a first light chain polypeptide (L1), and (b) a second heavy chain/light chain pair capable of binding to a second antigen, the second heavy chain/light chain pair comprising a second heavy chain polypeptide (H2) and a second light chain polypeptide (L2), wherein each H1 and H2 comprises a heavy chain variable domain (VH) and a heavy chain constant domain (CH1), and each L1 and L2 comprises a light chain variable domain (VL) and a light chain constant domain (CL); wherein the CH1 domain of H1 comprises an amino acid substitution at position S183 (EU numbering), and wherein the CL domain comprises an amino acid substitution mutation at position V133 (EU numbering). In certain embodiments, the CH1 domain of H1 consists of (such as consists essentially of) an amino acid substitution at position S183 (EU numbering), and wherein the CL domain consists of (such as consists essentially of) an amino acid substitution mutation at position V133 (EU numbering). In certain embodiments, the first antigen and the second antigen are the same. In certain embodiments, the first heavy chain/light chain pair and the second heavy chain/light chain pair each bind to a different epitope on the same antigen. In certain embodiments, the first antigen and the second antigen are different. In certain embodiments, the multispecific antigen-binding protein is a bispecific antibody that binds two different antigens. In certain embodiments, the bispecific antibody is an antagonist or an agonist antibody. In certain embodiments, the bispecific antibody is an antagonist to one or both antigens; while in other embodiments, the bispecific antibody is an agonist to one or both antigens. Antigen-binding fragments of the multispecific antigen-binding proteins (such as bispecific antibodies) provided herein are also contemplated.

[0180] In certain embodiments, the amino acid at position S183 (EU numbering) on the CH1 domain of H1 of the multispecific antigen-binding protein is replaced with a positively charged amino acid residue, and the amino acid at position V133 (EU numbering) on the CL domain of the multispecific antigen-binding protein is replaced with a negatively charged residue. In certain embodiments, the amino acid at position S183 (EU numbering) on the CH1 domain of H1 is replaced with a negatively charged amino acid residue, and the amino acid at position V133 (EU numbering) on the CL domain is replaced with a positively charged residue. In certain embodiments, the positively charged residue is selected from the group consisting of R or K. In certain embodiments, the negatively charged residue is selected from the group consisting of D and E.

[0181] In certain embodiments, the CH1 domain of the multispecific antigen-binding protein comprises an amino acid substitution selected from the group consisting of S183A, S183T, S183V, S183Y, S183F, S183H, S183N, S183D, S183E, S183R, and S183K (EU numbering), and wherein the CL domain comprises an amino acid substitution selected from the group consisting of V133E, V133S, V133L, V133W, V133K, V133R, and V133D (EU numbering).

[0182] In certain embodiments, the CH1 domain of the multispecific antigen-binding protein consists of (such as consists essentially of) an amino acid substitution selected from the group consisting of: S183A, S183T, S183V, S183Y, S183F, S183H, S183N, S183D, S183E, S183R, and S183K (EU numbering), and wherein the CL domain consists of (such as consists essentially of) an amino acid substitution selected from the group consisting of V133E, V133S, V133L, V133W, V133K, V133R, and V133D (EU numbering).

[0183] It will be apparent to those of ordinary skill in the art that the terms “H1” and “H2” are arbitrary designations, and that “H1” and “H2” in any of the embodiments above can be reversed. That is, any of the mutations above described as being in the CH1 domain of H1 and CL domain of L1 can, alternatively, be in the CH1 domain of H2 and the CL domain of L2.

[0184] Thus, all possible pair-wise combinations of substitution mutations at position S183 (EU numbering) on the CH1 domain of H1 and at position V133 (EU numbering) on the CL domain of L1 are contemplated. In certain embodiments, specific combinations of substitution mutations at position S183 (EU numbering) on the CH1 domain of H1 and at position V133 (EU numbering) on the CL domain of L1 are contemplated. Such combinations include, but are not limited to, those provided in Table 1 below:

Table 1

S183D/ V133K	S183A/ V133K	S183T/ V133W	S183V/ V133L	S183Y/ V133S	S183F/ V133E	S183F/ V133D
S183E/ V133K	S183A/ V133R	S183T/ V133K	S183V/ V133W	S183Y/ V133L	S183F/ V133S	S183H/ V133S
S183A/ V133E	S183A/ V133D	S183T/ V133R	S183V/ V133K	S183Y/ V133W	S183F/ V133L	S183H/ V133L
S183A/ V133S	S183T/ V133E	S183T/ V133D	S183V/ V133R	S183Y/ V133K	S183F/ V133W	S183H/ V133W
S183A/ V133L	S183T/ V133S	S183V/ V133E	S183V/ V133D	S183Y/ V133R	S183F/ V133K	S183N/ V133L
S183A/ V133W	S183T/ V133L	S183V/ V133S	S183Y/ V133E	S183Y/ V133D	S183F/ V133R	S183E/ V133L
S183T/ V133K	S183K/ V133E	S183Y/ V133K				

[0185] In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the S183D or S183E mutation (EU numbering), and a CL domain of L1 comprising the V133K mutation (EU numbering). In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 and a CL domain of L1, wherein the CH1 domain consists of the S183D or S183E mutation (EU numbering), and a CL domain of L1 consists of the V133K mutation (EU numbering).

[0186] Two exemplary IgG1 CH1 domain amino acid sequences (SEQ ID NO: 53 and SEQ ID NO: 109), an exemplary IgG2 CH1 domain amino acid sequence (SEQ ID NO: 109), an exemplary IgG2 CH1 domain sequence (SEQ ID NO: 110), an exemplary IgG3 CH1 domain amino acid sequence (SEQ ID NO: 111), an exemplary IgG4 CH1 domain amino acid sequence (SEQ ID NO: 112), an exemplary lambda CL domain amino acid sequence (SEQ ID NO: 113) and an exemplary kappa CL domain amino acid sequence (SEQ ID NO: 54) are provided below:

ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTPFAVLQSS GLYSLSSVVT
VPSSSLGTQT YICNVN HKPS NTKVDKKV (SEQ ID NO: 53)

TKGPSVFPLA PSSKSTSGGT AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP
SSSLGTQTYI CN (SEQ ID NO: 109)

TKGPSVFPLA PCSRSTSEST AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP
SSNFGTQTYT CN (SEQ ID NO: 110)

TKGPSVFPLA PCSRSTSGGT AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP
SSSLGTQTYT CN (SEQ ID NO: 111)

TKGPSVFPLA PCSRSTSEST AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP
SSSLGTQTYT CN (SEQ ID NO: 112)

GQPKAAPSVT LFPPSSEELQ ANKATLVCLI SDFYPGAVTV AWKADSSPVK AGVETTTPSK QSNNKYAASS
YLSLTPEQWK SHKSYSCQVT HEGSTVEKTV APTECS (SEQ ID NO: 113)

TVAAPSVFIF PPSDEQLKSG TASVVCLLNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYLSLSST
LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC (SEQ ID NO: 54, without the R residue at the N-terminus of the mature CL domain, as shown in SEQ ID NO:30, which is generated as the result of gene splicing)

[0187] The amino acid sequences of full-length 4D5 IgG1 heavy chain (SEQ ID NO: 55) and light chain (SEQ ID NO: 56) are provided below:

4D5 HC (Human IgG1):

EVQLVESGGG LVQPGGSLRL SCAASGFNIK DTYIHWVRQA PGKGLEWVAR IYPTNGYTRY ADSVKGRETI
 SADTSKNTAY LQMNSLRAED TAVYYCSRWG GDGFYAMDYW GQGT LVT VSS ASTKGPSVFP LAPSSKSTSG
 GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT YICNVNHNKPS
 NTKVDKKVEP KSCDKTHTCP PCPAPELLGG PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW
 YVDGVEVHNA KTKPREEQYN STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ
 VYTLPPSREE MTKNQVSLWC LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW
 QQGNVFSCSV MHEALHNHYT QKSLSLSPGK (SEQ ID NO: 55)

4D5 LC (Human Kappa):

DIQMTQSPSS LSASVGDRVIT ITCRASQDVN TAVAWYQQKP GKAPKLLIYS ASFLYSGVPS RFGSGRSGTD
 FTLTISSLQP EDFATYYCQQ HYTPPTFGQ GTKVEIKRTV AAPSVFIFPP SDEQLKSGTA SVVCLLNIFY
 PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSSLT LT LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEK (SEQ
 ID NO: 56)

[0188] In certain embodiments, the multispecific antigen-binding protein comprises a kappa light chain. In certain embodiments, the multispecific antigen-binding protein comprises a CL domain of L1 comprising the amino acid sequence set forth in SEQ ID NO: 1 or the amino acids 11-116 in the sequence set forth in SEQ ID NO: 1. In certain embodiments, the multispecific antigen-binding protein comprises a CL domain of L1 comprising the amino acid sequence set forth in SEQ ID NO: 2 or the amino acids 11-116 in the sequence set forth in SEQ ID NO: 2. In certain embodiments, the multispecific antigen-binding protein comprises a CL domain of L1 comprising the amino acid sequence set forth in SEQ ID NO: 3 or the amino acids 11-116 in the sequence set forth in SEQ ID NO: 3. In certain embodiments, the multispecific antigen-binding protein comprises a CL domain of L1 comprising the amino acid sequence set forth in SEQ ID NO: 4 or the amino acids 11-116 in the sequence set forth in SEQ ID NO: 4. In certain embodiments, the multispecific antigen-binding protein comprises a CL domain of L1 comprising the amino acid sequence set forth in SEQ ID NO: 5 or the amino acids 11-116 in the sequence set forth in SEQ ID NO: 5. In certain embodiments, the multispecific antigen-binding protein comprises a CL domain of L1 comprising the amino acid sequence set forth in SEQ ID NO: 6 or the amino acids 11-116 in the sequence set forth in SEQ ID NO: 6. In certain embodiments, the multispecific antigen-binding protein comprises a CL domain of L1 comprising the amino acid sequence set forth in SEQ ID NO: 7 or the amino acids 11-116 in the sequence set forth in SEQ ID NO: 7.

[0189] The amino acid sequences of SEQ ID NOs: 1-7 are provided in Table 2A below. In certain embodiments, the multispecific antigen-binding protein comprises a first light chain polypeptide L1 comprising a CL domain as set forth in any of these sequences. The CL domain as set forth in SEQ ID NO: 54 corresponds to amino acids 11-116 of SEQ ID NOs: 1-7. Accordingly, L1 may comprise a CL domain comprising amino acids 11-116 as set forth in any of SEQ ID Nos: 1-7.

Table 2A

V133E SEQ ID NO: 1	GQGTKVEIKR TVAAPSVFIF PPSDEQLKSG TASV E CLLNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSLSST LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC
V133S SEQ ID NO: 2	GQGTKVEIKR TVAAPSVFIF PPSDEQLKSG TASV S CLLNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSLSST LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC
V133L SEQ ID NO: 3	GQGTKVEIKR TVAAPSVFIF PPSDEQLKSG TASV L CLLNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSLSST LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC
V133W SEQ ID NO: 4	GQGTKVEIKR TVAAPSVFIF PPSDEQLKSG TASV W CLLNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSLSST LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC
V133K SEQ ID NO: 5	GQGTKVEIKR TVAAPSVFIF PPSDEQLKSG TASV K CLLNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSLSST LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC
V133R SEQ ID NO: 6	GQGTKVEIKR TVAAPSVFIF PPSDEQLKSG TASV R CLLNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSLSST LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC
V133D SEQ ID NO: 7	GQGTKVEIKR TVAAPSVFIF PPSDEQLKSG TASV D CLLNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSLSST LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC

[0190] Amino acid position 133 (EU numbering) in the CL domain of a kappa light chain corresponds to amino acid position 35 in SEQ ID NOs: 1-7.

[0191] In certain embodiments, the multispecific antigen-binding protein comprises a lambda light chain. In certain embodiments, the multispecific antigen-binding protein comprises a CL domain of L1 comprising the amino acid sequence set forth in SEQ ID NO: 114. In certain embodiments, the multispecific antigen-binding protein comprises a CL domain of L1 comprising the amino acid sequence set forth in SEQ ID NO: 115. In certain embodiments, the multispecific antigen-binding protein comprises a CL domain of L1 comprising the amino acid sequence set forth in SEQ ID NO: 116. In certain embodiments, the multispecific antigen-binding protein comprises a CL domain of L1 comprising the amino acid sequence set forth in SEQ ID NO: 117. In certain embodiments, the multispecific antigen-binding protein comprises a CL domain of L1 comprising the amino acid sequence set forth in SEQ ID NO: 118. In certain embodiments, the multispecific antigen-binding protein comprises a CL domain of L1 comprising the amino acid sequence set forth in SEQ ID NO: 119. In certain embodiments, the multispecific antigen-binding protein comprises a CL domain of L1 comprising the amino acid sequence set forth in SEQ ID NO: 120.

[0192] The amino acid sequences of SEQ ID NOs: 114-120 are provided in Table 2B below:

Table 2B

V133E SEQ ID NO: 114	GQPKAAPSVT LFPPSSEELQ ANKATL E CLI SDFYPGAVTV AWKADSSPVK AGVETTTPSK QSNNKYAASS YLSLTPEQWK SHKSYSCQVT HEGSTVEKTV APTECS
V133S SEQ ID NO: 115	GQPKAAPSVT LFPPSSEELQ ANKATL S CLI SDFYPGAVTV AWKADSSPVK AGVETTTPSK QSNNKYAASS YLSLTPEQWK SHKSYSCQVT HEGSTVEKTV APTECS
V133L SEQ ID NO: 116	GQPKAAPSVT LFPPSSEELQ ANKATL L CLI SDFYPGAVTV AWKADSSPVK AGVETTTPSK QSNNKYAASS YLSLTPEQWK SHKSYSCQVT HEGSTVEKTV APTECS
V133W SEQ ID NO: 117	GQPKAAPSVT LFPPSSEELQ ANKATL W CLI SDFYPGAVTV AWKADSSPVK AGVETTTPSK QSNNKYAASS YLSLTPEQWK SHKSYSCQVT HEGSTVEKTV APTECS
V133K SEQ ID NO: 118	GQPKAAPSVT LFPPSSEELQ ANKATL K CLI SDFYPGAVTV AWKADSSPVK AGVETTTPSK QSNNKYAASS YLSLTPEQWK SHKSYSCQVT HEGSTVEKTV APTECS
V133R SEQ ID NO: 119	GQPKAAPSVT LFPPSSEELQ ANKATL R CLI SDFYPGAVTV AWKADSSPVK AGVETTTPSK QSNNKYAASS YLSLTPEQWK SHKSYSCQVT HEGSTVEKTV APTECS
V133D SEQ ID NO: 120	GQPKAAPSVT LFPPSSEELQ ANKATL D CLI SDFYPGAVTV AWKADSSPVK AGVETTTPSK QSNNKYAASS YLSLTPEQWK SHKSYSCQVT HEGSTVEKTV APTECS

[0193] Amino acid position 133 (EU numbering) in the CL domain of a kappa light chain corresponds to amino acid position 133 (Kabat numbering) in the CL domain of a lambda light chain, which corresponds to amino acid position 27 in SEQ ID NOs: 114-120.

[0194] In certain embodiments, the multispecific antigen-binding protein comprises an IgG1 heavy chain, an IgG2 heavy chain, an IgG3 heavy chain, or an IgG4 heavy chain. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 8. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 9. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 10. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 11. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 12. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 13. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 14. In certain embodiments, the multispecific antigen-binding protein

comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 15. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 16. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 101. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 102. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 121. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 122. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 123. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 124. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 125. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 126.

[0195] The amino acid sequences of SEQ ID NOs: 8-16, 101-102, and 121-126 are provided in Table 3 below:

Table 3

S183A SEQ ID NO: 8	TKGPSVFPLA PSSKSTSGGT AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSL A SVVTVP SSSLGTQTYI CN
S183T SEQ ID NO: 9	TKGPSVFPLA PSSKSTSGGT AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSL T SVVTVP SSSLGTQTYI CN
S183V SEQ ID NO: 10	TKGPSVFPLA PSSKSTSGGT AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSL V SVVTVP SSSLGTQTYI CN
S183Y SEQ ID NO: 11	TKGPSVFPLA PSSKSTSGGT AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSL Y SVVTVP SSSLGTQTYI CN
S183F SEQ ID NO: 12	TKGPSVFPLA PSSKSTSGGT AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSL F SVVTVP SSSLGTQTYI CN
S183H SEQ ID NO: 13	TKGPSVFPLA PSSKSTSGGT AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSL H SVVTVP SSSLGTQTYI CN
S183N SEQ ID NO: 14	TKGPSVFPLA PSSKSTSGGT AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSL N SVVTVP SSSLGTQTYI CN

S183E IgG1 SEQ ID NO: 15	TKGPSVFPLA PSSKSTSGGT AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSL E SVVTVP SSSLGTQTYI CN
S183D SEQ ID NO: 16	TKGPSVFPLA PSSKSTSGGT AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSL D SVVTVP SSSLGTQTYI CN
S183E IgG2 SEQ ID NO: 121	TKGPSVFPLA PCSRSTSEST AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSL E SVVTVP SSNFGTQTYT CN
S183E IgG3 SEQ ID NO: 122	TKGPSVFPLA PCSRSTSGGT AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSL E SVVTVP SSSLGTQTYT CN
S183E IgG4 SEQ ID NO: 123	TKGPSVFPLA PCSRSTSEST AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSL E SVVTVP SSSLGTKTYT CN
S183R SEQ ID NO: 101	TKGPSVFPLA PSSKSTSGGT AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSL R SVVTVP SSSLGTQTYI CN
S183K IgG1 SEQ ID NO: 102	TKGPSVFPLA PSSKSTSGGT AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSL K SVVTVP SSSLGTQTYI CN
S183K IgG2 SEQ ID NO: 124	TKGPSVFPLA PCSRSTSEST AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSL K SVVTVP SSNFGTQTYT CN
S183K IgG3 SEQ ID NO: 125	TKGPSVFPLA PCSRSTSGGT AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSL K SVVTVP SSSLGTQTYT CN
S183K IgG4 SEQ ID NO: 126	TKGPSVFPLA PCSRSTSEST AALGCLVKDY FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSL K SVVTVP SSSLGTKTYT CN

[0196] Amino acid position 183 in the CH1 domain of IgG1, IgG2, IgG3, and IgG4 corresponds to amino acid position 64 in SEQ ID NOs: 8-16, 101-102, and 121-126.

[0197] All possible pair-wise combinations of SEQ ID NOs: 1-7 or amino acids 11-116 of SEQ ID Nos: 1-7 and 114-120 with SEQ ID NOs: 8-15, 101-102, and 121-126 are contemplated. In certain embodiments, specific combinations of SEQ ID NOs: 1-7 or amino acids 11-116 of SEQ ID Nos: 1-7 and 114-120 with SEQ ID NOs: 8-15 and 101 and 102 are contemplated. Such combinations include, but are not limited to, those provided in Table 4 below (HC is IgG1 HC unless indicated otherwise):

Table 4

SEQ ID NO: 16/ SEQ ID NO: 5* S183D/V133K kappa	SEQ ID NO: 8/ SEQ ID NO: 5* S183A/V133K kappa	SEQ ID NO: 9/ SEQ ID NO: 4* S183T/V133W kappa	SEQ ID NO: 10/ SEQ ID NO: 3* S183V/V133L kappa
SEQ ID NO: 15/	SEQ ID NO: 8/	SEQ ID NO: 9/	SEQ ID NO: 10/

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SEQ ID NO: 5* S183E/V133K IgG1/kappa	SEQ ID NO: 6* S183A/V133R kappa	SEQ ID NO: 5* S183T/V133K kappa	SEQ ID NO: 4* S183V/V133W kappa
SEQ ID NO: 8/ SEQ ID NO: 1* S183A/V133E kappa	SEQ ID NO: 8/ SEQ ID NO: 7* S183A/V133D kappa	SEQ ID NO: 9/ SEQ ID NO: 6* S183T/V133R kappa	SEQ ID NO: 10/ SEQ ID NO: 5* S183V/V133K kappa
SEQ ID NO: 8/ SEQ ID NO: 2* S183A/V133S kappa	SEQ ID NO: 9/ SEQ ID NO: 1* S183T/V133E kappa	SEQ ID NO: 9/ SEQ ID NO: 7* S183T/V133D kappa	SEQ ID NO: 10/ SEQ ID NO: 6* S183V/V133R kappa
SEQ ID NO: 8/ SEQ ID NO: 3* S183A/V133L kappa	SEQ ID NO: 9/ SEQ ID NO: 2* S183T/V133S kappa	SEQ ID NO: 10/ SEQ ID NO: 1* S183V/V133E kappa	SEQ ID NO: 10/ SEQ ID NO: 7* S183V/V133D kappa
SEQ ID NO: 8/ SEQ ID NO: 4* S183A/V133W kappa	SEQ ID NO: 9/ SEQ ID NO: 3* S183T/V133L kappa	SEQ ID NO: 10/ SEQ ID NO: 2* S183V/V133S kappa	SEQ ID NO: 11/ SEQ ID NO: 1* S183Y/V133E kappa
SEQ ID NO: 11/ SEQ ID NO: 2* S183Y/V133S kappa	SEQ ID NO: 12/ SEQ ID NO: 1* S183F/V133E kappa	SEQ ID NO: 12/ SEQ ID NO: 7* S183F/V133D kappa	SEQ ID NO: 11/ SEQ ID NO: 3* S183Y/V133L kappa
SEQ ID NO: 12/ SEQ ID NO: 2* S183F/V133S kappa	SEQ ID NO: 13/ SEQ ID NO: 2* S183H/V133S kappa	SEQ ID NO: 11/ SEQ ID NO: 4* S183Y/V133W kappa	SEQ ID NO: 12/ SEQ ID NO: 3* S183F/V133L kappa
SEQ ID NO: 13/ SEQ ID NO: 3* S183H/V133L kappa	SEQ ID NO: 11/ SEQ ID NO: 5* S183Y/V133K kappa	SEQ ID NO: 12/ SEQ ID NO: 4* S183F/V133W kappa	SEQ ID NO: 13/ SEQ ID NO: 4* S183H/V133W kappa
SEQ ID NO: 11/ SEQ ID NO: 6* S183Y/V133R kappa	SEQ ID NO: 12/ SEQ ID NO: 5* S183F/V133K kappa	SEQ ID NO: 14/ SEQ ID NO: 3* S183N/V133L kappa	SEQ ID NO: 11/ SEQ ID NO: 7* S183Y/V133D kappa
SEQ ID NO: 12/ SEQ ID NO: 6* S183F/V133R kappa	SEQ ID NO: 15/ SEQ ID NO: 3* S183E/V133L kappa	SEQ ID NO: 102/ SEQ ID NO: 1* S183K/V133E kappa	SEQ ID NO: 9/ SEQ ID NO: 5* S183T/V133K kappa
SEQ ID NO: 8/ SEQ ID NO: 114 S183A/V133E lambda	SEQ ID NO: 9/ SEQ ID NO: 114 S183T/V133E lambda	SEQ ID NO: 10/ SEQ ID NO: 114 S183V/V133E lambda	SEQ ID NO: 11/ SEQ ID NO: 114 S183Y/V133E lambda
SEQ ID NO: 12/ SEQ ID NO: 114 S183F/V133E lambda	SEQ ID NO: 102/ SEQ ID NO: 114 S183K/V133E IgG1/lambda	SEQ ID NO: 16/ SEQ ID NO: 118 S183D/V133K lambda	SEQ ID NO: 8/ SEQ ID NO: 118 S183A/V133K lambda
SEQ ID NO: 15/ SEQ ID NO: 118 S183E /V133K IgG1/lambda	SEQ ID NO: 9/ SEQ ID NO: 118 S183T/V133K lambda	SEQ ID NO: 10/ SEQ ID NO: 118 S183V/V133K lambda	SEQ ID NO: 11/ SEQ ID NO: 118 S183Y/V133K lambda
SEQ ID NO: 12/ SEQ ID NO: 118 S183F/V133K lambda	SEQ ID NO: 9/ SEQ ID NO: 118 S183T/V133K lambda	SEQ ID NO: 121/ SEQ ID NO: 5 S183E/V133K IgG2/kappa	SEQ ID NO: 122/ SEQ ID NO: 5 S183E/V133K IgG3/kappa
SEQ ID NO: 123/ SEQ ID NO: 5 S183E/V133K IgG4/kappa	SEQ ID NO: 121/ SEQ ID NO: 118 S183E /V133K IgG2/lambda	SEQ ID NO: 122/ SEQ ID NO: 118 S183E /V133K IgG3/lambda	SEQ ID NO: 123/ SEQ ID NO: 118 S183E /V133K IgG4/lambda
SEQ ID NO: 124/ SEQ ID NO: 1 S183K/V133E IgG2/kappa	SEQ ID NO: 125/ SEQ ID NO: 1 S183K/V133E IgG3/kappa	SEQ ID NO: 126/ SEQ ID NO: 1 S183K/V133E IgG4/kappa	SEQ ID NO: 124/ SEQ ID NO: 114 S183K/V133E IgG2/lambda
SEQ ID NO: 125/	SEQ ID NO: 126/		

SED ID NO: 114 S183K/V133E IgG3/lambda	SED ID NO: 114 S183K/V133E IgG4/lambda		
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* or amino acids 11-116 of the corresponding sequence

[0198] The first SEQ ID NO in each pair in Table 4 refers to a CH1 domain sequence, and the second SEQ ID NO in each pair in Table 4 refers to a CL domain sequence.

[0199] It will be apparent to those of ordinary skill in the art that the terms “H1” and “H2” are arbitrary designations, and that “H1” and “H2” in any of the embodiments above can be reversed. That is, any of the mutations above described as being in the CH1 domain of H1 and CL domain of L1 can, alternatively, be in the CH1 domain of H2 and the CL domain of L2.

[0200] In certain embodiments, the multispecific antigen-binding proteins comprise CH1/CL mutations and demonstrate correct protein folding and/or expression levels that are comparable or superior to the multispecific antigen-binding proteins without the mutations or each parental monospecific antigen-binding proteins without the mutations.

[0201] In certain embodiments, the CH1 domain of H2 and the CL domain of L2 of the multispecific antigen-binding protein do not comprise an amino acid substitution. In certain embodiments, the CH1 of H2 of the multispecific antigen-binding protein does not comprise a substitution at S183 (EU numbering), and the CL of L2 of the multispecific antigen-binding protein does not comprise a substitution at V133 (EU numbering).

[0202] In certain embodiments, the parental H1 from which an H1 of a multispecific antigen-binding protein provided herein is derived does not show a significant preference for a parental L1 from which an L1 of a multispecific antigen-binding protein provided herein is derived. In certain embodiments, the parental H1 from which an H1 of a multispecific antigen-binding protein provided herein is derived shows a preference for a parental L1 from which an L1 of a multispecific antigen-binding protein provided herein is derived.

[0203] It will be apparent to those of ordinary skill in the art that the terms “H1” and “H2” are arbitrary designations, and that “H1” and “H2” in any of the embodiments above can be reversed. That is, any of the mutations above described as being in the CH1 domain of H1 and CL domain of L1 can, alternatively, be in the CH1 domain of H2 and the CL domain of L2.

Strategy #2

[0204] Using a second strategy aided by computer-guided and human-guided designs, Applicants redesigned the interacting surfaces of a CH1 domain of a heavy chain and a CL domain of a light chain to generate CH1/CL mutant pairs that are sterically compatible (such as conformationally compatible) with

each other. The modified CH1 domains in each CH1/CL mutant pair are less sterically compatible (such as conformationally compatible) with wild-type CL, and demonstrate decreased pairing to wild-type CL. Correspondingly, the modified CL domains in each CH1/CL mutant pair are less sterically compatible (such as conformationally compatible) with wild-type CH1, and demonstrate decreased pairing to wild-type CH1. It was surprisingly discovered that the T_m of the Fabs comprising the modifications at the interface of the CH1 and CL domains were the same or substantially the same as the T_m of the Fabs without the corresponding mutations in the CH1/CL domains.

[0205] The mutations identified using the design strategy described below can be used independently of or in addition to the S183/V133 mutations discussed above (*i.e.*, Strategy #1).

[0206] In a first approach (*i.e.*, “Approach A”), one or more amino acid substitution mutations were introduced to the CL domain of a light chain to create a “knob” (or protuberance) on the surface of the CL domain that interacts with the CH1 domain. Correspondingly, one or more amino acid substitution mutations were introduced to the CH1 domain of a heavy chain to create a “hole” (or cavity) on the surface of the CH1 domain that interacts with the CL domain. *See, e.g.*, Figure 11A. In certain embodiments, the multispecific antigen-binding proteins comprising the modified CH1/CL sequences result in preferential pairing of the heavy and light chains with the amino acid substitution mutations in the CH1 and CL domains. In certain embodiments, the multispecific antigen-binding proteins comprising the modified CH1/CL sequences demonstrate increased protein expression levels as compared to the multispecific antigen-binding proteins without the corresponding CH1/CL mutations. In certain embodiments, the substituted amino acid(s) are not replaced with charged residue(s).

[0207] In a second approach (*i.e.*, “Approach B”), two or more amino acid substitution mutations were introduced to the CL domain of a light chain to create a “knob” (or protuberance) and a “hole” (or cavity) on the surface of the CL domain that interacts with the CH1 domain. Correspondingly, two or more mutations were introduced to the CH1 domain of a heavy chain to create a “hole” and a “knob” at the surface of the CH1 domain that interacts with the CL domain. *See, e.g.*, Figure 11B. In certain embodiments, the multispecific antigen-binding proteins comprising the modified CH1/CL sequences show preferential pairing of the heavy and light chains with the amino acid substitution mutations in the CH1 and CL domains. In certain embodiments, the multispecific antigen-binding proteins comprising the modified CH1/CL sequences show increased protein expression as compared to the multispecific antigen-binding proteins without the corresponding CH1/CL mutations. In certain embodiments, the substituted amino acid(s) are not replaced with charged residue(s).

[0208] Multispecific antigen-binding proteins comprising a modified CH1 domain of H1 and a modified CL domain of L1 demonstrate improved stability and improved specificity with regard to heavy chain/light chain pairing. Provided herein is a multispecific antigen-binding protein comprising: a) a first

heavy chain/light chain pair capable of binding to a first antigen, the first heavy chain/light chain pair comprising a first heavy chain polypeptide (H1) and a first light chain polypeptide (L1), and b) a second heavy chain/light chain pair capable of binding to a second antigen, the second heavy chain/light chain pair comprising a second heavy chain polypeptide (H2) and a second light chain polypeptide (L2), wherein each H1 and H2 comprises a heavy chain variable domain (VH) and a heavy chain constant domain (CH1), and each L1 and L2 comprises a light chain variable domain (VL) and a light chain constant domain (CL); wherein the CH1 domain of H1 comprises an amino acid substitution at position F170 (EU numbering), and wherein the CL domain comprises an amino acid substitution at position S176 (EU numbering). In certain embodiments, the first antigen and the second antigen are the same. In certain embodiments, the first heavy chain/light chain pair and the second heavy chain/light chain pair each bind to a different epitope on the same antigen. In certain embodiments, the first antigen and the second antigen are different. In certain embodiments, the CH1 domain of H1 of the multispecific antigen-binding protein further comprises one or more amino acid substitutions selected from the group consisting of: A141, S181, S183, and V185 (all EU numbering). In certain embodiments, the CL domain of L1 of the multispecific antigen-binding protein further comprises one or more amino acid substitutions selected from the group consisting of F116, S131, V133, L135, S162, S174, and T178 (all EU numbering). In certain embodiments, the CL domain of L1 of the multispecific antigen-binding protein further comprises one or more amino acid substitutions selected from the group consisting of F116, V133, L135, S162, S174, and T178 (all EU numbering). In certain embodiments, the CL domain of L1 of the multispecific antigen-binding protein further comprises one or more amino acid substitutions selected from the group consisting of F116, S131, L135, S162, S174, and T178 (all EU numbering). In certain embodiments, the CL domain of L1 of the multispecific antigen-binding protein further comprises one or more amino acid substitutions selected from the group consisting of F116, L135, S174, and T178 (all EU numbering). In certain embodiments, the CL domain of L1 of the multispecific antigen-binding protein further comprises one or more amino acid substitutions selected from the group consisting of F116, L135, S162, S174, and T178 (all EU numbering). In certain embodiments, the amino acid substitutions result in steric complementarity. In certain embodiments, the amino acid substitutions result in conformational complementarity. In certain embodiments, the substituted amino acid(s) are not replaced with charged residue(s).

[0209] In certain embodiments, the CH1 domain of H1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) one or more amino acid substitutions selected from the group consisting of: A141 and F170 (all EU numbering). In certain embodiments, the CL domain of L1 of the multispecific antigen-binding protein comprises one or more amino acid substitutions selected from the group consisting of F116, L135, S176, and T178 (all EU numbering). In certain embodiments, the amino acid substitutions result in steric complementarity. In certain embodiments, the amino acid substitutions result in conformational complementarity.

[0210] In certain embodiments, the CH1 domain of H1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) one or more amino acid substitutions selected from the group consisting of: F170, S181, and S183 (all EU numbering). In certain embodiments, the CL domain of L1 of the multispecific antigen-binding protein comprises one or more amino acid substitutions selected from the group consisting of F116 and S176 (all EU numbering). In certain embodiments, the amino acid substitutions result in steric complementarity. In certain embodiments, the amino acid substitutions result in conformational complementarity.

[0211] In certain embodiments, the CH1 domain of H1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) the amino acid substitution F170 (EU numbering). In certain embodiments, the CL domain of L1 of the multispecific antigen-binding protein comprises one or more amino acid substitutions selected from the group consisting of F116, L135, S174, S176, and T178 (all EU numbering). In certain embodiments, the amino acid substitutions result in steric complementarity. In certain embodiments, the amino acid substitutions result in conformational complementarity.

[0212] In certain embodiments, the CH1 domain of H1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) one or more amino acid substitutions selected from the group consisting of: F170, S183, and V185 (all EU numbering). In certain embodiments, the CL domain of L1 of the multispecific antigen-binding protein comprises one or more amino acid substitutions selected from the group consisting of F116, S176, and T178 (all EU numbering). In certain embodiments, the amino acid substitutions result in steric complementarity. In certain embodiments, the amino acid substitutions result in conformational complementarity.

[0213] In certain embodiments, the CH1 domain of H1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) one or more amino acid substitutions selected from the group consisting of: F170, S181, and V185 (all EU numbering). In certain embodiments, the CL domain of L1 of the multispecific antigen-binding protein comprises one or more amino acid substitutions selected from the group consisting of F116, L135, and S176 (all EU numbering). In certain embodiments, the amino acid substitutions result in steric complementarity. In certain embodiments, the amino acid substitutions result in conformational complementarity.

[0214] In certain embodiments, the CH1 domain of H1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) one or more amino acid substitutions selected from the group consisting of: A141 and F170 (all EU numbering). In certain embodiments, the CL domain of L1 of the multispecific antigen-binding protein comprises one or more amino acid substitutions selected from the group consisting of F116, L135, S174, S176, and T178 (all EU numbering). In certain

embodiments, the amino acid substitutions result in steric complementarity. In certain embodiments, the amino acid substitutions result in conformational complementarity.

[0215] In certain embodiments, the CH1 domain of H1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) one or more amino acid substitutions selected from the group consisting of: A141, F170, and S181 (all EU numbering). In certain embodiments, the CL domain of L1 of the multispecific antigen-binding protein comprises one or more amino acid substitutions selected from the group consisting of F116, L135, S174, S176, and T178 (all EU numbering). In certain embodiments, the amino acid substitutions result in steric complementarity. In certain embodiments, the amino acid substitutions result in conformational complementarity.

[0216] In certain embodiments, the CH1 domain of H1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) one or more amino acid substitutions selected from the group consisting of: F170, S181, S183, and V185 (all EU numbering). In certain embodiments, the CL domain of L1 of the multispecific antigen-binding protein comprises one or more amino acid substitutions selected from the group consisting of L135, S174, S176, and T178 (all EU numbering). In certain embodiments, the amino acid substitutions result in steric complementarity. In certain embodiments, the amino acid substitutions result in conformational complementarity.

[0217] In certain embodiments, the CH1 domain of H1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) one or more amino acid substitutions selected from the group consisting of: A141, F170, S183, and V185 (all EU numbering). In certain embodiments, the CL domain of L1 of the multispecific antigen-binding protein comprises one or more amino acid substitutions selected from the group consisting of F116, S174, S176, and T178 (all EU numbering). In certain embodiments, the amino acid substitutions result in steric complementarity. In certain embodiments, the amino acid substitutions result in conformational complementarity.

[0218] In certain embodiments, the CH1 domain of H1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) one or more amino acid substitutions selected from the group consisting of: A141, F170, S181, and V185 (all EU numbering). In certain embodiments, the CL domain of L1 of the multispecific antigen-binding protein comprises one or more amino acid substitutions selected from the group consisting of F116, L135, S176, and T178 (all EU numbering). In certain embodiments, the amino acid substitutions result in steric complementarity. In certain embodiments, the amino acid substitutions result in conformational complementarity.

[0219] In certain embodiments, the CH1 domain of H1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) one or more amino acid substitutions selected from the group consisting of A141, F170, S181, and S183 (all EU numbering). In certain embodiments,

the CL domain of L1 of the multispecific antigen-binding protein comprises one or more amino acid substitutions selected from the group consisting of F116, L135, S174, and S176 (all EU numbering). In certain embodiments, the amino acid substitutions result in steric complementarity. In certain embodiments, the amino acid substitutions result in conformational complementarity.

[0220] In certain embodiments, the CH1 domain of H1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) the amino acid substitution F170 (EU numbering). In certain embodiments, the CL domain of L1 of the multispecific antigen-binding protein comprises one or more amino acid substitutions selected from the group consisting of F116, L135, S176, and T178 (all EU numbering). In certain embodiments, the amino acid substitutions result in steric complementarity. In certain embodiments, the amino acid substitutions result in conformational complementarity.

[0221] In certain embodiments, the CH1 domain of H1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) one or more amino acid substitutions selected from the group consisting of: A141 F170, and V185 (EU numbering). In certain embodiments, the CL domain of L1 of the multispecific antigen-binding protein comprises one or more amino acid substitutions selected from the group consisting of F116 and S176 mutations (all EU numbering). In certain embodiments, the amino acid substitutions result in conformational complementarity.

[0222] In certain embodiments, the CH1 domain of H1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) one or more amino acid substitutions selected from the group consisting of: A141, F170, and S183 (EU numbering). In certain embodiments, the CL domain of L1 of the multispecific antigen-binding protein comprises one or more amino acid substitutions selected from the group consisting of F116 and S176 mutations (all EU numbering). In certain embodiments, the amino acid substitutions result in conformational complementarity.

[0223] In certain embodiments, the CH1 domain of H1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) one or more amino acid substitutions selected from the group consisting of: F170 and V185 (EU numbering). In certain embodiments, the CL domain of L1 of the multispecific antigen-binding protein comprises one or more amino acid substitutions selected from the group consisting of F116 and S176 mutations (all EU numbering). In certain embodiments, the amino acid substitutions result in conformational complementarity.

[0224] In certain embodiments, the CH1 domain of H1 and CL domain of L1 of the multispecific antigen-binding protein are altered so that within the CH1/CL interface, one or more amino acid residues of the CH1 domain are replaced with an equivalent number of amino acid residues, some or all having a larger side chain volume, thereby generating a protuberance on the surface of the CH1 domain, and one

or more amino acid residues of the CL domain are replaced with an equivalent number of amino acid residues, some or all having a smaller side chain volume, thereby generating a cavity on the surface of the CL domain. In certain embodiments, the modifications on the CH1 and CL domains provide steric complementarity at the CH1/CL interface. In certain embodiments, the modifications on the CH1 and CL domains provide conformational complementarity at the CH1/CL interface.

[0225] In certain embodiments, the CH1 domain of H1 and the CL domain of L1 of the multispecific antigen-binding protein are altered so that within the CH1/CL interface, one or more amino acid residues of the CL domain are replaced with an equivalent number of amino acid residues, some or all having a larger side chain volume, thereby generating a protuberance on the surface of the CL domain, and one or more amino acid residues of the CH1 domain are replaced with an equivalent number of amino acid residues, some or all having a smaller side chain volume, thereby generating a cavity on the surface of the CH1 domain. In certain embodiments, the one or more substituted amino acid residues of the CL domain comprise S176. In certain embodiments, the one or more substituted amino acid residues of the CH1 domain comprise F170. In certain embodiments, the modifications on the CH1 and CL domains provide steric complementarity at the interface. In certain embodiments, the modifications on the CH1 and CL domains provide conformational complementarity at the interface.

[0226] In certain embodiments, the CH1 domain of H1 comprises an amino acid substitution selected from the group consisting of F170S and F170A (EU numbering), and wherein the CL domain of L1 comprises an amino acid substitution selected from the group consisting of S176F (EU numbering).

[0227] In certain embodiments, the CH1 domain of H1 comprises the F170S mutation (EU numbering), and the CL domain of L1 comprises the S176F mutation (EU numbering). In certain embodiments, the CH1 domain of H1 comprises the F170A mutation (EU numbering), and the CL domain of L1 comprises the S176F mutation (EU numbering).

[0228] In certain embodiments a multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) A141I, F170S, S181M, S183V, and V185A mutations (EU numbering), and a CL domain of L1 comprising (including consisting of or consisting essentially of) F116A, V133I, L135V, S162M, S174A, S176F, and T178V mutations (EU numbering).

[0229] In certain embodiments a multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) A141I, F170S, S181M, S183A, and V185A mutations (EU numbering) and a CL domain of L1 comprising (including consisting of or consisting essentially of) F116A, S131D, L135V, S162A, S174A, S176F, and T178I mutations (EU numbering).

[0230] In certain embodiments a multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) A141I, F170S, S181M, S183A, and V185A mutations (EU numbering) and a CL domain of L1 comprising (including consisting of or consisting essentially of) F116A, L135V, S174A, S176F, and T178V mutations (EU numbering). In certain embodiments a multispecific antigen-binding protein comprises a CH1 domain of H1 consisting of (such as consisting essentially of) A141I, F170S, S181M, S183A, and V185A mutations (EU numbering) and a CL domain of L1 consisting of (such as consisting essentially of) F116A, L135V, S174A, S176F, and T178V mutations (EU numbering).

[0231] In certain embodiments a multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) A141I, F170A, S181M, S183V, and V185A mutations (EU numbering) and a CL domain of L1 comprising (including consisting of or consisting essentially of) F116A, L135V, S162M, S174A, S176F, and T178V mutations (EU numbering).

[0232] In certain embodiments a multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) F170S, S181M, S183A, and V185A mutations (EU numbering) and a CL domain of L1 comprising (including consisting of or consisting essentially of) L135V, S174A, S176F, and T178V mutations (EU numbering).

[0233] In certain embodiments a multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) A141I, F170S, S183A, and V185A mutations (EU numbering) and a CL domain of L1 comprising (including consisting of or consisting essentially of) F116A, S174A, S176F, and T178V mutations (EU numbering).

[0234] In certain embodiments a multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) A141I, F170S, S181M, and V185A mutations (EU numbering) and a CL domain of L1 comprising (including consisting of or consisting essentially of) F116A, L135V, S176F, and T178V mutations (EU numbering).

[0235] In certain embodiments a multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) A141I, F170S, S181M, and S183A mutations (EU numbering) and a CL domain of L1 comprising (including consisting of or consisting essentially of) F116A, L135V, S174A, and S176F mutations (EU numbering).

[0236] In certain embodiments a multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) F170S, S183A, and V185A mutations (EU numbering) and a CL domain of L1 comprising (including consisting of or consisting essentially of) F116A, S176F, and T178V mutations (EU numbering).

[0237] In certain embodiments a multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) F170S, S181M, and V185A mutations (EU numbering) and a CL domain of L1 comprising (including consisting of or consisting essentially of) F116A, L135V, and S176F mutations (EU numbering).

[0238] In certain embodiments a multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) F170S, S181M, and S183A mutations (EU numbering) and a CL domain of L1 comprising (including consisting of or consisting essentially of) F116A and S176F mutations (EU numbering).

[0239] In certain embodiments a multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) A141I, F170S, and V185A mutations (EU numbering) and a CL domain of L1 comprising (including consisting of or consisting essentially of) F116A and S176F mutations.

[0240] In certain embodiments a multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) A141I, F170S, and S183A mutations (EU numbering) and a CL domain of L1 comprising (including consisting of or consisting essentially of) F116A and S176F mutations.

[0241] In certain embodiments a multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) A141I, F170S, and S181M mutations (EU numbering) and a CL domain of L1 comprising (including consisting of or consisting essentially of) F116A, L135V, S174A, S176F, and T178V mutations (EU numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering).

[0242] In certain embodiments a multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) F170S and V185A mutations (EU

numbering) and a CL domain of L1 comprising (including consisting of or consisting essentially of) F116A and S176F mutations.

[0243] In certain embodiments a multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) A141I and F170S mutations (EU numbering) and a CL domain of L1 comprising (including consisting of or consisting essentially of) F116A, L135V, S174A, S176F, and T178V mutations (EU numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering).

[0244] In certain embodiments a multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) A141I and F170S mutations (EU numbering) and a CL domain of L1 comprising (including consisting of or consisting essentially of) F116A, L135V, S176F, and T178V mutations (EU numbering).

[0245] In certain embodiments a multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) A141I and F170S mutations (EU numbering) and a CL domain of L1 comprising (including consisting of or consisting essentially of) F116A, L135V, S174A, and S176F mutations (EU numbering).

[0246] In certain embodiments a multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) A141I and F170S mutations (EU numbering) and a CL domain of L1 comprising (including consisting of or consisting essentially of) F116A, S176F, and T178V mutations (EU numbering).

[0247] In certain embodiments a multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) A141I and F170S mutations (EU numbering) and a CL domain of L1 comprising (including consisting of or consisting essentially of) F116A, L135V, and S176F mutations (EU numbering).

[0248] In certain embodiments a multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) A141I and F170S mutations (EU numbering) and a CL domain of L1 comprising (including consisting of or consisting essentially of) F116A and S176F mutations (EU numbering).

[0249] In certain embodiments a multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) an F170S mutation (EU numbering), and a CL domain of L1 comprising (including consisting of or consisting essentially of) F116A, L135V, S174A, S176F, and T178V mutations (EU numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering).

[0250] In certain embodiments a multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) an F170S mutation (EU numbering), and a CL domain of L1 comprising (including consisting of or consisting essentially of) F116A, L135V, S176F, and T178V mutations (EU numbering).

[0251] In certain embodiments a multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) an F170S mutation (EU numbering) and a CL domain of L1 comprising (including consisting of or consisting essentially of) F116A, L135V, S174A, and S176F mutations (EU numbering).

[0252] In certain embodiments a multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) an F170S mutation (EU numbering) and a CL domain of L1 comprising (including consisting of or consisting essentially of) F116A, S176F, and T178V mutations (EU numbering).

[0253] In certain embodiments a multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) an F170S mutation (EU numbering)

and a CL domain of L1 comprising (including consisting of or consisting essentially of) F116A, L135V, and S176F mutations (EU numbering).

[0254] In certain embodiments a multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) an F170S mutation (EU numbering) and a CL domain of L1 comprising (including consisting of or consisting essentially of) F116A and S176F mutations (EU numbering).

[0255] In certain embodiments a multispecific antigen-binding protein comprises CH1 domain of H1 comprising no more than 1, no more than two, no more than three, no more than four, or no more than five amino acid mutations selected from the group consisting of: A141I, F170S, S181M, S183V, and V185A mutations (EU numbering).

