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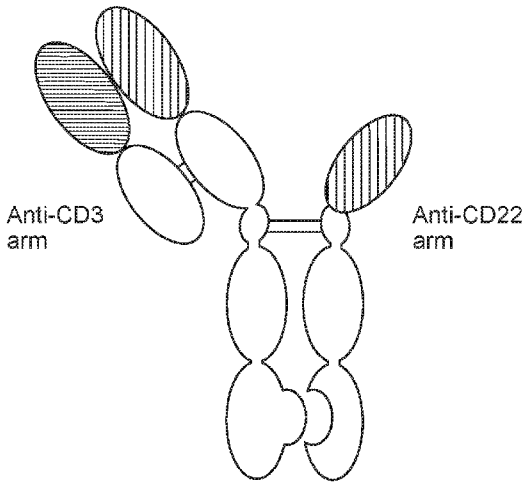


FIG. 14A

(57) Abstract: Multispecific, human heavy chain antibodies (e.g., UniAbs™) binding to CD22 and CD3 are disclosed, along with methods of making such antibodies, compositions, including pharmaceutical compositions, comprising such antibodies, and their use to treat disorders that are characterized by the expression of CD22.

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MULTISPECIFIC HEAVY CHAIN ANTIBODIES BINDING TO CD22 AND CD3

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority benefit of the filing date of US Provisional Patent Application Serial No. 62/861,708, filed on June 14, 2019, the disclosure of which application is herein incorporated by reference in its entirety.

FIELD OF THE INVENTION

[0002] The present invention concerns multispecific, human heavy chain antibodies (e.g., UniAbs™) binding to CD22 and CD3. The invention further concerns methods of making such antibodies, compositions, including pharmaceutical compositions, comprising such antibodies, and their use to treat disorders that are characterized by the expression of CD22.

BACKGROUND OF THE INVENTION

CD22

[0003] CD22, also known as SIGLEC-2 (UniProt P20273), is a cell-surface receptor that is expressed on mature B-cells. CD22 contains multiple Ig domains and is a member of the immunoglobulin superfamily. The extracellular domain of CD22 interacts with sialic acid moieties, including those present on the CD45 cell surface protein. CD22 is thought to function as an inhibitory receptor for B-cell receptor signaling. Along with CD20 and CD19, the restricted B-cell expression of CD22 makes it an attractive target for the therapeutic treatment of B-cell malignancies. Monoclonal antibodies specific to CD22 have been described in the literature (e.g., Jabbour, Elias, et al. "Monoclonal antibodies in acute lymphoblastic leukemia." *Blood* 125.26 (2015): 4010-4016) and have been used therapeutically as standard monoclonals (e.g., epratuzumab) as well as antibody-drug conjugates (inotuzumab ozogamicin). In addition, anti-CD22 chimeric antigen receptor T-cells have been used in the clinic to treat leukemia (Fry, Terry J., et al. "CD22-targeted CAR T cells induce remission in B-ALL that is naive or resistant to CD19-targeted CAR immunotherapy." *Nature medicine* (2017)).

Heavy Chain Antibodies

[0004] In a conventional IgG antibody, the association of the heavy chain and light chain is due in part to a hydrophobic interaction between the light chain constant region and the CH1 constant domain of the heavy chain. There are additional residues in the heavy chain framework 2 (FR2) and framework 4 (FR4) regions that also contribute to this hydrophobic interaction between the heavy and light chains.

[0005] It is known, however, that sera of camelids (sub-order Tylopoda which includes camels, dromedaries and llamas) contain a major type of antibodies composed solely of paired H-chains (heavy-chain only antibodies or UniAbs™). The UniAbs™ of *Camelidae* (*Camelus dromedarius, Camelus bactrianus, Lama glama, Lama guanaco, Lama alpaca* and *Lama vicugna*) have a unique structure consisting of a single variable domain (VHH), a hinge region and two constant domains (CH2 and CH3), which are highly homologous to the CH2 and CH3 domains of classical antibodies. These UniAbs™ lack the first domain of the constant region (CH1) which is present in the genome, but is spliced out during mRNA processing. The absence of the CH1 domain explains the absence of the light chain in the UniAbs™, since this domain is the anchoring place for the constant domain of the light chain. Such UniAbs™ naturally evolved to confer antigen-binding specificity and high affinity by three CDRs from conventional antibodies or fragments thereof (Muyldermans, 2001; *J Biotechnol* 74:277–302; Revets et al., 2005; *Expert Opin Biol Ther* 5:111–124). Cartilaginous fish, such as sharks, have also evolved a distinctive type of immunoglobulin, designated as IgNAR, which lacks the light polypeptide chains and is composed entirely by heavy chains. IgNAR molecules can be manipulated by molecular engineering to produce the variable domain of a single heavy chain polypeptide (vNARs) (Nuttall et al. *Eur. J. Biochem.* 270, 3543-3554 (2003); Nuttall et al. *Function and Bioinformatics* 55, 187-197 (2004); Dooley et al., *Molecular Immunology* 40, 25-33 (2003)).

[0006] The ability of heavy chain-only antibodies devoid of light chain to bind antigen was established in the 1960s (Jaton *et al.* (1968) *Biochemistry*, 7, 4185-4195). Heavy chain immunoglobulin physically separated from light chain retained 80% of antigen-binding activity relative to the tetrameric antibody. Sitia et al. (1990) *Cell*, 60, 781-790 demonstrated that removal of the CH1 domain from a rearranged mouse μ gene results in the production of a heavy chain-only antibody, devoid of light chain, in mammalian cell culture. The antibodies produced retained VH binding specificity and effector functions.

[0007] Heavy chain antibodies with a high specificity and affinity can be generated against a variety of antigens through immunization (van der Linden, R. H., et al. *Biochim. Biophys. Acta.* 1431, 37-46 (1999)) and the VHH portion can be readily cloned and expressed in yeast (Frenken, L. G. J., *et al. J. Biotechnol.* 78, 11-21 (2000)). Their levels of expression, solubility and stability are significantly higher than those of classical F(ab) or Fv fragments (Ghahroudi, M. A. et al. *FEBS Lett.* 414, 521-526 (1997)).

[0008] Mice in which the λ (lambda) light (L) chain locus and/or the λ and κ (kappa) L chain loci have been functionally silenced and antibodies produced by such mice are described in U.S. Patent Nos. 7,541,513 and 8,367,888. Recombinant production of heavy chain-only antibodies in mice and rats has been reported, for example, in WO2006008548; U.S. Application Publication No. 20100122358; Nguyen et al., 2003, *Immunology*; 109(1), 93-101; Brüggemann *et al.*, *Crit. Rev.*

Immunol.; 2006, 26(5):377-90; and Zou *et al.,* 2007, *J Exp Med*; 204(13): 3271–3283. The production of knockout rats via embryo microinjections of zinc-finger nucleases is described in Geurts et al., 2009, *Science*, 325(5939):433. Soluble heavy chain-only antibodies and transgenic rodents comprising a heterologous heavy chain locus producing such antibodies are described in U. S. Patent Nos. 8,883,150 and 9,365,655. CAR-T structures comprising single-domain antibodies as binding (targeting) domain are described, for example, in Iri-Sofla *et al.*, 2011, *Experimental Cell Research* 317:2630-2641 and Jamnani *et al.*, 2014, *Biochim Biophys Acta*, 1840:378-386.

SUMMARY OF THE INVENTION

[0009] Aspects of the invention relate to heavy chain antibodies, including but not limited to UniAbs™, with binding affinity to CD22. Further aspects of the invention relate to methods of making such antibodies, compositions comprising such antibodies, and their use in the treatment of disorders that are characterized by the expression of CD22.

[0010] Aspects of the invention include multi-specific binding compounds that bind to CD3, comprising: a heavy chain variable region comprising: (a) a CDR1 sequence having two or fewer substitutions in SEQ ID NO: 85; and/or (b) a CDR2 sequence having two or fewer substitutions in SEQ ID NO: 86; and/or (c) a CDR3 sequence having two or fewer substitutions in SEQ ID NO: 87; and a light chain variable region. In some embodiments, the heavy chain CDR1, CDR2 and CDR3 sequences are present in a human VH framework. In some embodiments, the heavy chain variable region comprises heavy chain CDR1, CDR2 and CDR3 sequences in a human VH framework, wherein each CDR sequence comprises a sequence with at least 85% identity to any one of SEQ ID NOs:85-87; and the binding compound also comprises a light chain variable region.