[0256] In certain embodiments a multispecific antigen-binding protein comprises CH1 domain of H1 comprising no more than one, no more than two, no more than three, no more than four, or no more than five amino acid mutations selected from the group consisting of: A141I, F170S, S181M, S183A, and V185A mutations (EU numbering).

[0257] In certain embodiments a multispecific antigen-binding protein comprises CH1 domain of H1 consisting of no more than one, no more than two, no more than three, no more than four, or no more than five amino acid mutations selected from the group consisting of: A141I, F170S, S181M, S183A, and V185A mutations (EU numbering).

[0258] In certain embodiments a multispecific antigen-binding protein comprises CH1 domain of H1 comprising no more than one, no more than two, no more than three, no more than four, or no more than five amino acid mutations selected from the group consisting of: A141I, F170A, S181M, S183V, and V185A mutations (EU numbering).

[0259] In certain embodiments a multispecific antigen-binding protein comprises a CL domain of L1 comprising no more than one, no more than two, no more than three, no more than four, no more than five, no more than six, or no more than seven amino acid mutations selected from the group consisting of: F116A, V133I, L135V, S162M, S174A, S176F, and T178V mutations (EU numbering).

[0260] In certain embodiments a multispecific antigen-binding protein comprises a CL domain of L1 comprising no more than one, no more than two, no more than three, no more than four, no more than five, no more than six, or no more than seven amino acid mutations selected from the group consisting of: F116A, S131D, L135V, S162A, S174A, S176F, and T178I mutations (EU numbering).

[0261] In certain embodiments a multispecific antigen-binding protein comprises a CL domain of L1 comprising no more than one, no more than two, no more than three, no more than four, or no more than

five amino acid mutations selected from the group consisting of: F116A, L135V, S174A, S176F, and T178V mutations (EU numbering).

[0262] In certain embodiments a multispecific antigen-binding protein comprises a CL domain of L1 consisting of no more than one, no more than two, no more than three, no more than four, or no more than five amino acid mutations selected from the group consisting of: F116A, L135V, S174A, S176F, and T178V mutations (EU numbering).

[0263] In certain embodiments a multispecific antigen-binding protein comprises a CL domain of L1 comprising no more than one, no more than two, no more than three, no more than four, no more than five, or no more than six amino acid mutations selected from the group consisting of: F116A, L135V, S162M, S174A, S176F, and T178V mutations (EU numbering).

[0264] All possible pair-wise combinations of CH1 domains and L1 domains described above are contemplated.

[0265] In certain embodiments, the multispecific antigen-binding protein comprises a kappa light chain. In certain embodiments, the multispecific antigen-binding protein comprises a first light chain polypeptide L1 comprising a CL domain as set forth in any of SEQ ID Nos: 17-27. The CL domain as set forth in SEQ ID NO: 54 corresponds to amino acids 11-116 of SEQ ID NOs: 17-27. Accordingly, L1 may comprise a CL domain comprising amino acids 11-116 as set forth in any of SEQ ID Nos: 17-27. In certain embodiments, the multispecific antigen-binding protein comprises a CL domain of L1 comprising the amino acid sequence set forth in SEQ ID NO: 17 or the amino acids 11-116 in the sequence set forth in SEQ ID NO: 17. In certain embodiments, the multispecific antigen-binding protein comprises a CL domain of L1 comprising the amino acid sequence set forth in SEQ ID NO: 18 or the amino acids 11-116 in the sequence set forth in SEQ ID NO: 18. In certain embodiments, the multispecific antigen-binding protein comprises a CL domain of L1 comprising the amino acid sequence set forth in SEQ ID NO: 19 or the amino acids 11-116 in the sequence set forth in SEQ ID NO: 19. In certain embodiments, the multispecific antigen-binding protein comprises a CL domain of L1 comprising the amino acid sequence set forth in SEQ ID NO: 20 or the amino acids 11-116 in the sequence set forth in SEQ ID NO: 20. In certain embodiments, the multispecific antigen-binding protein comprises a CL domain of L1 comprising the amino acid sequence set forth in SEQ ID NO: 21 or the amino acids 11-116 in the sequence set forth in SEQ ID NO: 21. In certain embodiments, the multispecific antigen-binding protein comprises a CL domain of L1 comprising the amino acid sequence set forth in SEQ ID NO: 22 or the amino acids 11-116 in the sequence set forth in SEQ ID NO: 22. In certain embodiments, the multispecific antigen-binding protein comprises a CL domain of L1 comprising the amino acid sequence set forth in SEQ ID NO: 23 or the amino acids 11-116 in the sequence set forth in SEQ ID NO: 23. In certain embodiments, the multispecific antigen-binding protein comprises a CL domain of L1 comprising the amino acid sequence

set forth in SEQ ID NO: 24 or the amino acids 11-116 in the sequence set forth in SEQ ID NO: 24. In certain embodiments, the multispecific antigen-binding protein comprises a CL domain of L1 comprising the amino acid sequence set forth in SEQ ID NO: 25 or the amino acids 11-116 in the sequence set forth in SEQ ID NO: 25. In certain embodiments, the multispecific antigen-binding protein comprises a CL domain of L1 comprising the amino acid sequence set forth in SEQ ID NO: 26 or the amino acids 11-116 in the sequence set forth in SEQ ID NO: 26. In certain embodiments, the multispecific antigen-binding protein comprises a CL domain of L1 comprising the amino acid sequence set forth in SEQ ID NO: 27 or the amino acids 11-116 in the sequence set forth in SEQ ID NO: 27.

[0266] In certain embodiments, the mutispecific antigen-binding protein comprises a lambda light chain. In certain embodiments, the the multispecific antigen-binding protein comprises a CL domain of L1 comprising the amino acid sequence set forth in SEQ ID NO: 127.

[0267] The amino acid sequences of SEQ ID NOs: 17-27 and 127 are provided in Table 5 below (LC is kappa LC unless indicated otherwise):

Table 5

YS08 LC SEQ ID NO: 17	GQG T KVEIKR TVAAPSV A IF PPSDEQLKSG TASV I C V LNN FYPREAKVQW KVDNALQSGN SQE M VTEQDS KDSTY A L F S V LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC
YS18 LC SEQ ID NO: 18	GQG T KVEIKR TVAAPSV A IF PPSDEQLKSG TA D VVC V LNN FYPREAKVQW KVDNALQSGN SQE A VTEQDS KDSTY A L F S I LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC
YT65 LC kappa SEQ ID NO: 19	GQG T KVEIKR TVAAPSV A IF PPSDEQLKSG TASVVC V LNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTY A L F S V LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC
YT65.1 LC SEQ ID NO: 20	GQG T KVEIKR TVAAPSVFIF PPSDEQLKSG TASVVC V LNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTY A L F S V LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC
YT65.2 LC SEQ ID NO: 21	GQG T KVEIKR TVAAPSV A IF PPSDEQLKSG TASVVC L LNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTY A L F S V LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC
YT65.3 LC SEQ ID NO: 22	GQG T KVEIKR TVAAPSV A IF PPSDEQLKSG TASVVC V LNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSL F S V LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC
YT65.4 LC SEQ ID NO: 23	GQG T KVEIKR TVAAPSV A IF PPSDEQLKSG TASVVC V LNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTY A L F ST LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC
YT65.5 LC SEQ ID NO: 24	GQG T KVEIKR TVAAPSV A IF PPSDEQLKSG TASVVC L LNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSL F S V LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC
YT65.6 LC SEQ ID NO: 25	GQG T KVEIKR TVAAPSV A IF PPSDEQLKSG TASVVC V LNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSL F ST LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC
YT65.7 LC SEQ ID NO: 26	GQG T KVEIKR TVAAPSV A IF PPSDEQLKSG TASVVC L LNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSL F ST LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC
YT34 LC SEQ ID NO: 27	GQG T KVEIKR TVAAPSV A IF PPSDEQLKSG TASVVC V LNN FYPREAKVQW KVDNALQSGN SQE M VTEQDS KDSTY A L F S V LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC
YT65 lambda SEQ ID NO: 127	GQPKAAPSV A LFPPSSEELQ ANKATLVC V I SDFYPGAVTV AWKADSSPVK AGVETTTPSK QSNNKY A AFS V LSLTPEQWK SHKSYSCQVT HEGSTVEKTV APTECS

[0268] Amino acid positions 116, 118, 131, 133, 135, 162, 164, 174, 176, and 178 in CL (EU numbering) correspond to amino acid positions 18, 20, 33, 35, 37, 64, 66, 76, 78, and 80 in SEQ ID NOs: 17-27, respectively. Amino acid positions 116, 118, 131, 133, 135, 162, 164, 174, 176, and 178 (EU numbering) in the CL domain of a kappa chain correspond to amino acid positions 116, 118, 131, 133, 135, 162, 164, 174, 176, and 178 (Kabat numbering) in the CL domain of a lambda light chain. Amino acid positions 116, 118, 131, 133, 135, 162, 164, 174, 176, and 178 (Kabat numbering) in the CL domain of a lambda light chain correspond to amino acid positions 10, 12, 25, 27, 29, 56, 59, 67, 69, and 71 in SEQ ID NO: 127, respectively.

[0269] In certain embodiments, the multispecific antigen-binding protein comprises an IgG1, IgG2, IgG3, or IgG4 heavy chain. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 28. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 29. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 31. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 32. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 33. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 34. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 35. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 36. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 37. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 38. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 39. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 40. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 41. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 42. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 43. In

certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 44. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 103. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 104. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 105.

The amino acid sequences of SEQ ID NOs: 28-44 are provided in Table 6 below (HC is of IgG1 isotype unless indicated otherwise):

Table 6

YS08 HC SEQ ID NO: 28	TKGPSVFPLA PSSKSTSGGT A <u>I</u> LGCLVKDY FPEPVTVSWN SGALTSGVHT <u>S</u> PAVLQSSGL Y <u>M</u> L <u>V</u> S <u>A</u> VTVP SSSLGTQTYI CN
YS18 HC/ YT65 HC IgG1 SEQ ID NO: 29	TKGPSVFPLA PSSKSTSGGT A <u>I</u> LGCLVKDY FPEPVTVSWN SGALTSGVHT <u>S</u> PAVLQSSGL Y <u>M</u> L <u>A</u> S <u>A</u> VTVP SSSLGTQTYI CN
YS18 HC/ YT65 HC IgG2 SEQ ID NO: 103	TKGPSVFPLA PCSRSTSEST A <u>I</u> LGCLVKDY FPEPVTVSWN SGALTSGVHT <u>S</u> PAVLQSSGL Y <u>M</u> L <u>A</u> S <u>A</u> VTVP SSNFGTQTYT CN
YS18 HC/ YT65 HC IgG3 SEQ ID NO: 104	TKGPSVFPLA PCSRSTSGGT A <u>I</u> LGCLVKDY FPEPVTVSWN SGALTSGVHT <u>S</u> PAVLQSSGL Y <u>M</u> L <u>A</u> S <u>A</u> VTVP SSSLGTQTYT CN
YS18 HC/ YT65 HC IgG4 SEQ ID NO: 105	TKGPSVFPLA PCSRSTSEST A <u>I</u> LGCLVKDY FPEPVTVSWN SGALTSGVHT <u>S</u> PAVLQSSGL Y <u>M</u> L <u>A</u> S <u>A</u> VTVP SSSLGTKTYT CN
YT65.1 HC SEQ ID NO: 31	TKGPSVFPLA PSSKSTSGGT AALGCLVKDY FPEPVTVSWN SGALTSGVHT <u>S</u> PAVLQSSGL Y <u>M</u> L <u>A</u> S <u>A</u> VTVP SSSLGTQTYI CN
YT65.2 HC SEQ ID NO: 32	TKGPSVFPLA PSSKSTSGGT A <u>I</u> LGCLVKDY FPEPVTVSWN SGALTSGVHT <u>S</u> PAVLQSSGL YSL <u>A</u> S <u>A</u> VTVP SSSLGTQTYI CN
YT65.3 HC SEQ ID NO: 33	TKGPSVFPLA PSSKSTSGGT A <u>I</u> LGCLVKDY FPEPVTVSWN SGALTSGVHT <u>S</u> PAVLQSSGL Y <u>M</u> LSS <u>A</u> VTVP SSSLGTQTYI CN
YT65.4 HC SEQ ID NO: 34	TKGPSVFPLA PSSKSTSGGT A <u>I</u> LGCLVKDY FPEPVTVSWN SGALTSGVHT <u>S</u> PAVLQSSGL Y <u>M</u> L <u>A</u> SVVTVP SSSLGTQTYI CN
YT65.5 HC	TKGPSVFPLA PSSKSTSGGT AALGCLVKDY FPEPVTVSWN SGALTSGVHT <u>S</u> PAVLQSSGL YSL <u>A</u> S <u>A</u> VTVP SSSLGTQTYI CN

SEQ ID NO: 35	
YT65.6 HC SEQ ID NO: 36	TKGPSVFPLA PSSKSTSGGT AALGCLVKDY FPEPVTVSWN SGALTSGVHT <u>S</u> PAVLQSSGL Y <u>M</u> LSS <u>A</u> VTVP SSSLGTQTYI CN
YT65.7 HC SEQ ID NO: 37	TKGPSVFPLA PSSKSTSGGT AALGCLVKDY FPEPVTVSWN SGALTSGVHT <u>S</u> PAVLQSSGL Y <u>M</u> L <u>A</u> SVVTVP SSSLGTQTYI CN
YT65.8 HC SEQ ID NO: 38	TKGPSVFPLA PSSKSTSGGT A <u>I</u> LGCLVKDY FPEPVTVSWN SGALTSGVHT <u>S</u> PAVLQSSGL YSLSS <u>A</u> VTVP SSSLGTQTYI CN
YT65.9 HC SEQ ID NO: 39	TKGPSVFPLA PSSKSTSGGT A <u>I</u> LGCLVKDY FPEPVTVSWN SGALTSGVHT <u>S</u> PAVLQSSGL YSL <u>A</u> SVVTVP SSSLGTQTYI CN
YT65.10 HC SEQ ID NO: 40	TKGPSVFPLA PSSKSTSGGT A <u>I</u> LGCLVKDY FPEPVTVSWN SGALTSGVHT <u>S</u> PAVLQSSGL Y <u>M</u> LSSVVTVP SSSLGTQTYI CN
YT65.11 HC SEQ ID NO: 41	TKGPSVFPLA PSSKSTSGGT AALGCLVKDY FPEPVTVSWN SGALTSGVHT <u>S</u> PAVLQSSGL YSLSS <u>A</u> VTVP SSSLGTQTYI CN
YT65.12 HC SEQ ID NO: 42	TKGPSVFPLA PSSKSTSGGT A <u>I</u> LGCLVKDY FPEPVTVSWN SGALTSGVHT <u>S</u> PAVLQSSGL YSLSSVVTVP SSSLGTQTYI CN
YT65.13 HC SEQ ID NO: 43	TKGPSVFPLA PSSKSTSGGT AALGCLVKDY FPEPVTVSWN SGALTSGVHT <u>S</u> PAVLQSSGL YSLSSVVTVP SSSLGTQTYI CN
YT34 HC SEQ ID NO: 44	TKGPSVFPLA PSSKSTSGGT A <u>I</u> LGCLVKDY FPEPVTVSWN SGALTSGVHT <u>A</u> PAVLQSSGL Y <u>M</u> L <u>V</u> <u>S</u> <u>A</u> VTVP SSSLGTQTYI CN

[0270] Amino acid positions 141, 170, 181, 183, and 185 (EU numbering) in CH1 correspond to amino acid positions 22, 51, 62, 64, and 66 of SEQ ID NOs: 28-44 and 103-105, respectively.

[0271] All possible pair-wise combinations of SEQ ID NOs: 17-27 or amino acids 11-116 of SEQ ID Nos: 17-27 and 127with SEQ ID NOs: 28-44 and 103-105 described above are contemplated. In certain embodiments, specific combinations of SEQ ID NOs: 17-27 or amino acids 11-116 of SEQ ID Nos: 17-27 and 127 with SEQ ID NOs: 28-44 and 103-105 are contemplated. Such combinations include, but are not limited to, those provided in Table 7 below:

Table 7

SEQ ID NO: 28/ SEQ ID NO: 17* YS08HC/YS08LC	SEQ ID NO: 40 / SEQ ID NO: 19* YT65.10HC/YT65LC	SEQ ID NO: 36/ SEQ ID NO: 25* YT65.6HC/YT65.6LC
SEQ ID NO: 29/ SEQ ID NO: 18* YS18HC/YS18LC	SEQ ID NO: 42/ SEQ ID NO: 19* YT65.12HC/YT65LC	SEQ ID NO: 32/ SEQ ID NO: 21* YT65.2HC/YT65.2LC

SEQ ID NO: 29/ SEQ ID NO: 19* YT65HC/YT65LC IgG1/kappa	SEQ ID NO: 43/ SEQ ID NO: 19* YT65.13HC/YT65LC	SEQ ID NO: 43/ SEQ ID NO: 22* YT65.13HC/YT65.3LC
SEQ ID NO: 34/ SEQ ID NO: 23* YT65.4HC/YT65.4LC	SEQ ID NO: 44/ SEQ ID NO: 27* YT34HC/YT34LC	SEQ ID NO: 37/ SEQ ID NO: 26* YT65.7HC/YT65.7LC
SEQ ID NO: 35/ SEQ ID NO: 24* YT65.5HC/YT65.5LC	SEQ ID NO: 31/ SEQ ID NO: 20* YT65.1HC/YT65.1 LC	SEQ ID NO: 33/ SEQ ID NO: 22* YT65.3HC/YT65.3LC
SEQ ID NO: 42/ SEQ ID NO: 22 YT65.12HC/YT65.3LC	SEQ ID NO: 38/ SEQ ID NO: 26 YT65.8HC/YT65.7LC	SEQ ID NO: 39/ SEQ ID NO: 26 YT65.9HC/YT65.7LC
SEQ ID NO: 41/ SEQ ID NO: 26 YT65.11HC /YT65.7LC	SEQ ID NO: 103/ SEQ ID NO: 19 YT65HC/YT65LC IgG2/kappa	SEQ ID NO: 104/ SEQ ID NO: 19 YT65HC IgG3/YT65LC IgG3/kappa
SEQ ID NO: 105/ SEQ ID NO: 19 YT65HC/YT65LC IgG4/kappa	SEQ ID NO: 29/ SEQ ID NO: 127 YT65HC/YT65LC IgG1/lambda	SEQ ID NO: 103/ SEQ ID NO: 127 YT65HC/YT65LC IgG2/kappa
SEQ ID NO: 104/ SEQ ID NO: 127 YT65HC IgG3/YT65LC IgG3/kappa	SEQ ID NO: 105/ SEQ ID NO: 127 YT65HC/YT65LC IgG4/lambda	

* or amino acids 11-116 of the corresponding sequence

[0272] The first SEQ ID NO in each pair in Table 7 refers to a CH1 domain sequence, and the second SEQ ID NO in each pair in Table 7 refers to a CL domain sequence.

[0273] In a related aspect, provided is a multispecific antigen binding protein comprising: a) a first heavy chain/light chain pair capable of binding a first antigen, the first heavy chain/light chain pair comprising a first heavy chain sequence (H1) and a first light chain sequence (L1), and b) a second heavy chain/light chain pair comprising a second heavy chain sequence (H2) and a second light chain sequence (L2), wherein each H1 and H2 comprises a heavy chain variable domain (VH) and a heavy chain constant domain (CH1), and each L1 and L2 comprises a light chain variable domain (VL) and a light chain constant domain (CL); wherein the CH1 domain of H1 and the CL domain of L1 of the multispecific antigen-binding protein are altered so that within the CH1/CL interface, one or more amino acid residues of the CH1 domain are replaced with an equivalent number of amino acid residues, some having a larger side chain volume and some having a smaller side chain volume, thereby generating a protuberance and a cavity on the surface of the CH1 domain, and one or more amino acid residues of the CL domain are replaced with an equivalent number of amino acid residues, some having a smaller side chain volume and some having a larger side chain volume, thereby generating a cavity and a protuberance on the surface of the CL domain. In certain embodiments, the modifications on the CH1 and CL domains provide steric complementarity (such as conformational complementarity) at the interface.

[0274] In certain embodiments, the CH1 domain of H1 comprises an amino acid substitutions at positions L128, and wherein the CL domain of L1 comprises an amino acid substitution at positions F118 and L135 (EU numbering). In certain embodiments, the first antigen and the second antigen are the same. In certain embodiments, the first heavy chain/light chain pair and the second heavy chain/light chain pair each bind to a different epitope on the same antigen. In certain embodiments, the first antigen and the second antigen are different. In certain embodiments, the CH1 domain of H1 comprises an amino acid substitutions at positions L128 and V185 (EU numbering), and wherein the CL domain of L1 comprises an amino acid substitution at positions F118 and L135 (EU numbering). In certain embodiments, the first antigen and the second antigen are the same. In certain embodiments, the first heavy chain/light chain pair and the second heavy chain/light chain pair each bind to a different epitope on the same antigen. In certain embodiments, the first antigen and the second antigen are different. In certain embodiments, the CH1 domain of H1 of the multispecific antigen-binding protein further comprises one or more amino acid substitutions selected from the group consisting of: A141, F170, S181, and S183 (all EU numbering). In certain embodiments, the CL domain of L1 of the multispecific antigen-binding protein further comprises one or more amino acid substitutions selected from the group consisting of S131, V133, S162, S176 and T178 (all EU numbering). In certain embodiments, the amino acid substitutions result in steric complementarity (such as conformational complementarity) comparable or greater than that of the wild-type sequences. In certain embodiments, the CL domain of L1 of the multispecific antigen-binding protein further comprises one or more amino acid substitutions selected from the group consisting of S131, V133, S162, T164, S176 and T178 (all EU numbering).

[0275] In certain embodiments the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) one or more amino acid substitution selected from F128, A141, F170, S181, and S183 (EU numbering). In certain embodiments the multispecific antigen-binding protein comprises a CL domain of L1 comprising (including consisting of or consisting essentially of) one or more amino acid substitution selected from V118, S131, V133, S135, S162, T164, S176 and T178 (EU numbering). In certain embodiments, the amino acid substitutions result in steric complementarity (such as conformational complementarity) comparable or greater than that of the wild-type sequences.

[0276] In certain embodiments the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) one or more amino acid substitution selected from F128, A141, F170, S181, S183, and V185 (EU numbering). In certain embodiments the multispecific antigen-binding protein comprises a CL domain of L1 comprising (including consisting of or consisting essentially of) one or more amino acid substitution selected from V118, S131, V133, S135, S162, T164, S176 and T178 (EU numbering). In certain embodiments, the amino acid substitutions result

in steric complementarity (such as conformational complementarity) comparable or greater than that of the wild-type sequences.

[0277] In certain embodiments the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) one or more amino acid substitution selected from F128, A141, F170, S181, S183, and V185 (EU numbering). In certain embodiments the multispecific antigen-binding protein comprises a CL domain of L1 comprising (including consisting of or consisting essentially of) one or more amino acid substitution selected from V118, S131, V133, S135, S162, S176 and T178 (EU numbering). In certain embodiments, the amino acid substitutions result in steric complementarity (such as conformational complementarity) comparable or greater than that of the wild-type sequences.

[0278] In certain embodiments the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) L128F, A141M, F170M, S181I and S183A mutations (EU numbering) and a CL domain of L1 comprising (including consisting of or consisting essentially of) F118V, S131T, V133A, L135Y, S162A, T164S, S176M, and T178L mutations (EU numbering).

[0279] In certain embodiments the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) L128F, A141M, F170Y, S181I, S183A, and V185A mutations (EU numbering) and a CL domain of L1 comprising (including consisting of or consisting essentially of) F118V, S131T, V133A, L135F, S162A, S176A, and T178L mutations (EU numbering).

[0280] In certain embodiments the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) L128F, A141T, F170M, S181T, S183A, and V185L mutations (EU numbering) and a CL domain of L1 comprising (including consisting of or consisting essentially of) F118V, S131T, V133A, L135F, S162A, T164S, S176T, and T178L mutations (EU numbering).

[0281] In certain embodiments the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising (including consisting of and consisting essentially of) L128F, A141M, F170M, S181T, and S183A mutations (EU numbering), and a CL domain of L1 comprising (including consisting of or consisting essentially of) F118V, S131T, V133A, L135F, S162M, T164S, S176M, and T178L mutations (EU numbering).

[0282] In certain embodiments the multispecific antigen-binding protein comprises CH1 domain of H1 comprising no more than one, no more than two, no more than three, no more than four, or no more

than five amino acid mutations selected from the group consisting of: L128F, A141M, F170M, S181I and S183A mutations (EU numbering).

[0283] In certain embodiments a multispecific antigen-binding protein comprises CH1 domain of H1 comprising no more than one, no more than two, no more than three, no more than four, no more than five, or no more than six amino acid mutations selected from the group consisting of: L128F, A141M, F170Y, S181I, S183A, and V185A mutations (EU numbering).

[0284] In certain embodiments a multispecific antigen-binding protein comprises CH1 domain of H1 comprising no more than one, no more than two, no more than three, no more than four, no more than five, or no more than six amino acid mutations selected from the group consisting of: L128F, A141T, F170M, S181T, S183A, and V185L mutations (EU numbering).

[0285] In certain embodiments a multispecific antigen-binding protein comprises CH1 domain of H1 comprising no more than one, no more than two, no more than three, no more than four, or no more than five amino acid mutations selected from the group consisting of: L128F, A141M, F170M, S181T, and S183A mutations (EU numbering).

[0286] In certain embodiments a multispecific antigen-binding protein comprises a CL domain of L1 comprising no more than one, no more than two, no more than three, no more than four, no more than five, no more than six, no more than seven, or no more than eight amino acid mutations selected from the group consisting of: F118V, S131T, V133A, L135Y, S162A, T164S, S176M, and T178L mutations (EU numbering).

[0287] In certain embodiments a multispecific antigen-binding protein comprises a CL domain of L1 comprising no more than one, no more than two, no more than three, no more than four, no more than five, no more than six, or no more than seven amino acid mutations selected from the group consisting of: F118V, S131T, V133A, L135F, S162A, S176A, and T178L mutations (EU numbering).

[0288] In certain embodiments a multispecific antigen-binding protein comprises a CL domain of L1 comprising no more than one, no more than two, no more than three, no more than four, no more than five, no more than six, no more than seven, or no more than eight amino acid mutations selected from the group consisting of: F118V, S131T, V133A, L135F, S162A, T164S, S176T, and T178L mutations (EU numbering).

[0289] In certain embodiments a multispecific antigen-binding protein comprises a CL domain of L1 comprising no more than one, no more than two, no more than three, no more than four, no more than five, no more than six, no more than seven, or no more than eight amino acid mutations selected from the

group consisting of: F118V, S131T, V133A, L135F, S162M, T164S, S176M, and T178L mutations (EU numbering).

[0290] All possible pair-wise combinations of the CH1 and L1 domains described above are contemplated.

[0291] In certain embodiments, the multispecific antigen-binding protein comprises a kappa light chain. In certain embodiments, the multispecific antigen-binding protein comprises a first light chain polypeptide L1 comprising a CL domain as set forth in any of SEQ ID NO:45-48. The CL domain as set forth in SEQ ID NO: 54 corresponds to amino acids 11-116 of SEQ ID NOs: 45-48. Accordingly, L1 may comprise a CL domain comprising amino acids 11-116 as set forth in any of SEQ ID Nos: 45-48. In certain embodiments, the multispecific antigen-binding protein comprises a CL domain of L1 comprising the amino acid sequence set forth in SEQ ID NO: 45 or the amino acids 11-116 in the sequence set forth in SEQ ID NO: 45. In certain embodiments, the multispecific antigen-binding protein comprises a CL domain of L1 comprising the amino acid sequence set forth in SEQ ID NO: 46 or the amino acids 11-116 in the sequence set forth in SEQ ID NO: 46. In certain embodiments, the multispecific antigen-binding protein comprises a CL domain of L1 comprising the amino acid sequence set forth in SEQ ID NO: 47 or the amino acids 11-116 in the sequence set forth in SEQ ID NO: 47. In certain embodiments, the multispecific antigen-binding protein comprises a CL domain of L1 comprising the amino acid sequence set forth in SEQ ID NO: 48 or the amino acids 11-116 in the sequence set forth in SEQ ID NO: 48.

[0292] In certain embodiments, the multispecific antigen binding protein comprises a lambda light chain. In certain embodiments, the multispecific antigen-binding protein comprises a CL domain of L1 comprising the amino acid sequence set forth in SEQ ID NO: 128.

[0293] In certain embodiments, the multispecific antigen-binding protein comprises an IgG1, IgG2, IgG3, or IgG4 heavy chain. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 49. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 50. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 51. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 52. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 106. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 107. In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 comprising the amino acid sequence set forth in SEQ ID NO: 108. The amino acid sequences of SEQ ID

NOs: 45-52 and 106-108 are provided in Table 8 below (LC is kappa LC unless indicated otherwise; HC is of IgG1 iotype unless indicated otherwise)..

Table 8

JS20 LC SEQ ID NO: 45	GQGTKVEIKR TVAAPSVFI <u>V</u> PPSDEQLKSG TAT <u>TV</u> <u>A</u> <u>C</u> <u>Y</u> LNN FYPREAKVQW KVDNALQSGN SQE <u>A</u> <u>V</u> SEQDS KDSTYSL <u>M</u> <u>S</u> <u>L</u> LTLSKADYЕК HKVYACEVTH QGLSSPVTKS FNRGEC
JS78 LC kappa SEQ ID NO: 46	GQGTKVEIKR TVAAPSVFI <u>V</u> PPSDEQLKSG TAT <u>TV</u> <u>A</u> <u>C</u> <u>F</u> LNN FYPREAKVQW KVDNALQSGN SQE <u>A</u> <u>V</u> TEQDS KDSTYSL <u>A</u> <u>S</u> <u>L</u> LTLSKADYЕК HKVYACEVTH QGLSSPVTKS FNRGEC
JS78 LC lambda SEQ ID NO: 128	GQPKAAPSVT LVPPSSEELQ ANKAT <u>L</u> <u>A</u> <u>C</u> <u>F</u> I SDFYPGAVTV AWKADSSPVK AGVET <u>A</u> TPSK QSNNKYAA <u>A</u> S <u>L</u> LSLTPEQWK SHKSYSCQVT HEGSTVEKTV APTECS
JT20 LC SEQ ID NO: 47	GQGTKVEIKR TVAAPSVFI <u>V</u> PPSDEQLKSG TAT <u>TV</u> <u>A</u> <u>C</u> <u>F</u> LNN FYPREAKVQW KVDNALQSGN SQE <u>A</u> <u>V</u> SEQDS KDSTYSL <u>T</u> <u>S</u> <u>L</u> LTLSKADYЕК HKVYACEVTH QGLSSPVTKS FNRGEC
JT25 LC SEQ ID NO: 48	GQGTKVEIKR TVAAPSVFI <u>V</u> PPSDEQLKSG TAT <u>TV</u> <u>A</u> <u>C</u> <u>F</u> LNN FYPREAKVQW KVDNALQSGN SQE <u>M</u> <u>V</u> SEQDS KDSTYSL <u>M</u> <u>S</u> <u>L</u> LTLSKADYЕК HKVYACEVTH QGLSSPVTKS FNRGEC
JS20 HC SEQ ID NO: 49	TKGPSVFPP <u>F</u> A PSSKSTSGGT <u>A</u> <u>M</u> <u>L</u> GCLVKDY FPEPVTVSWN SGALTSGVHT <u>M</u> PAVLQSSGL Y <u>I</u> <u>L</u> <u>A</u> SVVTVP SSSLGTQTYI CN
JS78 HC IgG1 SEQ ID NO: 50	TKGPSVFPP <u>F</u> A PSSKSTSGGT <u>A</u> <u>M</u> <u>L</u> GCLVKDY FPEPVTVSWN SGALTSGVHT <u>Y</u> PAVLQSSGL Y <u>I</u> <u>L</u> <u>A</u> <u>S</u> AVTVP SSSLGTQTYI CN
JS78 HC IgG2 SEQ ID NO: 106	TKGPSVFPP <u>F</u> A PCSRSTSEST <u>A</u> <u>M</u> <u>L</u> GCLVKDY FPEPVTVSWN SGALTSGVHT <u>Y</u> PAVLQSSGL Y <u>I</u> <u>L</u> <u>A</u> <u>S</u> AVTVP SSNFGTQTYT CN
JS78 HC IgG3 SEQ ID NO: 107	TKGPSVFPP <u>F</u> A PCSRSTSGGT <u>A</u> <u>M</u> <u>L</u> GCLVKDY FPEPVTVSWN SGALTSGVHT <u>Y</u> PAVLQSSGL Y <u>I</u> <u>L</u> <u>A</u> <u>S</u> AVTVP SSSLGTQTYT CN
JS78 HC IgG4 SEQ ID NO: 108	TKGPSVFPP <u>F</u> A PCSRSTSEST <u>A</u> <u>M</u> <u>L</u> GCLVKDY FPEPVTVSWN SGALTSGVHT <u>F</u> PAVLQSSGL Y <u>I</u> <u>L</u> <u>A</u> <u>S</u> AVTVP SSSLGTKTYT CN
JT20 HC SEQ ID NO: 51	TKGPSVFPP <u>F</u> A PSSKSTSGGT <u>A</u> <u>T</u> <u>L</u> GCLVKDY FPEPVTVSWN SGALTSGVHT <u>M</u> PAVLQSSGL Y <u>T</u> <u>L</u> <u>A</u> <u>S</u> <u>L</u> VTVP SSSLGTQTYI CN
JT25 HC SEQ ID NO: 52	TKGPSVFPP <u>F</u> A PSSKSTSGGT <u>A</u> <u>M</u> <u>L</u> GCLVKDY FPEPVTVSWN SGALTSGVHT <u>M</u> PAVLQSSGL Y <u>T</u> <u>L</u> <u>A</u> SVVTVP SSSLGTQTYI CN

[0294] Amino acid positions 116, 118, 131, 133, 135, 162, 164, 174, 176, and 178 in CL (EU numbering) correspond to amino acid positions 18, 20, 33, 35, 37, 64, 66, 76, 78, and 80 in SEQ ID NOs: 45-48, respectively. Amino acid positions 116, 118, 131, 133, 135, 162, 164, 174, 176, and 178 (EU numbering) in the CL domain of a kappa chain correspond to amino acid positions 116, 118, 131, 133, 135, 162, 164, 174, 176, and 178 (Kabat numbering) in the CL domain of a lambda light chain. Amino

acid positions 116, 118, 131, 133, 135, 162, 164, 174, 176, and 178 (Kabat numbering) in the CL domain of a lambda light chain correspond to amino acid positions 10, 12, 25, 27, 29, 56, 59, 67, 69, and 71 in SEQ ID NO: 128, respectively.

[0295] Amino acid positions 128, 141, 170, 181, 183, and 185 (EU numbering) in CH1 correspond to amino acid positions 9, 22, 51, 62, 64, and 66 of SEQ ID NOs: 49-52 and 106-108, respectively.

[0296] All possible pair-wise combinations of SEQ ID NOs: 45-48 or amino acids 11-116 of SEQ ID Nos: 45-48 and SEQ ID NOs: 49-52 are contemplated. In certain embodiments, the multispecific antigen-binding protein comprises a first light chain polypeptide L1 comprising a CL domain as set forth in any of SEQ ID NOs: 45-48. The CL domain as set forth in SEQ ID NO: 54 corresponds to amino acids 11-116 of SEQ ID NOs: 45-48. Accordingly, L1 may comprise a CL domain comprising amino acids 11-116 as set forth in any of SEQ ID Nos: 45-48. In certain embodiments, specific combinations of SEQ ID NOs: 45-48 or amino acids 11-116 of SEQ ID Nos: 45-48 and 128 with SEQ ID NOs: 49-52 and 106-108 are contemplated. Such combinations include, but are not limited to, SEQ ID NO: 49/SEQ ID NO: 45 or amino acids 11-116 of SEQ ID NO: 45; SEQ ID NO: 50/SEQ ID NO: 46 or amino acids 11-116 of SEQ ID NO: 46; SEQ ID NO: 106/SEQ ID NO: 46 or amino acids 11-116 of SEQ ID NO: 46; SEQ ID NO: 107/SEQ ID NO: 46 or amino acids 11-116 of SEQ ID NO: 46; SEQ ID NO: 108/SEQ ID NO: 46 or amino acids 11-116 of SEQ ID NO: 46; SEQ IS NO: 51/SEQ ID NO: 47 or amino acids 11-116 of SEQ ID NO: 47; SEQ ID NO: 50/SEQ ID NO: 128; SEQ ID NO: 106/SEQ ID NO: 128; SEQ ID NO: 107/SEQ ID NO: 128; SEQ ID NO: 108/SEQ ID NO: 128; and SEQ ID NO: 52/SEQ ID NO: 48 or amino acids 11-116 of SEQ ID NO: 48.

[0297] It will be apparent to those of ordinary skill in the art that the terms “H1” and “H2” are arbitrary designations, and that “H1” and “H2” in any of the embodiments above can be reversed. That is, any of the mutations above described as being in the CH1 domain of H1 and CL domain of L1 can, alternatively, be in the CH1 domain of H2 and the CL domain of L2.

[0298] As noted above, the mutations in the CH1/CL interface identified by Strategy #2 can be used independently of or in addition to the mutations in the CH1/CL interface identified by Strategy #1.

[0299] Thus, for example, provided herein is a multispecific antigen-binding protein comprising a CH1 domain of H1 that comprises A141I, F170S, S181M, S183A, and V185A substitution mutations (EU numbering), a CL domain of L1 that comprises F116A, L135V, S174A, S176F, and T178V substitution mutations (EU numbering), a CH1 domain of H2 that comprises an S183E substitution mutation (EU numbering), and a CL domain of L2 that comprises a V133K substitution mutation (EU numbering). Additionally, in certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H1 of the

multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering). In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 that comprises A141I, F170S, S181M, S183A, and V185A substitution mutations (EU numbering), a CL domain of L1 that comprises F116A, L135V, S174A, S176F, and T178V substitution mutations (EU numbering), a CH1 domain of H2 that consists of an S183E substitution mutation (EU numbering), and a CL domain of L2 that consists of a V133K substitution mutation (EU numbering). Additionally, in certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering). In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 that consists of A141I, F170S, S181M, S183A, and V185A substitution mutations (EU numbering), a CL domain of L1 that consists of F116A, L135V, S174A, S176F, and T178V substitution mutations (EU numbering), a CH1 domain of H2 that consists of an S183E substitution mutation (EU numbering), and a CL domain of L2 that consists of a V133K substitution mutation (EU numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering). In certain embodiments, the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering). Additionally, in certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering). In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 that comprises (or consisting of or consisting essentially of) the amino acid sequence of SEQ ID NO: 29, a CL domain of L1 that comprises

(or consisting of or consisting essentially of) SEQ ID NO: 19 or the amino acids 11-116 in the sequence set forth in SEQ ID NO: 19, a CH1 domain of H2 that comprises (or consists of or consisting essentially of) the amino acid sequence of SEQ ID NO: 15, and a CL domain of L2 that comprises (or consists of or consisting essentially of) SEQ ID NO: 5 or the amino acids 11-116 in the sequence set forth in SEQ ID NO: 5.

[0300] In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 that comprises A141I, F170S, S181M, S183A, and V185A substitution mutations (EU numbering), a CL domain of L1 that comprises F116A, L135V, S174A, S176F, and T178V substitution mutations (EU numbering), a CH1 domain of H2 that comprises an S183K substitution mutation (EU numbering), and a CL domain of L2 that comprises a V133E substitution mutation (EU numbering). In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 that comprises A141I, F170S, S181M, S183A, and V185A substitution mutations (EU numbering), a CL domain of L1 that comprises F116A, L135V, S174A, S176F, and T178V substitution mutations (EU numbering), a CH1 domain of H2 that consists of an S183K substitution mutation (EU numbering), and a CL domain of L2 that consists of a V133E substitution mutation (EU numbering). In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 that consists of A141I, F170S, S181M, S183A, and V185A substitution mutations (EU numbering), a CL domain of L1 that consists of F116A, L135V, S174A, S176F, and T178V substitution mutations (EU numbering), a CH1 domain of H2 that consists of an S183K substitution mutation (EU numbering), and a CL domain of L2 that consists of a V133E substitution mutation (EU numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering). In certain embodiments, the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering).

[0301] In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 that comprises A141I, F170S, S181M, S183A, and V185A substitution mutations (EU numbering), a CL domain of L1 that comprises F116A, L135V, S174A, S176F, and T178V substitution mutations (EU numbering), a CH1 domain of H2 that comprises L128F, A141M, F170M, S181I, and S183A substitution mutations (EU numbering), and a CL domain of L2 that comprises F118V, S131T, V133A, L135Y, S162A, T164S, S176M, and S178L substitution mutations (EU numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering).

[0302] In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 that comprises A141I, F170S, S181M, S183A, and V185A substitution mutations (EU numbering), a CL domain of L1 that comprises F116A, L135V, S174A, S176F, and T178V substitution mutations (EU numbering), a CH1 domain of H2 that comprises L128F, A141M, F170Y, S181I, S183A, and V185A substitution mutations (EU numbering), and a CL domain of L2 that comprises F118V, S131T, V133A, L135F, S162A, S176A, and T178L substitution mutations (EU numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering).

[0303] In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 that comprises A141I, F170S, S181M, S183A, and V185A mutations (EU numbering), a CL domain of L1 that comprises F116A, L135V, S174A, S176F, and T178V mutations (EU numbering), a CH1 domain of H2 that comprises L128F, A141T, F170M, S181T, S183A, and V185L substitution mutations (EU numbering), and a CL domain of L2 that comprises F118V, S131T, V133A, L135F, S162A, T164S, S176T, and T178L substitution mutations (EU numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering).

[0304] In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 that comprises A141I, F170S, S181M, S183A, and V185A substitution mutations (EU numbering), a CL domain of L1 that comprises F116A, L135V, S174A, S176F, and T178V substitution mutations (EU numbering), a CH1 domain of H2 that comprises L128F, A141M, F170M, S181T, and S183A substitution mutations (EU numbering), and a CL domain of L2 that comprises F118V, S131T, V133A, L135F, S162M, T164S, S176M, and T178L substitution mutations (EU numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering).

[0305] In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 that comprises A141I, F170S, S181M, S183A, and V185A substitution mutations (EU numbering), a CL domain of L1 that comprises F116A, L135V, S174A, S176F, and T178V substitution mutations (EU numbering), a CH1 domain of H2 that comprises A141I, F170S, S181M, S183V, and V185A substitution mutations (EU numbering), and a CL domain of L2 that comprises F116A, V133I, L135V, S162M, S174A, S176F, and T178V substitution mutations (EU numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering).

[0306] In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 that comprises A141I, F170S, S181M, S183A, and V185A substitution mutations (EU numbering), a CL domain of L1 that comprises F116A, L135V, S174A, S176F, and T178V substitution mutations (EU numbering), a CH1 domain of H2 that comprises A141I, F170S, S181M, S183A, and V185A substitution mutations (EU numbering), and a CL domain of L2 that comprises F116A, S131D, L135V, S162A, S174A, S176F, and T178I substitution mutations (EU numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering).

[0307] In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 that comprises A141I, F170S, S181M, S183A, and V185A substitution mutations (EU numbering), a CL domain of L1 that comprises F116A, L135V, S174A, S176F, and T178V substitution mutations (EU numbering), a CH1 domain of H2 that comprises A141I, F170A, S181M, S183V, and V185A substitution mutations (EU numbering), and a CL domain of L2 that comprises F116A, L135V, S162M, S174A, S176F, and T178V substitution mutations (EU numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering).

[0308] In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 that comprises L128F, A141M, F170Y, S181I, S183A, and V185A mutations (EU numbering), a CL domain of L1 that comprises F118V, S131T, V133A, L135F, S162A, S176A, and T178L mutations (EU numbering), a CH1 domain of H2 that comprises an S183E substitution mutation (EU numbering), and a CL domain of L2 that comprises a V133K substitution mutation (EU numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering).

[0309] In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 that comprises L128F, A141M, F170Y, S181I, S183A, and V185A mutations (EU numbering), a CL

domain of L1 that comprises F118V, S131T, V133A, L135F, S162A, S176A, and T178L mutations (EU numbering), a CH1 domain of H2 that comprises an S183K substitution mutation (EU numbering), and a CL domain of L2 that comprises a V133E substitution mutation (EU numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering).

[0310] In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 that comprises L128F, A141M, F170Y, S181I, S183A, and V185A substitution mutations (EU numbering), a CL domain of L1 that comprises F118V, S131T, V133A, L135F, S162A, S176A, and T178L substitution mutations (EU numbering), a CH1 domain of H2 that comprises L128F, A141M, F170M, S181I, and S183A substitution mutations (EU numbering), and a CL domain of L2 that comprises F118V, S131T, V133A, L135Y, S162A, T164S, S176M, and S178L substitution mutations (EU numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering).

[0311] In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 that comprises L128F, A141M, F170Y, S181I, S183A, and V185A substitution mutations (EU numbering), a CL domain of L1 that comprises F118V, S131T, V133A, L135F, S162A, S176A, and T178L substitution mutations (EU numbering), a CH1 domain of H2 that comprises A141I, F170S,

S181M, S183A, and V185A substitution mutations (EU numbering), a CL domain of L2 that comprises F116A, L135V, S174A, S176F, and T178V substitution mutations (EU numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering).

[0312] In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 that comprises L128F, A141M, F170Y, S181I, S183A, and V185A substitution mutations (EU numbering), a CL domain of L1 that comprises F118V, S131T, V133A, L135F, S162A, S176A, and T178L substitution mutations (EU numbering), a CH1 domain of H2 that comprises L128F, A141T, F170M, S181T, S183A, and V185L substitution mutations (EU numbering), and a CL domain of L2 that comprises F118V, S131T, V133A, L135F, S162A, T164S, S176T, and T178L substitution mutations (EU numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering).

[0313] In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 that comprises L128F, A141M, F170Y, S181I, S183A, and V185A substitution mutations (EU numbering), a CL domain of L1 that comprises F118V, S131T, V133A, L135F, S162A, S176A, and T178L substitution mutations (EU numbering), a CH1 domain of H2 that comprises L128F, A141M, F170M, S181T, and S183A substitution mutations (EU numbering), and a CL domain of L2 that

comprises F118V, S131T, V133A, L135F, S162M, T164S, S176M, and T178L substitution mutations (EU numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering).

[0314] In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 that comprises L128F, A141M, F170Y, S181I, S183A, and V185A substitution mutations (EU numbering), a CL domain of L1 that comprises F118V, S131T, V133A, L135F, S162A, S176A, and T178L substitution mutations (EU numbering), a CH1 domain of H2 that comprises A141I, F170S, S181M, S183V, and V185A substitution mutations (EU numbering), and a CL domain of L2 that comprises F116A, V133I, L135V, S162M, S174A, S176F, and T178V substitution mutations (EU numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering).

[0315] It will be apparent to those of ordinary skill in the art that the terms “H1” and “H2” are arbitrary designations, and that “H1” and “H2” in any of the embodiments above can be reversed. That is, any of the mutations above described as being in the CH1 domain and/or the VH domain of H1 and CL domain and/or the VL domain of L1 can, alternatively, be in the CH1 domain and/or VH domain of H2 and the CL domain and/or VL domain of L2.