[0011] In some embodiments, the multi-specific binding compound comprises: a heavy chain variable region comprising: (a) a CDR1 sequence having two or fewer substitutions in SEQ ID NO: 85; and (b) a CDR2 sequence having two or fewer substitutions in SEQ ID NO: 86; and (c) a CDR3 sequence having two or fewer substitutions in SEQ ID NO: 87; and the binding compound also comprises a light chain variable region.

[0012] In some embodiments, the multi-specific binding compound comprises: a heavy chain variable region comprising a CDR1 sequence of SEQ ID NO: 85, a CDR2 sequence of SEQ ID NO: 86, and a CDR3 sequence of SEQ ID NO: 87; and the binding compound also comprises a light chain variable region.

[0013] In some embodiments, the light chain variable region comprises a CDR1, CDR2 and CDR3 sequence in a human VL framework, wherein each CDR sequence comprises a sequence with 3 or fewer amino acid substitutions relative to a CDR sequence or set of CDR sequences in SEQ ID NO: 92; or wherein the CDR sequences comprise a sequence with at least 85% identity to a CDR sequence

or set of CDR sequences in SEQ ID NO: 92. In some embodiments, the light chain variable region comprises a CDR1 sequence of SEQ ID NO: 88, a CDR2 sequence of SEQ ID NO: 89, and a CDR3 sequence of SEQ ID NO: 90. In some embodiments, the heavy chain variable region comprises an amino acid sequence having at least 95% identity to SEQ ID NO: 91. In some embodiments, the heavy chain variable region comprises an amino acid sequence set forth in SEQ ID NO: 91. In some embodiments, the light chain variable region comprises an amino acid sequence having at least 95% identity to SEQ ID NO: 92. In some embodiments, the light chain variable region comprises an amino acid sequence of SEQ ID NO: 92.

[0014] Aspects of the invention include multi-specific binding compounds comprising a first binding unit having binding affinity to CD22 and a second binding unit having binding affinity to CD3, wherein the first binding unit comprises: (a) a CDR1 having two or fewer substitutions in any of the amino acid sequences of SEQ ID NOs: 1 to 10; and/or (b) a CDR2 having two or fewer substitutions in any of the amino acid sequences of SEQ ID NOs: 11 to 17; and/or (c) a CDR3 having two or fewer substitutions in any of the amino acid sequences of SEQ ID NOs: 18 to 23. In some embodiments, the CDR1, CDR2, and CDR3 sequences of the first binding unit are present in a human framework. In some embodiments, the first binding unit further comprises a heavy chain constant region sequence in the absence of a CH1 sequence.

[0015] In some embodiments, the first binding unit comprises a heavy chain variable region comprising: (a) a CDR1 sequence selected from the group consisting of SEQ ID NOs: 1 to 10; and/or (b) a CDR2 sequence selected from the group consisting of SEQ ID NOs: 11 to 17; and/or (c) a CDR3 sequence selected from the group consisting of SEQ ID NOs: 18 to 23.

[0016] In some embodiments, the multi-specific binding compound comprises: (a) a CDR1 sequence selected from the group consisting of SEQ ID NOs: 1 to 10; and (b) a CDR2 sequence selected from the group consisting of SEQ ID NOs: 11 to 17; and (c) a CDR3 sequence selected from the group consisting of SEQ ID NOs: 18 to 23.

[0017] In some embodiments, the multi-specific binding compound comprises: (a) a CDR1 sequence of SEQ ID NO: 1, a CDR2 sequence of SEQ ID NO: 11, and a CDR3 sequence of SEQ ID NO: 18; (b) a CDR1 sequence of SEQ ID NO: 1, a CDR2 sequence of SEQ ID NO: 12, and a CDR3 sequence of SEQ ID NO: 19; or (c) a CDR1 sequence of SEQ ID NO: 1, a CDR2 sequence of SEQ ID NO: 12, and a CDR3 sequence of SEQ ID NO: 20. In some embodiments, the multi-specific binding compound comprises a heavy chain variable region having at least 95% sequence identity to any one of the sequences of SEQ ID NOs: 24 to 84. In some embodiments, the multi-specific binding compound comprises a heavy chain variable region sequence selected from the group consisting of SEQ ID NOs: 24 to 84. In some embodiments, the multi-specific binding compound comprises a heavy chain variable region sequence of SEQ ID NO: 24.

[0018] Aspects of the invention include multi-specific binding compounds comprising a first binding unit having binding affinity to CD22 and a second binding unit having binding affinity to CD3, wherein the first binding unit comprises a heavy chain variable region comprising: (a) a CDR1 sequence of the formula: G X_1 S I X_2 X_3 X_4 X_5 X_6 Y (SEQ ID NO: 104), where X_1 is D or G; X_2 is S, T, I or N; X_3 is S or D; X_4 is G, S or N; X_5 is D, G or S; and X_6 is Y or H; and (b) a CDR2 sequence of the formula: X_7 X_8 Y X_9 G X_{10} X_{11} (SEQ ID NO: 105) where X_7 is I or V; X_8 is Y or H; X_9 is S or T; X_{10} is A, V or S; and X_{11} is T or A; and (c) a CDR3 sequence of the formula: X_{12} R X_{13} D S S X_{14} W R S (SEQ ID NO: 106) where X_{12} is T, A or K; X_{13} is D or E; and X_{14} is N or S.

[0019] Aspects of the invention include multi-specific binding compounds comprising a first binding unit having binding affinity to CD22 and a second binding unit having binding affinity to CD3, wherein the first binding unit comprises a heavy chain variable region comprising CDR1, CDR2 and CDR3 sequences in a human VH framework, wherein the CDR sequences comprise a sequence having two or fewer substitutions in a CDR sequence selected from the group consisting of SEQ ID NOs: 1-23.

[0020] Aspects of the invention include multi-specific binding compounds comprising a first binding unit having binding affinity to CD22 and a second binding unit having binding affinity to CD3, wherein the first binding unit comprises a heavy chain variable region comprising CDR1, CDR2 and CDR3 sequences in a human VH framework, wherein the CDR sequences are selected from the group consisting of SEQ ID NOs: 1-23.

[0021] Aspects of the invention include multi-specific binding compounds comprising a first binding unit having binding affinity to CD22 and a second binding unit having binding affinity to CD3, wherein the first binding unit comprises a heavy chain variable region comprising: (a) a CDR1 sequence of SEQ ID NO: 1, a CDR2 sequence of SEQ ID NO: 11, and a CDR3 sequence of SEQ ID NO: 18; or (b) a CDR1 sequence of SEQ ID NO: 1, a CDR2 sequence of SEQ ID NO: 12, and a CDR3 sequence of SEQ ID NO: 19; or (c) a CDR1 sequence of SEQ ID NO: 1, a CDR2 sequence of SEQ ID NO: 12, and a CDR3 sequence of SEQ ID NO: 20, in a human VH framework.

[0022] In some embodiments, the multi-specific binding compound is bispecific. In some embodiments, the multi-specific binding compound is in a CAR-T format.

[0023] Aspects of the invention include multi-specific binding compounds comprising: (i) a heavy chain variable region having binding affinity to CD3, comprising a CDR1 sequence of SEQ ID NO: 85, a CDR2 sequence of SEQ ID NO: 86, and CDR3 sequence of SEQ ID NO: 87, in a human VH framework; (ii) a light chain variable region comprising a CDR1 sequence of SEQ ID NO: 88, a CDR2 sequence of SEQ ID NO: 89, and CDR3 sequences of SEQ ID NO: 90, in a human VL framework; and (iii) an antigen-binding domain of an anti-CD22 heavy chain antibody, comprising a

CDR1 sequence of SEQ ID NO: 1, a CDR2 sequence of SEQ ID NO: 11, and a CDR3 sequence of SEQ ID NO: 18, in a human VH framework.