[0316] In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 that comprises L128F, A141M, F170Y, S181I, S183A, and V185A substitution mutations (EU numbering), a CL domain of L1 that comprises F118V, S131T, V133A, L135F, S162A, S176A, and T178L substitution mutations (EU numbering), a CH1 domain of H2 that comprises A141I, F170S, S181M, S183A, and V185A substitution mutations (EU numbering), and a CL domain of L2 that comprises F116A, S131D, L135V, S162A, S174A, S176F, and T178I substitution mutations (EU numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering).

[0317] In certain embodiments, the multispecific antigen-binding protein comprises a CH1 domain of H1 that comprises L128F, A141M, F170Y, S181I, S183A, and V185A substitution mutations (EU numbering), a CL domain of L1 that comprises F118V, S131T, V133A, L135F, S162A, S176A, and T178L substitution mutations (EU numbering), a CH1 domain of H2 that comprises A141I, F170A, S181M, S183V, and V185A substitution mutations (EU numbering), and a CL domain of L2 that comprises F116A, L135V, S162M, S174A, S176F, and T178V substitution mutations (EU numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering). In certain embodiments, the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering).

[0318] It will be apparent to those of ordinary skill in the art that the terms “H1” and “H2” are arbitrary designations, and that “H1” and “H2” in any of the embodiments above can be reversed. That is, any of the mutations above described as being in the CH1 domain and/or the VH domain of H1 and CL domain and/or the VL domain of L1 can, alternatively, be in the CH1 domain and/or VH domain of H2 and the CL domain and/or VL domain of L2.

[0319] In certain embodiments, a multispecific antigen-binding protein provided herein comprises a CH1 domain of H1 comprising no more than 1 amino acid substitution mutation, no more than 2 amino acid substitution mutations, no more than 3 amino acid substitution mutations, no more than 5 amino acid substitution mutations, or no more than 6 amino acid substitutions, no more than 7 amino acid substitutions, no more than 8 amino acid substitutions, no more than 9 amino acid substitutions, no more than 10 amino acid substitutions, no more than 11 amino acid substitutions, or no more than 12 amino acid substitutions.

[0320] In certain embodiments, a multispecific antigen-binding protein provided herein comprises a CL domain of L1 comprising no more than 1 amino acid substitution mutation, no more than 2 amino acid substitution mutations, no more than 3 amino acid substitution mutations, no more than 5 amino acid substitution mutations, or no more than 6 amino acid substitutions, no more than 7 amino acid substitutions, no more than 8 amino acid substitutions, or no more than 9 amino acid substitutions, no more than 10 amino acid substitutions, no more than 11 amino acid substitutions, or no more than 12 amino acid substitutions.

In certain embodiments the CH1 domain of H1 has at least about 70%, at least about 71%, at least about 72%, at least about 73%, at least about 74%, at least about 75%, at least about 76%, at least about 77%, at least about 78%, at least about 79%, at least about 80%, at least about 81%, at least about 82%, at least about 83%, at least about 84%, at least about 85%, at least about 86%, at least about 87%, at least about 88%, at least about 89%, at least about 90%, at least about 91 %, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% identical to a human germline or allotype heavy chain CH1 domain. *See* Jefferis *et al.* (2009) *Mabs* 1: 332-338. Provided below are the amino acid sequences of human IgG1 CH1 domain (*i.e.*, **SEQ ID NO: 57**) and human IgG4 S228P CH1 domain (*i.e.*, **SEQ ID NO: 58**). ASTKGPSVFP

LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT
YICNVNHKPS NTKVDKKVEP KSCDKHTTCP PCPAPELLGG PSVFLFPPKP KDTLMISRTF EVTCVVVDVS
HEDPEVKFNW YVDGVEVHNA KTKPREEQYN STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS
KAKGQPREPQ VYTLPPSREE MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTTTPV LDSDGSFFLY
SKLTVDKSRW QQGNVFSCSV MHEALHNHYT QKSLSLSPGK (**SEQ ID NO. 57**)

ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS GLYSLSSVVT
VPSSSLGTKT YTCNVNHHKPS NTKVDKRVES KYGPPCPPCP APEFLGGPSV FLFPPKPKDT LMISRTPEVT
CVVVDVSQED PEVQFNWYVD GVEVHNAKTK PREEQFNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKGLPS

SIKTISKAK GQPREPQVYT LPFSQEEMTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTTPVLDS
DGSFFLYSRL TVDKSRWQEG NVFSCSVME ALHNHYTQKS LSLSLGK (SEQ ID NO. 58)

[0321] In some embodiments, LC1 is a kappa light chain. In some embodiments, the CL domain of LC1 has at least about 70%, at least about 71%, at least about 72%, at least about 73%, at least about 74%, at least about 75%, at least about 76%, at least about 77%, at least about 78%, at least about 79%, at least about 80%, at least about 81%, at least about 82%, at least about 83%, at least about 84%, at least about 85%, at least about 86%, at least about 87%, at least about 88%, at least about 89%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% identical to a human germline or allotype kappa chain CL domain. Provided below is the amino acid sequence of human kappa light chain constant domain (*i.e.*, SEQ ID NO: 59).

[0322] RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG NSQESVTEQD SKDSTYSLSS
TLTSLKADYE KHKVYACEVT HQGLSSPVTK SFNRGEC (SEQ ID NO. 59) In some embodiments, LC1 is a lambda light chain. In some embodiments, the CL domain of LC1 has at least about 70%, at least about 71%, at least about 72%, at least about 73%, at least about 74%, at least about 75%, at least about 76%, at least about 77%, at least about 78%, at least about 79%, at least about 80%, at least about 81%, at least about 82%, at least about 83%, at least about 84%, at least about 85%, at least about 86%, at least about 87%, at least about 88%, at least about 89%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% identical to a human germline or allotype lambda CL domain. Provided below is the amino acid sequence of a human lambda light chain constant domain (*i.e.*, SEQ ID NO: 113).

GQPKAAPSVT LFPPSSEELQ ANKATLVCLI SDFYPGAVTV AWKADSSPVK AGVETTTPSK QSNKYAASS
YLSLTPEQWK SHKSYSCQVT HEGSTVEKTV APTECS (SEQ ID NO: 113)

[0323] In certain embodiments, the parental H1 from which an H1 of a multispecific antigen-binding protein provided herein is derived does not show a significant preference for a parental L1 from which an L1 of a multispecific antigen-binding protein provided herein is derived. In certain embodiments, the parental H1 from which an H1 of a multispecific antigen-binding protein provided herein is derived shows a preference for a parental L1 from which an L1 of a multispecific antigen-binding protein provided herein is derived.

[0324] It will be apparent to those of ordinary skill in the art that the terms "H1" and "H2" are arbitrary designations, and that "H1" and "H2" in any of the embodiments above can be reversed. That is, any of the mutations above described as being in the CH1 domain and/or the VH domain of H1 and

CL domain and/or the VL domain of L1 can, alternatively, be in the CH1 domain and/or VH domain of H2 and the CL domain and/or VL domain of L2.

Modifications to the VH and VL domains

[0325] In certain embodiments, the multispecific antigen-binding protein, or an antigen-binding fragment thereof, comprises amino acid modifications in the VH and VL domain(s), *i.e.*, independently of modifications in the CH1 and CL domains described herein. In certain embodiments, the multispecific antigen-binding proteins provided herein additionally comprise amino acid modifications in the VH and VL domain(s), *i.e.*, in combination with mutations in the CH1/CL interface identified by Strategy #1 and/or the mutations in the CH1/CL interface identified by Strategy #1.

[0326] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises an amino acid substitution at position Q39 (Kabat numbering), and the VL domain of L1 of the multispecific antigen-binding protein comprises an amino acid substitution at position Q38 (Kabat numbering). In certain embodiments, the amino acid at position Q39 (Kabat numbering) in the VH domain of H1 is replaced with a positively charged residue, and the amino acid at position Q38 (Kabat numbering) in the VL domain of L1 is replaced with a negatively charged residue. In certain embodiments, the amino acid at position Q39 (Kabat numbering) in the VH domain of H1 is replaced with a negatively charged residue, and wherein the amino acid at position Q38 (Kabat numbering) in the VL domain of L1 is replaced with a positively charged residue. In certain embodiments, the positively charged residue is selected from the group consisting of R, H, and K. In certain embodiments, the negatively charged residue is selected from the group consisting of D and E.

[0327] Additionally or alternatively, in certain embodiments, the VH domain of H2 of the multispecific antigen-binding protein comprises an amino acid substitution at position Q39 (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises an amino acid substitution at position Q38 (Kabat numbering). In certain embodiments, the amino acid at position Q39 (Kabat numbering) in the VH domain of H2 is replaced with a positively charged residue, and wherein the amino acid at position Q38 (Kabat numbering) in the VL domain of L2 is replaced with a negatively charged residue. In certain embodiments, the amino acid at position Q39 (Kabat numbering) in the VH domain of H2 is replaced with a negatively charged residue, and wherein the amino acid at position Q38 (Kabat numbering) in the VL domain of L2 is replaced with a positively charged residue. In certain embodiments, the positively charged residue is selected from the group consisting of R, H, and K. In certain embodiments, the negatively charged residue is selected from the group consisting of D and E.

[0328] In certain embodiments, specific combinations of substitution mutations at position Q39 (Kabat numbering) on the VH domain of H1 and at position Q38 (Kabat numbering) on the VL domain of L1 and/or at position Q39 (Kabat numbering) on the VH domain of H2 and at position Q38 (Kabat numbering) on the VL domain of L2 are contemplated. Such combinations include, but not limited, to those shown in Tables 9A and 9B below:

Table 9A

Q39D/Q38K	Q39R/Q38D
Q39E/Q38K	Q39K/Q38D
Q39D/Q38R	Q39R/Q38E
Q39E/Q38R	Q39K/Q38E
Q39D/Q38H	Q39H/Q38D
Q39E/Q38H	Q39H/Q38E

[0329] The first mutation in each pair in Table 9A refers to a modification in the VH domain sequence, and the second mutation in each pair in Table 9A refers to a modification in the VL domain sequence.

Table 9B

EKKE	KEEK	EKKD	KDEK
ERKE	KEER	ERKD	KDER
DKKE	KEDK	DKKD	KDDK
DRKE	KEDR	DRKD	KDDR
EKRE	REEK	EKRD	RDEK
ERRE	REER	ERRD	RDER
DKRE	REDK	DKRD	RDDK
DRRE	REDR	DRRD	RDDR

[0330] The four letter mutations in Table 9B refer to the amino acid substitutions at $Q39X_{VH1}/Q38X_{VL1}/Q39X_{VH2}/Q38X_{VL2}$, where “VH1” refers to the VH domain of H1, “VL” refers to the VL domain of L1, “VH2” refers to the VH domain of H2, and “VL2” refers to the VL domain of L2. It will be apparent to those of ordinary skill in the art that the terms “H1”/“L1” and “H2”/“L2” are arbitrary designations, and that “H1” and “L1” in any of the embodiments above can be reversed with “H2” and

“L2,” respectively. That is, any of the mutations above described as being in the VH domain of H1 and VL domain of L1 can, alternatively, be in the VH domain of H2 and the VL domain of L2.

[0331] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises an amino acid substitution at position Q39E (Kabat numbering), and the VL domain of L1 of the multispecific antigen-binding protein comprises an amino acid substitution at position Q38K (Kabat numbering). In certain embodiments, the VH domain of H2 of the multispecific antigen-binding protein comprises an amino acid substitution at position Q39K (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises an amino acid substitution at position Q38E (Kabat numbering). In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises an amino acid substitution at position Q39K (Kabat numbering), and the VL domain of L1 of the multispecific antigen-binding protein comprises an amino acid substitution at position Q38E (Kabat numbering). In certain embodiments, the VH domain of H2 of the multispecific antigen-binding protein comprises an amino acid substitution at position Q39E (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises an amino acid substitution at position Q38K (Kabat numbering). In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises an amino acid substitution at position Q39E (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises an amino acid substitution at position Q38K (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises an amino acid substitution at position Q39K (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises an amino acid substitution at position Q38E (Kabat numbering). In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises an amino acid substitution at position Q39K (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises an amino acid substitution at position Q38E (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises an amino acid substitution at position Q39E (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises an amino acid substitution at position Q38K (Kabat numbering).

[0332] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38R substitution mutation (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering).

[0333] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39D substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of

H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering).

[0334] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39D substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38R substitution mutation (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering).

[0335] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39R substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering).

[0336] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38R substitution mutation (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39R substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering).

[0337] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39D substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39R substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering).

[0338] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a substitution mutation Q39D (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38R substitution mutation (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39R substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering).

[0339] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38D substitution mutation (Kabat numbering).

[0340] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38R substitution mutation (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38D substitution mutation (Kabat numbering).

[0341] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39D substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38D substitution mutation (Kabat numbering).

[0342] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39D substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38R substitution mutation (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38D substitution mutation (Kabat numbering).

[0343] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39R substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38D substitution mutation (Kabat numbering).

[0344] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38R substitution mutation (Kabat numbering), the VH domain of

H2 of the multispecific antigen-binding protein comprises a Q39R substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38D substitution mutation (Kabat numbering).

[0345] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39D substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39R substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38D substitution mutation (Kabat numbering).

[0346] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39D substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38R substitution mutation (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39R substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38D substitution mutation (Kabat numbering).

[0347] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38R substitution mutation (Kabat numbering).

[0348] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39D substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering).

[0349] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39D substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38R substitution mutation (Kabat numbering).

[0350] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39R substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering).

[0351] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39R substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38R substitution mutation (Kabat numbering).

[0352] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39R substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39D substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering).

[0353] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39R substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39D substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38R substitution mutation (Kabat numbering).

[0354] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38D substitution mutation (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering).

[0355] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38D substitution mutation (Kabat numbering), the VH domain of

H2 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38R substitution mutation (Kabat numbering).

[0356] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38D substitution mutation (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39D substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering).

[0357] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38D substitution mutation (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39D substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38R substitution mutation (Kabat numbering).

[0358] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39R substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38D substitution mutation (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering).

[0359] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39R substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38D substitution mutation (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38R substitution mutation (Kabat numbering).

[0360] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39R substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38D substitution mutation (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39D substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering).

[0361] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39R substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38D substitution mutation (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39D substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38R substitution mutation (Kabat numbering).

[0362] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39H substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38D substitution mutation (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39D substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38H substitution mutation (Kabat numbering).

[0363] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39H substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38H substitution mutation (Kabat numbering).

[0364] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39D substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38H substitution mutation (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39H substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38D substitution mutation (Kabat numbering).

[0365] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38H substitution mutation (Kabat numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39H substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering).

[0366] It will be apparent to those of ordinary skill in the art that the terms “H1”/“L1” and “H2”/“L2” are arbitrary designations, and that “H1” and “L1” in any of the embodiments above can be reversed with

“H2” and “L2,” respectively. That is, any of the mutations above described as being in the VH domain of H1 and VL domain of L1 can, alternatively, be in the VH domain of H2 and the VL domain of L2.

[0367] As noted elsewhere herein, the multispecific antigen-binding proteins provided herein in some embodiments comprise amino acid modifications in the VH and VL domain(s), *i.e.*, such as the amino acid modifications described above, in combination with mutations in the CH1/CL interface identified by Strategy #1 and/or the mutations in the CH1/CL interface identified by Strategy #2.

[0368] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) an S183E substitution mutation (EU numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) a V133K substitution mutation (EU numbering).

[0369] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) an S183E substitution mutation (EU numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) a V133K substitution mutation (EU numbering).

[0370] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) an S183E substitution mutation (EU numbering), and the CL domain of L1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) a V133K substitution mutation (EU numbering).

[0371] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) an S183E substitution mutation (EU numbering), and the CL domain of L1 of the multispecific antigen-

binding protein comprises (such as consists of or consists essentially of) a V133K substitution mutation (EU numbering).

[0372] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) an S183E substitution mutation (EU numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) a V133K substitution mutation (EU numbering).

[0373] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) an S183K substitution mutation (EU numbering), and the CL domain of L1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) a V133E substitution mutation (EU numbering).

[0374] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) an S183E substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) a V133K substitution mutation (EU numbering).

[0375] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) an S183E substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) a V133K substitution mutation (EU numbering).

[0376] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) an S183F substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) a V133K substitution mutation (EU numbering).

[0377] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) an S183E substitution mutation (EU numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) an S183F substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) a V133K substitution mutation (EU numbering).

[0378] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) an S183T substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) a V133K substitution mutation (EU numbering).

[0379] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) an S183E substitution mutation (EU numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the CH1 domain of H2 of the

multispecific antigen-binding protein comprises (such as consists of or consists essentially of) an S183T substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) a V133K substitution mutation (EU numbering).

[0380] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) an S183Y substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) a V133K substitution mutation (EU numbering).

[0381] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) an S183E substitution mutation (EU numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) an S183Y substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) a V133K substitution mutation (EU numbering).

[0382] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) a V133E substitution mutation (EU numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) an S183E substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the CL domain of L2 of the

multispecific antigen-binding protein comprises (such as consists of or consists essentially of) a V133K substitution mutation (EU numbering).

[0383] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) an S183K substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) a V133E substitution mutation (EU numbering).

[0384] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) an S183K substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) a V133E substitution mutation (EU numbering).

[0385] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) an S183E substitution mutation (EU numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) a V133K substitution mutation (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering).

[0386] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) an S183E substitution mutation (EU numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), CL domain of L1 of the multispecific antigen-binding

protein comprises (such as consists of or consists essentially of) a V133K substitution mutation (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering).

[0387] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) an S183K substitution mutation (EU numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) a V133E substitution mutation (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering).

[0388] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) an S183K substitution mutation (EU numbering), and the CL domain of L1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) a V133E substitution mutation (EU numbering).

[0389] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) an S183K substitution mutation (EU numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises (such as consists of or consists essentially of) a V133E substitution mutation (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering).

[0390] In certain embodiments, the CH1 domain of H1 of the multispecific antigen-binding protein comprises a S183K substitution mutation (EU numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises a V133E substitution mutation (EU numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises an S183E substitution mutation (EU numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises a V133K

substitution mutation (EU numbering). In certain embodiments, the CH1 domain of H1 of the multispecific antigen-binding protein consists of a S183K substitution mutation (EU numbering), the CL domain of L1 of the multispecific antigen-binding protein consists of a V133E substitution mutation (EU numbering), the CH1 domain of H2 of the multispecific antigen-binding protein consists of an S183E substitution mutation (EU numbering), and the CL domain of L2 of the multispecific antigen-binding protein consists of a V133K substitution mutation (EU numbering).

[0391] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises a V133E substitution mutation (EU numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises an S183E substitution mutation (EU numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises a V133K substitution mutation (EU numbering).

[0392] In certain embodiments, the CH1 domain of H1 of the multispecific antigen-binding protein comprises a S183K substitution mutation (EU numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises a V133E substitution mutation (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises an S183E substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises a V133K substitution mutation (EU numbering).

[0393] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein comprises a S183K substitution mutation (EU numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises a V133E substitution mutation (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises an S183E substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises a V133K substitution mutation (EU numbering).

[0394] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific

antigen-binding protein consists of a S183K substitution mutation (EU numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the CL domain of L1 of the multispecific antigen-binding protein consists of a V133E substitution mutation (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein consists of an S183E substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein consists of a V133K substitution mutation (EU numbering).

[0395] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein comprises a S183K substitution mutation (EU numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises a V133E substitution mutation (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises an S183E substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises a V133K substitution mutation (EU numbering).

[0396] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein consists of a S183K substitution mutation (EU numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the CL domain of L1 of the multispecific antigen-binding protein consists of a V133E substitution mutation (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein consists of an S183E substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein consists of a V133K substitution mutation (EU numbering).

[0397] In certain embodiments, the CH1 domain of H1 of the multispecific antigen-binding protein comprises a S183E substitution mutation (EU numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises a V133K substitution mutation (EU numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises an S183K substitution mutation (EU

numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises a V133E substitution mutation (EU numbering).

[0398] In certain embodiments, the CH1 domain of H1 of the multispecific antigen-binding protein consists of a S183E substitution mutation (EU numbering), the CL domain of L1 of the multispecific antigen-binding protein consists of a V133K substitution mutation (EU numbering), the CH1 domain of H2 of the multispecific antigen-binding protein consists of an S183K substitution mutation (EU numbering), and the CL domain of L2 of the multispecific antigen-binding protein consists of a V133E substitution mutation (EU numbering).

[0399] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein comprises a S183E substitution mutation (EU numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises a V133K substitution mutation (EU numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises an S183K substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises a V133E substitution mutation (EU numbering).

[0400] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein consists of a S183E substitution mutation (EU numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the CL domain of L1 of the multispecific antigen-binding protein consists of a V133K substitution mutation (EU numbering), the VH domain of H2 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein consists of an S183K substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein consists of a V133E substitution mutation (EU numbering).

[0401] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein comprises a S183E substitution mutation (EU numbering), the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the

CL domain of L1 of the multispecific antigen-binding protein comprises a V133K substitution mutation (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises an S183K substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises a V133E substitution mutation (EU numbering).

[0402] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein consists of a S183E substitution mutation (EU numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the CL domain of L1 of the multispecific antigen-binding protein consists of a V133K substitution mutation (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein consists of an S183K substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein consists of a V133E substitution mutation (EU numbering).

[0403] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises a V133E substitution mutation (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises an S183E substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises a V133K substitution mutation (EU numbering).

[0404] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises an S183F substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a

Q38E substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises a V133K substitution mutation (EU numbering).

[0405] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises an S183T substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises a V133K substitution mutation (EU numbering).

[0406] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises an S183Y substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises a V133K substitution mutation (EU numbering).

[0407] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises a V133E substitution mutation (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises an S183F substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises a V133K substitution mutation (EU numbering).

[0408] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises a V133E substitution mutation (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding

protein comprises an S183T substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises a V133K substitution mutation (EU numbering).

[0409] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises a V133E substitution mutation (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises an S183Y substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises a V133K substitution mutation (EU numbering).

[0410] In certain embodiments, the VH domain of H1 the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein comprises an S183T substitution mutation (EU numbering) the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the CL domain of L1 of the multispecific antigen-binding protein comprises a V133K substitution mutation (EU numbering). In certain embodiments, the VH domain of H2 the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises an S183K substitution mutation (EU numbering) the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises a V133T substitution mutation (EU numbering).

[0411] In certain embodiments, the VH domain of H1 the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein comprises an S183E substitution mutation (EU numbering) the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the CL domain of L1 of the multispecific antigen-binding protein comprises a V133K substitution mutation (EU numbering). In certain embodiments, the VH domain of H2 the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises an S183K substitution mutation (EU numbering) the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation

(Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises a V133E substitution mutation (EU numbering).

[0412] In certain embodiments, the VH domain of H1 the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein comprises an S183E substitution mutation (EU numbering) the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the CL domain of L1 of the multispecific antigen-binding protein comprises a V133K substitution mutation (EU numbering). In certain embodiments, the VH domain of H2 the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises an S183K substitution mutation (EU numbering) the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises a V133E substitution mutation (EU numbering).

[0413] In certain embodiments, the VH domain of H1 the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein comprises an S183T substitution mutation (EU numbering) the VL domain of L1 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the CL domain of L1 of the multispecific antigen-binding protein comprises a V133K substitution mutation (EU numbering). In certain embodiments, the VH domain of H2 the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises an S183K substitution mutation (EU numbering) the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises a V133T substitution mutation (EU numbering).

[0414] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein comprises A141I, F170S, S181M, S183A, and V185A mutations (EU numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises F116A, L135V, S174A, S176F, and T178V mutations (EU numbering).

[0415] In certain embodiments, the CH1 domain of H1 of the multispecific antigen-binding protein comprises A141I, F170S, S181M, S183A, and V185A mutations (EU numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises F116A, L135V, S174A, S176F, and T178V mutations (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a

Q39K substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering).

[0416] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein comprises A141I, F170S, S181M, S183A, and V185A mutations (EU numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises F116A, L135V, S174A, S176F, and T178V mutations (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering).

[0417] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein consists of A141I, F170S, S181M, S183A, and V185A mutations (EU numbering), the CL domain of L1 of the multispecific antigen-binding protein consists of F116A, L135V, S174A, S176F, and T178V mutations (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering).

[0418] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein comprises A141I, F170S, S181M, S183A, and V185A mutations (EU numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises F116A, L135V, S174A, S176F, and T178V mutations (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering).

[0419] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein consists of A141I, F170S, S181M, S183A, and V185A mutations (EU numbering), the CL domain of L1 of the multispecific antigen-binding protein consists of

F116A, L135V, S174A, S176F, and T178V mutations (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), and the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering).

[0420] In certain embodiments, the CH1 domain of H1 of the multispecific antigen-binding protein comprises A141I, F170S, S181M, S183A, and V185A mutations (EU numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises F116A, L135V, S174A, S176F, and T178V mutations (EU numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises an S183E substitution mutation (EU numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises a V133K substitution mutation (EU numbering).

[0421] In certain embodiments, the CH1 domain of H1 of the multispecific antigen-binding protein comprises A141I, F170S, S181M, S183A, and V185A mutations (EU numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises F116A, L135V, S174A, S176F, and T178V mutations (EU numbering), the CH1 domain of H2 of the multispecific antigen-binding protein consists of an S183E substitution mutation (EU numbering), and the CL domain of L2 of the multispecific antigen-binding protein consists of a V133K substitution mutation (EU numbering).

[0422] In certain embodiments, the CH1 domain of H1 of the multispecific antigen-binding protein consists of A141I, F170S, S181M, S183A, and V185A mutations (EU numbering), the CL domain of L1 of the multispecific antigen-binding protein consists of F116A, L135V, S174A, S176F, and T178V mutations (EU numbering), the CH1 domain of H2 of the multispecific antigen-binding protein consists of an S183E substitution mutation (EU numbering), and the CL domain of L2 of the multispecific antigen-binding protein consists of a V133K substitution mutation (EU numbering).

[0423] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein comprises A141I, F170S, S181M, S183A, and V185A mutations (EU numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises F116A, L135V, S174A, S176F, and T178V mutations (EU numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises an S183E substitution mutation (EU numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises a V133K substitution mutation (EU numbering).

[0424] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 the multispecific

antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein comprises A141I, F170S, S181M, S183A, and V185A mutations (EU numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises F116A, L135V, S174A, S176F, and T178V mutations (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises an S183E substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises a V133K substitution mutation (EU numbering).

[0425] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein comprises A141I, F170S, S181M, S183A, and V185A mutations (EU numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises F116A, L135V, S174A, S176F, and T178V mutations (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein consists of an S183E substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein consists of a V133K substitution mutation (EU numbering).

[0426] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein consists of A141I, F170S, S181M, S183A, and V185A mutations (EU numbering), the CL domain of L1 of the multispecific antigen-binding protein consists of F116A, L135V, S174A, S176F, and T178V mutations (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein consists of an S183E substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein consists of a V133K substitution mutation (EU numbering).

[0427] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein comprises A141I, F170S, S181M, S183A, and V185A

mutations (EU numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises F116A, L135V, S174A, S176F, and T178V mutations (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises an S183E substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises a V133K substitution mutation (EU numbering).

[0428] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein comprises A141I, F170S, S181M, S183A, and V185A mutations (EU numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises F116A, L135V, S174A, S176F, and T178V mutations (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein consists of an S183E substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein consists of a V133K substitution mutation (EU numbering).

[0429] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein consists of A141I, F170S, S181M, S183A, and V185A mutations (EU numbering), the CL domain of L1 of the multispecific antigen-binding protein consists of F116A, L135V, S174A, S176F, and T178V mutations (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein consists of an S183E substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein consists of a V133K substitution mutation (EU numbering).

[0430] In certain embodiments, the CH1 domain of H1 of the multispecific antigen-binding protein comprises A141I, F170S, S181M, S183A, and V185A mutations (EU numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises F116A, L135V, S174A, S176F, and T178V mutations (EU numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises an S183K substitution mutation (EU numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises a V133E substitution mutation (EU numbering).

[0431] In certain embodiments, the CH1 domain of H1 of the multispecific antigen-binding protein comprises A141I, F170S, S181M, S183A, and V185A mutations (EU numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises F116A, L135V, S174A, S176F, and T178V mutations (EU numbering), the CH1 domain of H2 of the multispecific antigen-binding protein consists of an S183K substitution mutation (EU numbering), and the CL domain of L2 of the multispecific antigen-binding protein consists of a V133E substitution mutation (EU numbering).

[0432] In certain embodiments, the CH1 domain of H1 of the multispecific antigen-binding protein consists of A141I, F170S, S181M, S183A, and V185A mutations (EU numbering), the CL domain of L1 of the multispecific antigen-binding protein consists of F116A, L135V, S174A, S176F, and T178V mutations (EU numbering), the CH1 domain of H2 of the multispecific antigen-binding protein consists of an S183K substitution mutation (EU numbering), and the CL domain of L2 of the multispecific antigen-binding protein consists of a V133E substitution mutation (EU numbering).

[0433] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein comprises A141I, F170S, S181M, S183A, and V185A mutations (EU numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises F116A, L135V, S174A, S176F, and T178V mutations (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises an S183K substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises a V133E substitution mutation (EU numbering).

[0434] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein comprises A141I, F170S, S181M, S183A, and V185A mutations (EU numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises F116A, L135V, S174A, S176F, and T178V mutations (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein consists of an S183K substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein consists of a V133E substitution mutation (EU numbering).

[0435] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein consists of A141I, F170S, S181M, S183A, and V185A mutations (EU numbering), the CL domain of L1 of the multispecific antigen-binding protein consists of F116A, L135V, S174A, S176F, and T178V mutations (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein consists of an S183K substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein consists of a V133E substitution mutation (EU numbering).

[0436] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein comprises A141I, F170S, S181M, S183A, and V185A mutations (EU numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises F116A, L135V, S174A, S176F, and T178V mutations (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein comprises an S183K substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein comprises a V133E substitution mutation (EU numbering).

[0437] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L1 the multispecific antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein comprises A141I, F170S, S181M, S183A, and V185A mutations (EU numbering), the CL domain of L1 of the multispecific antigen-binding protein comprises F116A, L135V, S174A, S176F, and T178V mutations (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein consists of an S183K substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein consists of a V133E substitution mutation (EU numbering).

[0438] In certain embodiments, the VH domain of H1 of the multispecific antigen-binding protein comprises a Q39K substitution mutation (Kabat numbering), the VL domain of L1 the multispecific

antigen-binding protein comprises a Q38E substitution mutation (Kabat numbering), the CH1 domain of H1 of the multispecific antigen-binding protein consists of A141I, F170S, S181M, S183A, and V185A mutations (EU numbering), the CL domain of L1 of the multispecific antigen-binding protein consists of F116A, L135V, S174A, S176F, and T178V mutations (EU numbering), the VH domain of H2 the multispecific antigen-binding protein comprises a Q39E substitution mutation (Kabat numbering), the CH1 domain of H2 of the multispecific antigen-binding protein consists of an S183K substitution mutation (EU numbering), the VL domain of L2 of the multispecific antigen-binding protein comprises a Q38K substitution mutation (Kabat numbering), and the CL domain of L2 of the multispecific antigen-binding protein consists of a V133E substitution mutation (EU numbering).

[0439] Additional combinations of mutations in the CH1/CL interface identified by Strategy #2, mutations in the CH1/CL interface identified by Strategy #1, and mutations in the VH and VL domains, *i.e.*, not limited to those described above, are also contemplated.

[0440] It will be apparent to those of ordinary skill in the art that the terms “H1” and “H2” are arbitrary designations, and that “H1” and “H2” in any of the embodiments above can be reversed. That is, any of the mutations above described as being in the CH1 domain and/or the VH domain of H1 and CL domain and/or the VL domain of L1 can, alternatively, be in the CH1 domain and/or VH domain of H2 and the CL domain and/or VL domain of L2.

Fc Mutations

[0441] In certain embodiments, each of H1 and H2 of the multispecific antigen-binding protein comprises an Fc region comprising a CH2 and a CH3 domain. In certain embodiments, the Fc region of H1 and/or H2 is IgG1, IgG2 or IgG4 Fc. In certain embodiments, the CH3 domains of H1 and H2 each meet at an interface, and each of the CH3 domains comprises an amino acid substitution such that the Fc region of H1 preferentially pairs with that of H2 as compared to H1. In certain embodiments, the amino acid substitutions in the CH3 domains results in greater electrostatic complementarity than wild type without the substitutions in the CH3 domains. Methods of measuring electrostatic complementarity at protein/protein interfaces are known in the art and described in, *e.g.*, McCoy *et al.* (1997) *J Mol Biol* 268, 570–584; Lee *et al.*, (2001) *Protein Sci.* 10, 362-377; and Chau *et al.* (1994) *J Comp Mol Des* 8, 51325. In certain embodiments, the amino acid substitutions in the CH3 domains results in greater steric complementarity than wild type without the substitutions in the CH3 domains. Methods of measuring electrostatic complementarity at protein/protein interfaces are known in the art and described in, *e.g.*, Lawrence *et al.* (1993) *J Mol Biol* 234, 946–950; Walls *et al.* (1992) *J Mol Biol* 228, 277-297; and Schueler-Furman *et al.* (2005) *Proteins* 60, 187-194.

[0442] In certain embodiments, the CH3 domains of H1 and H2 (*e.g.*, H1 and H2 of any of the embodiments described herein) are altered, so that within the CH3/CH3 interface, one or more amino acid residues in the CH3 domain of H1 are replaced with one or more amino acid residues having a larger side chain volume, thereby generating a protuberance (or a knob) on the surface of the CH3 domain of H1, and one or more, preferably two or three, amino acid residues in the CH3 domain of H2 that interacts with the CH3 domain of H1 are modified and replaced with amino acid residues having a small side chain volume, thereby generating a cavity (or a hole) on the surface of the CH3 domain of H2 that interacts with the CH3 domain of H1. In certain embodiments, the CH3 domains of H1 and H2 (*e.g.*, H1 and H2 of any of the embodiments described herein) are altered, so that within the interface one or two amino acid residues in the CH3 domain of H2 are replaced with an equivalent number of amino acid residues having a larger side chain volume, thereby generating a protuberance (or a knob) within the interface of the CH3 domain of H2 which is positionable in a cavity (or a hole) within the surface of the CH3 domain of H1 and the CH3 domain of H1 is altered so that within the surface of the CH3 domain of H2 that meets the interface of the CH3 domain of H2 two or three amino acid residues are replaced with an equivalent number of amino acid residues having a smaller side chain volume, thereby generating a cavity within the interface of the CH3 domain of H1 within which a protuberance within the interface of the CH3 domain of H2 is positionable. In certain embodiments, the import residue with a larger side chain volume is phenylalanine (F), tyrosine (Y), arginine (R) or tryptophan (W). In certain embodiments, the protuberance or knob mutation comprises replacement of threonine at position 366 with tryptophan, amino acid numbering according to the EU numbering scheme of Kabat *et al.* (pp. 688-696 in *Sequences of proteins of immunological interest*, 5th ed., Vol. 1 (1991; NIH, Bethesda, MD)). In certain embodiments, the import residue with a smaller side chain volume is serine (S), alanine (A), valine (V), or threonine (T). In certain embodiments, the original residue is threonine. In certain embodiments, the original residue is leucine. In certain embodiments, the original residue is tyrosine. In certain embodiments, the import residue is not cysteine (C). In one embodiment, the import residue is alanine (A). A cavity can be generated by replacing one or more original residues of the CH3 domain. For example, in one embodiment, the CH3 domain comprising a cavity comprises replacement of two or more original amino acids selected from the group consisting of threonine, leucine and tyrosine. In certain embodiments, the CH3 domain comprising a cavity comprises two or more import residues selected from the group consisting of alanine, serine, threonine and valine. In certain embodiments, the modification for the knob mutation is T366W, and the modifications for the hole mutation is at least one, or at least two of T366S, L368A, and Y407V. In certain embodiments, the modification for the knob mutation is T366W, and the modifications for the hole mutation is T366S, L368A, and Y407V. *See, e.g.*, US 5,731,168, US 5,807,706, US 7,183,076, each incorporated herein by reference in its entirety.

Transferability

[0443] Although the specific amino acid modifications to CH1 domain of H1 and CL domain of L1 above have been described with respect to the EU numbering system, it is contemplated and that these amino acid modifications are transferable to other immunoglobulin heavy and light chains, resulting in similar patterns of preferential pairing of one immunoglobulin heavy chain with one of the two immunoglobulin light chains in view of the following.

[0444] The CH1/CL interface residues in the interface between immunoglobulin heavy and light chains are relatively well conserved (Padlan *et al.*, 1986, Mol. Immunol. 23(9): 951-960). This sequence conservation, a result of evolutionary constraints, increases the likelihood that functionally active antibody binding domains will be formed during combinatorial pairing of light and heavy chains. As a result of this sequence conservation, it follows that sequence modifications noted above which drive preferential pairing could transfer to other heavy and light chain pairs, as this region displays high sequence conservation across antibodies.

[0445] In certain embodiments, the amino acid modifications described herein are transferable to the immunoglobulin heavy and light chains of antibodies based on human or humanized IgG1/κ. In certain embodiments, the amino acid modifications described herein are transferable to the immunoglobulin heavy and light chains of antibodies based on human or humanized IgG2/κ. In certain embodiments, the amino acid modifications described herein are transferable to the immunoglobulin heavy and light chains of antibodies based on human or humanized IgG3/κ. In certain embodiments, the amino acid modifications described herein are transferable to the immunoglobulin heavy and light chains of antibodies based on human or humanized IgG4/κ. In certain embodiments, the amino acid modifications described herein are transferable to the immunoglobulin heavy and light chains of antibodies based on human or humanized IgA1/κ. In certain embodiments, the amino acid modifications described herein are transferable to the immunoglobulin heavy and light chains of antibodies based on human or humanized IgA2/κ. In certain embodiments, the amino acid modifications described herein are transferable to the immunoglobulin heavy and light chains of antibodies based on human or humanized IgD/κ. In certain embodiments, the amino acid modifications described herein are transferable to the immunoglobulin heavy and light chains of antibodies based on human or humanized IgE/κ. In certain embodiments, the amino acid modifications described herein are transferable to the immunoglobulin heavy and light chains of antibodies based on human or humanized IgG/κ. In certain embodiments, the amino acid modifications described herein are transferable to the immunoglobulin heavy and light chains of antibodies based on human or humanized IgM/κ.

[0446] In certain embodiments, the amino acid modifications described herein are transferable to the immunoglobulin heavy and light chains of antibodies based on human or humanized IgG1/ λ . In certain embodiments, the amino acid modifications described herein are transferable to the immunoglobulin heavy and light chains of antibodies based on human or humanized IgG2/ λ . In certain embodiments, the amino acid modifications described herein are transferable to the immunoglobulin heavy and light chains of antibodies based on human or humanized IgG3/ λ . In certain embodiments, the amino acid modifications described herein are transferable to the immunoglobulin heavy and light chains of antibodies based on human or humanized IgG4/ λ . In certain embodiments, the amino acid modifications described herein are transferable to the immunoglobulin heavy and light chains of antibodies based on human or humanized IgA1/ λ . In certain embodiments, the amino acid modifications described herein are transferable to the immunoglobulin heavy and light chains of antibodies based on human or humanized IgA2/ λ . In certain embodiments, the amino acid modifications described herein are transferable to the immunoglobulin heavy and light chains of antibodies based on human or humanized IgD/ λ . In certain embodiments, the amino acid modifications described herein are transferable to the immunoglobulin heavy and light chains of antibodies based on human or humanized IgE/ λ . In certain embodiments, the amino acid modifications described herein are transferable to the immunoglobulin heavy and light chains of antibodies based on human or humanized IgG/ λ . In certain embodiments, the amino acid modifications described herein are transferable to the immunoglobulin heavy and light chains of antibodies based on human or humanized IgM/ λ . In certain embodiments, the amino acid modifications described herein are transferable to the immunoglobulin heavy and light chains of antibodies having a framework close to germline. In certain embodiments, the amino acid modifications described herein are transferable to the immunoglobulin heavy and light chains of antibodies having canonical CL and CH1 domains.

[0447] In certain embodiments, the amino acid modifications described herein are introduced to the immunoglobulin heavy and light chains of mouse antibodies. In certain embodiments, the amino acid modifications described herein are introduced to the immunoglobulin heavy and light chains of antibodies based on mouse IgG2a/ λ . In certain embodiments, the amino acid modifications described herein are introduced to the immunoglobulin heavy and light chains of antibodies based on mouse IgG2a/ κ .

[0448] The amino acid sequence of the mouse IgG2a constant region is set forth in SEQ ID NO: 60 below:

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AKTTAPSVYP LAPVCGDTTG SSVTLGCLVK GYFPEPVTLT WNSGSLSSGV HTFPAVLQSD LYTLSSSVTV
TSSTWPSQSI TCNVAHPASS TKVDKKIEPR GPTIKPCPPC KCPAPNLLGG PSVFIFPPKI KDVLMISLSP
IVTCVVVDVS EDDPDVQISW FVNNVEVHTA QTQTHREDYN STLRVVSALP IQHQDWMSGK EFKCKVNNKD
LPAPIERTIS KPKGSVRAPQ VYVLPPPEEE MTKKQVTLTC MVTDFMPEDI YVEWTNNGKT ELNYKNTEPV
LDSGGSYFMY SKLRVEKKNW VERNYSYSCSV VHEGLHNHHT TKSFSRTPGK (SEQ ID NO: 60)
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[0449] The amino acid sequence of the mouse kappa light chain is set forth in SEQ ID NO: 61 below:

RADAAPTVSI FPPSSEQLTS GGASVVCFLN NFYPKDINVK WKIDGSERQN GVLNSWTDQD SKDSTYSMSS
TLTLTKDEYE RHNSYTCEAT HKTSTSPIVK SFNRNEC (SEQ ID NO: 61)

[0450] The amino acid sequence of the mouse lambda 1 light chain is set forth in SEQ ID NO: 62 below:

GQPKSSPSVT LFPPSSEELE TNKATLVCTI TDFYPGVTV DWKVDGTPVT QGMETTQPSK QSNNKYMASS
YLTLTARAWE RHSSYSCQVT HEGTVEKSL SRADCS (SEQ ID NO: 62)

[0451] The amino acid sequence of the mouse lambda 2 light chain is set forth in SEQ ID NO: 63 below:

GQPKSTPTLT VFPPSSEELK ENKATLVCLI SNFSPSGVTV AWKANGTPIT QGVDTSNPTK EGNKFMASSF
LHLTSDQWRS HNSFTCQVTH EGDTEKSL PAECL (SEQ ID NO: 63)

[0452] The amino acid sequence of the mouse lambda 3 light chain is set forth in SEQ ID NO: 64 below:

GQPKSTPTLT MFPPSPEELQ ENKATLVCLI SNFSPSGVTV AWKANGTPIT QGVDTSNPTK EDNKYMASSF
LHLTSDQWRS HNSFTCQVTH EGDTEKSL PAECL (SEQ ID NO: 64)

[0453] In certain embodiments, the amino acid modifications that are transferable (such as to any of the immunoglobulin heavy and light chains described above) comprise the following combination of substitution mutations: position Q39 (Kabat numbering) on the VH domain of H1; position Q38 on the VL domain of L1; position Q39 (Kabat numbering) on the VH domain of H2; position S183 (EU numbering) on the CH1 domain of H2; position Q38 (Kabat numbering) on the VL domain of L2; and position V133 (EU numbering) on the CL domain of L2.

[0454] In certain embodiments, the amino acid modifications that are transferable (such as to any of the immunoglobulin heavy and light chains described above) comprise the following combination of substitution mutations: position Q39 (Kabat numbering) on the VH domain of H1; position S183 (EU numbering) on the CH1 domain of H1; position Q38 on the VL domain of L1; position V133 (EU numbering) on the CL domain of L1; position Q39 (Kabat numbering) on the VH domain of H2; position S183 (EU numbering) on the CH1 domain of H2; position Q38 (Kabat numbering) on the VL domain of L2; and position V133 (EU numbering) on the CL domain of L2.

[0455] In certain embodiments, the amino acid modifications that are transferable (such as to any of the immunoglobulin heavy and light chains described above) comprise (such as consist or consist essentially of) the following combination of substitution mutations: position Q39E (Kabat numbering) on the VH domain of H1; position Q38K on the VL domain of L1; position Q39K (Kabat numbering) on the

VH domain of H2; position S183K (EU numbering) on the CH1 domain of H2; position Q38E (Kabat numbering) on the VL domain of L1; and V133E (EU numbering) on the CL domain of L2.

[0456] In certain embodiments, the amino acid modifications that are transferable (such as to any of the immunoglobulin heavy and light chains described above) comprise (such as consist or consist essentially of) the following combination of substitution mutations: position Q39K (Kabat numbering) on the VH domain of H1; position Q38E on the VL domain of L1; position Q39E (Kabat numbering) on the VH domain of H2; position S183K (EU numbering) on the CH1 domain of H2; position Q38K (Kabat numbering) on the VL domain of L1; and V133E (EU numbering) on the CL domain of L2.

[0457] In certain embodiments, the amino acid modifications that are transferable (such as to any of the immunoglobulin heavy and light chains described above) comprise (such as consist or consist essentially of) the following combination of substitution mutations: position Q39E (Kabat numbering) on the VH domain of H1; position Q38K on the VL domain of L1; position Q39K (Kabat numbering) on the VH domain of H2; position S183E (EU numbering) on the CH1 domain of H2; position Q38E (Kabat numbering) on the VL domain of L1; and V133K (EU numbering) on the CL domain of L2.

[0458] In certain embodiments, the amino acid modifications that are transferable (such as to any of the immunoglobulin heavy and light chains described above) comprise (such as consist or consist essentially of) the following combination of substitution mutations: position Q39K (Kabat numbering) on the VH domain of H1; position Q38E on the VL domain of L1; position Q39E (Kabat numbering) on the VH domain of H2; position S183E (EU numbering) on the CH1 domain of H2; position Q38K (Kabat numbering) on the VL domain of L1; and V133K (EU numbering) on the CL domain of L2.

[0459] In certain embodiments, the amino acid modifications that are introduced to different IgG molecules (such as to any of the immunoglobulin heavy and light chains described above) comprise a Q39E substitution mutation (Kabat numbering) in the the VH domain of H1; a Q38K substitution mutation (Kabat numbering) in the VL domain of L1; A141I, F170S, S181M, S183A, and V185A mutations (EU numbering) in the CH1 domain of H1; F116A, L135V, S174A, S176F, and T178V mutations (EU numbering) in the CL domain of L1; a Q39K substitution mutation (Kabat numbering) in the VH domain of H2; and a Q38E substitution mutation (Kabat numbering) in the VL domain of L2.

[0460] In certain embodiments, the amino acid modifications that are introduced to different IgG molecules (such as to any of the immunoglobulin heavy and light chains described above) comprise a Q39E substitution mutation (Kabat numbering) in the the VH domain of H1; comprise a Q38K substitution mutation (Kabat numbering) in the VL domain of L1; consist of A141I, F170S, S181M, S183A, and V185A mutations (EU numbering) in the CH1 domain of H1; consist of F116A, L135V, S174A, S176F, and T178V mutations (EU numbering) in the CL domain of L1; comprise a Q39K

substitution mutation (Kabat numbering) in the VH domain of H2; and comprise a Q38E substitution mutation (Kabat numbering) in the VL domain of L2..

[0461] In certain embodiments, the amino acid modifications that are introduced to different IgG molecules (such as to any of the immunoglobulin heavy and light chains described above) comprise: a Q39K substitution mutation (Kabat numbering) in the the VH domain of H1; a Q38E substitution mutation (Kabat numbering) in the VL domain of L1; A141I, F170S, S181M, S183A, and V185A mutations (EU numbering) in the CH1 domain of H1; F116A, L135V, S174A, S176F, and T178V mutations (EU numbering) in the CL domain of L1; a Q39E substitution mutation (Kabat numbering) in the VH domain of H2; and a Q38K substitution mutation (Kabat numbering) in the VL domain of L2.

[0462] In certain embodiments, the amino acid modifications that are introduced to different IgG molecules (such as to any of the immunoglobulin heavy and light chains described above) comprise a Q39K substitution mutation (Kabat numbering) in the the VH domain of H1; comprise a Q38E substitution mutation (Kabat numbering) in the VL domain of L1; consist of A141I, F170S, S181M, S183A, and V185A mutations (EU numbering) in the CH1 domain of H1; consist of F116A, L135V, S174A, S176F, and T178V mutations (EU numbering) in the CL domain of L1; comprise a Q39E substitution mutation (Kabat numbering) in the VH domain of H2; and comprise a Q38K substitution mutation (Kabat numbering) in the VL domain of L2.

[0463] In certain embodiments, the amino acid modifications that are introduced to different IgG molecules (such as to any of the immunoglobulin heavy and light chains described above) comprise: A141I, F170S, S181M, S183A, and V185A mutations (EU numbering) in the CH1 domain of H1; F116A, L135V, S174A, S176F, and T178V mutations (EU numbering) in the CL domain of L1, an S183E substitution mutation (EU numbering) in the CH1 domain of H2; and a V133K substitution mutation (EU numbering) in the CL domain of L2.

[0464] In certain embodiments, the amino acid modifications that are introduced to different IgG molecules (such as to any of the immunoglobulin heavy and light chains described above) comprise A141I, F170S, S181M, S183A, and V185A mutations (EU numbering) in the CH1 domain of H1; comprise F116A, L135V, S174A, S176F, and T178V mutations (EU numbering) in the CL domain of L1, consist of an S183E substitution mutation (EU numbering) in the CH1 domain of H2; and consist of a V133K substitution mutation (EU numbering) in the CL domain of L2.

[0465] In certain embodiments, the amino acid modifications that are introduced to different IgG molecules (such as to any of the immunoglobulin heavy and light chains described above) consist of A141I, F170S, S181M, S183A, and V185A mutations (EU numbering) in the CH1 domain of H1; F116A, L135V, S174A, S176F, and T178V mutations (EU numbering) in the CL domain of L1, of an

S183E substitution mutation (EU numbering) in the CH1 domain of H2; and a V133K substitution mutation (EU numbering) in the CL domain of L2.

[0466] In certain embodiments, the amino acid modifications that are introduced to different IgG molecules (such as to any of the immunoglobulin heavy and light chains described above) comprise: a Q39E substitution mutation (Kabat numbering) in the VH domain of H1; a Q38K substitution mutation (Kabat numbering) in the VL domain of L1; A141I, F170S, S181M, S183A, and V185A mutations (EU numbering) in the CH1 of H1; F116A, L135V, S174A, S176F, and T178V mutations (EU numbering) in the CL domain of H1; a Q39K substitution mutation (Kabat numbering) in the VH domain of H2; an S183E substitution mutation (EU numbering) in the CH1 of H2; a Q38E substitution mutation (Kabat numbering) in the VL domain of L2; and a V133K substitution mutation (EU numbering) in the CL domain of L2.

[0467] In certain embodiments, the amino acid modifications that are introduced to different IgG molecules (such as to any of the immunoglobulin heavy and light chains described above) comprise a Q39E substitution mutation (Kabat numbering) in the VH domain of H1; comprise a Q38K substitution mutation (Kabat numbering) in the VL domain of L1; comprise A141I, F170S, S181M, S183A, and V185A mutations (EU numbering) in the CH1 of H1; comprise F116A, L135V, S174A, S176F, and T178V mutations (EU numbering) in the CL domain of H1; comprise a Q39K substitution mutation (Kabat numbering) in the VH domain of H2; consist of an S183E substitution mutation (EU numbering) in the CH1 of H2; comprise a Q38E substitution mutation (Kabat numbering) in the VL domain of L2; and consist of a V133K substitution mutation (EU numbering) in the CL domain of L2.

[0468] In certain embodiments, the amino acid modifications that are introduced to different IgG molecules (such as to any of the immunoglobulin heavy and light chains described above) comprise a Q39E substitution mutation (Kabat numbering) in the VH domain of H1; comprise a Q38K substitution mutation (Kabat numbering) in the VL domain of L1; consist of A141I, F170S, S181M, S183A, and V185A mutations (EU numbering) in the CH1 of H1; consist of F116A, L135V, S174A, S176F, and T178V mutations (EU numbering) in the CL domain of H1; comprise a Q39K substitution mutation (Kabat numbering) in the VH domain of H2; consist of an S183E substitution mutation (EU numbering) in the CH1 of H2; comprise a Q38E substitution mutation (Kabat numbering) in the VL domain of L2; and consist of a V133K substitution mutation (EU numbering) in the CL domain of L2.

[0469] In certain embodiments, the amino acid modifications that are introduced to different IgG molecules (such as to any of the immunoglobulin heavy and light chains described above) comprise a Q39K substitution mutation (Kabat numbering) in the VH domain of H1; a Q38E substitution mutation (Kabat numbering) in the VL domain of L1; A141I, F170S, S181M, S183A, and V185A mutations (EU numbering) in the CH1 domain of H1; F116A, L135V, S174A, S176F, and T178V mutations (EU

numbering) in the CL domain of L1; a Q39E substitution mutation (Kabat numbering) in the VH domain of H2; an S183E substitution mutation (EU numbering) in the CH1 domain of H2; a Q38K substitution mutation (Kabat numbering) in the VL domain of L2; and a V133K substitution mutation (EU numbering) in the CL of L2.

[0470] In certain embodiments, the amino acid modifications that are introduced to different IgG molecules (such as to any of the immunoglobulin heavy and light chains described above) comprise a Q39K substitution mutation (Kabat numbering) in the VH domain of H1; comprise a Q38E substitution mutation (Kabat numbering) in the VL domain of L1; comprise A141I, F170S, S181M, S183A, and V185A mutations (EU numbering) in the CH1 domain of H1; comprise F116A, L135V, S174A, S176F, and T178V mutations (EU numbering) in the CL domain of L1; comprise a Q39E substitution mutation (Kabat numbering) in the VH domain of H2; consist of an S183E substitution mutation (EU numbering) in the CH1 domain of H2; comprise a Q38K substitution mutation (Kabat numbering) in the VL domain of L2; and consist of a V133K substitution mutation (EU numbering) in the CL of L2.

[0471] In certain embodiments, the amino acid modifications that are introduced to different IgG molecules (such as to any of the immunoglobulin heavy and light chains described above) comprise a Q39K substitution mutation (Kabat numbering) in the VH domain of H1; comprise a Q38E substitution mutation (Kabat numbering) in the VL domain of L1; consist of A141I, F170S, S181M, S183A, and V185A mutations (EU numbering) in the CH1 domain of H1; consist of F116A, L135V, S174A, S176F, and T178V mutations (EU numbering) in the CL domain of L1; comprise a Q39E substitution mutation (Kabat numbering) in the VH domain of H2; consist of an S183E substitution mutation (EU numbering) in the CH1 domain of H2; comprise a Q38K substitution mutation (Kabat numbering) in the VL domain of L2; and consist of a V133K substitution mutation (EU numbering) in the CL of L2.

[0472] In certain embodiments, the amino acid modifications that are introduced to different IgG molecules (such as to any of the immunoglobulin heavy and light chains described above) comprise A141I, F170S, S181M, S183A, and V185A mutations (EU numbering) in the CH1 domain of H1; F116A, L135V, S174A, S176F, and T178V mutations (EU numbering) in the CL domain of L1, an S183K substitution mutation (EU numbering) in the CH1 domain of H2, and a V133E substitution mutation (EU numbering) in the CL domain of L2.

[0473] In certain embodiments, the amino acid modifications that are introduced to different IgG molecules (such as to any of the immunoglobulin heavy and light chains described above) comprise A141I, F170S, S181M, S183A, and V185A mutations (EU numbering) in the CH1 domain of H1; comprise F116A, L135V, S174A, S176F, and T178V mutations (EU numbering) in the CL domain of L1, consist of an S183K substitution mutation (EU numbering) in the CH1 domain of H2, and consist of a V133E substitution mutation (EU numbering) in the CL domain of L2.

[0474] In certain embodiments, the amino acid modifications that are introduced to different IgG molecules (such as to any of the immunoglobulin heavy and light chains described above) consist of A141I, F170S, S181M, S183A, and V185A mutations (EU numbering) in the CH1 domain of H1; F116A, L135V, S174A, S176F, and T178V mutations (EU numbering) in the CL domain of L1, consist of an S183K substitution mutation (EU numbering) in the CH1 domain of H2, and consist of a V133E substitution mutation (EU numbering) in the CL domain of L2

[0475] In certain embodiments, the amino acid modifications that are introduced to different IgG molecules (such as to any of the immunoglobulin heavy and light chains described above) comprise a Q39E substitution mutation (Kabat numbering) in the VH domain of H1; a Q38K substitution mutation (Kabat numbering) in the VL domain of L1; A141I, F170S, S181M, S183A, and V185A mutations (EU numbering) in the CH1 domain of H1; F116A, L135V, S174A, S176F, and T178V mutations (EU numbering) in the CL domain of L1, a Q39K substitution mutation (Kabat numbering) in the VH domain of H2, an S183K substitution mutation (EU numbering) in the CH1 domain of H2, a Q38E substitution mutation (Kabat numbering) in the VL domain of L2, and a V133E substitution mutation (EU numbering) in the CL domain of L2.

[0476] In certain embodiments, the amino acid modifications that are introduced to different IgG molecules (such as to any of the immunoglobulin heavy and light chains described above) comprise a Q39E substitution mutation (Kabat numbering) in the VH domain of H1; comprise a Q38K substitution mutation (Kabat numbering) in the VL domain of L1; comprise A141I, F170S, S181M, S183A, and V185A mutations (EU numbering) in the CH1 domain of H1; comprise F116A, L135V, S174A, S176F, and T178V mutations (EU numbering) in the CL domain of L1; comprise a Q39K substitution mutation (Kabat numbering) in the VH domain of H2; consist of an S183K substitution mutation (EU numbering) in the CH1 domain of H2; comprise a Q38E substitution mutation (Kabat numbering) in the VL domain of L2; and consist of a V133E substitution mutation (EU numbering) in the CL domain of L2.

[0477] In certain embodiments, the amino acid modifications that are introduced to different IgG molecules (such as to any of the immunoglobulin heavy and light chains described above) comprise a Q39E substitution mutation (Kabat numbering) in the VH domain of H1; comprise a Q38K substitution mutation (Kabat numbering) in the VL domain of L1; consist of A141I, F170S, S181M, S183A, and V185A mutations (EU numbering) in the CH1 domain of H1; consist of F116A, L135V, S174A, S176F, and T178V mutations (EU numbering) in the CL domain of L1; comprise a Q39K substitution mutation (Kabat numbering) in the VH domain of H2; consist of an S183K substitution mutation (EU numbering) in the CH1 domain of H2; comprise a Q38E substitution mutation (Kabat numbering) in the VL domain of L2; and consist of a V133E substitution mutation (EU numbering) in the CL domain of L2.

[0478] In certain embodiments, the amino acid modifications that are introduced to different IgG molecules (such as to any of the immunoglobulin heavy and light chains described above) comprise a Q39K substitution mutation (Kabat numbering) in the VH domain of H1; a Q38E substitution mutation (Kabat numbering) in the VL domain of L1; A141I, F170S, S181M, S183A, and V185A mutations (EU numbering) in the CH1 domain of H1; F116A, L135V, S174A, S176F, and T178V mutations (EU numbering) in the CL domain of L1; a Q39E substitution mutation (Kabat numbering) in the VH domain of H2, an S183K substitution mutation (EU numbering) in the CH1 domain of H2; a Q38K substitution mutation (Kabat numbering) in the VL domain of L2; and a V133E substitution mutation (EU numbering) in the CL domain of L2.

[0479] In certain embodiments, the amino acid modifications that are introduced to different IgG molecules (such as to any of the immunoglobulin heavy and light chains described above) comprise a Q39K substitution mutation (Kabat numbering) in the VH domain of H1; comprise a Q38E substitution mutation (Kabat numbering) in the VL domain of L1; comprise A141I, F170S, S181M, S183A, and V185A mutations (EU numbering) in the CH1 domain of H1; comprise F116A, L135V, S174A, S176F, and T178V mutations (EU numbering) in the CL domain of L1; comprise a Q39E substitution mutation (Kabat numbering) in the VH domain of H2, consist of an S183K substitution mutation (EU numbering) in the CH1 domain of H2; comprise a Q38K substitution mutation (Kabat numbering) in the VL domain of L2; and consist of a V133E substitution mutation (EU numbering) in the CL domain of L2.

[0480] In certain embodiments, the amino acid modifications that are introduced to different IgG molecules (such as to any of the immunoglobulin heavy and light chains described above) comprise a Q39K substitution mutation (Kabat numbering) in the VH domain of H1; comprise a Q38E substitution mutation (Kabat numbering) in the VL domain of L1; consist of A141I, F170S, S181M, S183A, and V185A mutations (EU numbering) in the CH1 domain of H1; consist of F116A, L135V, S174A, S176F, and T178V mutations (EU numbering) in the CL domain of L1; comprise a Q39E substitution mutation (Kabat numbering) in the VH domain of H2, consist of an S183K substitution mutation (EU numbering) in the CH1 domain of H2; comprise a Q38K substitution mutation (Kabat numbering) in the VL domain of L2; and consist of a V133E substitution mutation (EU numbering) in the CL domain of L2.

[0481] In certain embodiments, the amino acid modifications that are introduced to different IgG molecules (such as to any of the immunoglobulin heavy and light chains described above) comprise (such as consist or consist essentially of) the following combination of substitution mutations: L128F, A141M, F170M, S181I and S183A mutations (EU numbering) on the CH1 domain of H1 and F118V, S131T, V133A, L135Y, S162A, T164S, S176M, and T178L mutations (EU numbering) on the CL domain of L1.

[0482] In certain embodiments, the amino acid modifications that are introduced to different IgG molecules (such as to any of the immunoglobulin heavy and light chains described above) comprise (such

as consist or consist essentially of) the following combination of substitution mutations: L128F, A141M, F170Y, S181I, S183A, and V185A mutations (EU numbering) on the CH1 domain of H1 and F118V, S131T, V133A, L135F, S162A, S176A, and T178L mutations (EU numbering) on the CL domain of L1.

[0483] In certain embodiments, the amino acid modifications that are introduced to different IgG molecules (such as to any of the immunoglobulin heavy and light chains described above) comprise (such as consist or consist essentially of) the following combination of substitution mutations: L128F, A141T, F170M, S181T, S183A, and V185L mutations (EU numbering) on the CH1 domain of H1 and F118V, S131T, V133A, L135F, S162A, T164S, S176T, and T178L mutations (EU numbering) on the CL domain of L1.

[0484] In certain embodiments, the amino acid modifications that are introduced to different IgG molecules (such as to any of the immunoglobulin heavy and light chains described above) comprise (such as consist or consist essentially of) the following combination of substitution mutations: L128F, A141M, F170M, S181T, and S183A mutations (EU numbering) on the CH1 domain of H1 and F118V, S131T, V133A, L135F, S162M, T164S, S176M, and T178L mutations (EU numbering) on the CL domain of L1.

[0485] In certain embodiments, the amino acid modifications that are introduced to different IgG molecules (such as to any of the immunoglobulin heavy and light chains described above) comprise (such as consist or consist essentially of) the following combination of substitution mutations: A141I, F170S, S181M, S183V, and V185A mutations (EU numbering) on the CH1 domain of H1 and F116A, V133I, L135V, S162M, S174A, S176F, and T178V mutations (EU numbering) on the CL domain of L1.

[0486] In certain embodiments, the amino acid modifications that are introduced to different IgG molecules (such as to any of the immunoglobulin heavy and light chains described above) comprise (such as consist or consist essentially of) the following combination of substitution mutations: A141I, F170S, S181M, S183A, and V185A mutations (EU numbering) on the CH1 domain of H1 and F116A, S131D, L135V, S162A, S174A, S176F, and T178I mutations (EU numbering) on the CL domain of L1.

[0487] In certain embodiments, the amino acid modifications that are introduced to different IgG molecules (such as to any of the immunoglobulin heavy and light chains described above) comprise the following combination of substitution mutations: A141I, F170S, S181M, S183A, and V185A mutations (EU numbering) on the CH1 domain of H1 and F116A, L135V, S174A, S176F, and T178V mutations (EU numbering) on the CL domain of L1.

[0488] In certain embodiments, the amino acid modifications that are introduced to different IgG molecules (such as to any of the immunoglobulin heavy and light chains described above) consist of the following combination of substitution mutations: A141I, F170S, S181M, S183A, and V185A mutations

(EU numbering) on the CH1 domain of H1 and F116A, L135V, S174A, S176F, and T178V mutations (EU numbering) on the CL domain of L1.

[0489] In certain embodiments, the amino acid modifications that are introduced to different IgG molecules (such as to any of the immunoglobulin heavy and light chains described above) comprise (such as consist or consist essentially of) the following combination of substitution mutations: A141I, F170A, S181M, S183V, and V185A mutations (EU numbering) on the CH1 domain of H1 and F116A, L135V, S162M, S174A, S176F, and T178V mutations (EU numbering) on the CL domain of L1.

[0490] Additional combinations of mutations in the CH1/CL interface identified by Strategy #2, mutations in the CH1/CL interface identified by Strategy #1, and mutations in the VH and VL domains, *i.e.*, not limited to those described above, are also contemplated. Such combinations include, but are not limited to those described below:

[0491] It will be apparent to those of ordinary skill in the art that the terms “H1” and “H2” are arbitrary designations, and that “H1” and “H2” in any of the embodiments above can be reversed. That is, any of the mutations above described as being in the CH1 domain and/or the VH domain of H1 and CL domain and/or the VL domain of L1 can, alternatively, be in the CH1 domain and/or VH domain of H2 and the CL domain and/or VL domain of L2.

Properties

Preferential Pairing/Preferential Assembly

[0492] “Preferential pairing” describes the pairing pattern of a first polypeptide (such as H1) with a second polypeptide (such as L1) when one or more additional, distinct polypeptides are present at the same time as the pairing occurs between the first and second polypeptide. Preferential pairing occurs between, *e.g.*, H1 and L1 of a multispecific antigen-binding protein provided herein, if the amount of the H1-L1 heavy chain-light chain pairing is greater than the amount of the H1-L2 pairing when H1 is co-expressed with at least L1, and L2. Likewise, preferential pairing occurs between, *e.g.*, H2 and L2 of a multispecific antigen-binding protein provided herein, if the amount of the H2-L2 heavy chain-light chain pairing was greater than the amount of the H2-L1 pairing when H2 is co-expressed with at least L1, and L2. In certain embodiments, the preferential pairing is resulted from amino acid modifications of the VH/VL domains and/or CH1/CL domains.

[0493] In certain embodiments, the H1 of a multispecific antigen-binding protein provided herein preferentially pairs with the L1. In certain embodiments, the H2 of a multispecific antigen-binding protein provided herein preferentially pairs with the L2. In certain embodiments, the H1 of a multispecific antigen-binding protein provided herein preferentially pairs with the L1 and the H2 of the

multispecific antigen-binding protein herein preferentially pairs with the L2. In certain embodiments, when H1 of a multispecific antigen-binding protein described herein is co-expressed with H2, L1, and L2, the multispecific antigen-binding protein comprising the desired pairings (e.g., H1-L1 and H2-L2) is produced with a relative yield of at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, at least about 55%, at least about 60%, at least about 70%, at least about 71%, at least about 71%, at least about 72%, at least about 73%, at least about 74%, at least about 75%, at least about 76%, at least about 77%, at least about 78%, at least about 79%, at least about 80%, at least about 81%, at least about 82%, at least about 83%, at least about 84%, at least about 85%, at least about 86%, at least about 87%, at least about 88%, at least about 89%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or more than about 99%, including any range in between these values. The relative yield of a multispecific antigen-binding protein comprising the desired pairings (e.g., H1-L1 and H2-L2) can be determined using, e.g., mass spectrometry, as described in the Examples.

[0494] In certain embodiments, the expressed polypeptides of a multispecific antigen-binding protein provided herein assemble with improved specificity to reduce generation of mispaired heavy chains and light chains. In certain embodiments, the CH1 domain of H1 of a multispecific antigen-binding protein provided herein assembles with the CL domain of L1 during production.

Methods of Assessing Preferential Pairing/Preferential Assembly

[0495] Preferential pairing and/or preferential assembly of the CH1 domain of H1 with the CL domain of L1 of the multispecific antigen-binding protein can be determined using any one of a variety of methods well known to those of ordinary skill in the art. For example, the degree of preferential pairing of the CH1 domain of H1 with the CL domain of L1 in a multispecific antigen-binding protein can be determined via Light Chain Competition Assay (LCCA). International patent application PCT/US2013/063306, filed October 3, 2013, describes various embodiments of LCCA and is herein incorporated by reference in its entirety for all purposes. The method allows quantitative analysis of the pairing of heavy chains with specific light chains within the mixture of co-expressed proteins and can be used to determine if one particular immunoglobulin heavy chain selectively associates with either one of two immunoglobulin light chains when the heavy chain and light chains are co-expressed. The method is briefly described as follows: At least one heavy chain and two different light chains are co-expressed in a cell, in ratios such that the heavy chain is the limiting pairing reactant; optionally separating the secreted proteins from the cell; separating the immunoglobulin light chain polypeptides bound to heavy chain from the rest of the secreted proteins to produce an isolated heavy chain paired fraction; detecting the amount of each different light chain in the isolated heavy chain fraction; and analyzing the relative amount of each different light chain in the isolated heavy chain fraction to determine the ability of the at least one heavy chain to selectively pair with one of the light chains.

[0496] In certain embodiments, preferential pairing of the CH1 domain of H1 with the CL domain of L1 of the multispecific antigen-binding protein is determined via mass spectrometry (such as liquid chromatography-mass spectrometry (LC-MS) native mass spectrometry, acidic mass spectrometry, *etc.*). Mass spectrometry is used to quantify the relative heterodimer populations including each light chain using differences in their molecular weight to identify each distinct species.

[0497] In certain embodiments, preferential pairing of the CH1 domain of H1 with the CL domain of L1 of the multispecific antigen-binding protein is determined by assaying the thermal stability of the heavy/light chain pairs of a multispecific antigen-binding protein provided herein. The thermal stability of a heavy/light chain pair in a multispecific antigen-binding protein can be determined according to methods known in the art. The melting temperature of a heavy/light chain pair in a multispecific antigen-binding protein is indicative of its thermal stability. The melting point of the heavy/light chain pair may be measured using techniques such as differential scanning calorimetry (Chen *et al* (2003) Pharm Res 20:1952-60; Ghirlando *et al* (1999) Immunol Lett 68:47-52). Alternatively, the thermal stability of the heavy/light chain pair may be measured using circular dichroism (Murray *et al.* (2002) J. Chromatogr Sci 40:343-9).

[0498] In certain embodiments, preferential pairing of the CH1 domain of H1 with the CL domain of L1 of the multispecific antigen-binding protein is determined via binding affinity of the heavy/light chain pairs for their respective targets. The on-rate and off-rate of the interaction can be determined by competitive binding assays according to methods well known in the art. In certain embodiments, the competitive binding assay is a radioimmunoassay comprising the incubation of labeled target (*e.g.*, ^3H or ^{125}I) with a multispecific antigen-binding protein provided herein in the presence of increasing amounts of unlabeled target, and the detection of the multispecific antigen-binding protein bound to the labeled target. In certain embodiments, the affinity of the multispecific antigen-binding protein for the target and the binding off-rates can be determined from the saturation data by Scatchard analysis.

[0499] In certain embodiments, preferential pairing of the CH1 domain of H1 with the CL domain of L1 of the multispecific antigen-binding protein is determined by measuring kinetic parameters, such as K_D , k_{off} , k_{on} , R_{max} . In certain embodiments, kinetic parameters are determined via surface plasmon resonance (SPR) based assays known in the art (*e.g.*, BIAcore kinetic analysis). For a review of SPR-based technology see Mullet *et al.*, 2000, Methods 22: 77-91; Dong *et al.*, 2002, Review in Mol. Biotech., 82: 303-23; Fivash *et al.*, 1998, Current Opinion in Biotechnology 9: 97-101; Rich *et al.*, 2000, Current Opinion In Biotechnology 11: 54-61. Additionally, any of the SPR instruments and SPR based methods for measuring protein-protein interactions described in U.S. Pat. Nos. 6,373,577; 6,289,286; 5,322,798; 5,341,215; 6,268,125 are contemplated.

[0500] In certain embodiments, fluorescence-activated cell sorting (FACS) is used to measure the affinity of a multispecific antigen-binding protein for its target(s), according to methods well known in the art. Other methods of assaying preferential pairing of CH1 domain of H1 with the CL domain of L1 are described in, *e.g.*, WO 2014/081955, WO 2014/082179, and WO 2014/150973, which are herein incorporated by reference in their entireties for all purposes.

Stability

[0501] In certain embodiments, the one or more amino acid substitution(s) present on the CH1 domain of H1 and the one or more amino acid substitution mutation(s) present on the CL of L1 do not decrease the stability of a multispecific antigen-binding protein provided herein. In certain embodiments, the one or more amino acid substitution(s) present on the CH1 domain of H1, the one or more amino acid substitution mutation(s) present on the CL of L1, the amino acid substitution mutation at position Q39 (Kabat numbering) on the VH of H1, and the amino acid substitution mutation at position Q38 (Kabat numbering) of the VL of L1 do not decrease the stability of a multispecific antigen-binding protein provided herein. In certain embodiments, the one or more amino acid substitution(s) present on the CH1 domain of H1, the one or more amino acid substitution mutation(s) present on the CL of L1, the amino acid substitution mutation at position Q39 (Kabat numbering) on the VH of H1, the amino acid substitution mutation at position Q38 (Kabat numbering) of the VL of L1, the amino acid substitution mutation at position Q39 (Kabat numbering) on the VH of H2, and the amino acid substitution mutation at position Q38 (Kabat numbering) of the VL of L2, do not decrease the stability of a multispecific antigen-binding protein provided herein.

[0502] In certain embodiments, the stability of a multispecific antigen-binding protein provided herein is at least about 80%, at least about 81%, at least about 82%, at least about 83%, at least about 84%, at least about 85%, at least about 86%, at least about 87%, at least about 88%, at least about 89%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or more than about 99% of the stability of a multispecific antigen-binding protein without the amino acid substitution mutations.

[0503] The stability of a multispecific antigen-binding protein can be determined using any one of a variety of techniques for assessing protein stability known to those of ordinary skill in the art. For example, circular dichroism (CD) is a spectroscopic technique widely that measures the absorption of circularly polarized light. As structures such as alpha helices and beta sheets are chiral, the absorption of circularly polarized light acts as a marker of the degree of foldedness of the protein ensemble. This technique has been used to measure equilibrium unfolding of the protein by measuring the change in this absorption as a function of temperature. The temperature at the transition midpoint, where the

concentration of native and denatured states is 1, is known as the melting temperature (T_m) of a protein. Further details regarding CD are described in, *e.g.*, Kelly *et al.* (2000) *Curr Prot and Peptide Sci* 1, 349-384; Correa *et al.* (2009) *African J Biochem Res* 3, 164-173; and Greenfield (2006) *Nat Protoc.* 1, 2527-2535.

[0504] In certain embodiments, a multispecific antigen-binding protein described herein (*e.g.*, comprising the CH1/CL modifications and/or VH/VL modifications described herein) has a melting temperature that is no more than about 10 °C, no more than about 9.5 °C, no more than about 9 °C, no more than about 8.5 °C, no more than about 8 °C, no more than about 7.5 °C, no more than about 7.0 °C, no more than about 6.5 °C, no more than about 6.0 °C, no more than about 5.5 °C, no more than about 5.0 °C, no more than about 4.5 °C, no more than about 4 °C, no more than about 3.5 °C, no more than about 3 °C, no more than about 2.5 °C no more than about 2 °C, no more than about 1.5 °C, no more than about 1 °C, no more than about 0.5 °C, or less than about 0.5 °C lower than the T_m of a wild type multispecific antigen binding protein that comprises no amino acid substitution mutations in the CH1/CL and/or VH/VL domains. In certain embodiments, a Fab of the multispecific antigen-binding protein described herein (*e.g.*, comprising the CH1/CL modifications and/or VH/VL modifications described herein) has a melting temperature that is no more than about 10 °C, no more than about 9.5 °C, no more than about 9 °C, no more than about 8.5 °C, no more than about 8 °C, no more than about 7.5 °C, no more than about 7.0 °C, no more than about 6.5 °C, no more than about 6.0 °C, no more than about 5.5 °C, no more than about 5.0 °C, no more than about 4.5 °C, no more than about 4 °C, no more than about 3.5 °C, no more than about 3 °C, no more than about 2.5 °C no more than about 2 °C, no more than about 1.5 °C, no more than about 1 °C, no more than about 0.5 °C, or less than about 0.5 °C lower than the T_m of a Fab of a wild type parent antibody of the multispecific antigen binding protein that comprises no amino acid substitution mutations in the CH1/CL and/or VH/VL domains.

[0505] Alternatively, the stability of a multispecific antigen-binding protein can be determined using, *e.g.*, differential scanning calorimetry (DSC), which measures the thermodynamic parameters that control non-covalent bond formation in proteins. Further details regarding DSC are described in, *e.g.*, Ionescu *et al.* (2008) *J Pharm Sci* 97, 1414–1426. The stability of a multispecific antigen-binding protein can also be determined using, *e.g.*, differential scanning fluorimetry (DSF or thermal shift assay), which measures the thermal stability of a target protein and the change in protein melting temperature upon the binding of the protein to, *e.g.*, a ligand or a second protein. Further details regarding DSF are described in, *e.g.*, Niesen, *et al.* (2007) *Nat Protoc* 2, 2212–2221.

Binding Affinity

[0506] In certain embodiments, the one or more amino acid substitution(s) present on the CH1 domain of H1 and the one or more amino acid substitution mutation(s) present on the CL of L1 do not

decrease the binding affinity of a multispecific antigen-binding protein provided herein to an antigen. In certain embodiments, the one or more amino acid substitution(s) present on the CH1 domain of H1, the one or more amino acid substitution mutation(s) present on the CL of L1, the amino acid substitution mutation at position Q39 (Kabat numbering) on the VH of H1, and the amino acid substitution mutation at position Q38 (Kabat numbering) of the VL of L1 do not decrease the binding affinity of a multispecific antigen-binding protein provided herein to an antigen. In certain embodiments, the one or more amino acid substitution(s) present on the CH1 domain of H1, the one or more amino acid substitution mutation(s) present on the CL of L1, the amino acid substitution mutation at position Q39 (Kabat numbering) on the VH of H1, the amino acid substitution mutation at position Q38 (Kabat numbering) of the VL of L1, the amino acid substitution mutation at position Q39 (Kabat numbering) on the VH of H2, and the amino acid substitution mutation at position Q38 (Kabat numbering) of the VL of L2, do not decrease the binding affinity of a multispecific antigen-binding protein provided herein to an antigen.

Methods of Measuring Binding Affinity

[0507] As noted elsewhere herein, antigen binding of a multispecific antigen binding protein provided herein can be assessed by measuring any one of a variety of binding kinetic parameters, including K_d , k_{on} , and/or k_{off} . K_d can be measured by using surface plasmon resonance assays using a BIAcore™-T100 or a BIAcore™-T200 (GE Healthcare, Piscataway, NJ) at 25°C with immobilized target (*e.g.*, antigen) CM5 chips at 100 response units (RU). Briefly, carboxymethylated dextran biosensor chips (CM5, BIAcore Inc.) are activated with N-ethyl-N'-(3-dimethylaminopropyl)-carbodiimide hydrochloride (EDC) and N-hydroxysuccinimide (NHS) according to the supplier's instructions. Antigen is diluted with 10 mM sodium acetate, pH 4.8, into 5 µg/ml (~0.2 µM) before injection at a flow rate of 5 µl/minute to achieve approximately 100 response units (RU) of coupled protein. Following the injection of antigen, 1M ethanolamine is injected to block unreacted groups. For kinetics measurements, two-fold serial dilutions of Fab (*e.g.*, 0.78 nM to 500 nM) are injected in PBS with 0.05% Tween 20 (PBST) at 25°C at a flow rate of approximately 25 µl/min. Association rates (k_{on}) and dissociation rates (k_{off}) are calculated using a simple one-to-one Langmuir binding model (BIAcore Evaluation Software) by simultaneous fitting the association and dissociation sensorgram. The equilibrium dissociation constant (K_d) is calculated as the ratio k_{off}/k_{on} . See, *e.g.*, Chen *et al.*, J. Mol. Biol. 293:865-881 (1999). If the on-rate exceeds $10^6 \text{ M}^{-1} \text{ s}^{-1}$ by the surface plasmon resonance assay above, then the on-rate can be determined by using a fluorescent quenching technique that measures the increase or decrease in fluorescence emission intensity (excitation = 295 nm; emission = 340 nm, 16 nm band-pass) at 25°C of a 20 nM anti-antigen antibody (Fab form) in PBS, pH 7.2, in the presence of increasing concentrations of antigen as measured in a spectrometer, such as a stop-flow equipped spectrophotometer (Aviv Instruments) or a 8000-series SLM-Aminco spectrophotometer (ThermoSpectronic) with a stirred cuvette.

[0508] In certain embodiments, the K_d of a multispecific antigen binding protein provided herein is at least no less than about 10%, about 15%, about 20%, about 25%, about 30%, about 35%, about 40%, about 45%, about 50%, or more than about 50% of the K_d of a wild type binding protein comprising no mutations at the CH1/CL interface.

Immunogenicity

[0509] In certain embodiments, a multispecific antigen-binding protein provided herein is non-immunogenic or substantially non-immunogenic in a human. In certain embodiments, the modification (such as one or more amino acid substitutions) of the CH1 region is non-immunogenic or substantially non-immunogenic in a human. In certain embodiments, the modification (such as one or more amino acid substitutions) of the CL region is non-immunogenic or substantially non-immunogenic in a human. In certain embodiments, the modification (such as one or more amino acid substitutions) of the CH1 region does not result in a human T-cell epitope. In certain embodiments, the modification (such as one or more amino acid substitutions) of the CL region does not result in a human T-cell epitope. The immunogenicity a multispecific antigen-binding protein provided herein can be evaluated using methods well known to those of ordinary skill in the art. In certain embodiments, the immunogenicity a multispecific antigen-binding protein provided herein is assessed via ELISA (*see, e.g., Yin et al. (2015) Cell Immunol. 295,118-126*). *See also, e.g., Hartmann et al. (2001) Clin Cancer Res. 7, 1873-1881.*

Pharmacokinetic Properties

[0510] In certain embodiments, the one or more amino acid substitution(s) present on the CH1 domain of H1 and the one or more amino acid substitution mutation(s) present on the CL of L1 do not significantly affect the pharmacokinetic properties of a multispecific antigen-binding protein provided herein, as compared to a multispecific antigen-binding protein that does not comprise such amino acid substitutions. In certain embodiments, the one or more amino acid substitution(s) present on the CH1 domain of H1, the one or more amino acid substitution mutation(s) present on the CL of L1, the amino acid substitution mutation at position Q39 (Kabat numbering) on the VH of H1, and the amino acid substitution mutation at position Q38 (Kabat numbering) of the VL of L1 do not significantly affect the pharmacokinetic properties of a multispecific antigen-binding protein provided herein, as compared to a multispecific antigen-binding protein that does not comprise such amino acid substitutions. In certain embodiments, the one or more amino acid substitution(s) present on the CH1 domain of H1, the one or more amino acid substitution mutation(s) present on the CL of L1, the amino acid substitution mutation at position Q39 (Kabat numbering) on the VH of H1, the amino acid substitution mutation at position Q38 (Kabat numbering) of the VL of L1, the amino acid substitution mutation at position Q39 (Kabat numbering) on the VH of H2, and the amino acid substitution mutation at position Q38 (Kabat numbering) of the VL of L2, do not significantly affect the pharmacokinetic properties of a multispecific

antigen-binding protein provided herein, as compared to a multispecific antigen-binding protein that does not comprise such amino acid substitutions. Such pharmacokinetic properties include, *e.g.*, C_{max}, AUC, CL (*i.e.*, drug clearance), $t_{1/2}$, V_d , V₁, and V_{ss}. In certain embodiments, C_{max} of a multispecific antigen-binding protein provided herein is about any one of 50%, 60%, 70%, 80%, 90%, 100%, 110%, 120%, 130%, 140%, 150%, or 160% (including any range in between these values) of a multispecific antigen-binding protein that does not comprise amino acid substitutions in the CH1 of H1, the VH of H1, the CL of L1, the VL of L1, the CH1 of H2, the VH of H2, the CL of L2, and/or the VL of L2. In certain embodiments, AUC of a multispecific antigen-binding protein provided herein is about any one of 50%, 60%, 70%, 80%, 90%, 100%, 110%, 120%, 130%, 140%, 150%, or 160% (including any range in between these values) of a multispecific antigen-binding protein that does not comprise amino acid substitutions in the CH1 of H1, the VH of H1, the CL of L1, the VL of L1, the CH1 of H2, the VH of H2, the CL of L2, and/or the VL of L2. In certain embodiments, CL (*i.e.*, drug clearance) of a multispecific antigen-binding protein provided herein is about any one of 50%, 60%, 70%, 80%, 90%, 100%, 110%, 120%, 130%, 140%, 150%, or 160% (including any range in between these values) of a multispecific antigen-binding protein that does not comprise amino acid substitutions in the CH1 of H1, the VH of H1, the CL of L1, the VL of L1, the CH1 of H2, the VH of H2, the CL of L2, and/or the VL of L2. In certain embodiments, $t_{1/2}$ of a multispecific antigen-binding protein provided herein is about any one of 50%, 60%, 70%, 80%, 90%, 100%, 110%, 120%, 130%, 140%, 150%, or 160% (including any range in between these values) of a multispecific antigen-binding protein that does not comprise amino acid substitutions in the CH1 of H1, the VH of H1, the CL of L1, the VL of L1, the CH1 of H2, the VH of H2, the CL of L2, and/or the VL of L2. In certain embodiments, the V₁ of a multispecific antigen-binding protein provided herein is about any one of 50%, 60%, 70%, 80%, 90%, 100%, 110%, 120%, 130%, 140%, 150%, or 160% (including any range in between these values) of a multispecific antigen-binding protein that does not comprise amino acid substitutions in the CH1 of H1, the VH of H1, the CL of L1, the VL of L1, the CH1 of H2, the VH of H2, the CL of L2, and/or the VL of L2. In certain embodiments, the V_{ss} of a multispecific antigen-binding protein provided herein is about any one of 50%, 60%, 70%, 80%, 90%, 100%, 110%, 120%, 130%, 140%, 150%, or 160% (including any range in between these values) of a multispecific antigen-binding protein that does not comprise amino acid substitutions in the CH1 of H1, the VH of H1, the CL of L1, the VL of L1, the CH1 of H2, the VH of H2, the CL of L2, and/or the VL of L2.

Multispecific Antibody Formats

[0511] The multispecific antigen-binding proteins provided herein can be used with any one of a variety of bispecific or multispecific antibody formats known in the art. Numerous formats have been developed in the art to address therapeutic opportunities afforded by molecules with multiple binding

specificities. Several approaches have been described to prepare bi-specific antibodies in which specific antibody light chains or fragment pair with specific antibody heavy chains or fragments.

[0512] For example, International Patent Application No. PCT/EP2011/056388 (WO 2011/131746) describes an in vitro method for generating a heterodimeric protein in which asymmetrical mutations are introduced into the CH3 regions of two monospecific starting proteins in order to drive directional “Fab-arm” or “half-molecule” exchange between two monospecific IgG4 or IgG4-like antibodies upon incubation under reducing conditions.

[0513] Schaefer *et al.* (Roche Diagnostics GmbH), describe a method to assemble two heavy and two light chains, derived from two existing antibodies, into human bivalent bispecific IgG antibodies without use of artificial linkers (PNAS (2011) 108(27): 11187-11192 and US 2009/0232811). The method involves exchanging one or more heavy chain and light chain domains within the antigen-binding fragment (Fab) of one half of the bi-specific antibody (CrossMab). Based on the knobs-into-holes technology that enables heterodimerization of the heavy chains, correct association of the light chains and their cognate heavy chains is achieved by exchange of heavy-chain and light-chain domains within the antigen binding fragment (Fab) of one half of the bispecific antibody. This “crossover” retains the antigen-binding affinity but makes the two arms so different that light-chain mispairing can no longer occur. See WO2009/080251, WO2009/080252, WO2009/080253, and WO2009/080254, each incorporated herein by reference in its entirety.

[0514] Knobs-into-holes is a heterodimerization technology for the CH3 domain of an antibody. Previously, knobs-into-holes technology has been applied to the production of human full-length bispecific antibodies with a single common light chain (LC) (Merchant *et al.* “An efficient route to human bispecific IgG.” Nat Biotechnol. 1998;16:677–81; Jackman *et al.* “Development of a two-part strategy to identify a therapeutic human bispecific antibody that inhibits IgE receptor signaling.” J Biol Chem. 2010;285:20850–9.) See also WO1996027011, which is herein incorporated by reference in its entirety for all purposes.

[0515] Strop *et al.* (Rinat-Pfizer Inc.), describe a method of producing stable bi-specific antibodies by expressing and purifying two antibodies of interest separately, and then mixing them together under specified redox conditions (J. Mol. Biol. (2012) 420:204-19).

[0516] Other heterodimerization domain having a strong preference for forming heterodimers over homodimers can be incorporated into the instant multispecific antigen-binding proteins. Illustrative examples include but are not limited to, for example, WO2007147901 (Kjærgaard *et al.* – Novo Nordisk: describing ionic interactions); WO 2009089004 (Kannan *et al.* – Amgen: describing electrostatic steering effects); WO 2010/034605 (Christensen *et al.* – Genentech; describing coiled coils). See also, for

example, Pack, P. & Plueckthun, A., *Biochemistry* 31, 1579-1584 (1992) describing leucine zipper or Pack *et al.*, *Bio/Technology* 11, 1271-1277 (1993) describing the helix-turn-helix motif. The phrase “heteromultimerization domain” and “heterodimerization domain” are used interchangeably herein. In certain embodiments, the multispecific antigen-binding protein comprises one or more heterodimerization domains.

[0517] Zhu *et al.* (Genentech) have engineered mutations in the VL/VH interface of a diabody construct consisting of variant domain antibody fragments completely devoid of constant domains, and generated a heterodimeric diabody (*Protein Science* (1997) 6:781-788). Similarly, Igawa *et al.* (Chugai) have also engineered mutations in the VL/VH interface of a single-chain diabody to promote selective expression and inhibit conformational isomerization of the diabody (*Protein Engineering, Design & Selection* (2010) 23:667-677).

[0518] US Patent Publication No. 2009/0182127 (Novo Nordisk, Inc.) describes the generation of bispecific antibodies by modifying amino acid residues at the Fc interface and at the CH1:CL interface of light-heavy chain pairs that reduce the ability of the light chain of one pair to interact with the heavy chain of the other pair.

[0519] Another format, used for Bispecific T cell Engager (BiTE) molecules (*see, e.g., Wolf et al.* (2005) *Drug Discovery Today* 10:1237-1244)), is based on single chain variable fragment (scFv) modules. An scFv consists of an antibody's light and heavy chain variable regions fused via a flexible linker, which generally can fold appropriately and so that the regions can bind the cognate antigen. A BiTE concatenates two scFv's of different specificities in tandem on a single chain. This configuration precludes the production of molecules with two copies of the same heavy chain variable region. In addition, the linker configuration is designed to ensure correct pairing of the respective light and heavy chains.

[0520] Reviews of various bispecific and multispecific antibody formats are provided in Klein *et al.*, (2012) *mAbs* 4:6, 653-663 and Spiess *et al.* (2015) “Alternative molecular formats and therapeutic applications for bispecific antibodies.” *Mol. Immunol.* Published online January 27, 2015; doi:10.1016/j.molimm.2015.01.003.

The multispecific antigen-binding proteins described herein can be incorporated into any one of the formats described above. In certain embodiments, the CH1/CL and VH/VL mutations described herein can be combined with the CrossMab technology to further ensure correct heavy/light chain pairing.

*Polynucleotides, Vectors, and Host Cells**Polynucleotides*

[0521] Provided herein are nucleic acids encoding heavy and/or light chain constant and/or variable domains described herein. In certain embodiments, an isolated nucleic acid provided herein encodes at least one polypeptide sequence of a multispecific antigen-binding protein described herein. In certain embodiments, an isolated nucleic acid provided herein encodes at least two polypeptide sequences of a multispecific antigen-binding protein described herein. In certain embodiments, an isolated nucleic acid provided herein encodes at least three polypeptide sequences of a multispecific antigen-binding protein described herein. In certain embodiments, an isolated nucleic acid provided herein encodes at least four polypeptide sequences of a multispecific antigen-binding protein described herein. In certain embodiments, an isolated nucleic acid provided herein encodes more than four polypeptide sequences of a multispecific antigen-binding protein described herein.

[0522] Nucleic acid molecules provided herein include DNA and RNA in both single-stranded and double-stranded form, as well as the corresponding complementary sequences. DNA includes, for example, cDNA, genomic DNA, chemically synthesized DNA, DNA amplified by PCR, and combinations thereof. The nucleic acid molecules provided herein include full-length genes or cDNA molecules as well as a combination of fragments thereof. In certain embodiments, the nucleic acids provided herein are derived from human sources. In certain embodiments, the nucleic acids provided herein are derived from mouse sources.

[0523] As noted elsewhere herein, an “isolated” nucleic acid is a nucleic acid that has been separated from adjacent genetic sequences present in the genome of the organism from which the nucleic acid was isolated, in the case of nucleic acids isolated from naturally-occurring sources. In the case of nucleic acids synthesized enzymatically from a template or chemically, such as PCR products, cDNA molecules, or oligonucleotides for example, it is understood that the nucleic acids resulting from such processes are isolated nucleic acids. An isolated nucleic acid molecule refers to a nucleic acid molecule in the form of a separate fragment or as a component of a larger nucleic acid construct.

[0524] In certain embodiments, the nucleic acids are substantially free from contaminating endogenous material. The nucleic acid molecule has preferably been derived from DNA or RNA isolated at least once in substantially pure form and in a quantity or concentration enabling identification, manipulation, and recovery of its component nucleotide sequences by standard biochemical methods (such as those outlined in Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1989)). Such sequences are preferably provided and/or constructed in the form of an open reading frame uninterrupted by internal non-translated

sequences, or introns, that are typically present in eukaryotic genes. Sequences of nontranslated DNA can be present 5' or 3' from an open reading frame, where the same do not interfere with manipulation or expression of the coding region.