[0024] Aspects of the invention include multi-specific binding compounds comprising: (i) a heavy chain variable region having binding affinity to CD3, comprising a CDR1 sequence of SEQ ID NO: 85, a CDR2 sequence of SEQ ID NO: 86, and CDR3 sequence of SEQ ID NO: 87, in a human VH framework; (ii) a light chain variable region comprising a CDR1 sequence of SEQ ID NO: 88, a CDR2 sequence of SEQ ID NO: 89, and CDR3 sequences of SEQ ID NO: 90, in a human VL framework; and (iii) an antigen-binding domain of an anti-CD22 heavy chain antibody, comprising a CDR1 sequence of SEQ ID NO: 1, a CDR2 sequence of SEQ ID NO: 12, and a CDR3 sequence of SEQ ID NO: 19, in a human VH framework.

[0025] Aspects of the invention include multi-specific binding compound comprising: (i) a heavy chain variable region having binding affinity to CD3, comprising a CDR1 sequence of SEQ ID NO: 85, a CDR2 sequence of SEQ ID NO: 86, and CDR3 sequence of SEQ ID NO: 87, in a human VH framework; (ii) a light chain variable region comprising a CDR1 sequence of SEQ ID NO: 88, a CDR2 sequence of SEQ ID NO: 89, and CDR3 sequences of SEQ ID NO: 90, in a human VL framework; and (iii) an antigen-binding domain of an anti-CD22 heavy chain antibody, comprising a CDR1 sequence of SEQ ID NO: 1, a CDR2 sequence of SEQ ID NO: 12, and a CDR3 sequence of SEQ ID NO: 20, in a human VH framework.

[0026] In some embodiments, the multispecific binding compound comprises a human IgG1 Fc region. In some embodiments, the human IgG1 Fc region is a silenced human IgG1 Fc region. In some embodiments, the multispecific binding compound comprises a human IgG4 Fc region. In some embodiments, the human IgG4 Fc region is a silenced human IgG4 Fc region.

[0027] Aspects of the invention include pharmaceutical compositions comprising a multi-specific binding compound as described herein.

[0028] Aspects of the invention include methods for the treatment of a B-cell disorder characterized by expression of CD22, comprising administering to a subject with said disorder a multi-specific binding compound or a pharmaceutical composition as described herein.

[0029] Aspects of the invention include use of a multi-specific binding compound in the preparation of a medicament for the treatment of a B-cell disorder characterized by expression of CD22.

[0030] In some embodiments, the disorder is diffuse large B cell lymphoma (DLBCL). In some embodiments, the disorder is non-Hodgkin's lymphoma (NHL). In some embodiments, the disorder is systemic lupus erythematosus (SLE). In some embodiments, the disorder is rheumatoid arthritis (RA). In some embodiments, the disorder is multiple sclerosis (MS).

[0031] Aspects of the invention include polynucleotides encoding a multi-specific binding compound as described herein. Aspects of the invention include vectors comprising the polynucleotides as described herein. Aspects of the invention include cells comprising the vectors as described herein.

[0032] Aspects of the invention include methods of producing a multi-specific binding compound as described herein, comprising growing a cell as described herein under conditions permissive for expression of the binding compound, and isolating the binding compound from the cell.

[0033] Aspects of the invention include methods of making a multi-specific binding compound as described herein, comprising immunizing a UniRat animal with CD22 and identifying CD22-binding heavy chain sequences.

[0034] Aspects of the invention include methods of treatment, comprising administering to an individual an effective dose of a multi-specific binding compound as described herein, or a pharmaceutical composition as described herein.

[0035] These and further aspects will be further explained in the rest of the disclosure, including the Examples.

BRIEF DESCRIPTION OF THE DRAWINGS

[0036] FIG. 1A is a graph depicting T cell mediated cytotoxicity of CD22 positive cells (Daudi) using resting human pan T cells.

[0037] FIG. 1B is a graph depicting dose response curves of cytokine release by resting human pan T cells incubated with CD22 positive cells (Daudi) and treated with an anti-CD22xCD3_F2F multispecific binding compound and a positive control.

[0038] FIG. 2A is a graph depicting T cell mediated cytotoxicity of CD22 positive cells (SUDHL10) using resting human pan T cells.

[0039] FIG. 2B is a graph depicting dose response curves of cytokine release by resting human pan T cells incubated with CD22 positive cells (SUDHL10) and treated with an anti-CD22xCD3_F2F multispecific binding compound and a positive control.

[0040] FIG. 3A shows a series of graphs depicting T cell mediated cytotoxicity of CD22 positive cells (RI-1) using resting human pan T cells.

[0041] FIG. 3B shows a series of graphs depicting dose response curves of cytokine release by resting human pan T cells incubated with CD22 positive cells (RI-1) and treated with an anti-CD22xCD3_F2F multispecific binding compound and a positive control.

[0042] FIG. 4 shows a series of graphs depicting T cell mediated cytotoxicity of CD22 positive cells using activated human pan T cells.

[0043] FIG. 5 shows a series of graphs depicting cell binding of bispecific antibodies against CD22 and CD3.

[0044] FIG. 6 shows a treatment plan to determine the *in vivo* efficacy of an anti-CD22xCD3_F2F multispecific binding compound in Daudi xenografts.

[0045] FIG. 7 is a graph depicting mean tumor volume as a function of days post tumor implant in mouse Daudi xenografts.

[0046] FIG. 8 is a graph depicting body weight as a function of days post tumor implant in mouse Daudi xenografts.

[0047] FIG. 9 is a graph depicting percent body weight change as a function of days post tumor implant in mouse Daudi xenografts.

[0048] FIG. 10 is a graph depicting mean tumor volume as a function of days post tumor implant in mouse Daudi xenografts.

[0049] FIG. 11 shows a series of graphs depicting individual tumor measurements as a function of days post tumor implant in mouse Daudi xenografts.

[0050] FIG. 12 is a graph depicting body weight as a function of days post tumor implant in mouse Daudi xenografts.

[0051] FIG. 13 is a graph depicting percent body weight change as a function of days post tumor implant in mouse Daudi xenografts.

[0052] FIG. 14A is a schematic illustration of a bispecific binding compound having one binding unit that specifically binds to CD3 and one binding unit the specifically binds to CD22.

[0053] FIG. 14B is an illustration of various CAR-T constructs that can incorporate one or more binding domains in accordance with embodiments of the present invention.

[0054] FIG. 15A is a schematic illustration of a bispecific binding molecule having one binding unit that specifically binds to CD3 and one binding unit the specifically binds to CD22 (monovalent, monospecific for CD22).

[0055] FIG. 15B is a schematic illustration of a bispecific binding molecule having one binding unit that specifically binds to CD3 and two binding units that specifically bind to CD22 (bivalent, monospecific for CD22).

[0056] FIG. 15C is a schematic illustration of a bispecific binding molecule having one binding unit that specifically binds to CD3 and two binding units that specifically bind to CD22 (bivalent, biparatopic for CD22).

[0057] FIG. 16 is table showing data for various biological activities of anti-CD22 antibodies in accordance with embodiments of the invention.

[0058] FIG. 17 is a series of graphs showing serum titer as a function of dilution.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

[0059] The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology (including recombinant techniques), microbiology, cell biology, biochemistry, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature, such as, "Molecular Cloning: A Laboratory Manual", second edition (Sambrook et al., 1989); "Oligonucleotide Synthesis" (M. J. Gait, ed., 1984); "Animal Cell Culture" (R. I. Freshney, ed., 1987); "Methods in Enzymology" (Academic Press, Inc.); "Current Protocols in Molecular Biology" (F. M. Ausubel et al., eds., 1987, and periodic updates); "PCR: The Polymerase Chain Reaction", (Mullis et al., ed., 1994); "A Practical Guide to Molecular Cloning" (Perbal Bernard V., 1988); "Phage Display: A Laboratory Manual" (Barbas et al., 2001); Harlow, Lane and Harlow, Using Antibodies: A Laboratory Manual: Portable Protocol No. I, Cold Spring Harbor Laboratory (1998); and Harlow and Lane, Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory; (1988).

[0060] Where a range of values is provided, it is understood that each intervening value, to the tenth of the unit of the lower limit unless the context clearly dictates otherwise, between the upper and lower limit of that range and any other stated or intervening value in that stated range is encompassed within the invention. The upper and lower limits of these smaller ranges may independently be included in the smaller ranges is also encompassed within the invention, subject to any specifically excluded limit in the stated range. Where the stated range includes one or both of the limits, ranges excluding either or both of those included limits are also included in the invention.