[0525] Nucleic acid variants are ordinarily prepared by site specific mutagenesis of nucleotides in the DNA encoding the polypeptide, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the recombinant DNA in cell culture as outlined herein. However, antibodies or antigen-binding fragments thereof comprising variant CDRs having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, *e.g.*, binding to antigen, although variants can also be selected which have modified characteristics.

[0526] As will be appreciated by those in the art, due to the degeneracy of the genetic code, an extremely large number of nucleic acids may be made, all of which encode the CDRs and heavy and light chains or other components of a multimeric antigen-binding protein described herein. Thus, having identified a particular amino acid sequence, those skilled in the art could make any number of different nucleic acids, by simply modifying the sequence of one or more codons in a way which does not change the amino acid sequence of the encoded multimeric antigen-binding protein.

Vectors

[0527] Provided are expression systems and constructs in the form of plasmids, expression vectors, transcription or expression cassettes which comprise at least one polynucleotide described herein. In certain embodiments, a plasmid, expression vector, transcription or expression cassette provided herein comprises a polynucleotide encoding at least one polypeptide (*e.g.*, a first heavy chain, a first light chain, a second heavy chain, or a second light chain) of a multispecific antigen-binding protein provided herein. In certain embodiments, a plasmid, expression vector, transcription or expression cassette provided herein comprises a polynucleotide encoding at least two polypeptides (*e.g.*, a first heavy chain and a first light chain, or a second heavy chain and a second light chain) of a multispecific antigen-binding protein provided herein. In certain embodiments, a plasmid, expression vector, transcription or expression cassette provided herein comprises a polynucleotide encoding at least four polypeptides (*e.g.*, a first heavy chain, a first light chain, a second heavy chain, and a second light chain) of a multispecific antigen-binding protein provided herein.

[0528] Typically, expression vectors used in the host cells will contain sequences for plasmid maintenance and for cloning and expression of exogenous nucleotide sequences. Such sequences, collectively referred to as "flanking sequences," in certain embodiments will typically include one or more of the following nucleotide sequences: a promoter, one or more enhancer sequences, an origin of replication, a transcriptional termination sequence, a complete intron sequence containing a donor and

acceptor splice site, a sequence encoding a leader sequence for polypeptide secretion, a ribosome binding site, a polyadenylation sequence, a polylinker region for inserting the nucleic acid encoding the polypeptide to be expressed, and a selectable marker element. Each of these sequences is discussed below.

[0529] Optionally, the vector may contain a “tag”-encoding sequence, *i.e.*, an oligonucleotide molecule typically located at the 5’ or 3’ end of the polypeptide coding sequence; the oligonucleotide sequence encodes polyHis (such as hexaHis (SEQ ID NO: 66)), or another “tag” such as FLAG, HA (hemagglutinin influenza virus), or myc, for which commercially available antibodies exist. This tag is typically fused to the polypeptide upon expression of the polypeptide, and can serve as a means for affinity purification or detection of the polypeptide from the host cell. Affinity purification can be accomplished, for example, by column chromatography using antibodies against the tag as an affinity matrix. Optionally, the tag can subsequently be removed from the purified polypeptide by various means such as using certain peptidases for cleavage.

[0530] Flanking sequences may be homologous (*i.e.*, from the same species and/or strain as the host cell), heterologous (*i.e.*, from a species other than the host cell species or strain), hybrid (*i.e.*, a combination of flanking sequences from more than one source), synthetic or native. As such, the source of a flanking sequence may be any prokaryotic or eukaryotic organism, any vertebrate or invertebrate organism, or any plant, provided that the flanking sequence is functional in, and can be activated by, the host cell machinery.

[0531] Flanking sequences useful in the vectors provided herein may be obtained by any of several methods well known in the art. Typically, flanking sequences useful herein will have been previously identified by mapping and/or by restriction endonuclease digestion and can thus be isolated from the proper tissue source using the appropriate restriction endonucleases. In some cases, the full nucleotide sequence of a flanking sequence may be known. Here, the flanking sequence may be synthesized using the methods described herein for nucleic acid synthesis or cloning.

[0532] Whether all or only a portion of the flanking sequence is known, it may be obtained using polymerase chain reaction (PCR) and/or by screening a genomic library with a suitable probe such as an oligonucleotide and/or flanking sequence fragment from the same or another species. Where the flanking sequence is not known, a fragment of DNA containing a flanking sequence may be isolated from a larger piece of DNA that may contain, for example, a coding sequence or even another gene or genes. Isolation may be accomplished by restriction endonuclease digestion to produce the proper DNA fragment followed by isolation using agarose gel purification, Qiagen® column chromatography (Chatsworth, CA), or other methods known to the skilled artisan. The selection of suitable enzymes to accomplish this purpose will be readily apparent to one of ordinary skill in the art.

[0533] An origin of replication is typically a part of those prokaryotic expression vectors purchased commercially, and the origin aids in the amplification of the vector in a host cell. If the vector of choice does not contain an origin of replication site, one may be chemically synthesized based on a known sequence, and ligated into the vector. For example, the origin of replication from the plasmid pBR322 (New England Biolabs, Beverly, MA) is suitable for most gram-negative bacteria, and various viral origins (*e.g.*, SV40, polyoma, adenovirus, vesicular stomatitis virus (VSV), or papillomaviruses such as HPV or BPV) are useful for cloning vectors in mammalian cells. Generally, the origin of replication component is not needed for mammalian expression vectors (for example, the SV40 origin is often used only because it also contains the virus early promoter).

[0534] A transcription termination sequence is typically located 3' to the end of a polypeptide coding region and serves to terminate transcription. Usually, a transcription termination sequence in prokaryotic cells is a G-C rich fragment followed by a poly-T sequence. While the sequence is easily cloned from a library or even purchased commercially as part of a vector, it can also be readily synthesized using methods for nucleic acid synthesis such as those described herein.

[0535] A selectable marker gene encodes a protein necessary for the survival and growth of a host cell grown in a selective culture medium. Typical selection marker genes encode proteins that (a) confer resistance to antibiotics or other toxins, *e.g.*, ampicillin, tetracycline, or kanamycin for prokaryotic host cells; (b) complement auxotrophic deficiencies of the cell; or (c) supply critical nutrients not available from complex or defined media. Specific selectable markers are the kanamycin resistance gene, the ampicillin resistance gene, and the tetracycline resistance gene. Advantageously, a neomycin resistance gene may also be used for selection in both prokaryotic and eukaryotic host cells.

[0536] Other selectable genes may be used to amplify the gene that will be expressed. Amplification is the process wherein genes that are required for production of a protein critical for growth or cell survival are reiterated in tandem within the chromosomes of successive generations of recombinant cells. Examples of suitable selectable markers for mammalian cells include dihydrofolate reductase (DHFR) and promoterless thymidine kinase genes. Mammalian cell transformants are placed under selection pressure wherein only the transformants are uniquely adapted to survive by virtue of the selectable gene present in the vector. Selection pressure is imposed by culturing the transformed cells under conditions in which the concentration of selection agent in the medium is successively increased, thereby leading to the amplification of both the selectable gene and the DNA that encodes another gene, such as an antibody light or heavy chain. As a result, increased quantities of a polypeptide are synthesized from the amplified DNA.

[0537] A ribosome-binding site is usually necessary for translation initiation of mRNA and is characterized by a Shine-Dalgarno sequence (prokaryotes) or a Kozak sequence (eukaryotes). The

element is typically located 3' to the promoter and 5' to the coding sequence of the polypeptide to be expressed. In certain embodiments, one or more coding regions may be operably linked to an internal ribosome binding site (IRES), allowing translation of two open reading frames from a single RNA transcript.

[0538] In some cases, such as where glycosylation is desired in a eukaryotic host cell expression system, one may manipulate the various pre- or prosequences to improve glycosylation or yield. For example, one may alter the peptidase cleavage site of a particular signal peptide, or add prosequences, which also may affect glycosylation. The final protein product may have, in the -1 position (relative to the first amino acid of the mature protein) one or more additional amino acids incident to expression, which may not have been totally removed. For example, the final protein product may have one or two amino acid residues found in the peptidase cleavage site, attached to the amino-terminus. Alternatively, use of some enzyme cleavage sites may result in a slightly truncated form of the desired polypeptide, if the enzyme cuts at such area within the mature polypeptide.

[0539] Expression and cloning vectors provided herein will typically contain a promoter that is recognized by the host organism and operably linked to the molecule encoding the polypeptide. Promoters are untranscribed sequences located upstream (*i.e.*, 5') to the start codon of a structural gene (generally within about 100 to 1000 bp) that control transcription of the structural gene. Promoters are conventionally grouped into one of two classes: inducible promoters and constitutive promoters. Inducible promoters initiate increased levels of transcription from DNA under their control in response to some change in culture conditions, such as the presence or absence of a nutrient or a change in temperature. Constitutive promoters, on the other hand, uniformly transcribe gene to which they are operably linked, that is, with little or no control over gene expression. A large number of promoters, recognized by a variety of potential host cells, are well known. A suitable promoter is operably linked to the DNA encoding *e.g.*, heavy chain or light chain, by removing the promoter from the source DNA by restriction enzyme digestion and inserting the desired promoter sequence into the vector.

[0540] Suitable promoters for use with yeast hosts are also well known in the art. Yeast enhancers are advantageously used with yeast promoters. Suitable promoters for use with mammalian host cells are well known and include, but are not limited to, those obtained from the genomes of viruses such as polyoma virus, fowlpox virus, adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, retroviruses, hepatitis-B virus and most preferably Simian Virus 40 (SV40). Other suitable mammalian promoters include heterologous mammalian promoters, for example, heat-shock promoters and the actin promoter.

[0541] Additional promoters which may be of interest include, but are not limited to: SV40 early promoter (Benoist and Chambon, 1981, Nature 290:304-310); CMV promoter (Thomsen *et al.*, 1984,

Proc. Natl. Acad. U.S.A. 81:659-663); the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto *et al.*, 1980, Cell 22:787-797); herpes thymidine kinase promoter (Wagner *et al.*, 1981, Proc. Natl. Acad. Sci. U.S.A. 78:1444-1445); promoter and regulatory sequences from the metallothionein gene Prinster *et al.*, 1982, Nature 296:39-42); and prokaryotic promoters such as the beta-lactamase promoter (Villa-Kamaroff *et al.*, 1978, Proc. Natl. Acad. Sci. U.S.A. 75:3727-3731); or the tac promoter (DeBoer *et al.*, 1983, Proc. Natl. Acad. Sci. U.S.A. 80:21-25). Also of interest are the following animal transcriptional control regions, which exhibit tissue specificity and have been utilized in transgenic animals: the elastase I gene control region that is active in pancreatic acinar cells (Swift *et al.*, 1984, Cell 38:639-646; Omitz *et al.*, 1986, Cold Spring Harbor Symp. Quant. Biol. 50:399-409; MacDonald, 1987, Hepatology 7:425-515); the insulin gene control region that is active in pancreatic beta cells (Hanahan, 1985, Nature 315: 115-122); the immunoglobulin gene control region that is active in lymphoid cells (Grosschedl *et al.*, 1984, Cell 38:647-658; Adames *et al.*, 1985, Nature 318:533-538; Alexander *et al.*, 1987, Mol. Cell. Biol. 7:1436-1444); the mouse mammary tumor virus control region that is active in testicular, breast, lymphoid and mast cells (Leder *et al.*, 1986, Cell 45:485-495); the albumin gene control region that is active in liver (Pinkert *et al.*, 1987, Genes and Devel. 1 :268-276); the alpha-feta-protein gene control region that is active in liver (Krumlauf *et al.*, 1985, Mol. Cell. Biol. 5:1639-1648; Hammer *et al.*, 1987, Science 253:53-58); the alpha 1-antitrypsin gene control region that is active in liver (Kelsey *et al.*, 1987, Genes and Devel. 1: 161-171); the beta-globin gene control region that is active in myeloid cells (Mogram *et al.*, 1985, Nature 315:338-340; Kollias *et al.*, 1986, Cell 46:89-94); the myelin basic protein gene control region that is active in oligodendrocyte cells in the brain (Readhead *et al.*, 1987, Cell 48:703-712); the myosin light chain-2 gene control region that is active in skeletal muscle (Sani, 1985, Nature 314:283-286); and the gonadotropic releasing hormone gene control region that is active in the hypothalamus (Mason *et al.*, 1986, Science 234: 1372-1378).

[0542] An enhancer sequence may be inserted into the vector to increase transcription of DNA encoding a light chain or a heavy chain provided herein by higher eukaryotes. Enhancers are cis-acting elements of DNA, usually about 10-300 bp in length, that act on the promoter to increase transcription. Enhancers are relatively orientation and position independent, having been found at positions both 5' and 3' to the transcription unit. Several enhancer sequences available from mammalian genes are known (*e.g.*, globin, elastase, albumin, alphafeto-protein and insulin). Typically, however, an enhancer from a virus is used. The SV40 enhancer, the cytomegalovirus early promoter enhancer, the polyoma enhancer, and adenovirus enhancers known in the art are exemplary enhancing elements for the activation of eukaryotic promoters. While an enhancer may be positioned in the vector either 5' or 3' to a coding sequence, it is typically located at a site 5' from the promoter. A sequence encoding an appropriate native or heterologous signal sequence (leader sequence or signal peptide) can be incorporated into an expression vector, to promote extracellular secretion of the multispecific antigen-binding protein. The choice of signal peptide or leader depends on the type of host cells in which the multispecific antigen-binding

protein is to be produced, and a heterologous signal sequence can replace the native signal sequence. Examples of signal peptides that are functional in mammalian host cells include the following: the signal sequence for interleukin-7 (IL-7) described in US Patent No. 4,965,195; the signal sequence for interleukin-2 receptor described in Cosman *et al.*, 1984, Nature 312:768; the interleukin-4 receptor signal peptide described in EP Patent No. 0367 566; the type I interleukin-I receptor signal peptide described in U.S. Patent No. 4,968,607; the type II interleukin- I receptor signal peptide described in EP Patent No. 0 460 846.

[0543] The vector may contain one or more elements that facilitate expression when the vector is integrated into the host cell genome. Examples include an EASE element (Aldrich *et al.* 2003 Biotechnol Prog. 19: 1433-38) and a matrix attachment region (MAR). MARs mediate structural organization of the chromatin and may insulate the integrated vector from “position” effect. Thus, MARs are particularly useful when the vector is used to create stable transfectants. A number of natural and synthetic MAR-containing nucleic acids are known in the art, *e.g.*, U.S. Pat. Nos. 6,239,328; 7,326,567; 6,177,612; 6,388,066; 6,245,974; 7,259,010; 6,037,525; 7,422,874; 7,129,062.

[0544] Expression vectors provided herein may be constructed from a starting vector such as a commercially available vector. Such vectors may or may not contain all of the desired flanking sequences. Where one or more of the flanking sequences described herein are not already present in the vector, they may be individually obtained and ligated into the vector. Methods used for obtaining each of the flanking sequences are well known to one skilled in the art.

[0545] After the vector has been constructed and a nucleic acid molecule encoding a light chain, a heavy chain, or a light chain and a heavy chain sequence has been inserted into the proper site of the vector, the completed vector may be inserted into a suitable host cell for amplification and/or polypeptide expression. The transformation of an expression vector into a selected host cell may be accomplished by well-known methods including transfection, infection, calcium phosphate co-precipitation, electroporation, microinjection, lipofection, DEAE-dextran mediated transfection, or other known techniques. The method selected will in part be a function of the type of host cell to be used. These methods and other suitable methods are well known to the skilled artisan, and are set forth, for example, in Sambrook *et al.*, 2001, *supra*. In certain embodiments, one or more vectors capable of expressing a first heavy chain, a first light chain, a second heavy chain and a first light chain are introduced into a host cell.

Host Cells

[0546] In addition, provided are host cells comprising the expression systems or constructs described above. In certain embodiments, the multispecific antigen-binding protein is expressed from a single host cell. A host cell, when cultured under appropriate conditions, synthesizes multispecific antigen-binding

protein that can subsequently be collected from the culture medium (if the host cell secretes it into the medium) or directly from the host cell producing it (if it is not secreted). The selection of an appropriate host cell will depend upon various factors, such as desired expression levels, polypeptide modifications that are desirable or necessary for activity (such as glycosylation or phosphorylation) and ease of folding into a biologically active molecule. A host cell may be eukaryotic or prokaryotic.

[0547] Mammalian cell lines available as hosts for expression are well known in the art and include, but are not limited to, immortalized cell lines available from the American Type Culture Collection (ATCC) and any cell lines used in an expression system known in the art can be used to make the recombinant polypeptides provided herein. In general, host cells are transformed with a recombinant expression vector that comprises DNA encoding a desired multispecific antigen-binding protein. Among the host cells that may be employed are prokaryotes, yeast or higher eukaryotic cells. Prokaryotes include gram negative or gram positive organisms, for example *E. coli* or bacilli. Higher eukaryotic cells include insect cells and established cell lines of mammalian origin. Examples of suitable mammalian host cell lines include the COS-7 line of monkey kidney cells (ATCC CRL 1651) (Gluzman *et al.*, 1981, Cell 23:175), L cells, 293 cells, C127 cells, 3T3 cells (ATCC CCL 163), Chinese hamster ovary (CHO) cells, or their derivatives such as Veggie CHO and related cell lines which grow in serum-free media (Rasmussen *et al.*, 1998, Cytotechnology 28: 31), HeLa cells, BHK (ATCC CRL10) cell lines, and the CVI/EBNA cell line derived from the African green monkey kidney cell line CVI (ATCC CCL 70) as described by McMahan *et al.*, 1991, EMBO J. 10: 2821, human embryonic kidney cells such as 293, 293 EBNA or MSR 293, human epidermal A431 cells, human Colo205 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HL-60, U937, HaK or Jurkat cells. Optionally, mammalian cell lines such as HepG2/3B, KB, NIH 3T3 or S49, for example, can be used for expression of the polypeptide when it is desirable to use the polypeptide in various signal transduction or reporter assays. Alternatively, it is possible to produce the polypeptide in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Suitable yeasts include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida* strains, *Pichia* strains, or any yeast strain capable of expressing heterologous polypeptides. Suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous polypeptides.

[0548] In certain embodiments, provided is a cell line expressing a multispecific antigen-binding protein described herein. In certain embodiments, the cell line is a prokaryotic cell line. In certain embodiments, the cell line is an *E. coli* cell line. In certain embodiments, HC1, LC1, HC2, and LC2 are coexpressed in the same prokaryotic cell. In certain embodiments, HC1, LC1, HC2, and LC2 are coexpressed in the same *E. coli* cell. In certain embodiments, HC1, LC1, HC2, and LC2 are coexpressed in the same eukaryotic cell. In certain embodiments, the cell line is an eukaryotic cell line. In certain

embodiments, the cell line is a stable cell line. In certain embodiments, the stable cell line is a mammalian cell line. In certain embodiments, the stable cell line is a CHO cell line. In certain embodiments, at least about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or more than about 99% of the multispecific antigen-binding protein expressed by the stable cell line is correctly assembled (*i.e.*, wherein LC1 is paired with HC1, and wherein LC2 is paired with HC2). Stable cell line can be generated by methods known in the art. In certain embodiments, the stable cell line is generated by random or targeted integration of polynucleotide(s) expressing HC1, LC1, HC2, and LC2 into the host cell genome.

[0549] If the multispecific antigen-binding protein made in yeast or bacteria, it may be desirable to modify the product produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain a functional product. Such covalent attachments can be accomplished using known chemical or enzymatic methods. A polypeptide can also be produced by operably linking the isolated nucleic acid provided herein to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, Calif., U.S.A. (the MaxBac kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), and Luckow and Summers, *Bio/Technology* 6:47 (1988). Cell-free translation systems could also be employed to produce polypeptides, such as antibodies or fragments, using RNAs derived from nucleic acid constructs disclosed herein. Appropriate cloning and expression vectors for use with bacterial, fungal, yeast, and mammalian cellular hosts are described by Pouwels *et al.* (*Cloning Vectors: A Laboratory Manual*, Elsevier, New York, 1985). A host cell that comprises an isolated nucleic acid provided herein, preferably operably linked to at least one expression control sequence, is a “recombinant host cell”.

[0550] In certain embodiments, cell lines may be selected through determining which cell lines have high expression levels and constitutively produce multispecific antigen-binding proteins with the desired binding properties. In another embodiment, a cell line from the B cell lineage that does not make its own antibody but has a capacity to make and secrete a heterologous multispecific antigen-binding protein can be selected.

Production and Purification of Multispecific Antigen-binding Proteins

Culturing Host Cells

[0551] In certain embodiments, provided is a method of producing a multispecific antigen-binding protein described herein comprising (a) introducing a set of polynucleotides encoding H1, H2, L1, and L2

into a host cell; and (b) culturing the host cell to produce multispecific antigen-binding protein. In certain embodiments, the polynucleotides encoding L1 and L2 are introduced into the host cell at a predetermined ratio (*e.g.*, a molar ratio or a weight ratio). In certain embodiments, polynucleotides encoding L1 and L2 are introduced into the host cell such that the ratio (*e.g.*, a molar ratio or a weight ratio) of L1:L2 is about 1:1, about 1:1.5, about 1:2, about 1:2.5, about 1:3, about 1:3.5, about 1:4, about 1:4.5, about 1:5, about 1:5.5, about 1.5:1, about 2:1, about 2.5:1, about 3:1, about 3.5:1, about 4:1, about 4.5:1, about 5:1, or about 5.5:1, including any range in between these values. In certain embodiments, the ratio is a molar ratio. In certain embodiments the ratio is a weight ratio. In certain embodiments, the polynucleotides encoding H1 and H1 are introduced into the host cell at a predetermined ratio (*e.g.*, a molar ratio or a weight ratio). In certain embodiments, polynucleotides encoding H1 and H2 are introduced into the host cell such that the ratio (*e.g.*, a molar ratio or a weight ratio) of H1:H2 is about 1:1, about 1:1.5, about 1:2, about 1:2.5, about 1:3, about 1:3.5, about 1:4, about 1:4.5, about 1:5, about 1:5.5, about 1.5:1, about 2:1, about 2.5:1, about 3:1, about 3.5:1, about 4:1, about 4.5:1, about 5:1, or about 5.5:1, including any range in between these values. In certain embodiments, the ratio is molar ratio. In certain embodiments the ratio is a weight ratio. In certain embodiments, the polynucleotides encoding H1, H2, L1 and L2 are introduced into the host cell at a predetermined ratio (*e.g.*, a molar ratio or a weight ratio). In certain embodiments, polynucleotides encoding H1, H2, L1, and L2 are introduced into the host cell such that the ratio (*e.g.*, a molar ratio or a weight ratio) of H1 + H2 : L1 + L2 is about 5:1, about 5:2, about 5:3, about 5:4, about 1:1, about 4:5, about 3:5, about 2:5, or about 1:5, including any range in between these values. In certain embodiments, polynucleotides encoding LC1, LC2, HC1, and HC2 are introduced into the host cell such that the ratio (*e.g.*, a molar ratio or a weight ratio) of LC1:LC2:HC1:HC2 is about 1:1:1:1, about 2.8:1:1:1, about 1.4:1:1:1, about 1:1.4:1:1, about 1:2.8:1:1, about 1:1:2.8:1, about 1:1:1.4:1, about 1:1:1:2.8, or about 1:1:1:1.4, including any range in between these values. In certain embodiments, the ratio is molar ratio. In certain embodiments the ratio is a weight ratio.

[0552] In certain embodiments, the method of producing a multispecific antigen-binding protein further comprises determining an optimal ratio of the polynucleotides for introduction into the cell. In certain embodiments, mass spectrometry is used to determine multispecific antigen-binding protein yield (such as bispecific antibody yield), and optimal chain ratio is adjusted to maximize multispecific antigen-binding protein yield (such as bispecific antibody yield). In certain embodiments, dual antigen ELISA is used to determine multispecific antigen-binding protein yield (such as bispecific antibody yield), and optimal chain ratio is adjusted to maximize yield. In certain embodiments, the method of producing a multispecific antigen-binding protein further comprises harvesting or recovering the multispecific antigen-binding protein from the cell culture. In certain embodiments, the method of producing a multispecific antigen-binding protein further comprises purifying the harvested or recovered multispecific antigen-binding protein.

DEMANDE OU BREVET VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET COMPREND PLUS D'UN TOME.

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NOM DU FICHER / FILE NAME :

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What is claimed is:

1. A multispecific antigen binding protein comprising: a) a first heavy chain/light chain pair binding to a first antigen which comprises a first heavy chain polypeptide (H1) and a first light chain polypeptide (L1), and b) a second heavy chain/light chain pair binding to a second antigen which comprises a second heavy chain polypeptide (H2) and a second light chain polypeptide (L2), wherein each H1 and H2 comprises a heavy chain variable domain (VH) and a heavy chain constant domain (CH1), and each L1 and L2 comprises a light chain variable domain (VL) and a light chain constant domain (CL); wherein the CH1 domain of H1 comprises an amino acid substitution at S183 (EU numbering), and wherein the CL domain of L1 comprises an amino acid substitution at V133 (EU numbering).
2. The multispecific antigen binding protein of claim 1, wherein the S183 substitution is selected from the group consisting of S183A, S183T, S183V, S183Y, S183F, S183H, S183N, S183D, S183E, S183R, and S183K, and wherein the V133 substitution is selected from the group consisting of V133E, V133S, V133L, V133W, V133K, V133R, and V133D.
3. The multispecific antigen binding protein of claim 1 or 2, wherein the amino acid at EU position S183 on the CH1 domain of H1 is replaced with a positively charged residue, and wherein the amino acid at V133 on the CL domain of L1 is replaced with a negatively charged residue.
4. The multispecific antigen binding protein of claim 1 or 2, wherein the amino acid at EU position S183 on the CH1 domain of H1 is replaced with a negatively charged residue, and wherein the amino acid at V133 on the CL domain of L1 is replaced with a positively charged residue.
5. The multispecific antigen binding protein of claim 3 or 4, wherein the positively charged residue is selected from the group consisting of R and K.
6. The multispecific antigen binding protein of any one of claims 3-5, wherein the negatively charged residue is selected from the group consisting of D and E.
7. The multispecific antigen binding protein of any one of claims 1-6 wherein the CH1 domain consists of an amino acid substitution at S183 (EU numbering), and wherein the CL domain of L1 consists of an amino acid substitution at V133 (EU numbering).
8. The multispecific antigen binding protein of any one of claims 1-7, wherein:
 - (a) the CH1 domain of H1 comprises the S183D mutation, and wherein the CL domain of L1 comprises the V133K mutation;

- (b) the CH1 domain of H1 comprises the S183E mutation, and wherein the CL domain of L1 comprises the V133K mutation;
- (c) the CH1 domain of H1 comprises the S183A mutation, and wherein the CL domain of L1 comprises the V133E mutation;
- (d) the CH1 domain of H1 comprises the S183A mutation, and wherein the CL domain of L1 comprises the V133S mutation;
- (e) the CH1 domain of H1 comprises the S183A mutation, and wherein the CL domain of L1 comprises the V133L mutation;
- (f) the CH1 domain of H1 comprises the S183A mutation, and wherein the CL domain of L1 comprises the V133W mutation;
- (g) the CH1 domain of H1 comprises the S183A mutation, and wherein the CL domain of L1 comprises the V133K mutation;
- (h) the CH1 domain of H1 comprises the S183A mutation, and wherein the CL domain of L1 comprises the V133R mutation;
- (i) the CH1 domain of H1 comprises the S183A mutation, and wherein the CL domain of L1 comprises the V133D mutation;
- (j) the CH1 domain of H1 comprises the S183T mutation, and wherein the CL domain of L1 comprises the V133E mutation;
- (k) the CH1 domain of H1 comprises the S183T mutation, and wherein the CL domain of L1 comprises the V133S mutation;
- (l) the CH1 domain of H1 comprises the S183T mutation, and wherein the CL domain of L1 comprises the V133L mutation;
- (m) the CH1 domain of H1 comprises the S183T mutation, and wherein the CL domain of L1 comprises the V133W mutation;
- (n) the CH1 domain of H1 comprises the S183T mutation, and wherein the CL domain of L1 comprises the V133K mutation;
- (o) the CH1 domain of H1 comprises the S183T mutation, and wherein the CL domain of L1 comprises the V133R mutation;
- (p) the CH1 domain of H1 comprises the S183T mutation, and wherein the CL domain of L1 comprises the V133D mutation;
- (q) the CH1 domain of H1 comprises the S183V mutation, and wherein the CL domain of L1 comprises the V133E mutation;
- (r) the CH1 domain of H1 comprises the S183V mutation, and wherein the CL domain of L1 comprises the V133S mutation;
- (s) the CH1 domain of H1 comprises the S183V mutation, and wherein the CL domain of L1 comprises the V133L mutation;

- (t) the CH1 domain of H1 comprises the S183V mutation, and wherein the CL domain of L1 comprises the V133W mutation;
- (u) the CH1 domain of H1 comprises the S183V mutation, and wherein the CL domain of L1 comprises the V133K mutation;
- (v) the CH1 domain of H1 comprises the S183V mutation, and wherein the CL domain of L1 comprises the V133R mutation;
- (w) the CH1 domain of H1 comprises the S183V mutation, and wherein the CL domain of L1 comprises the V133D mutation;
- (x) the CH1 domain of H1 comprises the S183Y mutation, and wherein the CL domain of L1 comprises the V133E mutation;
- (y) the CH1 domain of H1 comprises the S183Y mutation, and wherein the CL domain of L1 comprises the V133S mutation;
- (z) the CH1 domain of H1 comprises the S183Y mutation, and wherein the CL domain of L1 comprises the V133L mutation;
- (aa) the CH1 domain of H1 comprises the S183Y mutation, and wherein the CL of L1 domain comprises the V133W mutation;
- (bb) the CH1 domain of H1 comprises the S183Y mutation, and wherein the CL of L1 domain comprises the V133K mutation;
- (cc) the CH1 domain of H1 comprises the S183Y mutation, and wherein the CL domain of L1 comprises the V133R mutation;
- (dd) the CH1 domain of H1 comprises the S183Y mutation, and wherein the CL domain of L1 comprises the V133D mutation;
- (ee) the CH1 domain of H1 comprises the S183F mutation, and wherein the CL domain of L1 comprises the V133E mutation;
- (ff) the CH1 domain of H1 comprises the S183F mutation, and wherein the CL domain of L1 comprises the V133S mutation;
- (gg) the CH1 domain of H1 comprises the S183F mutation, and wherein the CL domain of L1 comprises the V133L mutation;
- (hh) the CH1 domain of H1 comprises the S183F mutation, and wherein the CL domain of L1 comprises the V133W mutation;
- (ii) the CH1 domain of H1 comprises the S183F mutation, and wherein the CL domain of L1 comprises the V133K mutation;
- (jj) the CH1 domain of H1 comprises the S183F mutation, and wherein the CL domain of L1 comprises the V133R mutation;
- (kk) the CH1 domain of H1 comprises the S183F mutation, and wherein the CL of L1 domain comprises the V133D mutation;

(ll) the CH1 domain of H1 comprises the S183H mutation, and wherein the CL domain of L1 comprises the V133S mutation;

(mm) the CH1 domain of H1 comprises the S183H mutation, and wherein the CL domain of L1 comprises the V133L mutation;

(nn) the CH1 domain of H1 comprises the S183H mutation, and wherein the CL domain of L1 comprises the V133W mutation;

(oo) the CH1 domain of H1 comprises the S183N mutation, and wherein the CL domain of L1 comprises the V133L mutation; or

(pp) the CH1 domain of H1 comprises the S183E mutation, and wherein the CL domain of L1 comprises the V133L mutation. the CH1 domain of H1 comprises the S183K mutation, and wherein the CL domain of L1 comprises the V133E mutation.

9. The multispecific antigen binding protein of claim 8, wherein:

(a) the CH1 domain of H1 comprises or consists of the S183D mutation, and wherein the CL domain of L1 comprises or consists of the V133K mutation;

(b) the CH1 domain of H1 comprises or consists of the S183E mutation, and wherein the CL domain of L1 comprises or consists of the V133K mutation;

(c) the CH1 domain of H1 comprises or consists of the S183T mutation, and wherein the CL domain of L1 comprises or consists of the V133K mutation; or

(d) the CH1 domain of H1 comprises or consists of the S183V mutation, and wherein the CL domain of L1 comprises or consists of the V133E mutation

(e) the CH1 domain of H1 comprises or consists of the S183K mutation, and wherein the CL domain of L1 comprises or consists of the V133E mutation.

10. The multispecific antigen binding protein of any one of claims 1-9, wherein the CH1 domain of H2 and/or the CL domain of L2 does not comprise an amino acid substitution.

11. The multispecific antigen binding protein of any one of claims 1-9, wherein the CH1 domain of H2 does not comprise a substitution at S183 and the CL domain of L2 do not comprise substitution at V133.

12. The multispecific antigen binding protein of any one of claims 1-11, wherein the VH domain of H1 and/or H2 comprises an amino acid substitution at position Q39 (Kabat numbering), and wherein the VL domain of L1 and/or L2 comprises an amino acid substitution at position Q38 (Kabat numbering).

13. The multispecific antigen binding protein of claim 12, wherein the amino acid at Q39 in the VH domain is replaced with a positively charged residue, and wherein the amino acid at Q38 in the VL domain is replaced with a negatively charged residue (Kabat numbering).

14. The multispecific antigen binding protein of claim 4, wherein the amino acid at Q39 in the VH domain is replaced with a positively charged residue, and wherein the amino acid at Q38 in the VL domain is replaced with a negatively charged residue (Kabat numbering).
15. The multispecific antigen binding protein of claim 12, wherein the amino acid at Q39 in the VH domain is replaced with a negatively charged residue, and wherein the amino acid at Q38 in the VL domain is replaced with a positively charged residue (Kabat numbering).
16. The multispecific antigen binding protein of claim 3, wherein the amino acid at Q39 in the VH domain is replaced with a negatively charged residue, and wherein the amino acid at Q38 in the VL domain is replaced with a positively charged residue (Kabat numbering).
17. The multispecific antigen binding protein of any one of claims 13-16, wherein the positively charged residue is selected from the group consisting of R and K.
18. The multispecific antigen binding protein of any one of claims 13-17, wherein the negatively charged residue is selected from the group consisting of D and E.
19. The multispecific antigen binding protein of any one of claims 1-12, wherein the VH domain of H1 comprises a Q39E substitution mutation (Kabat numbering), and wherein the VL domain of L1 comprises a Q38K substitution mutation (Kabat numbering).
20. The multispecific antigen binding protein of any one of claims 1-12, wherein the VH domain of H1 comprises a Q39E substitution mutation, wherein the VL domain of L1 comprises a Q38K substitution mutation, and wherein the VH domain of H2 comprises a Q39K substitution mutation (Kabat numbering).
21. The multispecific antigen binding protein of any one of claims 1-12, wherein the VH domain of H1 comprises a Q39E substitution mutation, wherein the VL domain of L1 comprises the Q38K substitution mutation, wherein the VH domain of H2 comprises a Q39K substitution mutation, and wherein the VL domain of L2 comprises a Q38E substitution mutation (Kabat numbering).
22. The multispecific antigen binding protein of any one of claims 1-12, wherein the VH domain of H1 comprises a Q39K substitution mutation (Kabat numbering), and wherein the VL domain of L1 comprises a Q38E substitution mutation (Kabat numbering).
23. The multispecific antigen binding protein of any one of claims 1-12 and 20, wherein the VH domain of H1 comprises a Q39K substitution mutation, wherein the VL domain of L1 comprises a Q38E substitution mutation, and wherein the VH domain of H2 comprises a Q39E substitution mutation (all Kabat numbering).

24. The multispecific antigen binding protein of any one of claims 1-12, wherein the VH domain of H1 comprises a Q39K substitution mutation, wherein the VH domain of H2 comprises a Q39E substitution mutation, and wherein the VL domain of L2 comprises a Q38K substitution mutation (all Kabat numbering).
25. The multispecific antigen binding protein of any one of claims 1-12 and 20-21, wherein the VH domain of H1 comprises the Q39K substitution mutation, wherein the VL domain of L1 comprises the Q38E substitution mutation, wherein the VH domain of H2 comprises a Q39E substitution mutation, and wherein the VL domain of L2 comprises a Q38K substitution mutation (all Kabat numbering).
26. The multispecific antigen binding protein of any one of claims 1-25, wherein the interaction between the two substituted amino acids is via hydrogen bonds.
27. The multispecific antigen binding protein of any one of claims 1-26, wherein the interaction between the two substituted amino acids is via electrostatic interaction.
28. The multispecific antigen binding protein of any one of claims 1-9, 12-13, 15, 17-18, 22-23, and 25-26, wherein the VH domain of H1 comprises a Q39K substitution mutation and the CH1 domain of H1 comprises the S183E substitution mutation, wherein the VL domain of L1 comprises a Q38E substitution mutation and the CL domain of L1 comprises the V133K mutation, wherein the VH domain of H2 comprises the Q39E substitution mutation, and wherein the VL domain of L2 comprises the Q38K substitution mutation.
29. The multispecific antigen binding protein of any one of claims 1-9, 12-13, 15, 17-18, 22-23, and 25-26, wherein the VH domain of H1 comprises a Q39K substitution mutation and the CH1 domain of H1 comprises the S183T substitution mutation, wherein the VL domain of L1 comprises a Q38E substitution mutation and the CL domain of L1 comprises the V133K mutation, wherein the VH domain of H2 comprises the Q39E substitution mutation, and wherein the VL domain of L2 comprises the Q38K substitution mutation.
30. The multispecific antigen binding protein of any one of claims 1-9, 12-13, 15, 17-18, 22-23, and 25-26 wherein the VH domain of H1 comprises a Q39K substitution mutation and the CH1 domain of H1 comprises the S183Y substitution mutation, wherein the VL domain of L1 comprises a Q38E substitution mutation and the CL domain of L1 comprises the V133K mutation, wherein the VH domain of H2 comprises the Q39E substitution mutation, and wherein the VL domain of L2 comprises the Q38K substitution mutation.
31. The multispecific antigen binding protein of any one of claims 1-9, 12-13, 15, 17-18, 22-23, and 25-26, wherein the VH domain of H1 comprises a Q39K substitution mutation and the CH1 domain of H1

comprises the S183F substitution mutation, wherein the VL domain of L1 comprises a Q38E substitution mutation and the CL domain of L1 comprises the V133K mutation, wherein the VH domain of H2 comprises the Q39E substitution mutation, and wherein the VL domain of L2 comprises the Q38K substitution mutation.

32. The multispecific antigen binding protein of any one of claims 1-9, 12-13, 15, 17-21, and 25-26, wherein the VH domain of H1 comprises a Q39E substitution mutation and the CH1 domain of H1 comprises the S183E substitution mutation, wherein the VL domain of L1 comprises a Q38K substitution mutation and the CL domain of L1 comprises the V133K mutation, wherein the VH domain of H2 comprises the Q39K substitution mutation, and wherein the VL domain of L2 comprises the Q38E substitution mutation.

33. The multispecific antigen binding protein of any one of claims 1-9, 12-13, 15, 17-18, 22-23, and 25-26, wherein the VH domain of H1 comprises a Q39K substitution mutation, wherein the VL domain of L1 comprises a Q38E substitution mutation, wherein the VH domain of H2 comprises the Q39E substitution mutation and the CH1 domain of H2 comprises the S183E substitution mutation, and wherein the VL domain of L2 comprises the Q38K substitution mutation and the CL domain of L1 comprises the V133K mutation.

34. The multispecific antigen binding protein of any one of claims 1-9, 12-13, 15, 17-21, and 25-26, wherein the VH domain of H1 comprises the Q39E substitution mutation and the CH1 domain of H1 comprises the S183K substitution mutation, wherein the VL domain of L1 comprises the Q38K substitution mutation and the CL domain of L1 comprises the V133E substitution mutation, wherein the VH domain of H2 comprises a Q39K substitution mutation and the CH1 domain of H2 comprises the S183E substitution mutation, and wherein the VL domain of L2 comprises a Q38E substitution mutation and the CL domain of L2 comprises the V133K mutation.

35. The multispecific antigen binding protein of any one of claims 1-9, 12-13, 15, 17-18, 22-23, and 25-26, wherein the VH domain of H1 comprises the Q39E substitution mutation and the CH1 domain of H1 comprises the S183E substitution mutation, wherein the VL domain of L1 comprises the Q38K substitution mutation and the CL domain of L1 comprises the V133K substitution mutation, wherein the VH domain of H2 comprises a Q39K substitution mutation and the CH1 domain of H2 comprises the S183K substitution mutation, and wherein the VL domain of L2 comprises a Q38E substitution mutation and the CL domain of L2 comprises the V133E mutation.

36. The multispecific antigen binding protein of any one of claims 1-9, 12-13, 15, 17-18, 22-23, and 25-26, wherein the VH domain of H1 comprises the Q39K substitution mutation and the CH1 domain of H1 comprises the S183K substitution mutation, wherein the VL domain of L1 comprises the Q38E

substitution mutation and the CL domain of L1 comprises the V133E substitution mutation, wherein the VH domain of H2 comprises a Q39E substitution mutation and the CH1 domain of H2 comprises the S183E substitution mutation, and wherein the VL domain of L2 comprises a Q38K substitution mutation and the CL domain of L2 comprises the V133K mutation.

37. The multispecific antigen binding protein of any one of claims 1-9, 12-13, 15, 17-18, 22-23, and 25-26, wherein the VH domain of H1 comprises the Q39K substitution mutation and the CH1 domain of H1 comprises the S183E substitution mutation, wherein the VL domain of L1 comprises the Q38E substitution mutation and the CL domain of L1 comprises the V133K substitution mutation, wherein the VH domain of H2 comprises a Q39E substitution mutation and the CH1 domain of H2 comprises the S183K substitution mutation, and wherein the VL domain of L2 comprises a Q38K substitution mutation and the CL domain of L2 comprises the V133E mutation.

38. The multispecific antigen binding protein of any one of claims 1-37, wherein each of H1 and/or H2 comprises an Fc region comprising a CH2 and a CH3 domain.

39. The multispecific antigen binding protein of claim 38, wherein the Fc region of H1 and/or H2 is human IgG1, human IgG2 or human IgG4 Fc.

40. The multispecific antigen binding protein of claim 38, wherein the Fc region of H1 and/or H2 is mouse IgG1, mouse IgG2 or mouse IgG4 Fc.

41. The multispecific antigen binding protein of any one of claims 1-40, wherein the CH3 domains of H1 and H2 each meet at an interface, and wherein each of the CH3 domains comprises an amino acid substitution such that the Fc region of H1 preferentially pairs with that of H2 as compared to H1.

42. The multispecific antigen binding protein of claim 41, wherein the amino acid substitutions in the CH3 domains result in greater electrostatic complementarity.

43. The multispecific antigen binding protein of claim 41, wherein the amino acid substitutions in the CH3 domains result in greater steric complementarity.

44. The multispecific antigen binding protein of claim 41,
wherein the CH3 domain of H1 is altered, so that within the CH3/CH3 interface, one or more amino acid residues are replaced with one or more amino acid residues having a larger side chain volume, thereby generating a protuberance on the surface of the CH3 domain of H1 that interacts with the CH3 domain of H2 and

wherein the CH3 domain of H2 is altered so that within the CH3/CH3 interface one or more amino acid residues are replaced with amino acid residues having a smaller side chain volume, thereby generating a cavity on the surface of the CH3 domain of H2 that interacts with the CH3 domain of H1.

45. The multispecific antigen binding protein of claim 41,

wherein the CH3 domain of H2 is altered, so that within the CH3/CH3 interface, one or more amino acid residues are replaced with one or more amino acid residues having a larger side chain volume, thereby generating a protuberance on the surface of the CH3 domain of H2 that interacts with the CH3 domain of H1

and

wherein the CH3 domain of H1 is altered so that within the CH3/CH3 interface, one or more amino acid residues are replaced with amino acid residues having a smaller side chain volume, thereby generating a cavity on the surface of the CH3 domain of H1 that interacts with the CH3 domain of H2.

46. The multispecific antigen binding protein of claim 44 or 45, wherein the protuberance is a knob mutation.

47. The multispecific binding protein of claim 46, wherein the knob mutation comprises T366W (EU numbering).

48. The multispecific antigen binding protein of claim 44 or 45 wherein the cavity is a hole mutation.

49. The multispecific antigen binding protein of claim 48, wherein the hole mutation comprises at least one, at least two, or all three of T366S, L368A, and Y407V (EU numbering).

50. A multispecific antigen binding protein comprising: a) a first heavy chain/light chain pair comprising a first heavy chain polypeptide (H1) and a first light chain polypeptide (L1), and b) a second heavy chain/light chain pair comprising a second heavy chain polypeptide (H2) and a second light chain polypeptide (L2), wherein each H1 and H2 comprises a heavy chain variable domain (VH) and a heavy chain constant domain (CH1), and each L1 and L2 comprises a light chain variable domain (VL) and a light chain constant domain (CL); wherein the CH1 domain of H1 comprises an amino acid substitution at F170 (EU numbering), and wherein the CL domain of L1 comprises an amino acid substitution at S176 (EU numbering).

51. The multispecific antigen binding protein of claim 50, wherein the CH1 domain of H1 further comprises one or more amino acid substitutions at a position selected from the group consisting of: A141, S181, S183, and V185 (EU numbering).

52. The multispecific antigen binding protein of any one of claims 50-51, wherein the CL domain of L1 further comprises one or more amino acid substitutions at a position selected from the group consisting of F116, S131, V133, L135, S162, S174, and T178 (EU numbering).
53. The multispecific antigen binding protein of any one of claims 50-52, wherein the one or more amino acid substitutions at a position selected from the group consisting of A141, F170, S181, S183, and V185 (EU numbering) of CH1 and/or the one or more amino acid substitutions at a position selected from the group consisting of F116, S131, V133, L135, S162, S174, S176, and T178 (EU numbering) of CL1 are not substituted with charged amino acid residues.
54. The multispecific antigen binding protein of any one of claims 50-53, wherein the amino acid substitutions result in steric complementarity.
55. The multispecific antigen binding protein of any one of claims 50-54, wherein the CH1 domain of H1 comprises an amino acid substitution selected from the group consisting of F170S and F170A, and wherein the CL domain of L1 comprises an amino acid substitution of S176F.
56. The multispecific antigen binding protein of any one of claims 50-54, wherein:
- (a) the CH1 domain of H1 comprises the F170S mutation, and the CL domain of L1 comprises the S176F mutation; or
 - (b) the CH1 domain of H1 comprises the F170A mutation, and the CL domain of L1 comprises the S176F mutation.
57. The multispecific antigen binding protein of claim 56, wherein the CH1 domain of H1 comprises the F170S mutation, and wherein the CL domain of L1 comprises the S176F mutation.
58. The multispecific antigen binding protein of any one of claims 50-57, wherein:
- (a) the CH1 domain of H1 comprises the A141I, F170S, S181M, S183V, and V185A mutations, and the CL domain of L1 comprises the F116A, V133I, L135V, S162M, S174A, S176F, and T178V mutations;
 - (b) the CH1 domain of H1 comprises the A141I, F170S, S181M, S183A, and V185A mutations and the CL domain of L1 comprises the F116A, S131D, L135V, S162A, S174A, S176F, and T178I mutations;
 - (c) the CH1 domain of H1 comprises the A141I, F170S, S181M, S183A, and V185A mutations and the CL domain of L1 comprises the F116A, L135V, S174A, S176F, and T178V mutations; or
 - (d) the CH1 domain of H1 comprises the A141I, F170A, S181M, S183V, and V185A mutations and the CL domain of L1 comprises the F116A, L135V, S162M, S174A, S176F, and T178V mutations.

59. The multispecific antigen binding protein of any one of claims 50-57, wherein the CH1 domain of H1 comprises A141I, F170S, S181M, S183A, and V185A mutations and the CL domain of L1 comprises F116A, L135V, S174A, S176F, and T178V mutations.
60. The multispecific antigen binding protein of claim 59, wherein the VH domain of H1 comprises a Q39E mutation (Kabat numbering), the VL domain of L1 comprises a Q38K mutation (Kabat numbering), the VH domain of H2 comprises a Q39K mutation (Kabat numbering), and the the VL domain of L2 comprises a Q38E mutation (Kabat numbering).
61. The multispecific antigen binding protein of claim 59 or 60, wherein the CH1 domain of H2 comprises an S183E mutation (EU numbering) and the CL domain of L2 comprises a V133K mutation (EU numbering).
62. The multispecific antigen binding protein of claim 59, wherein the VH domain of H1 comprises a Q39K mutation (Kabat numbering), the VL domain of L1 comprises a Q38E mutation (Kabat numbering), wherein the VH domain of H2 comprises a Q39E mutation (Kabat numbering), and the VL domain of L2 comprises a Q38K mutation (Kabat numbering).
63. The multispecific antigen binding protein of claim 59 or 62, wherein the CH1 domain of H2 comprises an S183K mutation (EU numbering) and the CL domain of L2 comprises a V133K mutation (EU numbering).
64. The multispecific antigen binding protein of any one of claims 50-55, wherein:
- (a) the CH1 domain of H1 comprises F170S, S181M, S183A, and V185A mutations and the CL domain of L1 comprises L135V, S174A, S176F, and T178V mutations;
 - (b) the CH1 domain of H1 comprises A141I, F170S, S183A, and V185A mutations and the CL domain of L1 comprises F116A, S174A, S176F, and T178V mutations;
 - (c) the CH1 domain of H1 comprises A141I, F170S, S181M, and V185A mutations and the CL domain of L1 comprises F116A, L135V, S176F, and T178V mutations;
 - (d) the CH1 domain of H1 comprises A141I, F170S, S181M, and S183A mutations and the CL domain of L1 comprises F116A, L135V, S174A, and S176F mutations;
 - (e) the CH1 domain of H1 comprises F170S, S183A, and V185A mutations and the CL domain of L1 comprises F116A, S176F, and T178V mutations;
 - (f) the CH1 domain of H1 comprises F170S, S181M, and V185A mutations and the CL domain of L1 comprises F116A, L135V, and S176F mutations;
 - (g) the CH1 domain of H1 comprises F170S, S181M, and S183A mutations and the CL domain of L1 comprises F116A and S176F mutations;

- (h) the CH1 domain of H1 comprises A141I, F170S, and V185A mutations and the CL domain of L1 comprises F116A and S176F mutations;
- (i) the CH1 domain of H1 comprises A141I, F170S, and S183A mutations and the CL domain of L1 comprises F116A and S176F mutations;
- (j) the CH1 domain of H1 comprises A141I, F170S, and S181M mutations and the CL domain of L1 comprises F116A, L135V, S174A, S176F, and T178V mutations;
- (k) the CH1 domain of H1 comprises F170S and V185A mutations and the CL domain of L1 comprises F116A and S176F mutations;
- (l) the CH1 domain of H1 comprises A141I and F170S mutations and the CL domain of L1 comprises F116A, L135V, S174A, S176F, and T178V mutations;
- (m) the CH1 domain of H1 comprises A141I and F170S mutations and the CL domain of L1 comprises F116A, L135V, S176F, and T178V mutations;
- (n) the CH1 domain of H1 comprises A141I and F170S mutations and the CL domain of L1 comprises F116A, L135V, S174A, and S176F mutations;
- (o) the CH1 domain of H1 comprises A141I and F170S mutations and the CL domain of L1 comprises F116A, S176F, and T178V mutations;
- (p) the CH1 domain of H1 comprises A141I and F170S mutations and the CL domain of L1 comprises F116A, L135V, and S176F mutations;
- (q) the CH1 domain of H1 comprises A141I and F170S mutations and the CL domain of L1 comprises F116A and S176F mutations;
- (r) the CH1 domain of H1 comprises the F170S mutation and the CL domain of L1 comprises F116A, L135V, S174A, S176F, and T178V mutations;
- (s) the CH1 domain of H1 comprises the F170S mutation and the CL domain of L1 comprises F116A, L135V, S176F, and T178V mutations;
- t) the CH1 domain of H1 comprises the F170S mutation and the CL domain of L1 comprises F116A, L135V, S174A, and S176F mutations;
- (u) the CH1 domain of H1 comprises the F170S mutation and the CL domain of L1 comprises F116A, S176F, and T178V mutations;
- (v) the CH1 domain of H1 comprises the F170S mutation and the CL domain of L1 comprises F116A, L135V, and S176F mutations; or
- (w) the CH1 domain of H1 comprises the F170S mutation and the CL domain of L1 comprises F116A and S176F mutations.

65. The multispecific antigen binding protein of claim 64, wherein the CH1 domain of H1 comprises A141I, F170S, and S181M mutations and the CL domain of L1 comprises F116A, L135V, S174A, S176F, and T178V mutations.

66. The multispecific antigen binding protein of claim 64, wherein the CH1 domain of H1 comprises A141I and F170S mutations and the CL domain of L1 comprises F116A, L135V, S174A, S176F, and T178V mutations.
67. The multispecific antigen binding protein of claim 64, wherein the CH1 domain of H1 comprises the F170S mutation and the CL domain of L1 comprises F116A, L135V, S174A, S176F, and T178V mutations.
68. A multispecific antigen binding protein comprising: a) a first heavy chain/light chain pair comprising a first heavy chain sequence (H1) and a first light chain sequence (L1), and b) a second heavy chain/light chain pair comprising a second heavy chain sequence (H2) and a second light chain sequence (L2), wherein each H1 and H2 comprises a heavy chain variable domain (VH) and a heavy chain constant domain (CH1), and each L1 and L2 comprises a light chain variable domain (VL) and a light chain constant domain (CL); wherein the CH1 domain of H1 comprises an amino acid substitution at L128 (EU numbering) and wherein the CL domain of C1 comprises amino acid substitutions at F118 and L135 (EU numbering).
69. The multispecific antigen binding protein of claim 68, wherein the CH1 domain of H1 further comprises an amino acid substitution at V185 (EU numbering).
70. The multispecific antigen binding protein of claim 68 or 69, wherein the CH1 domain of H1 further comprises one or more amino acid substitutions at a position selected from the group consisting of: A141, F170, S181, and S183 (EU numbering).
71. The multispecific antigen binding protein of any one of claims 68-70, wherein the CL domain of L1 further comprises one or more amino acid substitutions at a position selected from the group consisting of S131, V133, S162, T164, S176 and T178 (EU numbering).
72. The multispecific antigen binding protein of any one of claims 68-71, wherein the one or more amino acid substitutions at a position selected from the group consisting of L128 A141, F170, S181, S183, V185 (EU numbering) of CH1 and/or the one or more amino acid substitutions at a position selected from the group consisting of F118 S131, V133, and L135 S162, T164, S176 and T178 (EU numbering) of CL1 are not substituted with charged amino acid residues.
73. The multispecific antigen binding protein of any one of claims 68-72, wherein the amino acid substitutions result in greater steric complementarity.
74. The multispecific antigen binding protein of any one of claims 68-73, wherein the CH1 domain of H1 comprises an amino acid substitution at a position selected from the group consisting of A141,

F170, S181, and S183, and wherein the CL domain comprises an amino acid substitution at a position selected from the group consisting of S131, V133, S162, T164, S176 and T178.

75. The multispecific antigen binding protein of claim 74, wherein

(a) the CH1 domain of H1 comprises L128F, A141M, F170M, S181I and S183A mutations and the CL domain comprises F118V, S131T, V133A, L135Y, S162A, T164S, S176M, and T178L mutations;

(b) the CH1 domain of H1 comprises L128F, A141M, F170Y, S181I, S183A, and V185A mutations and the CL domain comprises F118V, S131T, V133A, L135F, S162A, S176A, and T178L mutations;

(c) the CH1 domain of H1 comprises L128F, A141T, F170M, S181T, S183A, and V185L mutations and the CL domain comprises F118V, S131T, V133A, L135F, S162A, T164S, S176T, and T178L mutations; or

(d) the CH1 domain of H1 comprises L128F, A141M, F170M, S181T, and S183A, mutations and the CL domain comprises F118V, S131T, V133A, L135F, S162M, T164S, S176M, and T178L mutations.

76. The multispecific antigen binding protein of claim 75, wherein the CH1 domain of H1 comprises the L128F, A141M, F170Y, S181I, S183A, and V185A mutations, and wherein the CL domain comprises the F118V, S131T, V133A, L135F, S162A, S176A, and T178L mutations.

77. The multispecific antigen binding protein of any one of claims 1-49, wherein the CH1 domain of H2 is altered so that within the CH1/CL interface, two or more amino acid residues are replaced with an equivalent number of amino acid residues having a larger side chain volume, thereby generating a protuberance on the surface of the CH1 domain of H2 that interacts with the CL domain of L2,
and

wherein the CL domain of L2 is altered so that within the CH1/CL interface, two or more amino acid residues are replaced with an equivalent number of amino acid residues having a smaller side chain volume, thereby generating a cavity on the surface of the CL domain of L2 that interacts with the CH1 domain of H2.

78. The multispecific antigen binding protein of claim any one of claims 1-49, Wherein the CL domain of L2 is altered so that within the CH1/CL interface, two or more amino acid residues are replaced with amino acid residues having a larger side chain volume, thereby generating a protuberance on the surface of the CL domain that interacts with the CH1 domain of H2,
and

wherein the CH1 domain of H2 is altered so that within the CH1/CL interface, two or more amino acid residues are replaced with amino acid residues having a smaller side chain volume, thereby generating a cavity on the surface of the CH1 domain of H2 that interacts with the CL domain.

79. The multispecific antigen-binding protein of claim 59, wherein the CH1 domain of H2 comprises an amino acid substitution mutation at S183 (EU numbering) and the CL domain of L2 comprises an amino acid substitution mutation V133K (EU numbering).

80. The multispecific antigen-binding protein of claim 79, wherein the amino acid at position S183 in the CH1 domain of H2 is replaced with a positively charged amino acid, and wherein the amino acid at position V133 in the CL domain of L2 is replaced with a negatively charged amino acid.

81. The multispecific antigen-binding protein of claim 79, wherein the amino acid at position S183 in the CH1 domain of H2 is replaced with a negatively charged amino acid, and wherein the amino acid at position V133 in the CL domain of L2 is replaced with a positively charged amino acid.

82. The multispecific antigen-binding protein of claim 79, wherein the CH1 domain of H2 comprises S183E mutation, and wherein the CL domain of L2 comprises V133K mutation.

83. The multispecific antigen-binding protein of claim 82, further comprising in the VH domain of H1 Q39E mutation, in the VL domain of L1 Q38K mutation, in the VH domain of H2 Q39K mutation and in the VL domain of L2 Q38E mutation.

84. The multispecific antigen-binding protein of claim 79, wherein the CH1 domain of H2 comprises S183K mutation, and wherein the CL domain of L2 comprises V133E mutation.

85. The multispecific antigen-binding protein of claim 84, further comprising in the VH domain of H1 Q39K mutation, in the VL domain of L1 Q38E mutation, in the VH domain of H2 Q39E mutation and in the VL domain of L2 Q38K mutation.

86. The multispecific antigen binding protein of any one of claims 50-59 and 64-78, wherein the CH1 domain of H2 comprises an amino acid substitution at EU position S183, and wherein the CL domain of L2 comprises an amino acid substitution at EU position V133.

87. The multispecific antigen binding protein of claim 85, wherein the interaction between the amino acid substitution at EU position S183 on the CH1 domain of H2 and the amino acid substitution at EU position V133 on the CL domain of L2 is via electrostatic interaction.

88. The multispecific antigen binding protein of claim 87, wherein the amino acid at EU position S183 on the CH1 domain of H2 is replaced with a positively charged residue, and wherein the amino acid at EU position V133 on the CL domain of L2 is replaced with a negatively charged residue.

89. The multispecific antigen binding protein of claim 87, wherein the amino acid at EU position S183 on the CH1 domain of H2 is replaced with a negatively charged residue, and wherein the amino acid at EU position V133 on the CL domain of L2 is replaced with a positively charged residue.

90. The multispecific antigen binding protein of any one of claims 86-89, wherein the CH1 domain of H2 comprises an amino acid substitution at a position selected from the group consisting of EU position S183A, S183T, S183V, S183Y, S183F, S183H, S183N, S183D, S183E, S183R, and S183K, and wherein the CL domain of L2 comprises an amino acid substitution at a position selected from the group consisting of EU position V133E, V133S, V133L, V133W, V133K, V133R, and V133D.

91. The multispecific antigen binding protein of claim 90, wherein:

- (a) the CH1 domain of H2 comprises the EU position S183D mutation, and wherein the CL domain of L2 comprises the EU position V133K mutation;
- (b) the CH1 domain of H2 comprises the EU position S183E mutation, and wherein the CL domain of L1 comprises the EU position V133K mutation;
- (c) the CH1 domain of H2 comprises the EU position S183A mutation, and wherein the CL domain of L2 comprises the EU position V133E mutation;
- (d) the CH1 domain of H2 comprises the EU position S183A mutation, and wherein the CL domain of L2 comprises the EU position V133S mutation;
- (e) the CH1 domain of H2 comprises the EU position S183A mutation, and wherein the CL domain of L2 comprises the EU position V133L mutation;
- (f) the CH1 domain of H2 comprises the EU position S183A mutation, and wherein the CL domain of L2 comprises the EU position V133W mutation;
- (g) the CH1 domain of H2 comprises the EU position S183A mutation, and wherein the CL domain of L2 comprises the EU position V133K mutation;
- (h) the CH1 domain of H2 comprises the EU position S183A mutation, and wherein the CL domain of L2 comprises the EU position V133R mutation;
- (i) the CH1 domain of H2 comprises the EU position S183A mutation, and wherein the CL domain of L2 comprises the EU position V133D mutation;
- (j) the CH1 domain of H2 comprises the EU position S183T mutation, and wherein the CL domain of L2 comprises the EU position V133E mutation;
- (k) the CH1 domain of H2 comprises the EU position S183T mutation, and wherein the CL domain of L2 comprises the EU position V133S mutation;

- (l) the CH1 domain of H2 comprises the EU position S183T mutation, and wherein the CL domain of L2 comprises the EU position V133L mutation;
- (m) the CH1 domain of H2 comprises the EU position S183T mutation, and wherein the CL domain of L2 comprises the EU position V133W mutation;
- (n) the CH1 domain of H2 comprises the EU position S183T mutation, and wherein the CL domain of L2 comprises the EU position V133K mutation;
- (o) the CH1 domain of H2 comprises the EU position S183T mutation, and wherein the CL domain of L2 comprises the EU position V133R mutation;
- (p) the CH1 domain of H2 comprises the EU position S183T mutation, and wherein the CL domain of L2 comprises the EU position V133D mutation;
- (q) the CH1 domain of H2 comprises the EU position S183V mutation, and wherein the CL domain of L2 comprises the EU position V133E mutation;
- (r) the CH1 domain of H2 comprises the EU position S183V mutation, and wherein the CL domain of L2 comprises the EU position V133S mutation;
- (s) the CH1 domain of H2 comprises the EU position S183V mutation, and wherein the CL domain of L2 comprises the EU position V133L mutation;
- (t) the CH1 domain of H2 comprises the EU position S183V mutation, and wherein the CL domain of L2 comprises the EU position V133W mutation;
- (u) the CH1 domain of H2 comprises the EU position S183V mutation, and wherein the CL domain of L2 comprises the EU position V133K mutation;
- (v) the CH1 domain of H2 comprises the EU position S183V mutation, and wherein the CL domain of L2 comprises the EU position V133R mutation;
- (w) the CH1 domain of H2 comprises the EU position S183V mutation, and wherein the CL domain of L2 comprises the EU position V133D mutation;
- (x) the CH1 domain of H2 comprises the EU position S183Y mutation, and wherein the CL domain of L2 comprises the EU position V133E mutation;
- (y) the CH1 domain of H2 comprises the EU position S183Y mutation, and wherein the CL domain of L2 comprises the EU position V133S mutation;
- (z) the CH1 domain of H2 comprises the EU position S183Y mutation, and wherein the CL domain of L2 comprises the EU position V133L mutation;
- (aa) the CH1 domain of H2 comprises the EU position S183Y mutation, and wherein the CL of L2 domain comprises the EU position V133W mutation;
- (bb) the CH1 domain of H2 comprises the EU position S183Y mutation, and wherein the CL of L2 domain comprises the EU position V133K mutation;
- (cc) the CH1 domain of H2 comprises the EU position S183Y mutation, and wherein the CL domain of L2 comprises the EU position V133R mutation;

- (dd) the CH1 domain of H2 comprises the EU position S183Y mutation, and wherein the CL domain of L2 comprises the EU position V133D mutation;
- (ee) the CH1 domain of H2 comprises the EU position S183F mutation, and wherein the CL domain of L2 comprises the EU position V133E mutation;
- (ff) the CH1 domain of H2 comprises the EU position S183F mutation, and wherein the CL domain of L2 comprises the EU position V133S mutation;
- (gg) the CH1 domain of H2 comprises the EU position S183F mutation, and wherein the CL domain of L2 comprises the EU position V133L mutation;
- (hh) the CH1 domain of H2 comprises the EU position S183F mutation, and wherein the CL domain of L2 comprises the EU position V133W mutation;
- (ii) the CH1 domain of H2 comprises the EU position S183F mutation, and wherein the CL domain of L2 comprises the EU position V133K mutation;
- (jj) the CH1 domain of H2 comprises the EU position S183F mutation, and wherein the CL domain of L2 comprises the EU position V133R mutation;
- (kk) the CH1 domain of H2 comprises the EU position S183F mutation, and wherein the CL of L2 domain comprises the EU position V133D mutation;
- (ll) the CH1 domain of H2 comprises the EU position S183H mutation, and wherein the CL domain of L2 comprises the EU position V133S mutation;
- (mm) the CH1 domain of H2 comprises the EU position S183H mutation, and wherein the CL domain of L2 comprises the EU position V133L mutation;
- (nn) the CH1 domain of H2 comprises the EU position S183H mutation, and wherein the CL domain of L2 comprises the EU position V133W mutation;
- (oo) the CH1 domain of H2 comprises the EU position S183N mutation, and wherein the CL domain of L2 comprises the EU position V133L mutation;
- (pp) the CH1 domain of H2 comprises the EU position S183E mutation, and wherein the CL domain of L2 comprises the EU position V133L mutation; or
- (qq) the CH1 domain of H2 comprises the S183K mutation, and wherein the CL domain of L2 comprises the V133E mutation..

92. The multispecific antigen binding protein of claim 91, wherein the CH1 domain of H2 comprises the

- (a) the CH1 domain of H2 comprises the EU position S183D mutation, and wherein the CL domain of L2 comprises the EU position V133K mutation;
- (b) the CH1 domain of H2 comprises the EU position S183E mutation, and wherein the CL domain of L2 comprises the EU position V133K mutation;
- (c) the CH1 domain of H2 comprises the EU position S183T mutation, and wherein the CL domain of L2 comprises the EU position V133K mutation;

(d) the CH1 domain of H2 comprises the EU position S183V mutation, and wherein the CL domain of L2 comprises the EU position V133E mutation;

(e) the CH1 domain of H2 comprises the EU position S183K mutation, and wherein the CL domain of L2 comprises the EU position V133E mutation.

93. The multispecific antigen binding protein of any one of claims 50-59 and 64-78 wherein the CH1 domain of H2 and the CL domain of L2 do not comprise an amino acid substitution.

94. The multispecific antigen binding protein of any one of claims 50-59 and 64-93, wherein the VH domain of H1 comprises an amino acid substitution at Kabat position Q39, and wherein the VL domain of V1 comprises an amino acid substitution at Kabat position Q38.

95. The multispecific antigen binding protein of claim 94, wherein the amino acid at Kabat position Q39 on the VH domain of H1 is replaced with a positively charged residue, and wherein the amino acid at Kabat position Q38 on the VL domain of L1 is replaced with a negatively charged residue.

96. The multispecific antigen binding protein of claim 94, wherein the amino acid at Kabat position Q39 on the VH domain of H1 is replaced with a negatively charged residue, and wherein the amino acid at Kabat position Q38 on the VL domain of L1 is replaced with a positively charged residue.

97. The multispecific antigen binding protein of any one of claims 94-96, wherein the positively charged residue is selected from the group consisting of R and K.

98. The multispecific antigen binding protein of any one of claims 94-97, wherein the negatively charged residue is selected from the group consisting of D and E.

99. The multispecific antigen binding protein of any one of claims 50-59 and 64-93, wherein the VH domain of H1 comprises a Kabat position Q39E substitution mutation, wherein the VL domain of L1 comprises a Kabat position Q38K substitution.

100. The multispecific antigen binding protein of any one of claims 50-59 and 64-93, wherein the VH domain of H1 comprises a Kabat position Q39E substitution mutation, wherein the VL domain of L1 comprises a Kabat position Q38K substitution, and wherein the VH domain of H2 comprises a Kabat position Q39K substitution mutation.

101. The multispecific antigen binding protein of any one of claims 50-59 and 64-93, wherein the VH domain of H1 comprises a Kabat position Q39E substitution mutation, wherein the VL domain of L1 comprises a Kabat position Q38K substitution, wherein the VH domain of H2 comprises a Kabat position Q39K substitution mutation, and wherein the VL domain of L2 comprises a Kabat position Q38E substitution mutation.

102. The multispecific antigen binding protein of any one of claims 50-59 and 64-93, wherein the VH domain of H1 comprises a Kabat position Q39K substitution mutation, wherein the VL domain of L1 comprises a Kabat position Q38E substitution.
103. The multispecific antigen binding protein of any one of claims 50-59 and 64-93, wherein the VH domain of H1 comprises a Kabat position Q39K substitution mutation, wherein the VL domain of L1 comprises a Kabat position Q38E substitution, and wherein the VH domain of H2 comprises a Kabat position Q39E substitution mutation.
104. The multispecific antigen binding protein of any one of claims 50-59 and 64-93, wherein the VH domain of H1 comprises a Kabat position Q39K substitution mutation, wherein the VL domain of L1 comprises a Kabat position Q38E substitution, wherein the VH domain of H2 comprises a Kabat position Q39E substitution mutation, and wherein the VL domain of L2 comprises a Kabat position Q38K substitution mutation.
105. The multispecific antigen binding protein of any one of claims 50-103, wherein each of H1 comprises an Fc region comprising a CH2 and a CH3 domain.
106. The multispecific antigen binding protein of any one of claims 50-105, wherein the Fc region of H1 and/or H2 is human IgG1, human IgG2 or human IgG4 Fc.
107. The multispecific antigen binding protein of claim 50-105, wherein the Fc region of H1 and/or H2 is mouse IgG1, mouse IgG2 or mouse IgG4 Fc.
108. The multispecific antigen binding protein of claim 106 or 107 wherein the CH3 domains of H1 and H2 each meet at an interface, and wherein each of the CH3 domains comprises an amino acid substitution such that the Fc region of H1 preferentially pairs with that of H2 as compared to H1.
109. The multispecific antigen binding protein of claim 108, wherein the amino acid substitutions in the CH3 domains result in greater electrostatic complementarity.
110. The multispecific antigen binding protein of claim 108, wherein the amino acid substitutions in the CH3 domains result in greater steric complementarity.
111. The multispecific antigen binding protein of claim 108,
wherein the CH3 domain of H1 is altered, so that within the CH3/CH3 interface, one or more amino acid residues are replaced with one or more amino acid residues having a larger side chain volume, thereby generating a protuberance on the surface of the CH3 domain of H1 that interacts with the CH3 domain of H2 and

wherein the CH3 domain of H2 is altered so that within the CH3/CH3 interface one or more amino acid residues are replaced with amino acid residues having a smaller side chain volume, thereby generating a cavity within on the surface of the CH3 domain of H2 that interacts with the CH3 domain of H1.

112. The multispecific antigen binding protein of claim 108

wherein the CH3 domain of H2 is altered, so that within the CH3/CH3 interface, one or more amino acid residues are replaced with one or more amino acid residues having a larger side chain volume, thereby generating a protuberance on the surface of the CH3 domain of H2 that interacts with the CH3 domain of H1

and

wherein the CH3 domain of H1 is altered so that within the CH3/CH3 interface, one or more amino acid residues are replaced with amino acid residues having a smaller side chain volume, thereby generating a cavity on the surface of the CH3 domain of H1 that interacts with the CH3 domain of H2.

113. The multispecific antigen binding protein of claim 111 or 112, wherein the protuberance is a knob mutation.

114. The multispecific binding protein of claim 113, wherein the knob mutation comprises T366W (EU numbering).

115. The multispecific antigen binding protein of claim 111 or 112, wherein the cavity is a hole mutation.

116. The multispecific antigen binding protein of claim 115, wherein the hole mutation comprises at least one, at least two or all three of T366S, L368A, and Y407V (EU numbering).

117. The multispecific antigen binding protein of any one of claims 1-116, wherein H1 preferentially pairs with L1 as compared to L2, and wherein H2 preferentially pairs with L2 as compared to L1.

118. The multispecific antigen binding protein of any one of claims 1-117, wherein the first antigen and the second antigen are the same.

119. The multispecific antigen binding protein of claim 1-118, wherein the first heavy chain/light chain pair and the second heavy chain/light chain pair each bind to a different epitope on the same antigen.

120. The multispecific antigen binding protein of any one of claims 1-117, wherein the first antigen and the second antigen are different.

121. A pharmaceutical composition comprising the multispecific antigen binding protein of any one of claims 1-120 and a pharmaceutically acceptable carrier.
122. A method of treating a disease in an individual, comprising administering to the individual an effective amount of the pharmaceutical composition of claim 121.
123. Isolated nucleic acids(s) encoding at least one polypeptide sequence of the multispecific antigen binding protein of any one of claims 1-122.
124. A vector comprising the nucleic acid(s) of claim 123.
125. An isolated host cell comprising the nucleic acid(s) of claim 123 or the vector of claim 124.
126. The host cell of claim 125, wherein the host cell is a prokaryotic host cell, and E. coli cell, a eukaryotic host cell, a yeast cell, a mammalian cell, or a CHO cell.
127. A method of producing the multispecific antigen binding protein of any one of claims 1-120, comprising:
- (a) obtaining the H1, H2, L1, and L2 polypeptides;
 - (b) allowing H1 to pair preferentially with L1 as compared to L2, and H2 to pair preferentially with L2 as compared to L1 so as to form the multispecific antigen binding protein.
128. A method of producing the multispecific antigen binding protein of any one of claims 1-120, comprising:
- (a) introducing a set of polynucleotides encoding H1, L1, H2, and L2 into a host cell; and
 - (b) culturing the host cell to produce the multispecific antigen binding protein.
129. The method of claim 128, wherein the set of polynucleotides encoding H1, L1, H2, and L2 are introduced into the host cell at a predetermined ratio.
130. The method of claim 129, further comprising determining an optimal ratio of the polynucleotides for introduction into the host cell.
131. The method of any one of claims 127-130 wherein the multispecific antigen binding protein is produced with a relative yield of 60% or higher.
132. The method of any one of claims 127-131 wherein the multispecific antigen binding protein is produced with a relative yield of at least about 70%, at least about 71%, at least about 71%, at least about 72%, at least about 73%, at least about 74%, at least about 75%, at least about 76%, at least about 77%, at least about 78%, at least about 79%, at least about 80%, at least about 81%, at least about 82%, at least about 83%, at least about 84%, at least about 85%, at least about 86%, at least about 87%, at least about

88%, at least about 89%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 99%, or more than about 99%.

133. A method of producing a multispecific antigen binding protein comprising culturing the host cell of any one of claims 125-126 and producing the multispecific antigen binding protein.

134. The method of any one of claims 127-133, further comprising recovering the multispecific antigen binding protein.

135. The multispecific antigen binding protein produced by the methods of any one of claims 127-134.

136. A library comprising a plurality of polynucleotides encoding a plurality of multispecific antigen binding proteins of any one of claims 1-120.

137. A method of screening for a multispecific antigen binding protein that binds to a first antigen and a second antigen, comprising:

- (a) obtaining a plurality of multispecific antigen binding proteins from the library of claim 123;
- (b) assaying for binding of the plurality of multispecific antigen binding proteins to the first and second antigen; and
- (c) identifying the multispecific antigen binding protein that binds to the first and second antigen.

138. A computer readable medium for evaluating a multispecific antigen binding protein comprising 1) a first heavy chain/light chain pair binding to a first antigen which comprises a first heavy chain sequence (H1) and a first light chain sequence (L1), and 2) a second heavy chain/light chain pair binding to a second antigen which comprises a second heavy chain sequence (H2) and a second light chain sequence (L2), wherein each H1 and H2 comprises a heavy chain variable domain (VH) and a heavy chain constant domain (CH1), and each L1 and L2 comprises a light chain variable domain (VL) and a light chain constant domain (CL); comprising:

- a) a dataset comprising data representing amino acid substitutions in H1, L1, H2, and L2, wherein at least one of the amino acid substitutions in the CH1 domain of H1 comprises an amino acid substitution at EU position F170 or L128 and wherein the CL domain comprises an amino acid substitution at EU position S176 or F118 and L135; and/or
- b) a dataset comprising data representing amino acid substitutions in H1, L1, H2, and L2, wherein at least one of the amino acid substitutions in the CH1 domain of H1 comprises an amino acid substitution at EU position S183, and wherein the CL domain of L1 comprises an amino acid substitution at EU position V133; and

(b) computer executable code for determining the likelihood that H1 will preferentially pair with L1 as compared to L2 and/or H2 will preferentially pair with L2 as compared to L1.

139. The computer readable medium of claim 138, wherein the at least one of the amino acid substitutions in the CH1 domain of H1 comprises an amino acid substitution at EU position F170 or L128 and V185.

FIG. 1A

FIG. 1B

FIG. 1A

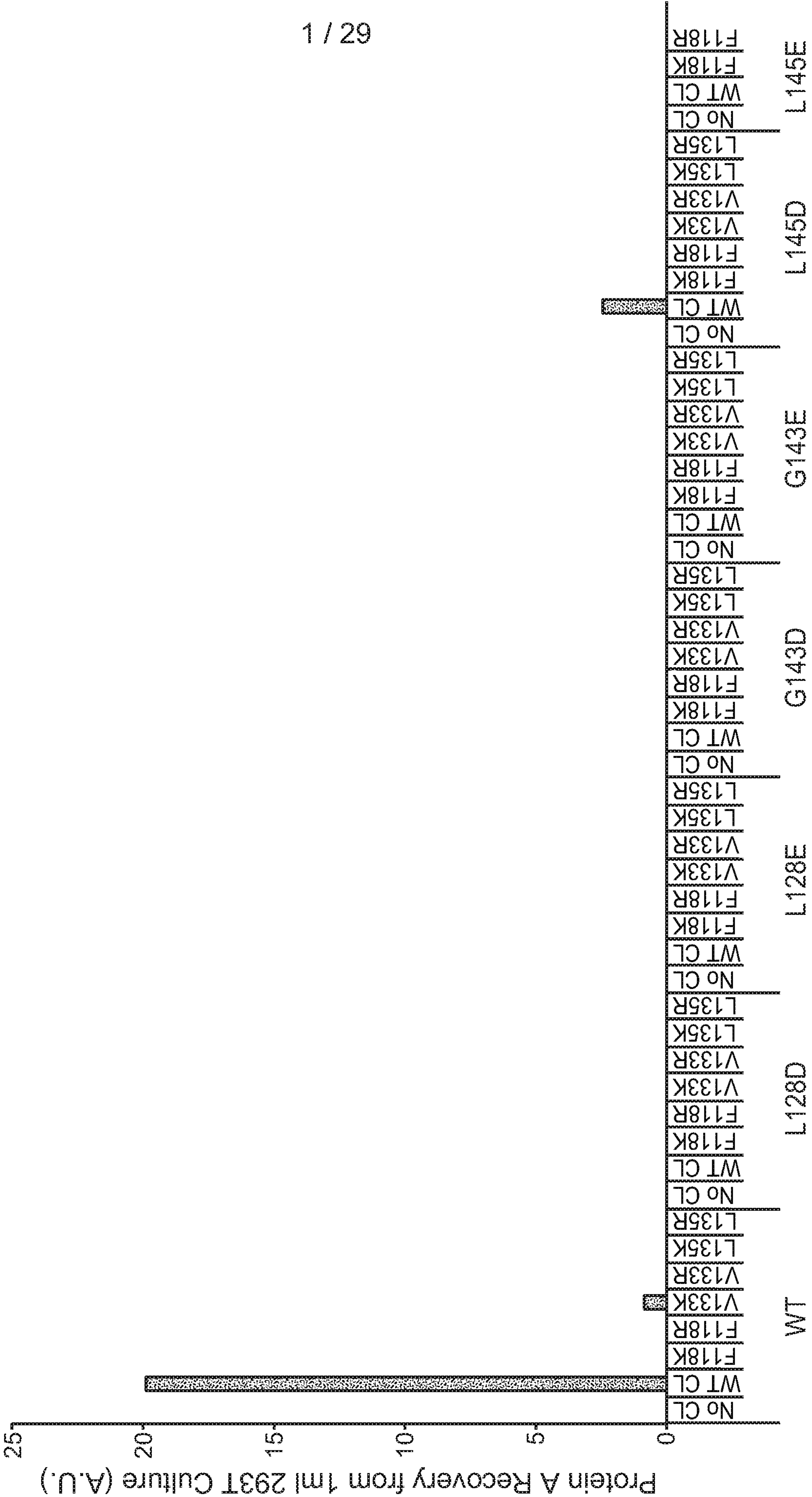
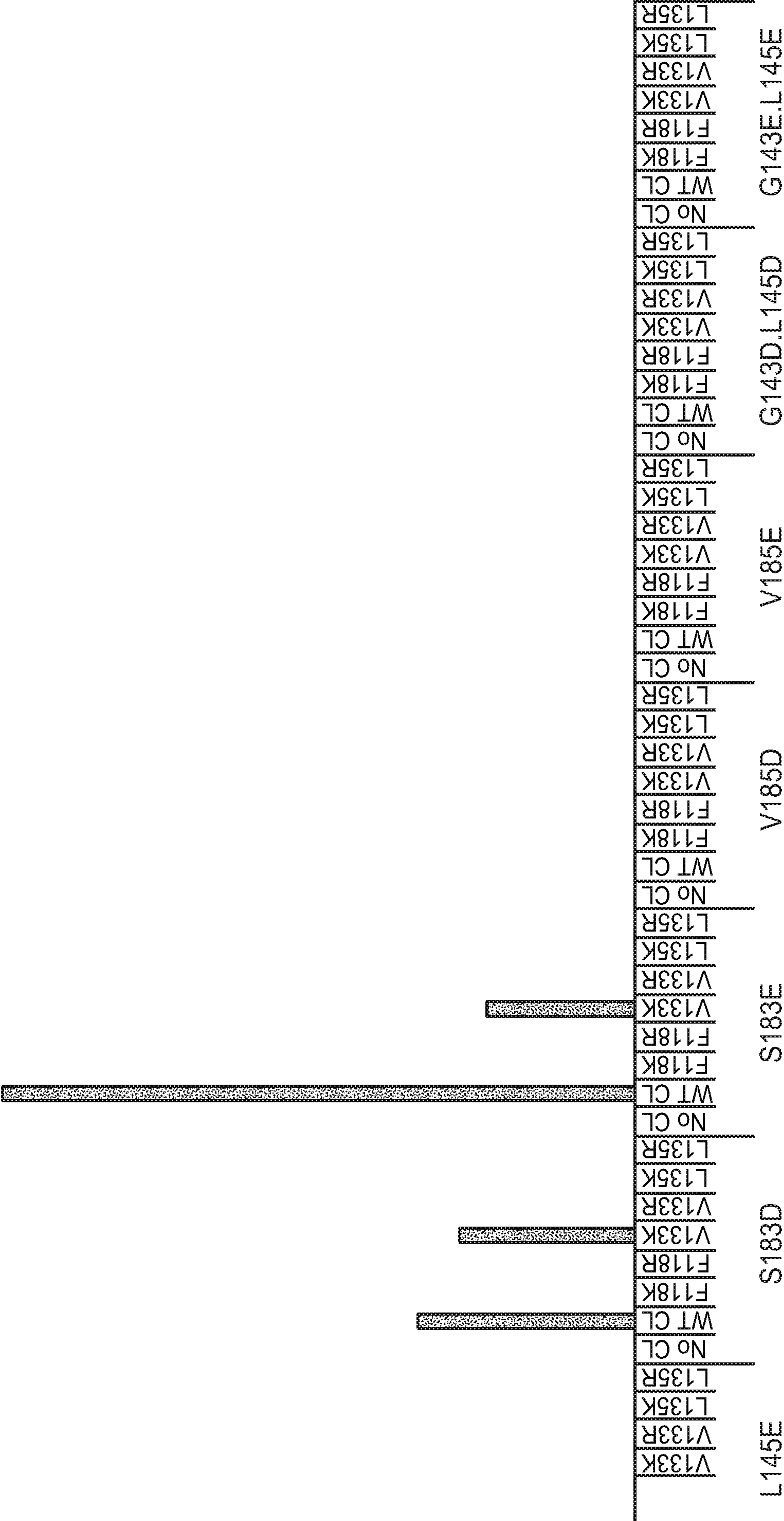


FIG. 1B



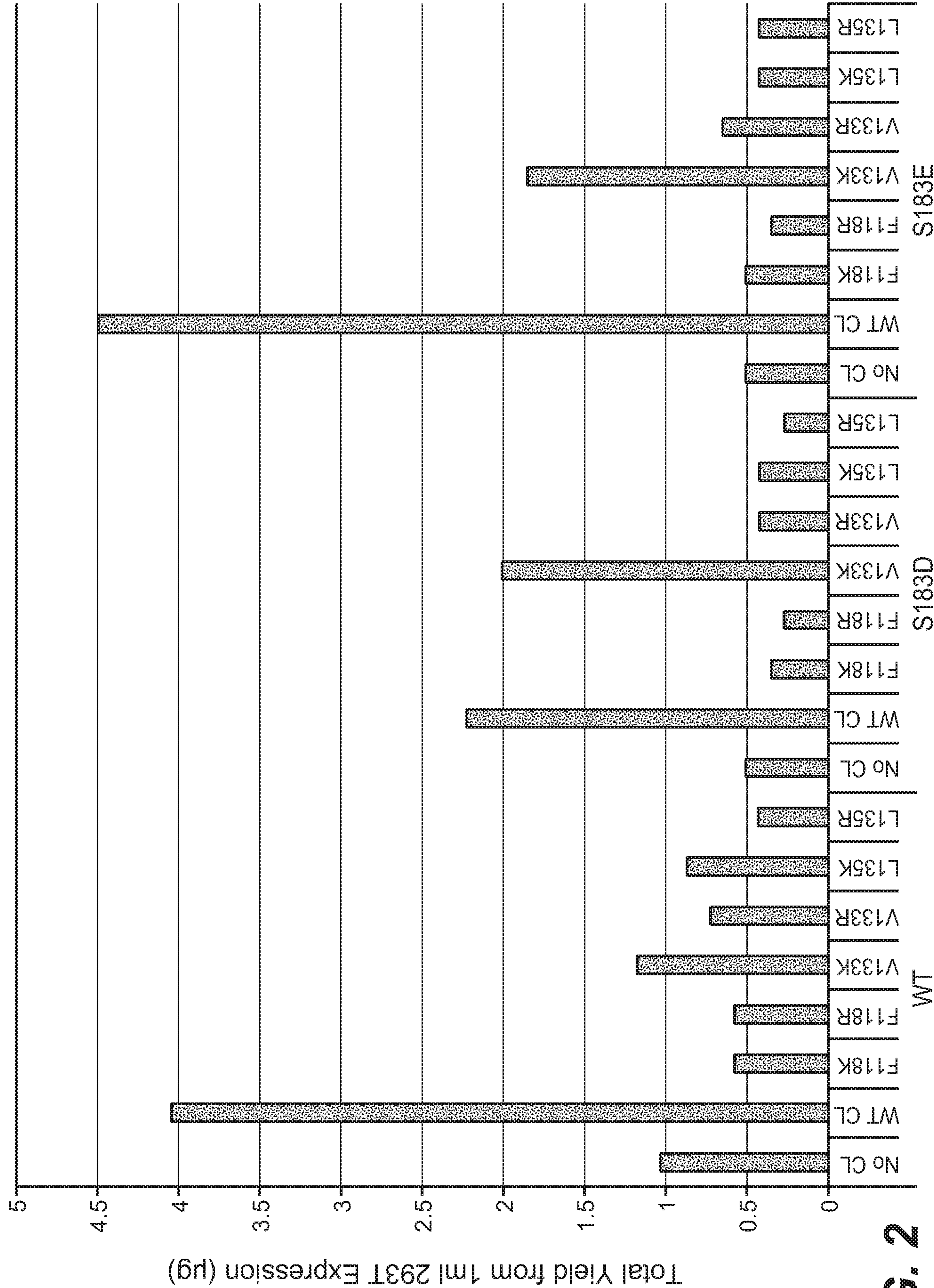


FIG. 2

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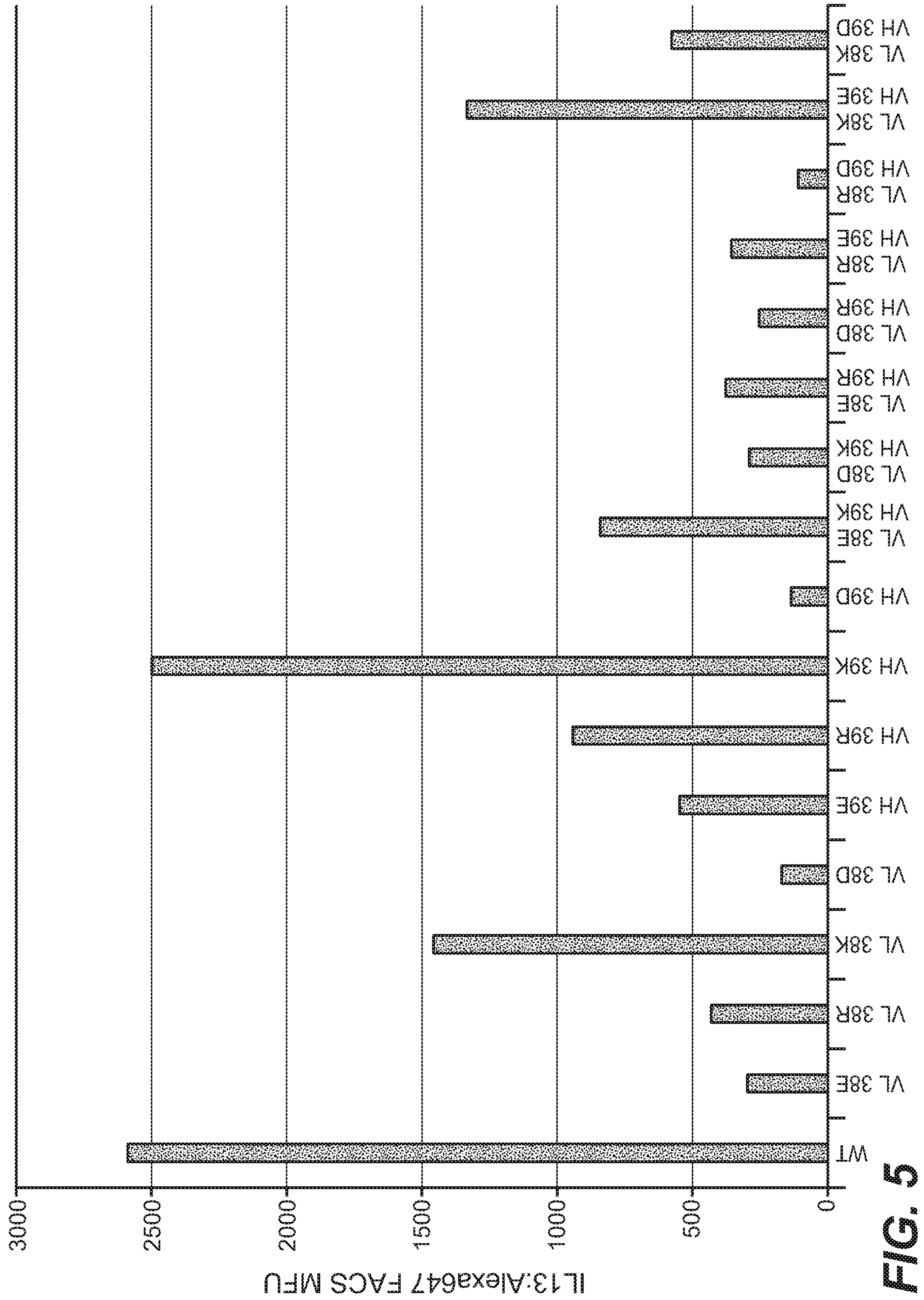