[0061] Unless indicated otherwise, antibody residues herein are numbered according to the Kabat numbering system (*e.g.*, Kabat *et al.*, Sequences of Immunological Interest. 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md. (1991)).

[0062] In the following description, numerous specific details are set forth to provide a more thorough understanding of the present invention. However, it will be apparent to one of skill in the art that the present invention may be practiced without one or more of these specific details. In other instances, well-known features and procedures well known to those skilled in the art have not been described in order to avoid obscuring the invention.

[0063] All references cited throughout the disclosure, including patent applications and publications, are incorporated by reference herein in their entirety.

I. Definitions

[0064] By "comprising" it is meant that the recited elements are required in the composition/method/kit, but other elements may be included to form the composition/method/kit etc. within the scope of the claim.

[0065] By "consisting essentially of", it is meant a limitation of the scope of composition or method described to the specified materials or steps that do not materially affect the basic and novel characteristic(s) of the subject invention.

[0066] By "consisting of", it is meant the exclusion from the composition, method, or kit of any element, step, or ingredient not specified in the claim.

[0067] Antibody residues herein are numbered according to the Kabat numbering system and the EU numbering system. The Kabat numbering system is generally used when referring to a residue in the variable domain (approximately residues 1-113 of the heavy chain) (*e.g.*, Kabat *et al.*, Sequences of Immunological Interest. 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md. (1991)). The "EU numbering system" or "EU index" is generally used when referring to a residue in an immunoglobulin heavy chain constant region (e.g., the EU index reported in Kabat et al., supra). The "EU index as in Kabat" refers to the residue numbering of the human IgG1 EU antibody. Unless stated otherwise herein, references to residue numbers in the variable domain of antibodies mean residue numbering by the Kabat numbering system. Unless stated otherwise herein, references to residue numbers in the constant domain of antibodies mean residue numbering by the EU numbering system.

[0068] Antibodies, also referred to as immunoglobulins, conventionally comprise at least one heavy chain and one light chain, where the amino terminal domain of the heavy and light chains is variable in sequence, hence is commonly referred to as a variable region domain, or a variable heavy (VH) or variable light (VH) domain. The two domains conventionally associate to form a specific binding region, although as will be discussed here, specific binding can also be obtained with heavy chain-only variable sequences, and a variety of non-natural configurations of antibodies are known and used in the art.

[0069] A "functional" or "biologically active" antibody or antigen-binding molecule (including heavy chain-only antibodies and multi-specific (e.g., bispecific) three-chain antibody-like molecules (TCAs), described herein) is one capable of exerting one or more of its natural activities in structural, regulatory, biochemical or biophysical events. For example, a functional antibody or other binding molecule, e.g., a TCA, may have the ability to specifically bind an antigen and the binding may in turn elicit or alter a cellular or molecular event such as signal transduction or enzymatic activity. A functional antibody or other binding molecule, e.g., a TCA, may also block ligand activation of a receptor or act as an agonist or antagonist. The capability of an antibody or other binding molecule, e.g., a TCA, to exert one or more of its natural activities depends on several factors, including proper folding and assembly of the polypeptide chains.

[0070] The term "antibody" herein is used in the broadest sense and specifically covers monoclonal antibodies, polyclonal antibodies, monomers, dimers, multimers, multispecific antibodies (e.g.,

bispecific antibodies), heavy chain-only antibodies, three chain antibodies, single chain Fv (scFv), nanobodies, etc., and also includes antibody fragments, so long as they exhibit the desired biological activity (Miller et al (2003) Jour. of Immunology 170:4854-4861). Antibodies may be murine, human, humanized, chimeric, or derived from other species.

[0071] The term antibody may reference a full-length heavy chain, a full length light chain, an intact immunoglobulin molecule; or an immunologically active portion of any of these polypeptides, i.e., a polypeptide that comprises an antigen binding site that immunospecifically binds an antigen of a target of interest or part thereof, such targets including but not limited to, a cancer cell, or cells that produce autoimmune antibodies associated with an autoimmune disease. The immunoglobulin disclosed herein can be of any type (e.g., IgG, IgE, IgM, IgD, and IgA), class (e.g., IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2) or subclass of immunoglobulin molecule, including engineered subclasses with altered Fc portions that provide for reduced or enhanced effector cell activity. The immunoglobulins can be derived from any species. In one aspect, the immunoglobulin is of largely human origin.

[0072] The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally occurring mutations that may be present in minor amounts. Monoclonal antibodies are highly specific, being directed against a single antigenic site. Furthermore, in contrast to conventional (polyclonal) antibody preparations which typically include different antibodies directed against different determinants (epitopes), each monoclonal antibody is directed against a single determinant on the antigen. Monoclonal antibodies in accordance with the present invention can be made by the hybridoma method first described by Kohler et al. (1975) *Nature* 256:495, and can also be made via recombinant protein production methods (see, *e.g.*, U.S. Patent No. 4,816,567), for example.

[0073] The term "variable", as used in connection with antibodies, refers to the fact that certain portions of the antibody variable domains differ extensively in sequence among antibodies and are used in the binding and specificity of each particular antibody for its particular antigen. However, the variability is not evenly distributed throughout the variable domains of antibodies. It is concentrated in three segments called hypervariable regions both in the light chain and the heavy chain variable domains. The more highly conserved portions of variable domains are called the framework regions (FRs). The variable domains of native heavy and light chains each comprise four FRs, largely adopting a β-sheet configuration, connected by three hypervariable regions, which form loops connecting, and in some cases forming part of, the β-sheet structure. The hypervariable regions in each chain are held together in close proximity by the FRs and, with the hypervariable regions from the other chain, contribute to the formation of the antigen-binding site of antibodies (see Kabat *et al., Sequences of Proteins of Immunological Interest*, 5th Ed. Public Health Service, National Institutes of

Health, Bethesda, MD. (1991)). The constant domains are not involved directly in binding an antibody to an antigen, but exhibit various effector functions, such as participation of the antibody in antibody dependent cellular cytotoxicity (ADCC).

[0074] The term "hypervariable region" when used herein refers to the amino acid residues of an antibody which are responsible for antigen-binding. The hypervariable region generally comprises amino acid residues from a "complementarity determining region" or "CDR" (e.g., residues 31-35 (H1), 50-65 (H2) and 95-102 (H3) in the heavy chain variable domain; Kabat et al., *Sequences of Proteins of Immunological Interest*, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD. (1991)) and/or those residues from a "hypervariable loop" residues 26-32 (H1), 53-55 (H2) and 96-101 (H3) in the heavy chain variable domain; Chothia and Lesk *J. Mol. Biol.* 196:901-917 (1987)). "Framework Region" or "FR" residues are those variable domain residues other than the hypervariable region residues as herein defined.

[0075] Exemplary CDR designations are shown herein, however one of skill in the art will understand that a number of definitions of the CDRs are commonly in use, including the Kabat definition (see "Zhao et al. A germline knowledge based computational approach for determining antibody complementarity determining regions." *Mol Immunol.* 2010;47:694–700), which is based on sequence variability and is the most commonly used. The Chothia definition is based on the location of the structural loop regions (Chothia et al. "Conformations of immunoglobulin hypervariable regions." *Nature.* 1989; 342:877–883). Alternative CDR definitions of interest include, without limitation, those disclosed by Honegger, "Yet another numbering scheme for immunoglobulin variable domains: an automatic modeling and analysis tool." *J Mol Biol.* 2001;309:657–670; Ofran et al. "Automated identification of complementarity determining regions (CDRs) reveals peculiar characteristics of CDRs and B cell epitopes." *J Immunol.* 2008;181:6230–6235; Almagro "Identification of differences in the specificity-determining residues of antibodies that recognize antigens of different size: implications for the rational design of antibody repertoires." *J Mol Recognit.* 2004;17:132–143; and Padlanet al. "Identification of specificity-determining residues in antibodies." Faseb J. 1995;9:133–139., each of which is herein specifically incorporated by reference.