FIG. 3

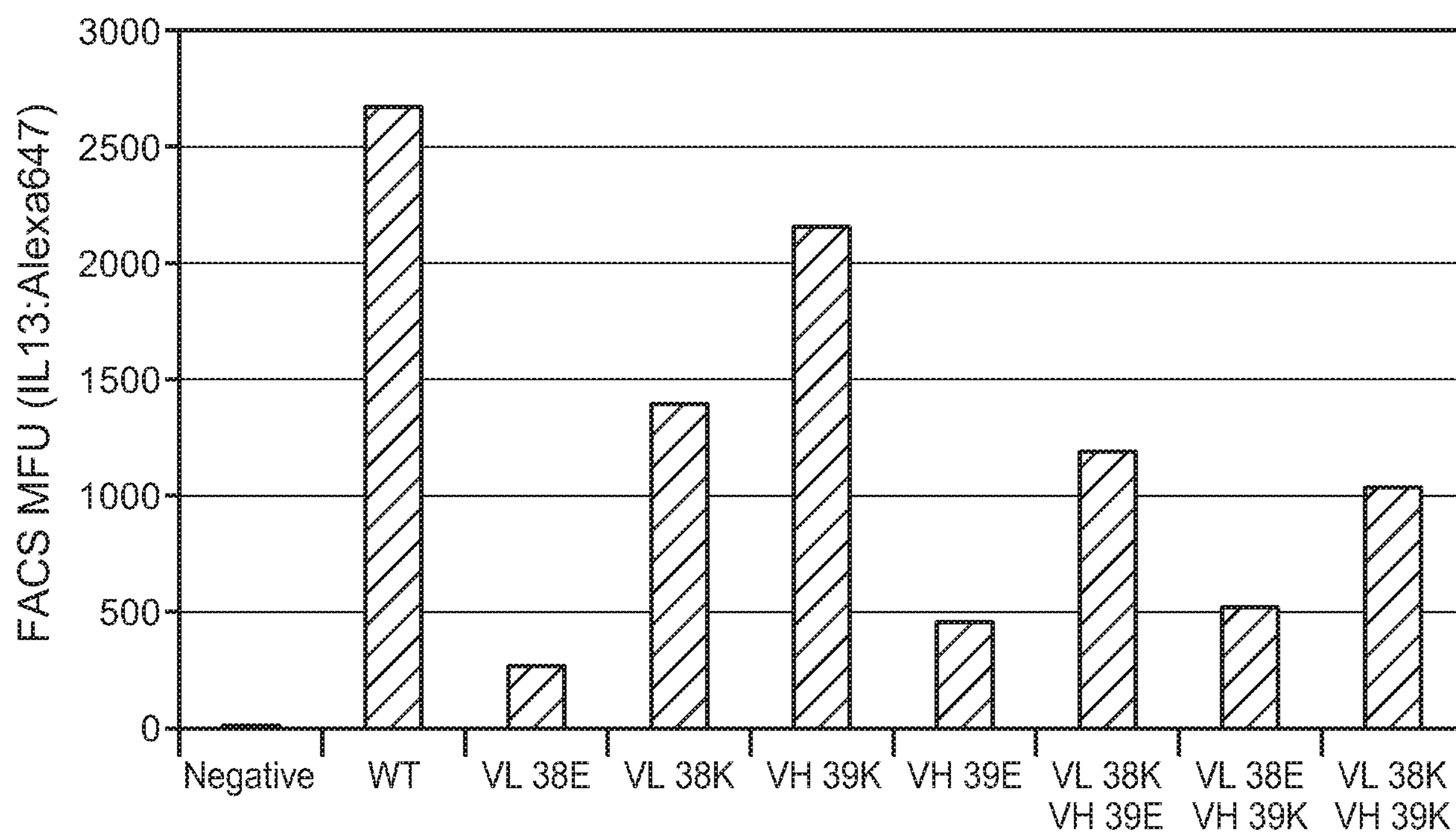
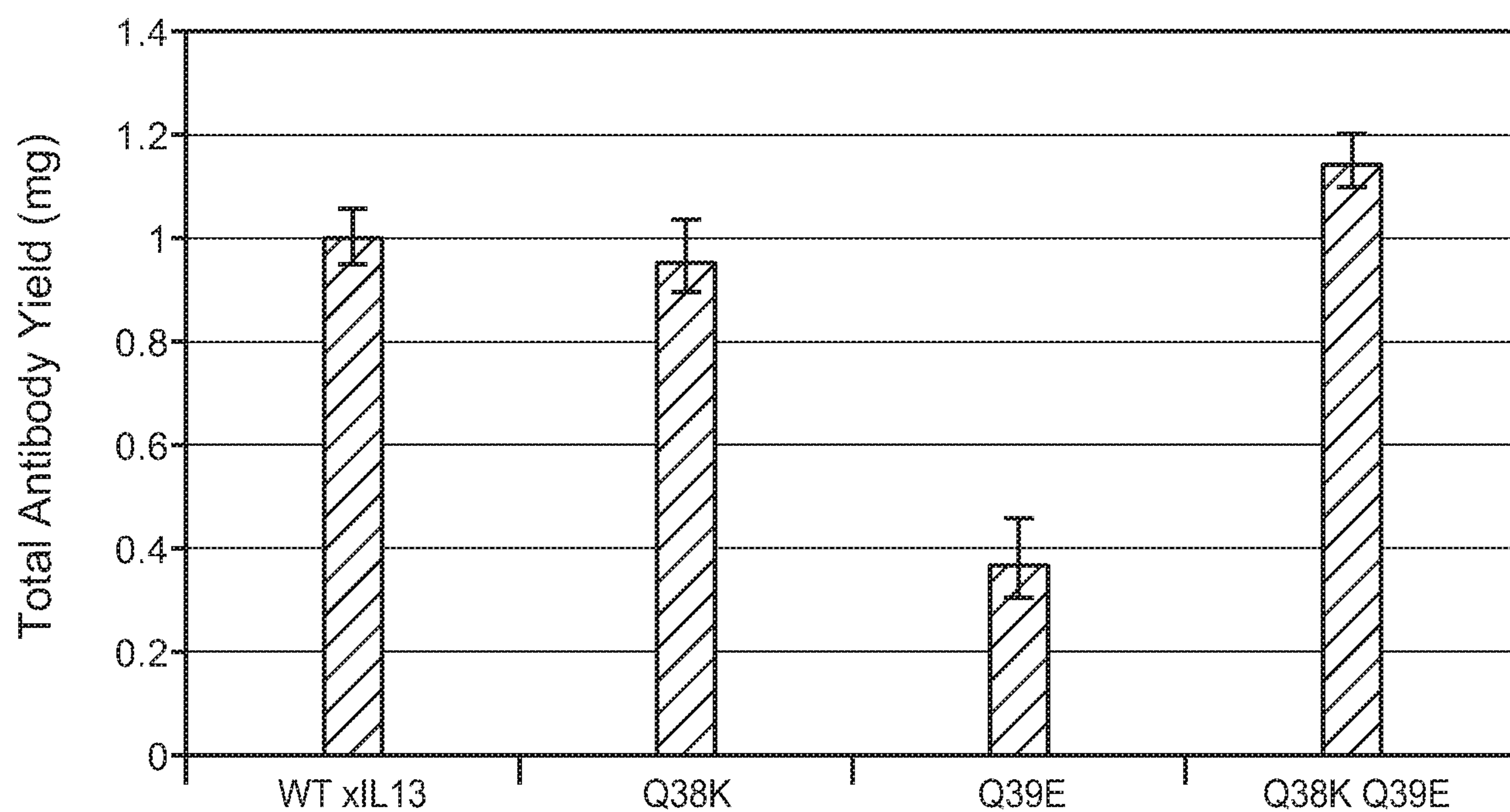
Yield (mg)/30ml 293T		Heavy Chain											
	WT	S183A	S183T	S183V	S183Y	S183F	S183H	S183N	S183D	S183E	S183R	S183K	
WT	2.8	2.7	2.9	2.8	3.2	3.2	1.8	1.6	0.3	2.0	0.2	0.7	
V133E	1.7	2.3	3.6	4.5	2.9	4.4	0.1	0.0	0.0	0.0	0.2	0.2	
V133S	1.4	1.9	3.0	3.0	3.4	3.8	1.1	0.4	0.0	0.3	0.2	0.2	
V133L	1.8	2.6	2.3	2.9	3.2	3.0	1.8	1.1	0.2	1.0	0.1	0.2	
V133W	1.1	2.2	2.6	2.8	3.4	3.4	0.8	0.2	0.0	0.0	0.1	0.1	
V133K	0.4	1.4	2.6	2.2	2.4	3.6	0.0	0.0	0.4	0.2	0.1	0.1	
V133R	0.2	1.0	1.8	2.2	2.1	3.1	0.0	0.0	0.0	0.0	0.1	0.1	
V133D	0.3	1.1	2.0	2.0	1.7	3.2	0.1	0.0	0.0	0.0	0.2	0.2	

FIG. 4

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**FIG. 6****FIG. 7**

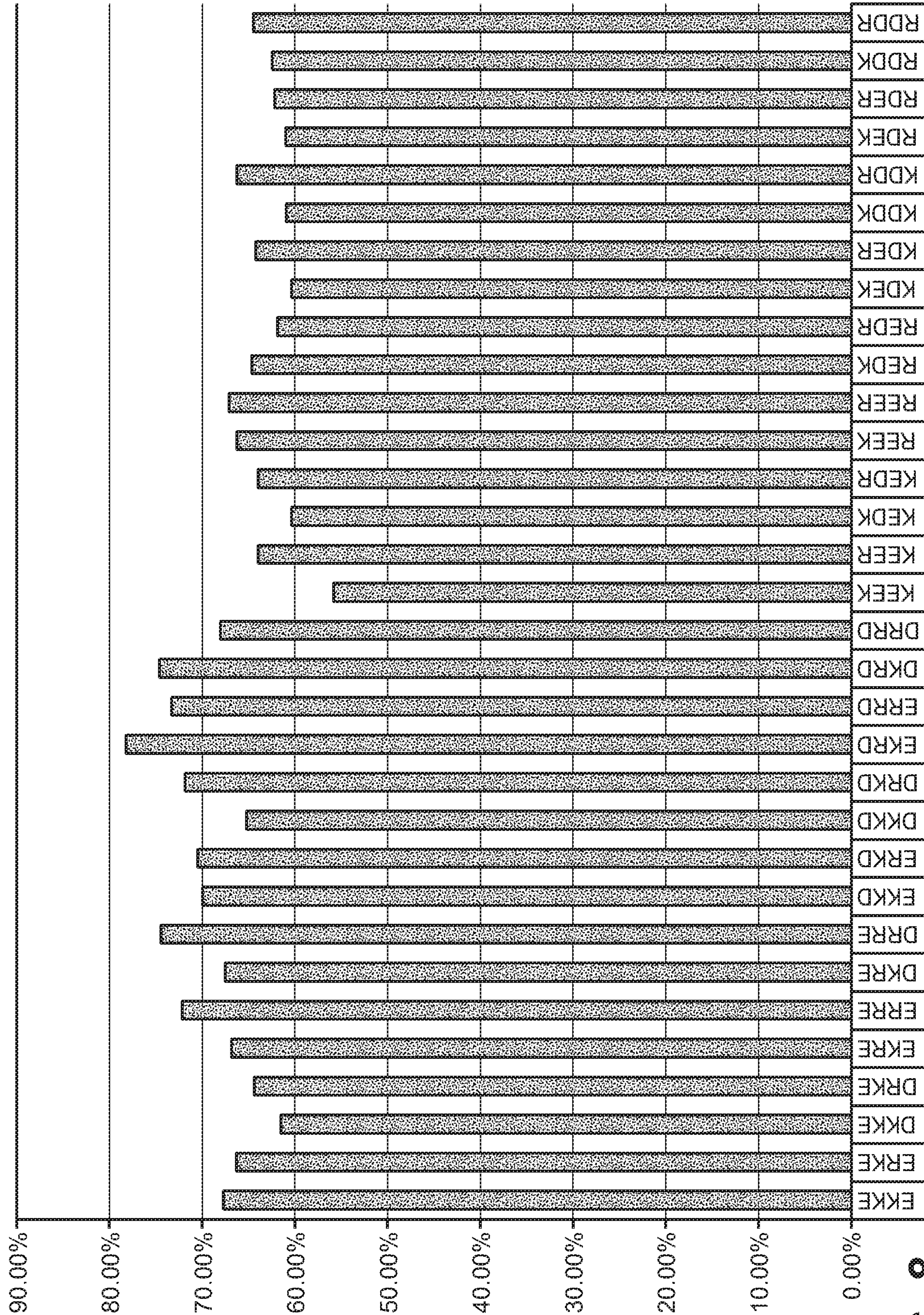


FIG. 8

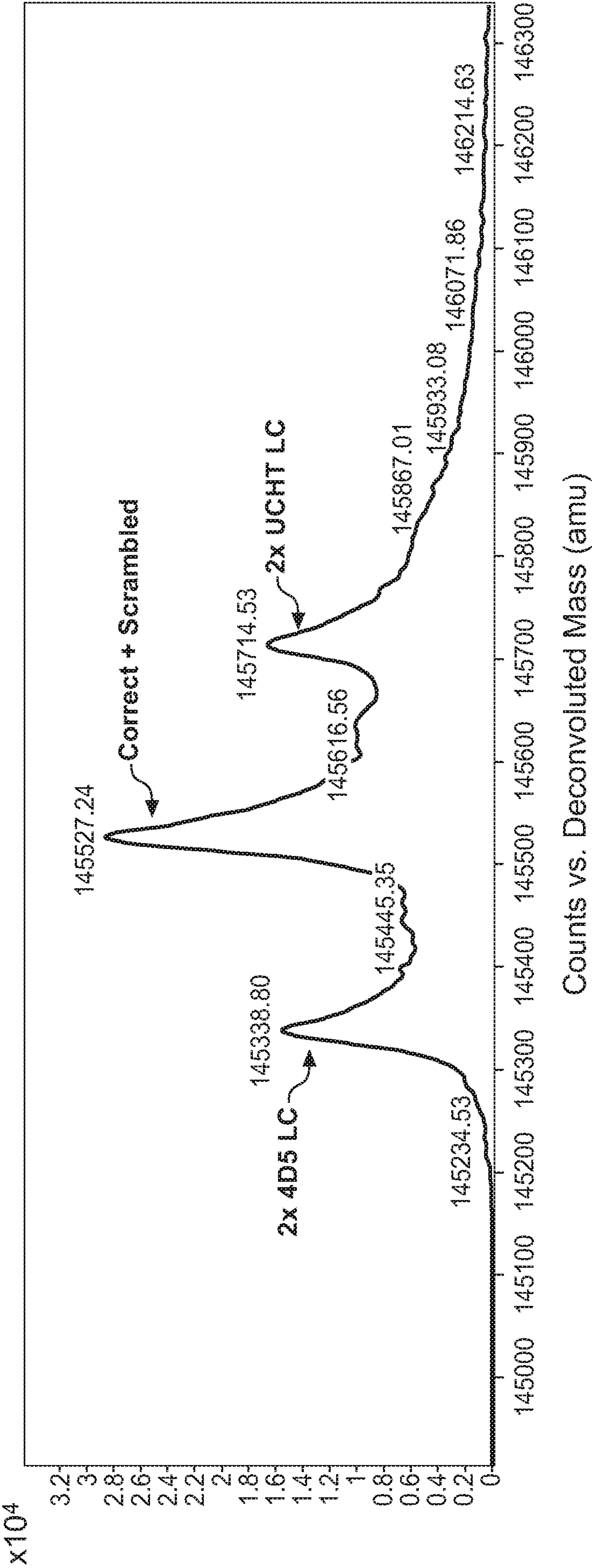


FIG. 9A

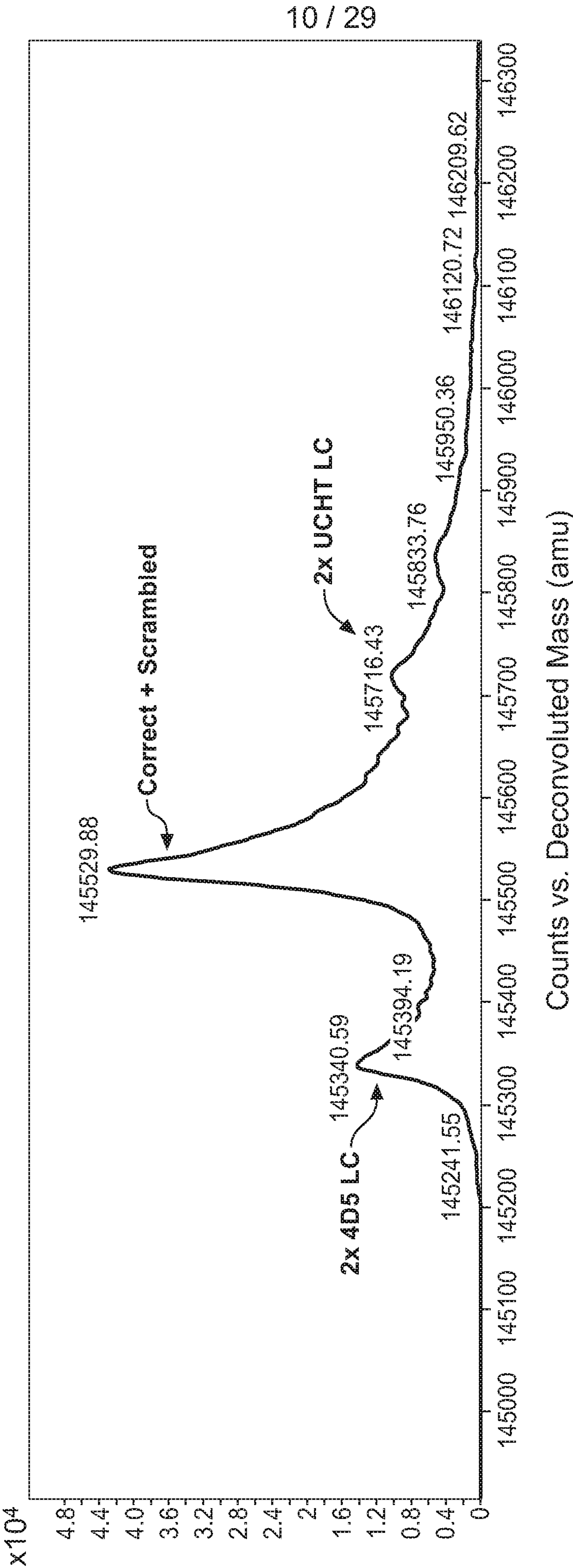
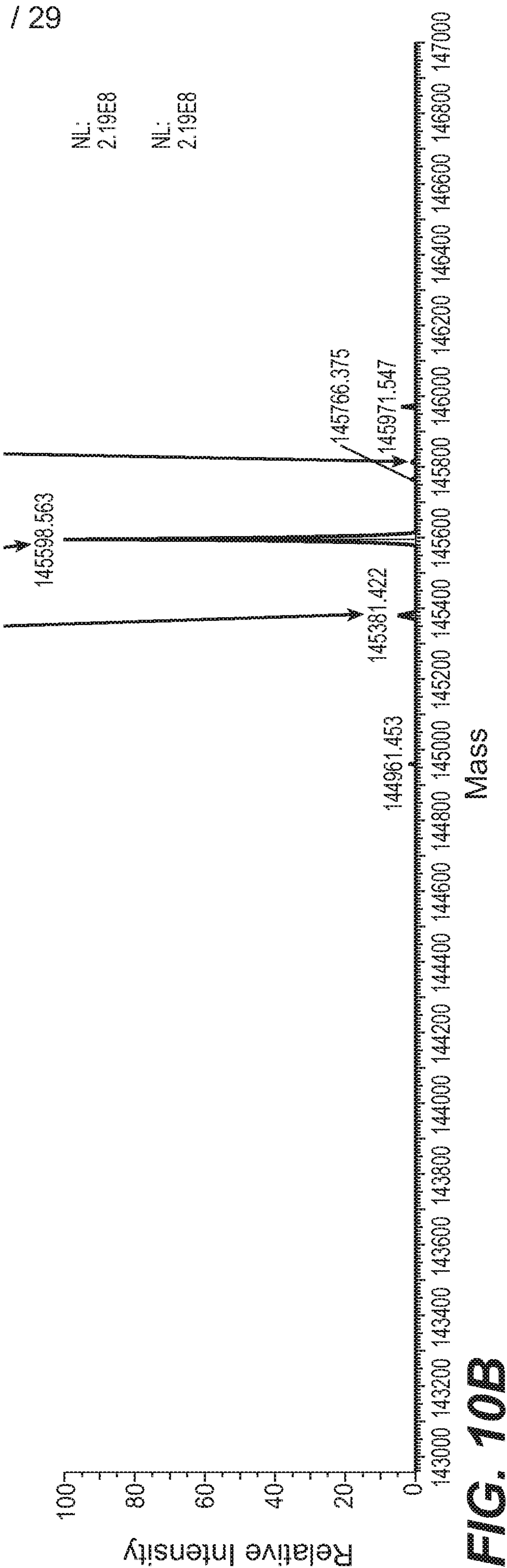
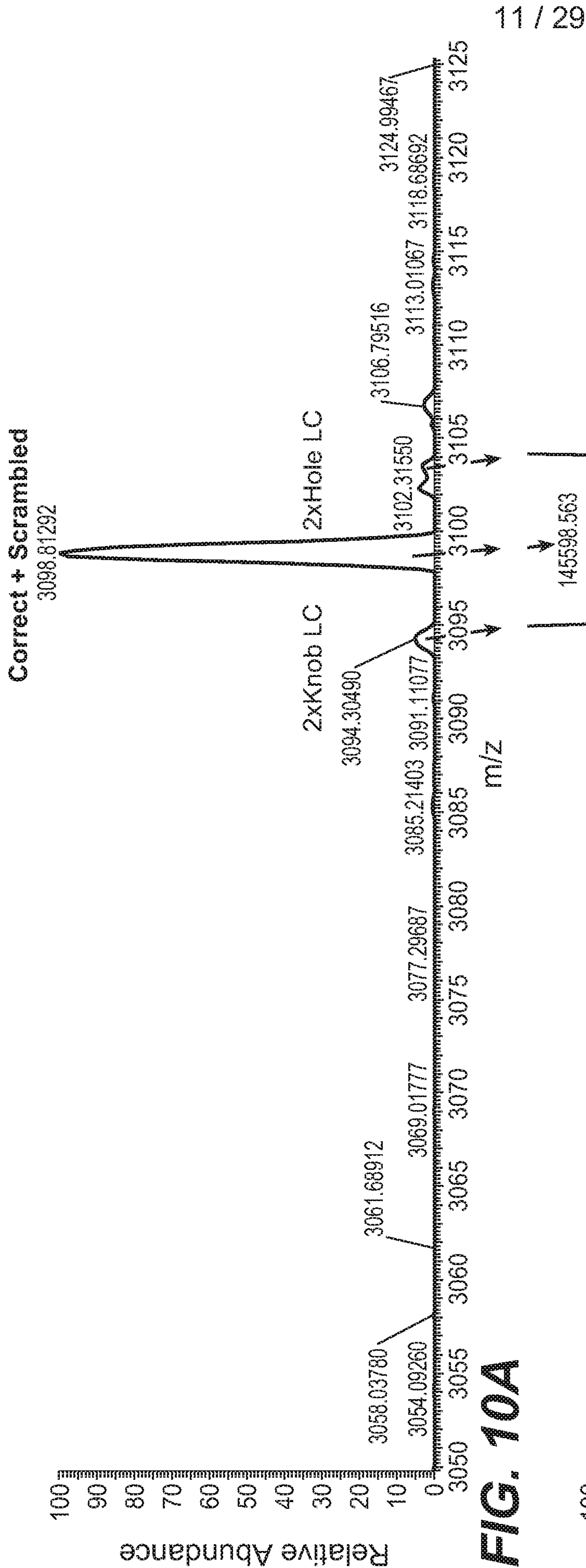
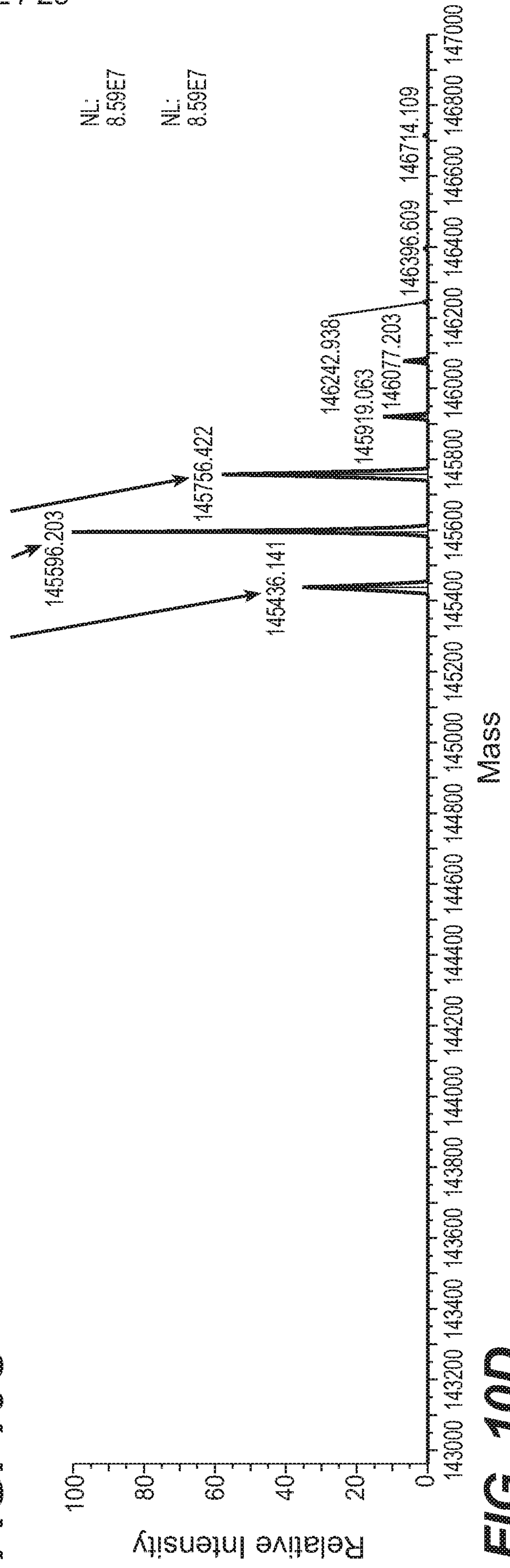
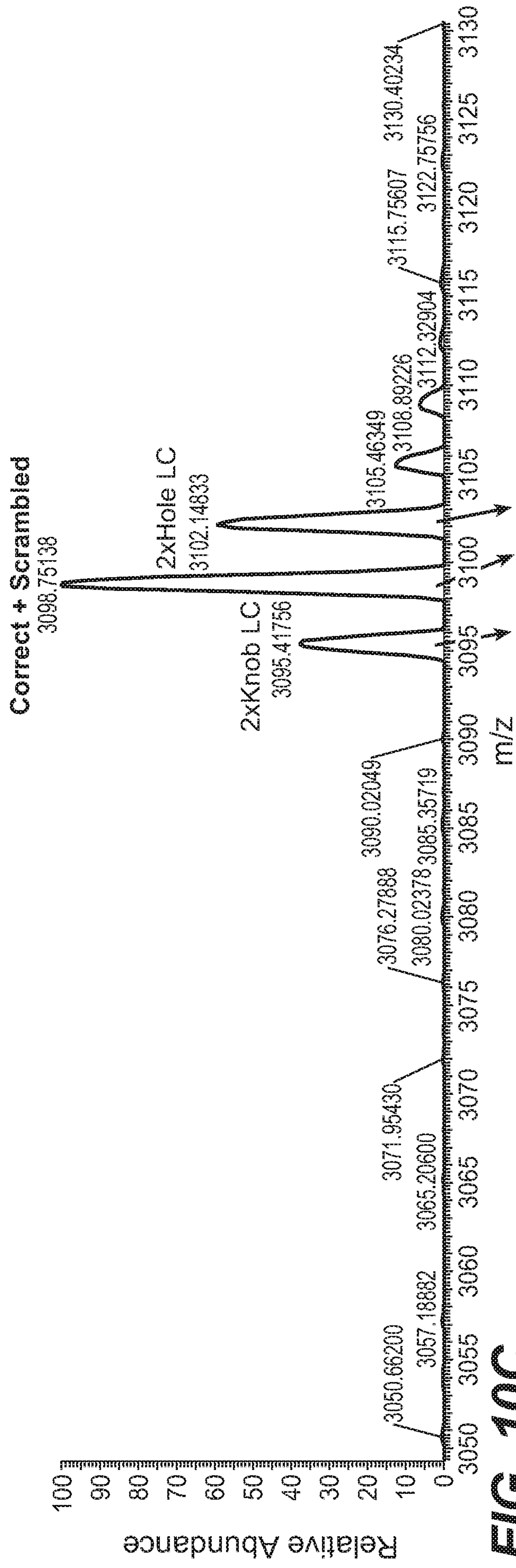
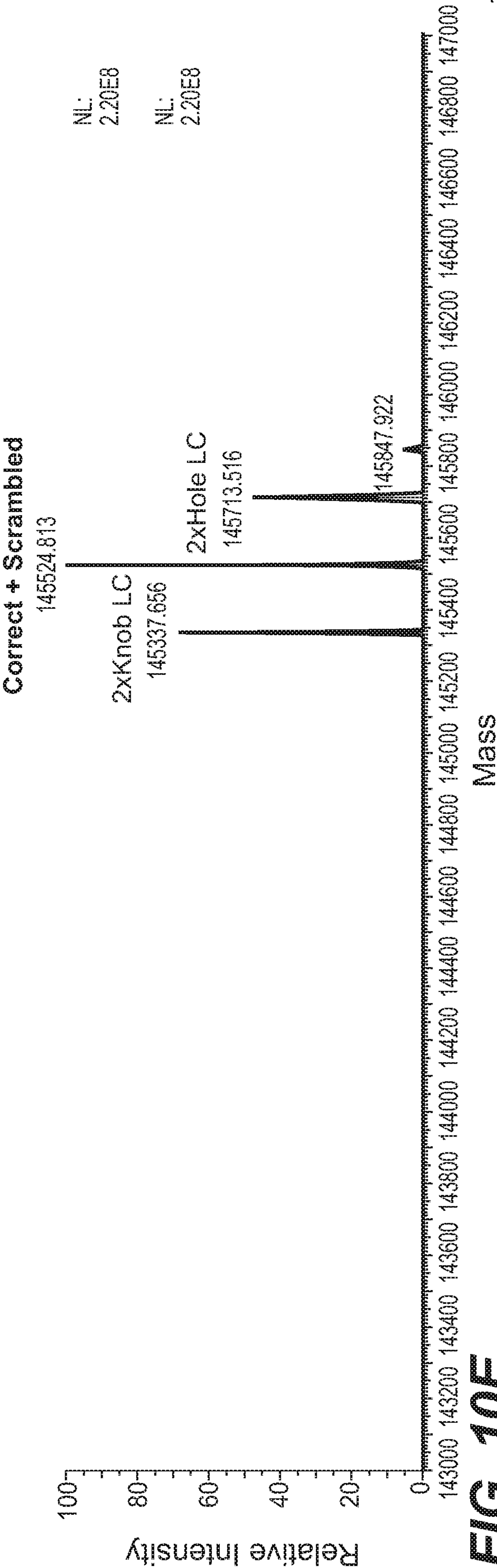


FIG. 9B



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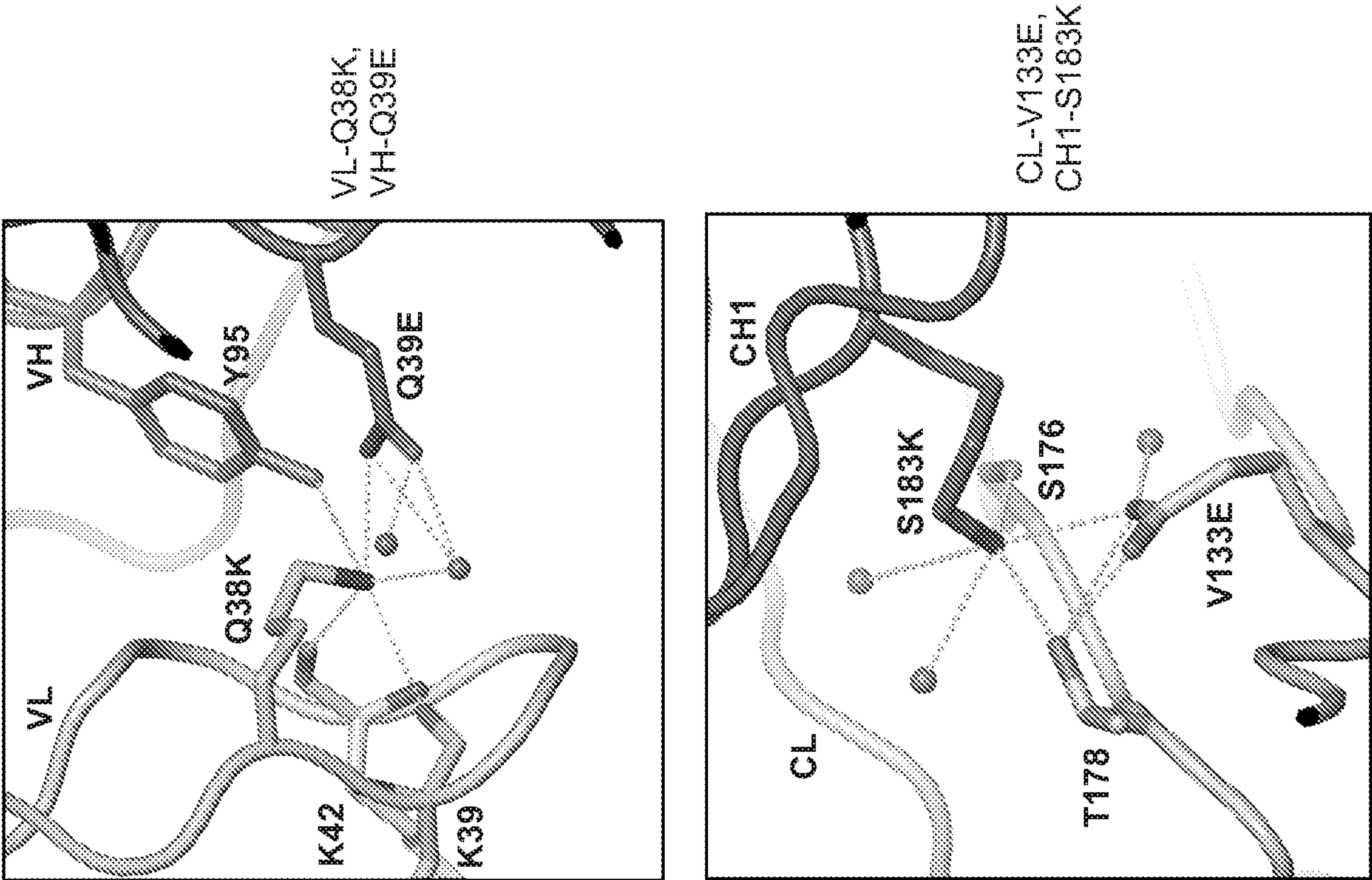


FIG. 11B

FIG. 11C

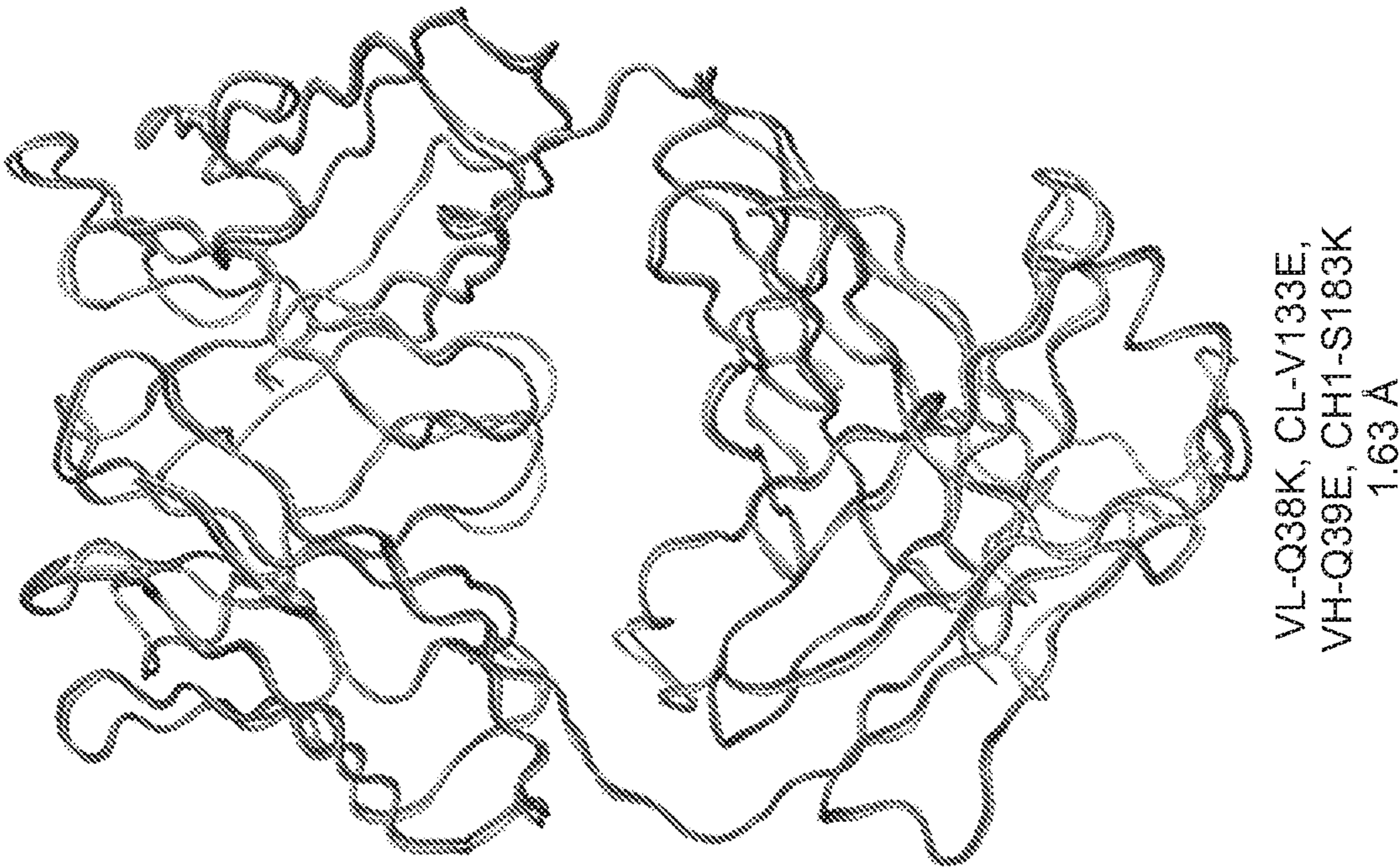


FIG. 11A

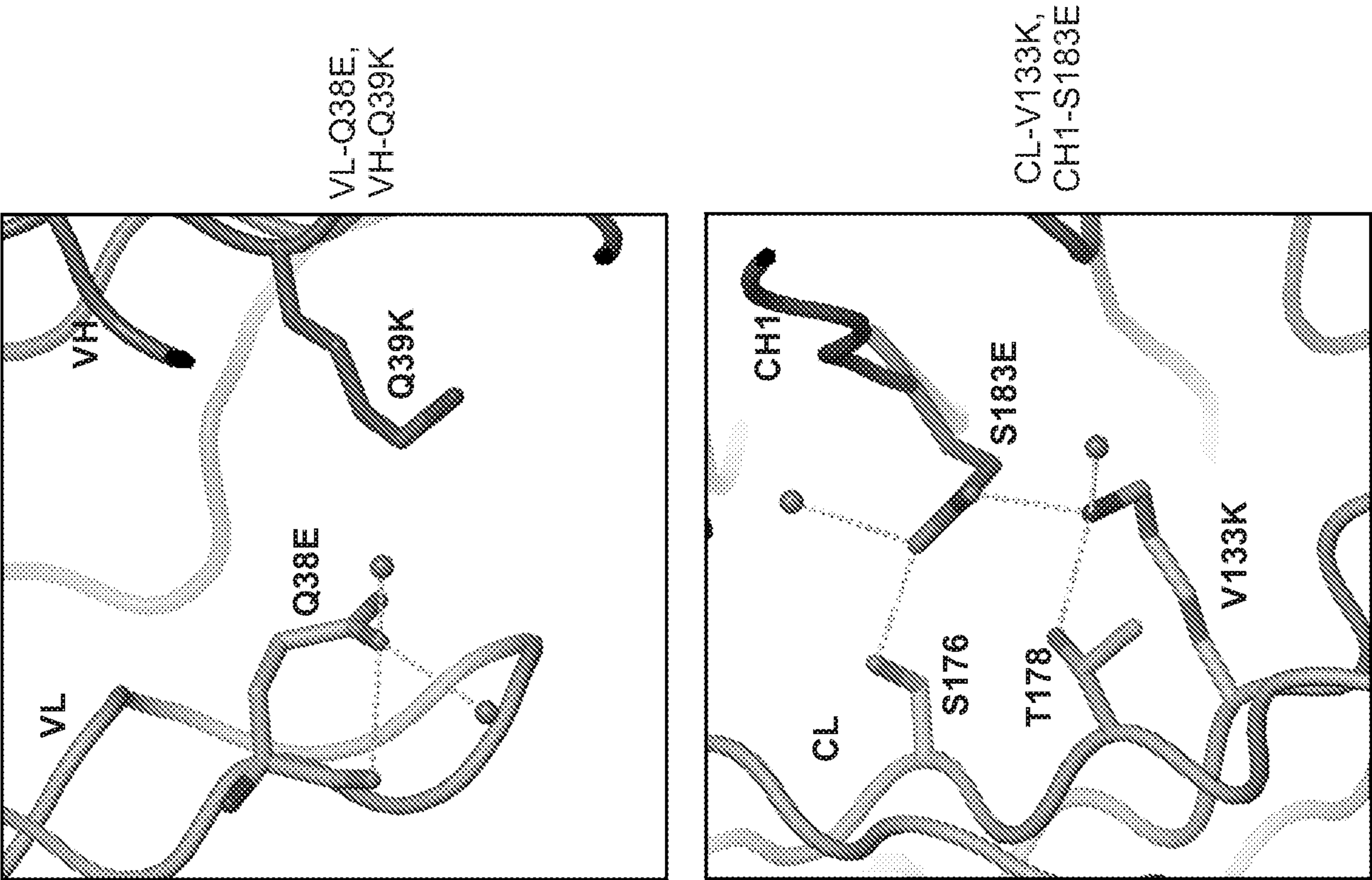


FIG. 12B

FIG. 12C

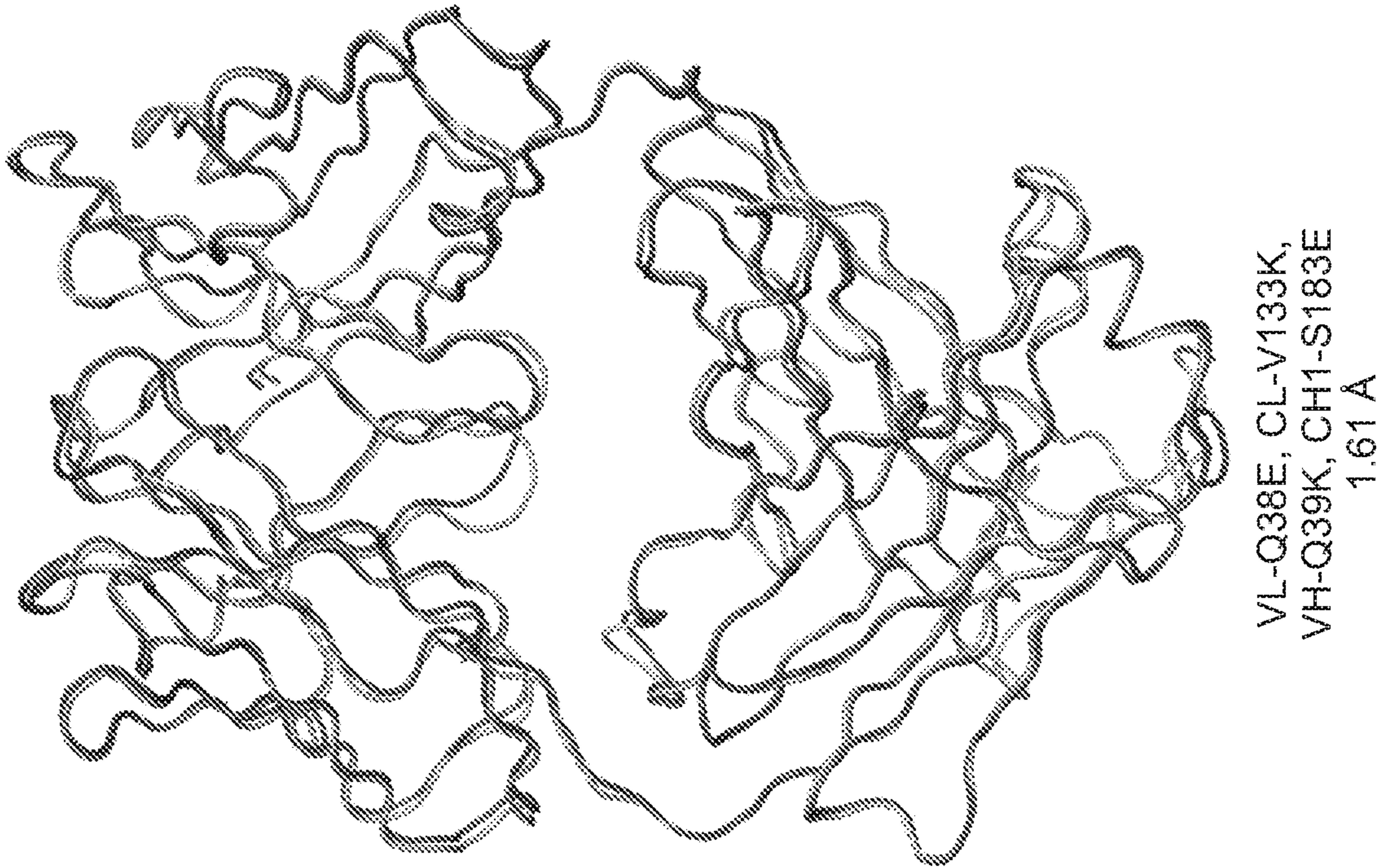


FIG. 12A

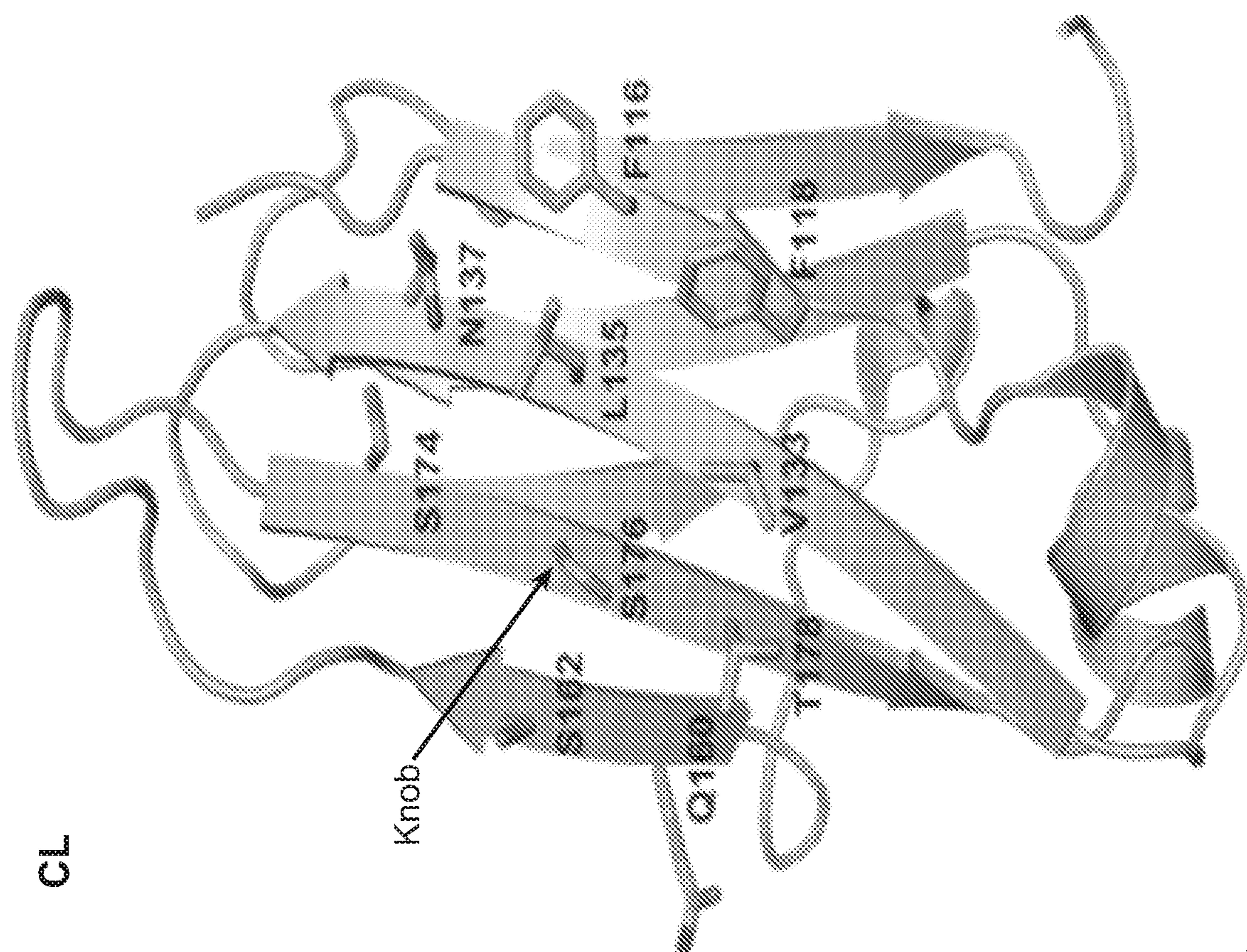
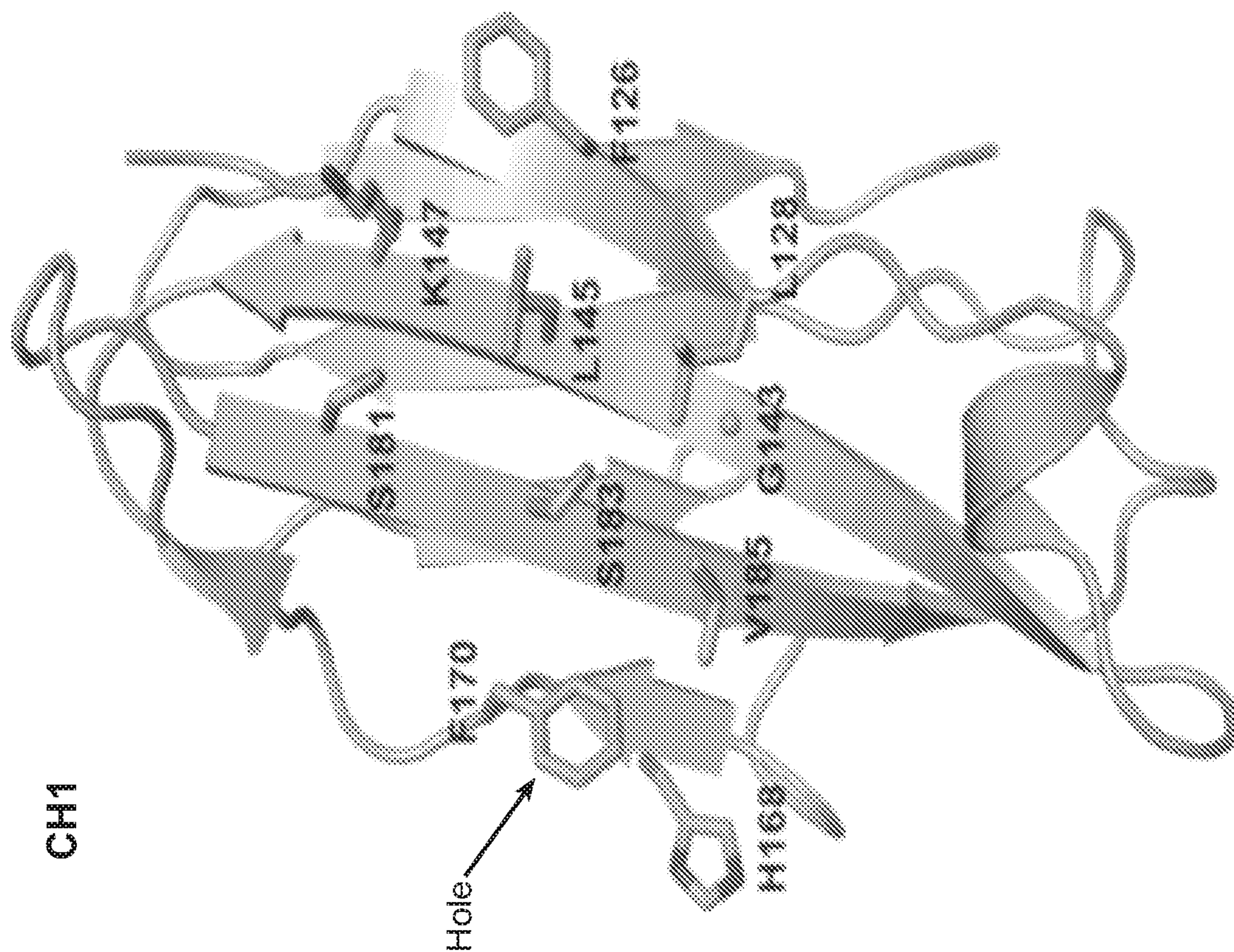
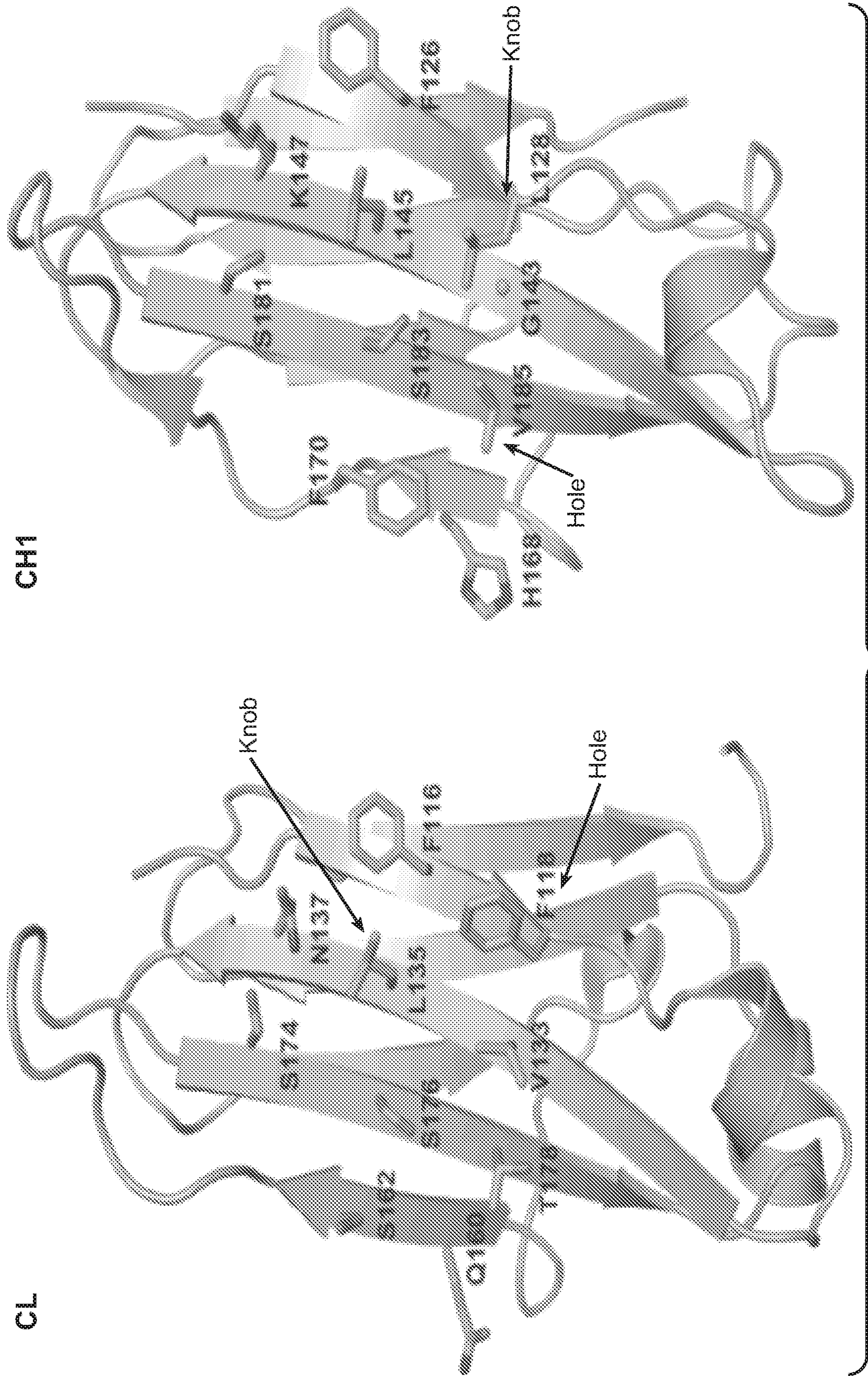


FIG. 13A



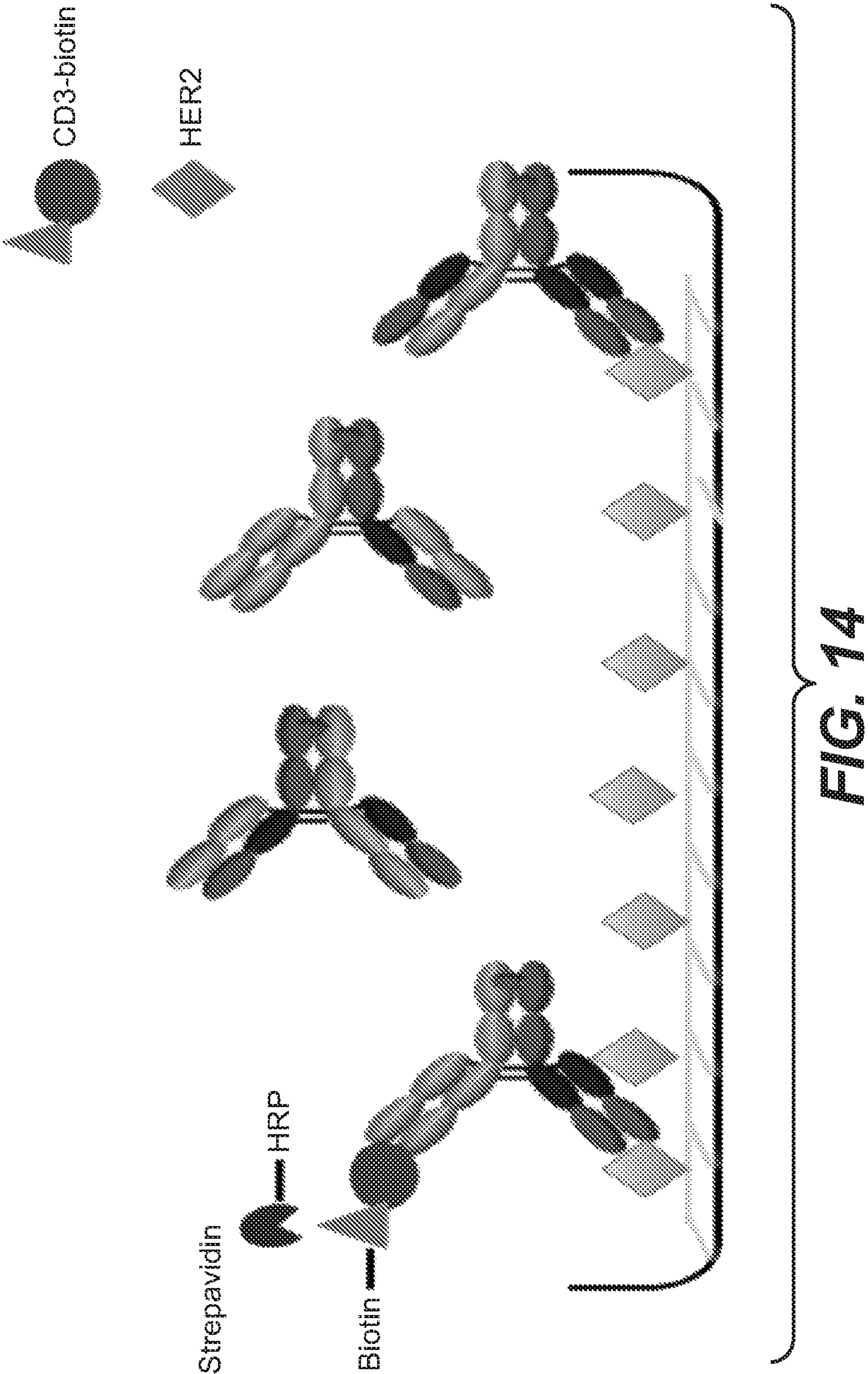
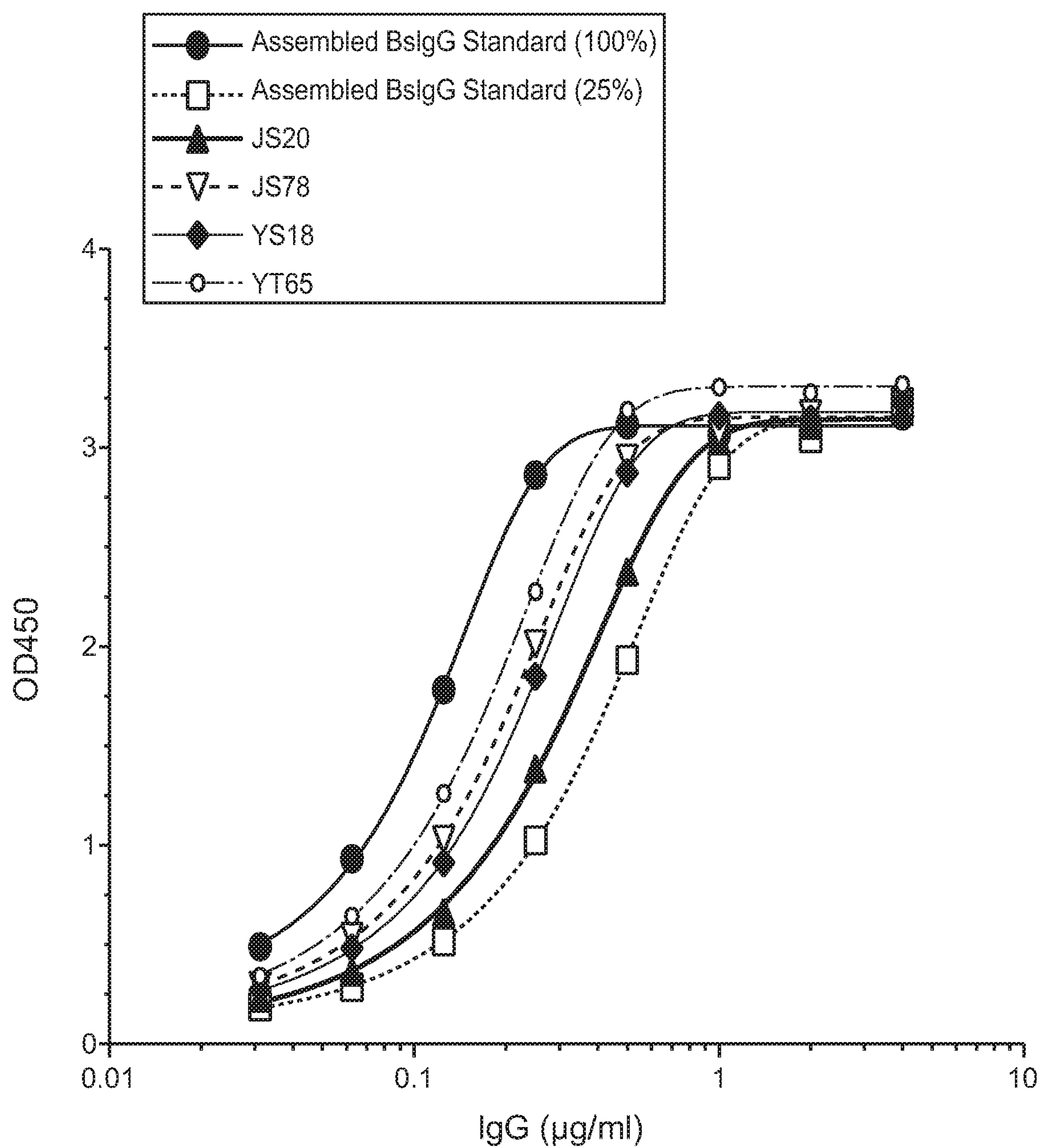


FIG. 14

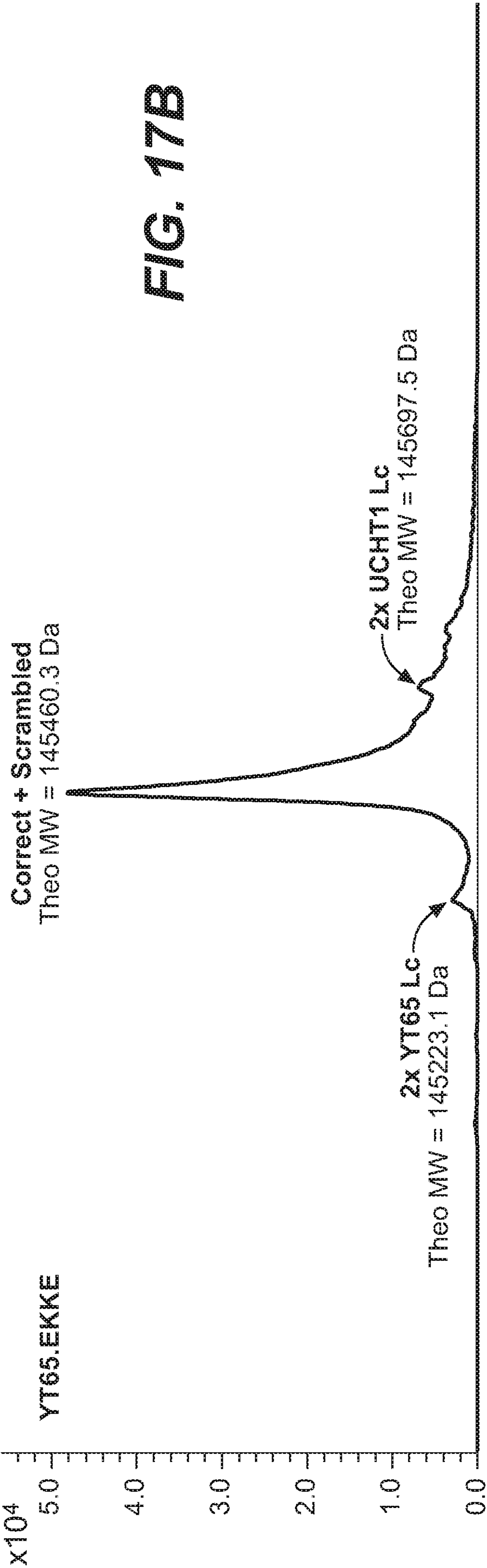
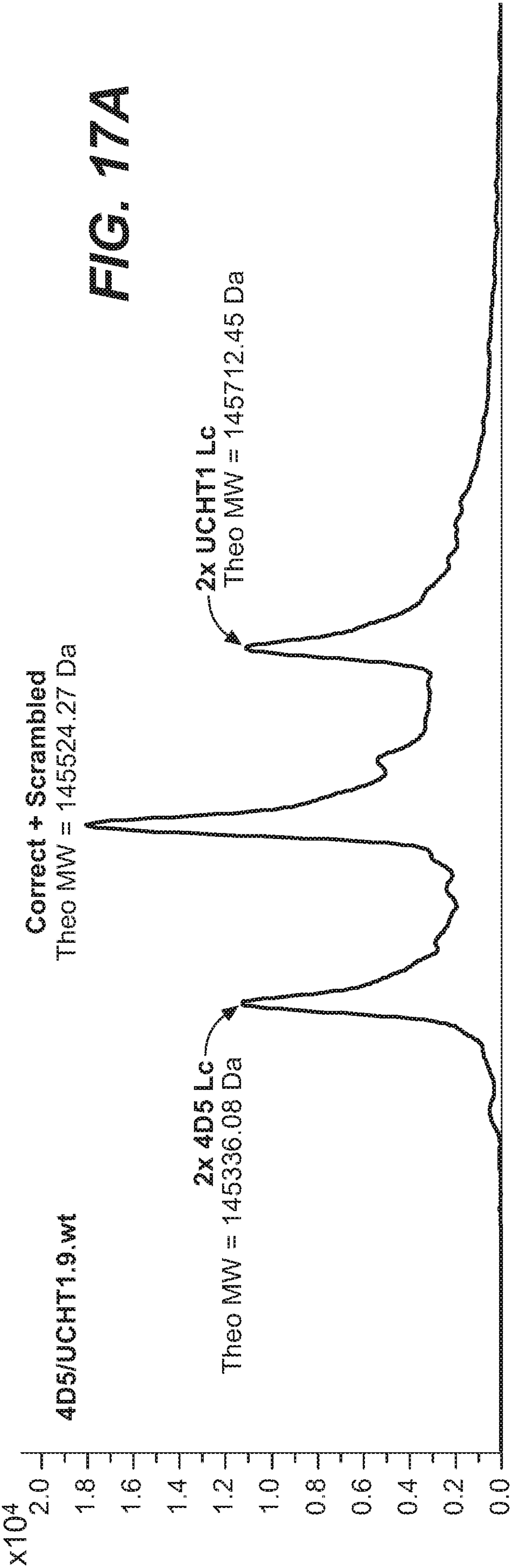
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**FIG. 15**

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4D5wt-LC	116	118	131	133	135	162	164	174	176	178
GQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL										
JS20	V.....	T.A.Y.....	T.A.F.....	T.A.F.....	T.A.F.....	M.S.....	M.L.....	A.F.V.....	A.F.V.....	A.F.V.....
JS78	V.....	T.A.F.....	T.A.F.....	T.A.F.....	T.A.F.....	M.S.....	M.L.....	A.F.V.....	A.F.V.....	A.F.V.....
JT20	V.....	T.A.F.....	T.A.F.....	T.A.F.....	T.A.F.....	M.S.....	M.L.....	A.F.V.....	A.F.V.....	A.F.V.....
JT25	V.....	T.A.F.....	T.A.F.....	T.A.F.....	T.A.F.....	M.S.....	M.L.....	A.F.V.....	A.F.V.....	A.F.V.....
YS8	A.....	I.V.....	I.V.....	I.V.....	I.V.....	M.....	M.....	A.F.V.....	A.F.V.....	A.F.V.....
YS18	A.....	D.....	D.....	D.....	D.....	A.....	A.....	A.F.V.....	A.F.V.....	A.F.V.....
YT65	A.....	V.....	V.....	V.....	V.....	M.....	M.....	A.F.V.....	A.F.V.....	A.F.V.....
YT34	A.....	V.....	V.....	V.....	V.....	M.....	M.....	A.F.V.....	A.F.V.....	A.F.V.....

FIG. 16B



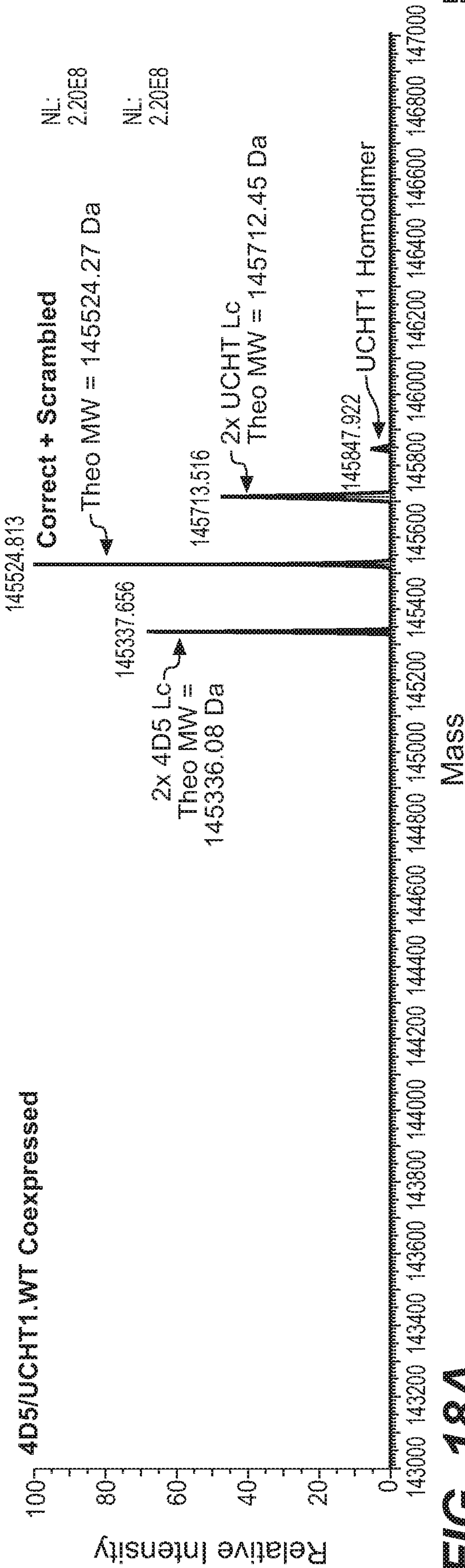


FIG. 18A

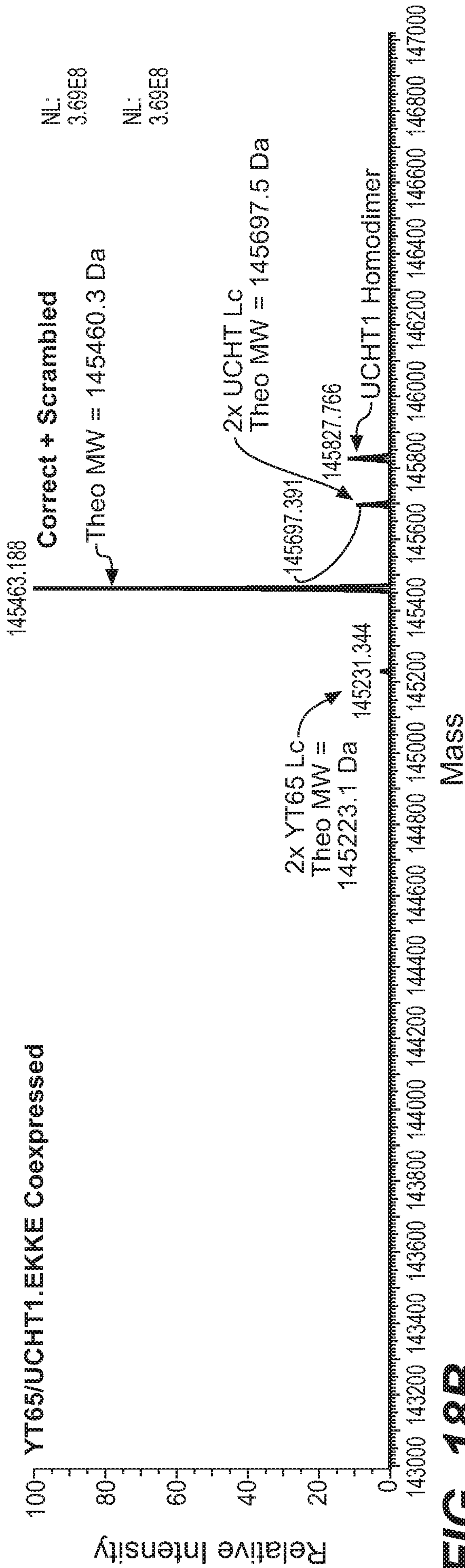


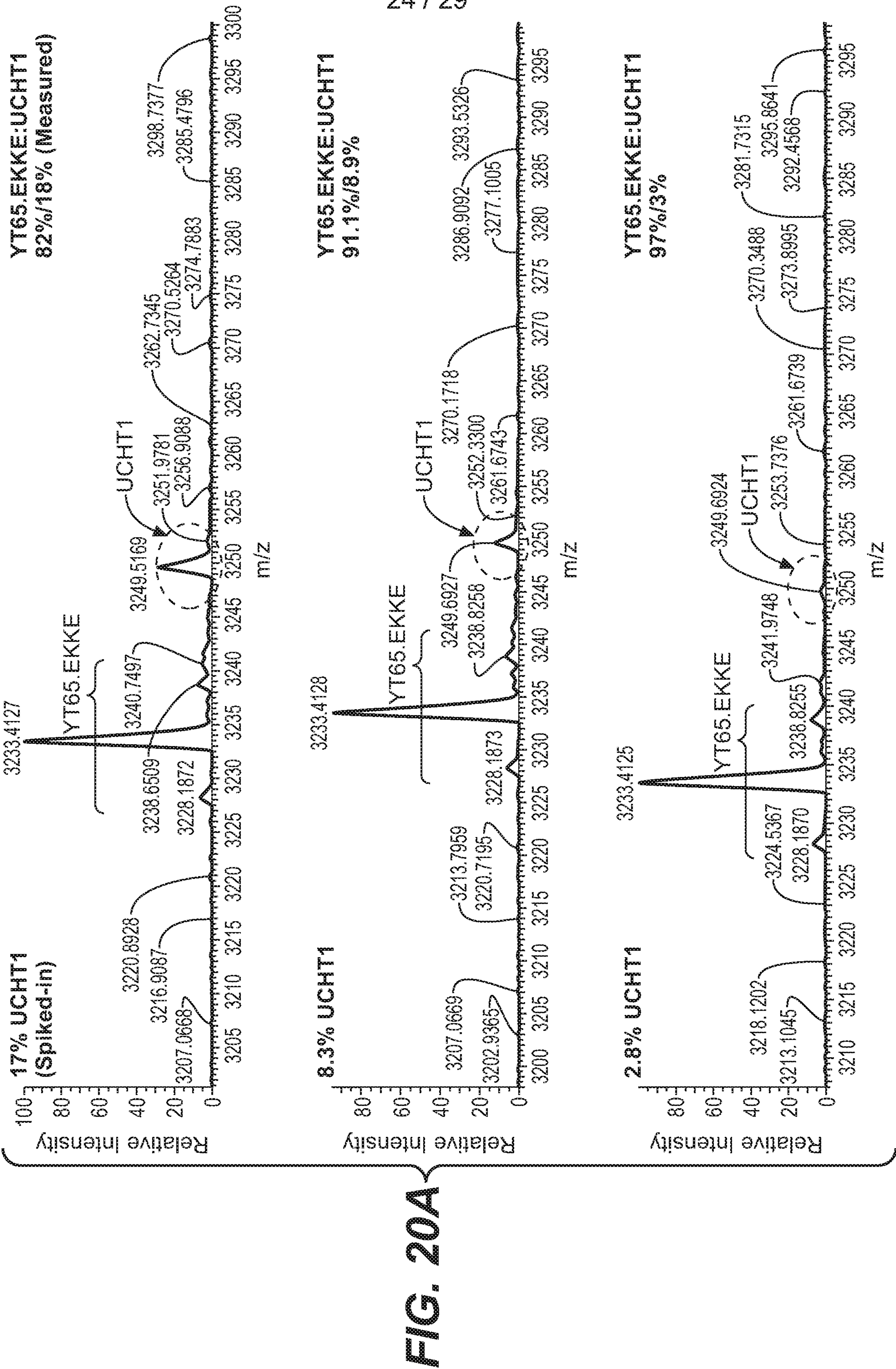
FIG. 18B

	141	170	180	181	182
4D5wt-HC	SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSVVTVPPSS				
YT65-HC	I.....S.....M.A.A.....				
YT65-HC.1	I.....S.....M.A.A.....				
YT65-HC.2	I.....S.....A.A.....				
YT65-HC.3	I.....S.....M.A.....				
YT65-HC.4	I.....S.....M.A.....				
YT65-HC.5	I.....S.....A.A.....				
YT65-HC.6	I.....S.....M.A.....				
YT65-HC.7	I.....S.....M.A.....				
YT65-HC.8	I.....S.....A.....				
YT65-HC.9	I.....S.....A.....				
YT65-HC.10	I.....S.....M.....				
YT65-HC.11	I.....S.....A.....				
YT65-HC.12	I.....S.....				
YT65-HC.13	I.....S.....				

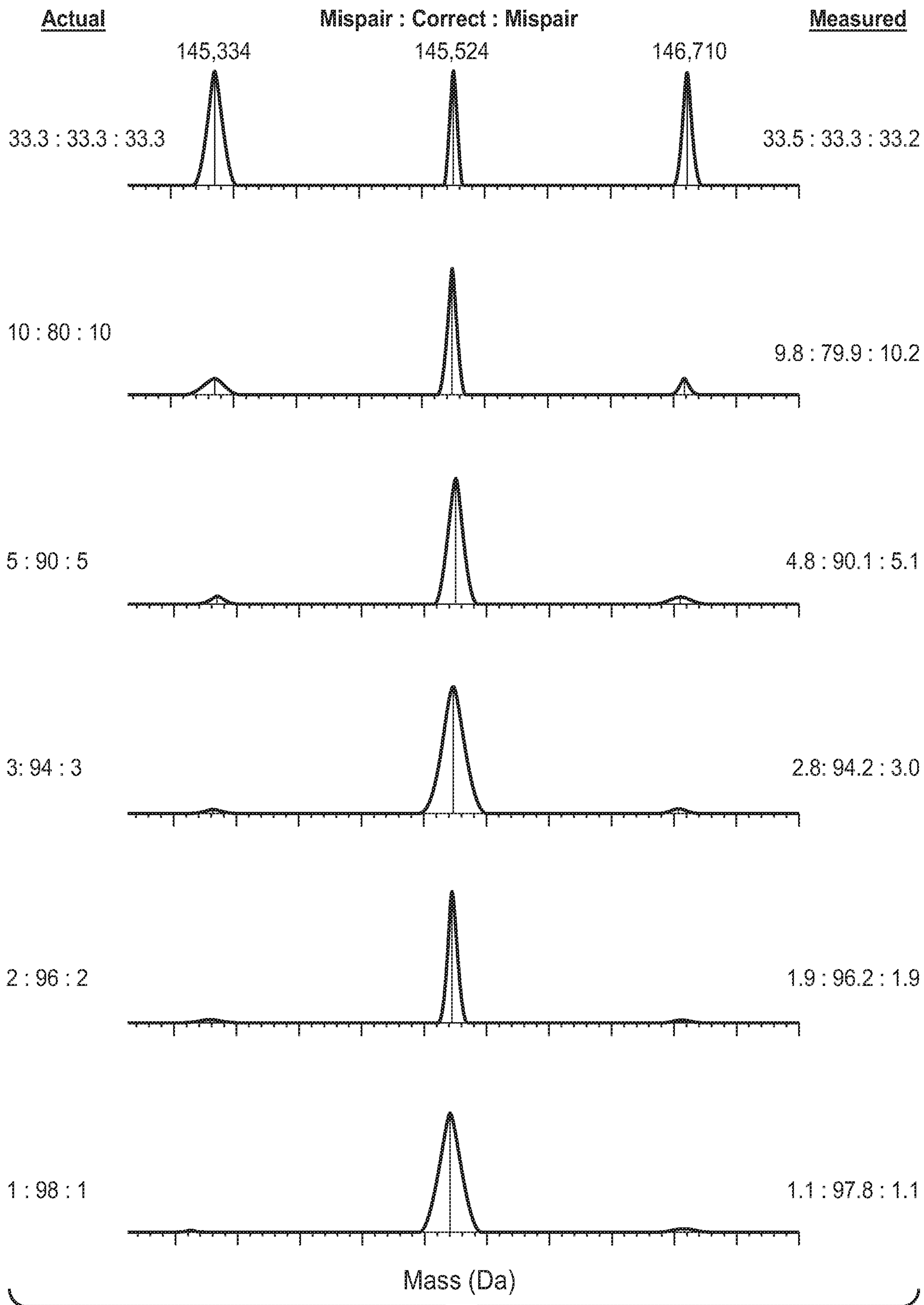
FIG. 19A

	180	181	182	183	184	185	186	187	188
4D5wt-LC	PSVFIFPPSDEQLKSGTASVVCCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT								
YT65-LC	...A.....V.....A.F.V..								
YT65-LC.1	...A.....V.....A.F.V..								
YT65-LC.2	...A.....V.....A.F.V..								
YT65-LC.3	...A.....V.....F.V..								
YT65-LC.4	...A.....V.....A.F..								
YT65-LC.5	...A.....V.....F.V..								
YT65-LC.6	...A.....V.....F..								
YT65-LC.7	...A.....V.....F..								

FIG. 19B



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**FIG. 20B**

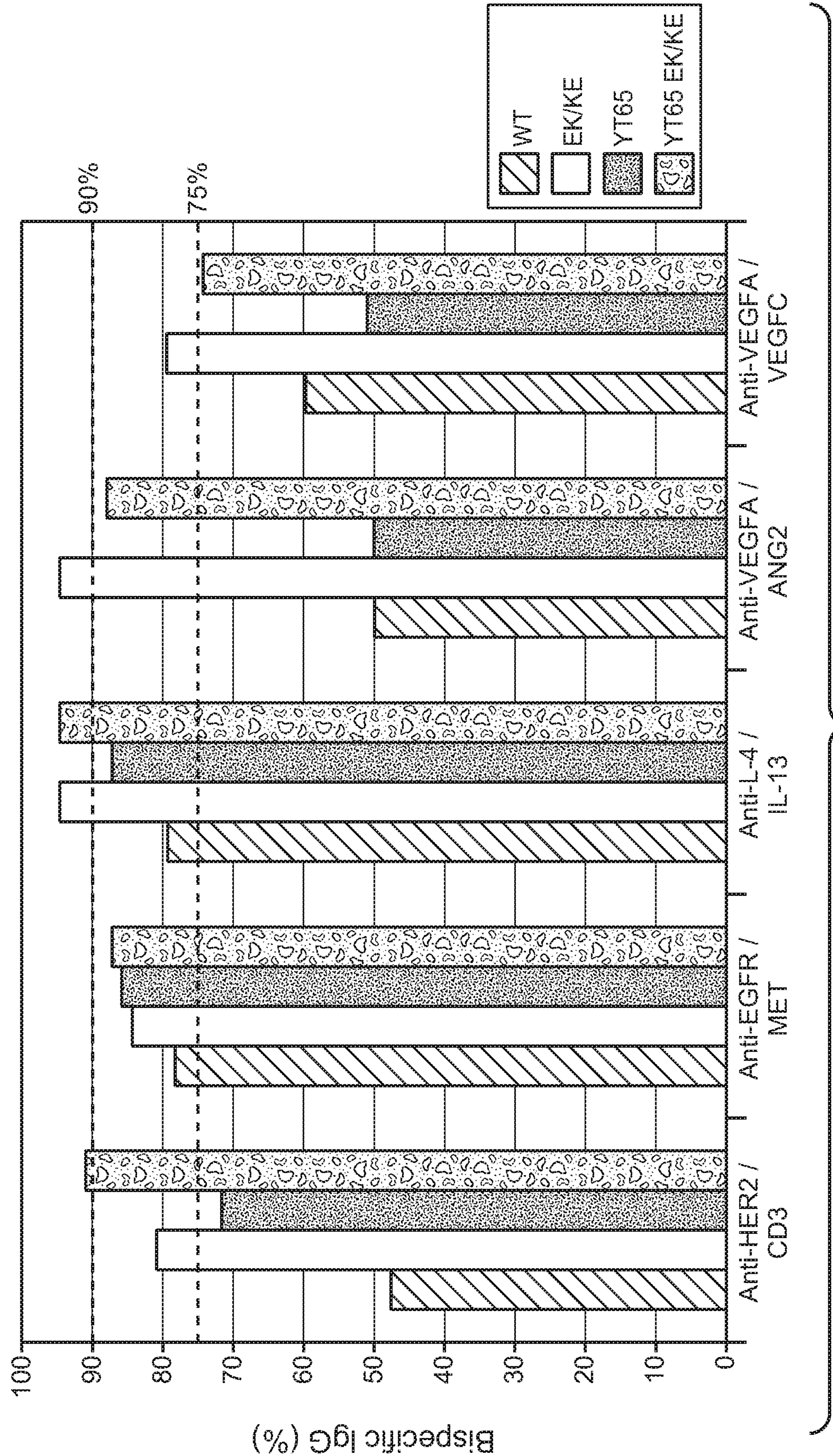


FIG. 21



FIG. 22A VL-Q38K, VH-Q39E, YT65
1.72 Å

FIG. 22B YT65 Mutations
WT Residues

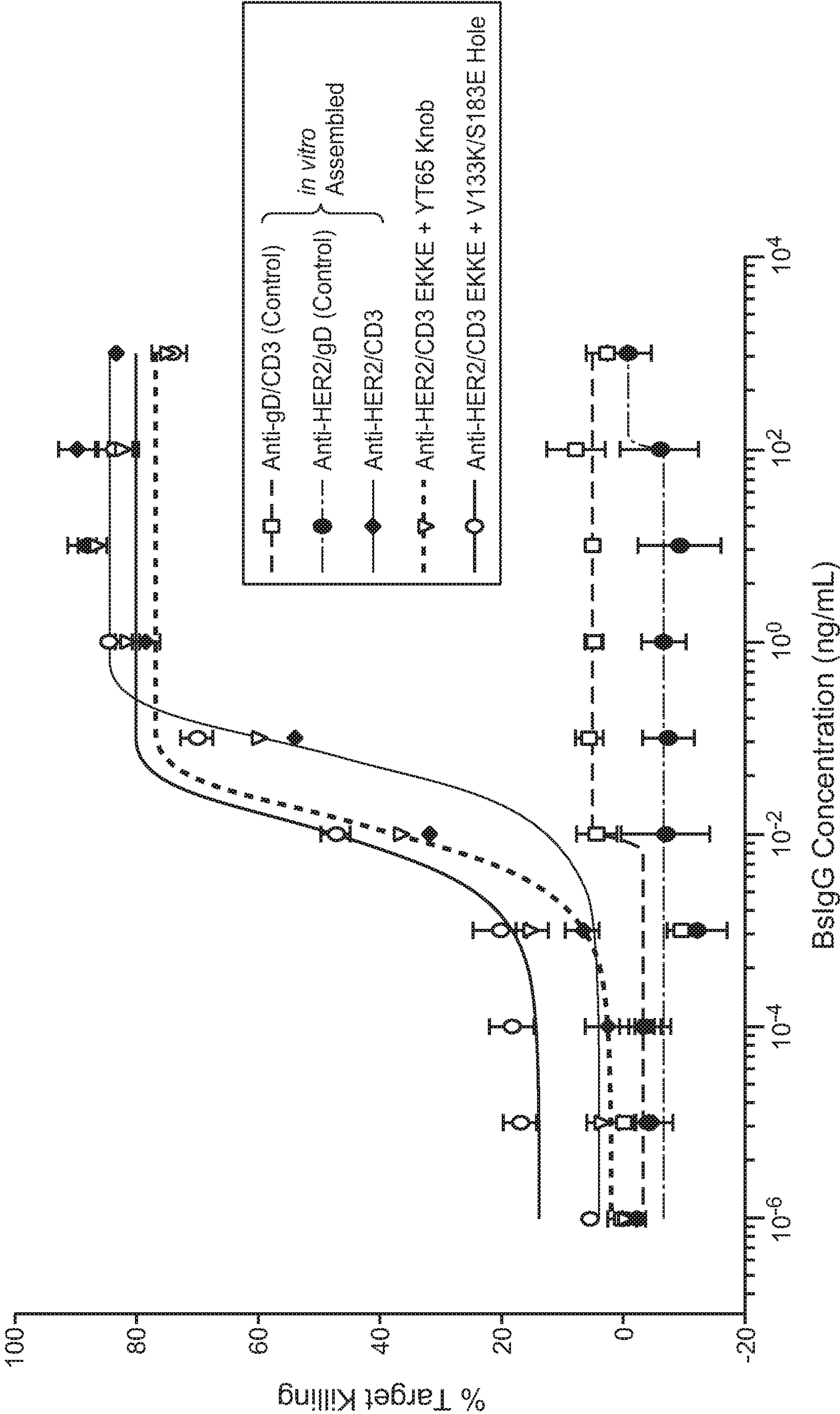
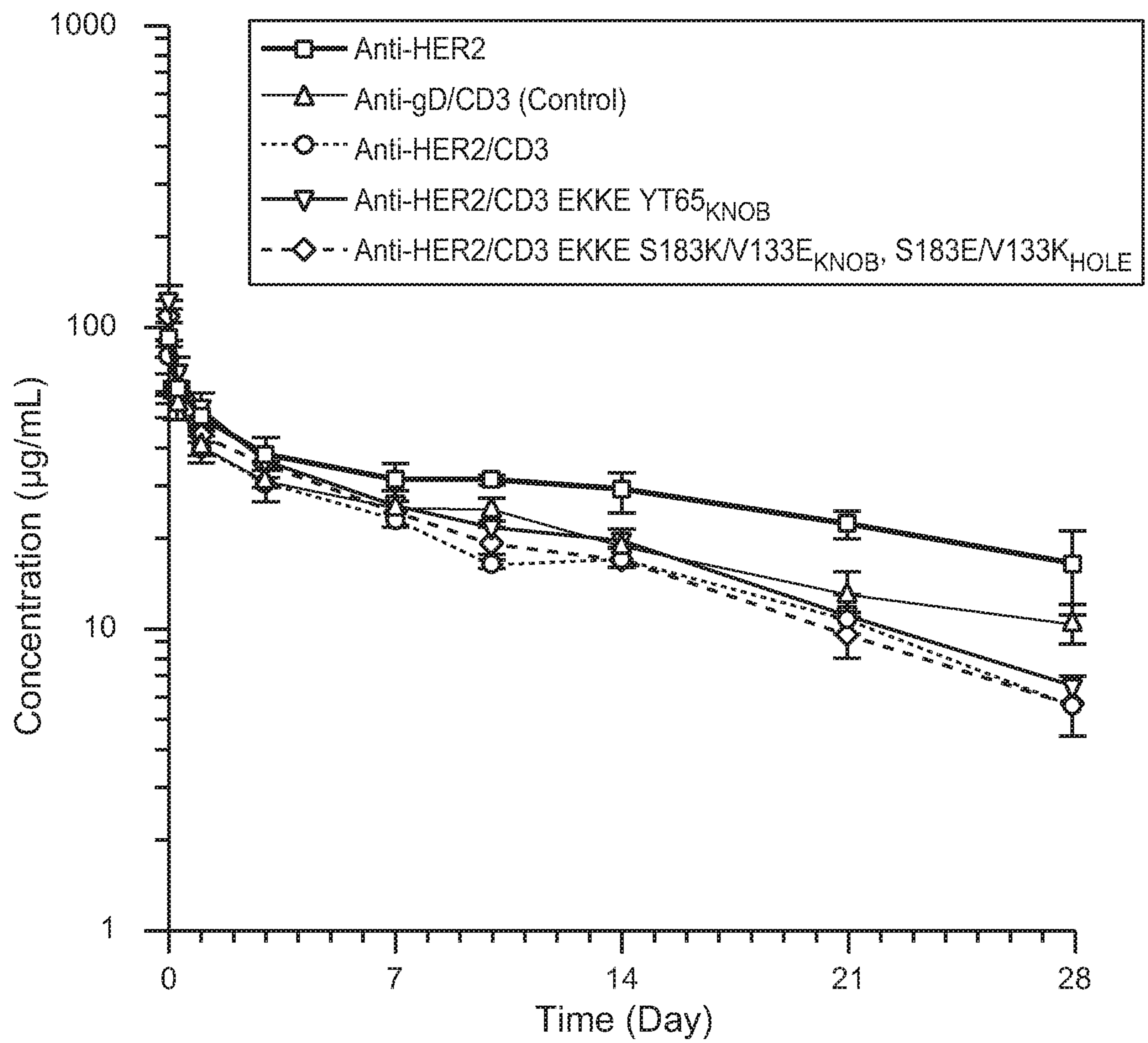


FIG. 23

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**FIG. 24**