[0076] The terms "heavy chain-only antibody," and "heavy-chain antibody" are used interchangeably herein and refer, in the broadest sense, to antibodies lacking the light chain of a conventional antibody. The terms specifically include, without limitation, homodimeric antibodies comprising the VH antigen-binding domain and the CH2 and CH3 constant domains, in the absence of the CH1 domain; functional (antigen-binding) variants of such antibodies, soluble VH variants, Ig-NAR comprising a homodimer of one variable domain (V-NAR) and five C-like constant domains (C-NAR) and functional fragments thereof; and soluble single domain antibodies (sUniDabs™). In one embodiment, a heavy chain-only antibody is composed of the variable region antigen-binding domain

composed of framework 1, CDR1, framework 2, CDR2, framework 3, CDR3, and framework 4. In another embodiment, the heavy chain-only antibody is composed of an antigen-binding domain, at least part of a hinge region and CH2 and CH3 domains. In another embodiment, the heavy chain-only antibody is composed of an antigen-binding domain, at least part of a hinge region and a CH2 domain. In a further embodiment, the heavy chain-only antibody is composed of an antigen-binding domain, at least part of a hinge region and a CH3 domain. Heavy chain-only antibodies in which the CH2 and/or CH3 domain is truncated are also included herein. In a further embodiment the heavy chain is composed of an antigen binding domain, and at least one CH (CH1, CH2, CH3, or CH4) domain but no hinge region. In a further embodiment the heavy chain is composed of an antigen binding domain, at least one CH (CH1, CH2, CH3, or CH4) domain, and at least a portion of a hinge region. The heavy chain-only antibody can be in the form of a dimer, in which two heavy chains are disulfide bonded or otherwise, covalently or non-covalently, attached with each other. The heavy chain-only antibody may belong to the IgG subclass, but antibodies belonging to other subclasses, such as IgM, IgA, IgD and IgE subclass, are also included herein. In a particular embodiment, the heavy-chain antibody is of the IgG1, IgG2, IgG3, or IgG4 subtype, in particular the IgG1 subtype. In one embodiment, the heavy-chain antibody is of the IgG4 subtype, wherein one or more of the CH domains are modified to alter an effector function of the antibody. In one embodiment, the heavy-chain antibody is of the IgG1 subtype, wherein one or more of the CH domains are modified to alter an effector function of the antibody. Modifications of CH domains that alter effector function are further described herein. Non-limiting examples of heavy-chain antibodies are described, for example, in WO2018/039180, the disclosure of which is incorporated herein by reference in its entirety.

[0077] In one embodiment, the heavy chain-only antibodies herein are used as a binding (targeting) domain of a chimeric antigen receptor (CAR). The definition specifically includes human heavy chain-only antibodies produced by human immunoglobulin transgenic rats (UniRat™), called UniAbs™. The variable regions (VH) of UniAbs™ are called UniDabs™, and are versatile building blocks that can be linked to Fc regions or serum albumin for the development of novel therapeutics with multi-specificity, increased potency and extended half-life. Since the homodimeric UniAbs™ lack a light chain and thus a VL domain, the antigen is recognized by one single domain, i.e., the variable domain (antigen-binding domain) of the heavy chain of a heavy-chain antibody (VH).

[0078] An "intact antibody chain" as used herein is one comprising a full length variable region and a full length constant region (Fc). An intact "conventional" antibody comprises an intact light chain and an intact heavy chain, as well as a light chain constant domain (CL) and heavy chain constant domains, CH1, hinge, CH2 and CH3 for secreted IgG. Other isotypes, such as IgM or IgA may have different CH domains. The constant domains may be native sequence constant domains (e.g., human native sequence constant domains) or amino acid sequence variants thereof. The intact antibody may

have one or more "effector functions" which refer to those biological activities attributable to the Fc constant region (a native sequence Fc region or amino acid sequence variant Fc region) of an antibody. Examples of antibody effector functions include C1q binding; complement dependent cytotoxicity; Fc receptor binding; antibody-dependent cell-mediated cytotoxicity (ADCC); phagocytosis; and down regulation of cell surface receptors. Constant region variants include those that alter the effector profile, binding to Fc receptors, and the like.

[0079] Depending on the amino acid sequence of the Fc (constant domain) of their heavy chains, antibodies and various antigen-binding proteins can be provided as different classes. There are five major classes of heavy chain Fc regions: IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into "subclasses" (isotypes), e.g., IgG1, IgG2, IgG3, IgG4, IgA, and IgA2. The Fc constant domains that correspond to the different classes of antibodies may be referenced as α, δ, ε, γ, and μ, respectively. The subunit structures and three-dimensional configurations of different classes of immunoglobulins are well known. Ig forms include hinge-modifications or hingeless forms (Roux et al (1998) J. Immunol. 161:4083-4090; Lund et al (2000) Eur. J. Biochem. 267:7246-7256; US 2005/0048572; US 2004/0229310). The light chains of antibodies from any vertebrate species can be assigned to one of two types, called κ and λ, based on the amino acid sequences of their constant domains.

[0080] A "functional Fc region" possesses an "effector function" of a native-sequence Fc region. Non-limiting examples of effector functions include C1q binding; CDC; Fc-receptor binding; ADCC; ADCP; down-regulation of cell-surface receptors (e.g., B-cell receptor), etc. Such effector functions generally require the Fc region to interact with a receptor, e.g., the FcγRI; FcγRIIA; FcγRIIB1; FcγRIIB2; FcγRIIIA; FcγRIIIB receptors, and the low affinity FcRn receptor; and can be assessed using various assays known in the art. A "dead" or "silenced" Fc is one that has been mutated to retain activity with respect to, for example, prolonging serum half-life, but which does not activate a high affinity Fc receptor, or which has a reduced affinity to an Fc receptor.

[0081] 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, for example, 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.

[0082] A "variant Fc region" comprises an amino acid sequence that 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% homology therewith.

[0083] Variant Fc sequences may include three amino acid substitutions in the CH2 region to reduce FcγRI binding at EU index positions 234, 235, and 237 (see Duncan et al., (1988) Nature 332:563). Two amino acid substitutions in the complement C1q binding site at EU index positions 330 and 331 reduce complement fixation (see Tao et al., J. Exp. Med. 178:661 (1993) and Canfield and Morrison, J. Exp. Med. 173:1483 (1991)). Substitution into human IgG1 or IgG2 residues at positions 233-236 and IgG4 residues at positions 327, 330 and 331 greatly reduces ADCC and CDC (see, for example, Armour KL. *et al.*, 1999 Eur J Immunol. 29(8):2613-24; and Shields RL. *et al.*, 2001. J Biol Chem. 276(9):6591-604). The human IgG1 amino acid sequence (UniProtKB No. P01857) is provided herein as SEQ ID NO: 93. The human IgG4 amino acid sequence (UniProtKB No. P01861) is provided herein as SEQ ID NO: 94. Silenced IgG1 is described, for example, in Boesch, A.W., et al., "Highly parallel characterization of IgG Fc binding interactions." MAbs, 2014. 6(4): p. 915-27, the disclosure of which is incorporated herein by reference in its entirety.

[0084] Other Fc variants are possible, including, without limitation, one in which a region capable of forming a disulfide bond is deleted, or in which certain amino acid residues are eliminated at the N-terminal end of a native Fc, or a methionine residue is added thereto. Thus, in some embodiments, one or more Fc portions of a binding compound can comprise one or more mutations in the hinge region to eliminate disulfide bonding. In yet another embodiment, the hinge region of an Fc can be removed entirely. In still another embodiment, a binding compound can comprise an Fc variant.

[0085] Further, an Fc variant can be constructed to remove or substantially reduce effector functions by substituting (mutating), deleting or adding amino acid residues to effect complement binding or Fc receptor binding. For example, and not limitation, a deletion may occur in a complement-binding site, such as a C1q-binding site. Techniques for preparing such sequence derivatives of the immunoglobulin Fc fragment are disclosed in International Patent Publication Nos. WO 97/34631 and WO 96/32478. In addition, the Fc domain may be modified by phosphorylation, sulfation, acylation, glycosylation, methylation, farnesylation, acetylation, amidation, and the like.

[0086] The term "Fc-region-comprising antibody" refers to an antibody that comprises an Fc region. The C-terminal lysine (residue 447 according to the EU numbering system) of the Fc region may be removed, for example, during purification of the antibody or by recombinant engineering of the nucleic acid encoding the antibody. Accordingly, an antibody having an Fc region according to this invention can comprise an antibody with or without K447.

[0087] Aspects of the invention include binding compounds having multi-specific configurations, which include, without limitation, bispecific, trispecific, etc. A large variety of methods and protein configurations are known and used in bispecific monoclonal antibodies (BsMAB), tri-specific antibodies, etc.

[0088] Various methods for the production of multivalent artificial antibodies have been developed by recombinantly fusing variable domains of two or more antibodies. In some embodiments, a first and a second antigen-binding domain on a polypeptide are connected by a polypeptide linker. One non-limiting example of such a polypeptide linker is a GS linker, having an amino acid sequence of four glycine residues, followed by one serine residue, and wherein the sequence is repeated n times, where n is an integer ranging from 1 to about 10, such as 2, 3, 4, 5, 6, 7, 8, or 9. Non-limiting examples of such linkers include GGGGS (SEQ ID NO: 102) (n=1) and GGGGSGGGGS (SEQ ID NO: 103) (n=2). Other suitable linkers can also be used, and are described, for example, in Chen et al., Adv Drug Deliv Rev. 2013 October 15; 65(10): 1357-69, the disclosure of which is incorporated herein by reference in its entirety.

[0089] The term "three-chain antibody like molecule" or "TCA" is used herein to refer to antibody-like molecules comprising, consisting essentially of, or consisting of three polypeptide subunits, two of which comprise, consist essentially of, or consist of one heavy and one light chain of a monoclonal antibody, or functional antigen-binding fragments of such antibody chains, comprising an antigen-binding region and at least one CH domain. This heavy chain/light chain pair has binding specificity for a first antigen. The third polypeptide subunit comprises, consists essentially of, or consists of a heavy-chain only antibody comprising an Fc portion comprising CH2 and/or CH3 and/or CH4 domains, in the absence of a CH1 domain, and one or more antigen binding domains (e.g., two antigen binding domains) that binds an epitope of a second antigen or a different epitope of the first antigen, where such binding domain is derived from or has sequence identity with the variable region of an antibody heavy or light chain. Parts of such variable region may be encoded by V_H and/or V_L gene segments, D and J_H gene segments, or J_L gene segments. The variable region may be encoded by rearranged V_HDJ_H, V_LDJ_H, V_HJ_L, or V_LJ_L gene segments. A TCA protein makes use of a heavy chain-only antibody as hereinabove defined.

[0090] A TCA binding compound makes use of a "heavy chain only antibody" or "heavy chain antibody" or "heavy chain polypeptide" which, as used herein, mean a single chain antibody comprising heavy chain constant regions CH2 and/or CH3 and/or CH4 but no CH1 domain. In one embodiment, the heavy chain antibody is composed of an antigen-binding domain, at least part of a hinge region and CH2 and CH3 domains. In another embodiment, the heavy chain antibody is composed of an antigen-binding domain, at least part of a hinge region and a CH2 domain. In a further embodiment, the heavy chain antibody is composed of an antigen-binding domain, at least part

of a hinge region and a CH3 domain. Heavy chain antibodies in which the CH2 and/or CH3 domain is truncated are also included herein. In a further embodiment, the heavy chain is composed of an antigen binding domain, and at least one CH (CH1, CH2, CH3, or CH4) domain but no hinge region. The heavy chain only antibody can be in the form of a dimer, in which two heavy chains are disulfide bonded other otherwise covalently or non-covalently attached with each other, and can optionally include an asymmetric interface between two or more of the CH domains to facilitate proper pairing between polypeptide chains. The heavy-chain antibody may belong to the IgG subclass, but antibodies belonging to other subclasses, such as IgM, IgA, IgD and IgE subclass, are also included herein. In a particular embodiment, the heavy chain antibody is of the IgG1, IgG2, IgG3, or IgG4 subtype, in particular the IgG1 subtype or the IgG4 subtype. Non-limiting examples of a TCA binding compound are described in, for example, WO2017/223111 and WO2018/052503, the disclosures of which are incorporated herein by reference in their entirety.

[0091] Heavy-chain antibodies constitute about one fourth of the IgG antibodies produced by the camelids, e.g., camels and llamas (Hamers-Casterman C., et al. Nature. 363, 446-448 (1993)). These antibodies are formed by two heavy chains but are devoid of light chains. As a consequence, the variable antigen binding part is referred to as the VHH domain and it represents the smallest naturally occurring, intact, antigen-binding site, being only around 120 amino acids in length (Desmyter, A., et al. J. Biol. Chem. 276, 26285-26290 (2001)). Heavy chain antibodies with a high specificity and affinity can be generated against a variety of antigens through immunization (van der Linden, R. H., et al. Biochim. Biophys. Acta. 1431, 37-46 (1999)) and the VHH portion can be readily cloned and expressed in yeast (Frenken, L. G. J., et al. J. Biotechnol. 78, 11-21 (2000)). Their levels of expression, solubility and stability are significantly higher than those of classical F(ab) or Fv fragments (Ghahroudi, M. A. et al. FEBS Lett. 414, 521-526 (1997)). Sharks have also been shown to have a single VH-like domain in their antibodies, termed VNAR. (Nuttall et al. Eur. J. Biochem. 270, 3543-3554 (2003); Nuttall et al. Function and Bioinformatics 55, 187-197 (2004); Dooley et al., Molecular Immunology 40, 25-33 (2003)).

[0092] The terms “CD22” and “cluster of differentiation-22” as used herein refer to a molecule belonging to the SIGLEC family of lectins, found on the surface of mature B cells, and to a lesser extent on some immature B cells. The term “CD22” includes a CD22 protein of any human and non-human animal species, and specifically includes human CD22 as well as CD22 of non-human mammals.

[0093] The term “human CD22” as used herein includes any variants, isoforms and species homologs of human CD22 (UniProt P20273), regardless of its source or mode of preparation. Thus, “human CD22” includes human CD22 naturally expressed by cells and CD22 expressed on cells transfected with the human CD22 gene.

[0094] The terms "anti-CD22 heavy chain-only antibody," "CD22 heavy chain-only antibody," "anti-CD22 heavy chain antibody" and "CD22 heavy chain antibody" are used herein interchangeably to refer to a heavy chain-only antibody as hereinabove defined, immunospecifically binding to CD22, including human CD22, as hereinabove defined. The definition includes, without limitation, human heavy chain antibodies produced by transgenic animals, such as transgenic rats or transgenic mice expressing human immunoglobulin, including UniRats™ producing human anti-CD22 UniAb™ antibodies, as hereinabove defined.

[0095] "Percent (%) amino acid sequence identity" with respect to a reference polypeptide sequence is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the reference polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for aligning sequences, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2.

[0096] An "isolated" antibody is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody 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. Isolated antibody includes the antibody *in situ* within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

[0097] Antibodies of the invention include multi-specific antibodies. Multi-specific antibodies have more than one binding specificity. The term "multi-specific" specifically includes "bispecific" and "trispecific," as well as higher-order independent specific binding affinities, such as higher-order polyepitopic specificity, as well as tetravalent antibodies and antibody fragments. The terms "multi-specific antibody," "multi-specific heavy chain-only antibody," "multi-specific heavy chain antibody," "multi-specific UniAb™", and "multi-specific binding compound" are used herein in the

broadest sense and cover all antibodies with more than one binding specificity. The multi-specific heavy chain anti-CD22 antibodies of the present invention specifically include antibodies immunospecifically binding to one single epitope on a CD22 protein, such as a human CD22, and to an epitope on a different protein, such as, for example, a CD3 protein (i.e., bivalent and monoparatopic). The multi-specific heavy chain anti-CD22 antibodies of the present invention specifically include antibodies immunospecifically binding to two or more non-overlapping epitopes on a CD22 protein, such as a human CD22 (i.e., bivalent and biparatopic). The multi-specific heavy chain anti-CD22 antibodies of the present invention also specifically include antibodies immunospecifically binding to an epitope on a CD22 protein, such as human CD22 and to an epitope on a different protein, such as, for example, a CD3 protein, such as human CD3 (i.e., bivalent and biparatopic). The multi-specific heavy chain anti-CD22 antibodies of the present invention also specifically include antibodies immunospecifically binding to two or more non-overlapping or partially overlapping epitopes on a CD22 protein, such as a human CD22 protein, and to an epitope on a different protein, such as, for example, a CD3 protein, such as human CD3 protein (i.e., trivalent and biparatopic).

[0098] Antibodies of the invention include monospecific antibodies, having one binding specificity. Monospecific antibodies specifically include antibodies comprising a single binding specificity, as well as antibodies comprising more than one binding unit having the same binding specificity. The terms "monospecific antibody," "monospecific heavy chain-only antibody," "monospecific heavy chain antibody," and "monospecific UniAb™" are used herein in the broadest sense and cover all antibodies with one binding specificity. The monospecific heavy chain anti-CD22 antibodies of the present invention specifically include antibodies immunospecifically binding to one epitope on a CD22 protein, such as a human CD22 (monovalent and monospecific). The monospecific heavy chain anti-CD22 antibodies of the present invention also specifically include antibodies having more than one binding unit (e.g., multivalent antibodies) immunospecifically binding to an epitope on a CD22 protein, such as human CD22. For example, a monospecific antibody in accordance with embodiments of the invention can include a heavy chain variable region comprising two antigen-binding domains, wherein each antigen-binding domain binds to the same epitope on a CD22 protein (i.e., bivalent and monospecific).

[0099] An "epitope" is the site on the surface of an antigen molecule to which a single antibody molecule binds. Generally, an antigen has several or many different epitopes and reacts with many different antibodies. The term specifically includes linear epitopes and conformational epitopes.

[0100] "Epitope mapping" is the process of identifying the binding sites, or epitopes, of antibodies on their target antigens. Antibody epitopes may be linear epitopes or conformational epitopes. Linear epitopes are formed by a continuous sequence of amino acids in a protein. Conformational epitopes

are formed of amino acids that are discontinuous in the protein sequence, but which are brought together upon folding of the protein into its three-dimensional structure.

[0101] "Polyepitopic specificity" refers to the ability to specifically bind to two or more different epitopes on the same or different target(s). As noted above, the present invention specifically includes anti-CD22 heavy chain antibodies with polyepitopic specificities, i.e., anti-CD22 heavy chain antibodies binding to one or more non-overlapping epitopes on a CD22 protein, such as a human CD22; and anti-CD22 heavy chain antibodies binding to one or more epitopes on a CD22 protein and to an epitope on a different protein, such as, for example, a CD3 protein. The term "non-overlapping epitope(s)" or "non-competitive epitope(s)" of an antigen is defined herein to mean epitope(s) that are recognized by one member of a pair of antigen-specific antibodies but not the other member. Pairs of antibodies, or antigen-binding regions targeting the same antigen on a multi-specific antibody, recognizing non-overlapping epitopes, do not compete for binding to that antigen and are able to bind that antigen simultaneously.

[0102] An antibody binds "essentially the same epitope" as a reference antibody, when the two antibodies recognize identical or sterically overlapping epitopes. The most widely used and rapid methods for determining whether two epitopes bind to identical or sterically overlapping epitopes are competition assays, which can be configured in all number of different formats, using either labeled antigen or labeled antibody. Usually, the antigen is immobilized on a 96-well plate, and the ability of unlabeled antibodies to block the binding of labeled antibodies is measured using radioactive or enzyme labels.

[0103] The term "valent" as used herein refers to a specified number of binding sites in an antibody molecule.

[0104] A "monovalent" antibody has one binding site. Thus a monovalent antibody is also monospecific.

[0105] A "multi-valent" antibody has two or more binding sites. Thus, the terms "bivalent", "trivalent", and "tetravalent" refer to the presence of two binding sites, three binding sites, and four binding sites, respectively. Thus, a bispecific antibody according to the invention is at least bivalent and may be trivalent, tetravalent, or otherwise multi-valent. A bivalent antibody in accordance with embodiments of the invention may have two binding sites to the same epitope (i.e., bivalent, monoparatopic), or to two different epitopes (i.e., bivalent, biparatopic).

[0106] A large variety of methods and protein configurations are known and used for the preparation of bispecific monoclonal antibodies (BsMAB), tri-specific antibodies, and the like.

[0107] The term "chimeric antigen receptor" or "CAR" is used herein in the broadest sense to refer to an engineered receptor, which grafts a desired binding specificity (e.g., the antigen-binding region of a monoclonal antibody or other ligand) to membrane-spanning and intracellular-signaling domains.

Typically, the receptor is used to graft the specificity of a monoclonal antibody onto a T cell to create a chimeric antigen receptor (CAR). (*J Natl Cancer Inst,* 2015; 108(7):dvj439; and Jackson et al., *Nature Reviews Clinical Oncology*, 2016; 13:370–383).

[0108] The term "human antibody" is used herein to include antibodies having variable and constant regions derived from human germline immunoglobulin sequences. The human antibodies herein may include amino acid residues not encoded by human germline immunoglobulin sequences, e.g., mutations introduced by random or site-specific mutagenesis *in vitro* or by somatic mutation *in vivo*. The term "human antibody" specifically includes heavy chain-only antibodies having human heavy chain variable region sequences, produced by transgenic animals, such as transgenic rats or mice, in particular UniAbs™ produced by UniRats™, as defined above.

[0109] By a "chimeric antibody" or a "chimeric immunoglobulin" is meant an immunoglobulin molecule comprising amino acid sequences from at least two different Ig loci, e.g., a transgenic antibody comprising a portion encoded by a human Ig locus and a portion encoded by a rat Ig locus. Chimeric antibodies include transgenic antibodies with non-human Fc-regions or artificial Fc-regions, and human idiotypes. Such immunoglobulins can be isolated from animals of the invention that have been engineered to produce such chimeric antibodies.

[0110] As used herein, the term "effector cell" refers to an immune cell which is involved in the effector phase of an immune response, as opposed to the cognitive and activation phases of an immune response. Some effector cells express specific Fc receptors and carry out specific immune functions. In some embodiments, an effector cell such as a natural killer cell is capable of inducing antibody-dependent cellular cytotoxicity (ADCC). For example, monocytes andmacrophages, which express FcR, are involved in specific killing of target cells and presenting antigens to other components of the immune system, or binding to cells that present antigens. In some embodiments, an effector cell may phagocytose a target antigen or target cell.

[0111] "Human effector cells" are leukocytes which express receptors such as T cell receptors or FcRs and perform effector functions. Preferably, the cells express at least FcγRIII and perform ADCC effector function. Examples of human leukocytes which mediate ADCC include natural killer (NK) cells, monocytes, cytotoxic T cells and neutrophils, with NK cells being preferred. The effector cells may be isolated from a native source thereof, e.g., from blood or PBMCs as described herein.

[0112] The term "immune cell" is used herein in the broadest sense, including, without limitation, cells of myeloid or lymphoid origin, for instance lymphocytes (such as B cells and T cells including cytolytic T cells (CTLs)), killer cells, natural killer (NK) cells, macrophages, monocytes, eosinophils, polymorphonuclear cells, such as neutrophils, granulocytes, mast cells, and basophils.

[0113] 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. Examples of

antibody effector functions include C1q binding; complement dependent cytotoxicity (CDC); Fc receptor binding; antibody-dependent cell-mediated cytotoxicity (ADCC); phagocytosis; down regulation of cell surface receptors (e.g., B cell receptor; BCR), etc.

[0114] "Antibody-dependent cell-mediated cytotoxicity" and "ADCC" refer to a cell-mediated reaction in which nonspecific cytotoxic cells that express Fc receptors (FcRs) (e.g., Natural Killer (NK) cells, neutrophils, and macrophages) recognize bound antibody on a target cell and subsequently cause lysis of the target cell. 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 US Patent No. 5,500,362 or 5,821,337 may 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 may be assessed *in vivo*, e.g., in an animal model such as that disclosed in Clynes *et al. PNAS (USA)* 95:652-656 (1998).

[0115] "Complement dependent cytotoxicity" or "CDC" refers to the ability of a molecule to lyse a target in the presence of complement. The complement activation pathway is initiated by the binding of the first component of the complement system (C1q) to a molecule (*e.g.* an antibody) complexed with a cognate antigen. To assess complement activation, a CDC assay, e.g., as described in Gazzano-Santoro *et al.*, *J. Immunol. Methods* 202:163 (1996), may be performed.

[0116] "Binding affinity" refers to the strength of the sum total of noncovalent interactions between a single binding site of a molecule (e.g., an antibody) 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 (Kd). Affinity can be measured by common methods known in the art. 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.

[0117] As used herein, the "Kd" or "Kd value" refers to a dissociation constant determined by BioLayer Interferometry, using an Octet QK384 instrument (Fortebio Inc., Menlo Park, CA) in kinetics mode. For example, anti-mouse Fc sensors are loaded with mouse-Fc fused antigen and then dipped into antibody-containing wells to measure concentration dependent association rates (kon). Antibody dissociation rates (koff) are measured in the final step, where the sensors are dipped into wells containing buffer only. The Kd is the ratio of koff/kon. (For further details see, Concepcion, J, et al., *Comb Chem High Throughput Screen*, 12(8), 791-800, 2009).

[0118] The terms "treatment", "treating" and the like are used herein to generally mean obtaining a desired pharmacologic and/or physiologic effect. The effect may be prophylactic in terms of completely or partially preventing a disease or symptom thereof and/or may be therapeutic in terms of a partial or complete cure for a disease and/or adverse effect attributable to the disease. "Treatment" as used herein covers any treatment of a disease in a mammal, and includes: (a) preventing the disease from occurring in a subject which may be predisposed to the disease but has not yet been diagnosed as having it; (b) inhibiting the disease, i.e., arresting its development; or (c) relieving the disease, i.e., causing regression of the disease. The therapeutic agent may be administered before, during or after the onset of disease or injury. The treatment of ongoing disease, where the treatment stabilizes or reduces the undesirable clinical symptoms of the patient, is of particular interest. Such treatment is desirably performed prior to complete loss of function in the affected tissues. The subject therapy may be administered during the symptomatic stage of the disease, and in some cases after the symptomatic stage of the disease.

[0119] A "therapeutically effective amount" is intended for an amount of active agent which is necessary to impart therapeutic benefit to a subject. For example, a "therapeutically effective amount" is an amount which induces, ameliorates or otherwise causes an improvement in the pathological symptoms, disease progression or physiological conditions associated with a disease or which improves resistance to a disorder.

[0120] The terms "B-cell neoplasms" or "mature B-cell neoplasms" in the context of the present invention include small lymphocytic lymphoma, B-cell prolymphocytic lymphoma, B-cell chronic lymphocytic leukemia, mantle cell lymphoma, Burkitt's lymphoma, follicular lymphoma, diffuse large B-cell lymphoma (DLBCL), multiple myeloma, lymphoplasmacytic lymphoma, splenic marginal zone lymphoma, plasma cell neoplasms, such as plasma cell myeloma, plasmacytoma, monoclonal immunoglobulin deposition disease, heavy chain disease, MALT lymphoma, nodal marginal B cell lymphoma, intravascular large B cell lymphoma, primary effusion lymphoma, lymphomatoid granulomatosis, non-Hodgkins lymphoma, Hodgkins lymphoma, hairy cell leukemia, primary effusion lymphoma and AIDS-related non-Hodgkins lymphoma.

[0121] The term "characterized by expression of CD22" broadly refers to any disease or disorder in which CD22 expression is associated with or involved with one or more pathological processes that are characteristic of the disease or disorder. Such disorders include, but are not limited to, B-cell neoplasms.

[0122] The terms "subject," "individual," and "patient" are used interchangeably herein to refer to a mammal being assessed for treatment and/or being treated. In an embodiment, the mammal is a human. The terms "subject," "individual," and "patient" encompass, without limitation, individuals having cancer, individuals with autoimmune diseases, with pathogen infections, and the like. Subjects

may be human, but also include other mammals, particularly those mammals useful as laboratory models for human disease, e.g., mouse, rat, etc.

[0123] The term "pharmaceutical formulation" refers to a preparation which is in such form as to permit the biological activity of the active ingredient to be effective, and which contains no additional components which are unacceptably toxic to a subject to which the formulation would be administered. Such formulations are sterile. "Pharmaceutically acceptable" excipients (vehicles, additives) are those which can reasonably be administered to a subject mammal to provide an effective dose of the active ingredient employed.

[0124] A "sterile" formulation is aseptic or free or essentially free from all living microorganisms and their spores. A "frozen" formulation is one at a temperature below 0 °C.

[0125] A "stable" formulation is one in which the protein therein essentially retains its physical stability and/or chemical stability and/or biological activity upon storage. Preferably, the formulation essentially retains its physical and chemical stability, as well as its biological activity upon storage. The storage period is generally selected based on the intended shelf-life of the formulation. Various analytical techniques for measuring protein stability are available in the art and are reviewed in Peptide and Protein Drug Delivery, 247-301. Vincent Lee Ed., Marcel Dekker, Inc., New York, N.Y., Pubs. (1991) and Jones. A. Adv. Drug Delivery Rev. 10: 29-90) (1993), for example. Stability can be measured at a selected temperature for a selected time period. Stability can be evaluated qualitatively and/or quantitatively in a variety of different ways, including evaluation of aggregate formation (for example using size exclusion chromatography, by measuring turbidity, and/or by visual inspection); by assessing charge heterogeneity using cation exchange chromatography, image capillary isoelectric focusing (icIEF) or capillary zone electrophoresis; amino-terminal or carboxy-terminal sequence analysis; mass spectrometric analysis; SDS-PAGE analysis to compare reduced and intact antibody; peptide map (for example tryptic or LYS-C) analysis; evaluating biological activity or antigen binding function of the antibody; etc. Instability may involve any one or more of: aggregation, deamidation (e.g., Asn deamidation), oxidation (e.g., Met oxidation), isomerization (e.g., Asp isomeriation), clipping/hydrolysis/fragmentation (e.g., hinge region fragmentation), succinimide formation, unpaired cysteine(s), N-terminal extension, C-terminal processing, glycosylation differences, etc.

II. Detailed Description

Anti-CD22 Antibodies

[0126] Aspects of the invention include multispecific binding compounds that comprise an anti-CD22 binding domain. A family of closely related heavy chain-only antibody binding domains that bind to human CD22 are provided herein. The antibodies of this family comprise a set of CDR sequences as defined herein and shown in Table 1, and are exemplified by the provided heavy chain

variable region (VH) sequences of SEQ ID NOs: 24 to 84 set forth in Table 2. The antibodies described herein provide a number of benefits that contribute to utility as clinically therapeutic agent(s). The antibodies include members with a range of binding affinities, allowing the selection of a specific sequence with a desired binding affinity.

Table 1: Anti-CD22 heavy chain antibody unique CDR amino acid sequences.

SEQ_aa_CDR1	SEQ_aa_CDR2	SEQ_aaCDR3
GDSISSGDYY (SEQ ID NO: 1)	IYYSGVT (SEQ ID NO: 11)	TREDSSNWRS (SEQ ID NO: 18)
GDSISSGGYY (SEQ ID NO: 2)	IYYSGAT (SEQ ID NO: 12)	TRDDSSNWRS (SEQ ID NO: 19)
GGSISSGDYY (SEQ ID NO: 3)	IYYSGAT (SEQ ID NO: 13)	TREDSSSWRS (SEQ ID NO: 20)
GGSISSSSYY (SEQ ID NO: 4)	IYYTGST (SEQ ID NO: 14)	AREDSSSWRS (SEQ ID NO: 21)
GGSFSGYY (SEQ ID NO: 5)	VYYTGAT (SEQ ID NO: 15)	KRDDSSNWRS (SEQ ID NO: 22)
GDSISSSSYY (SEQ ID NO: 6)	IHYSGST (SEQ ID NO: 16)	ARDDSSNWRS (SEQ ID NO: 23)
GGSITSSSYY (SEQ ID NO: 7)	IYYSGSA (SEQ ID NO: 17)	
GGSISSSSHY (SEQ ID NO: 8)		
GGSIISSSYY (SEQ ID NO: 9)		
GGSINDNSHY (SEQ ID NO: 10)		

Table 2. Anti-CD22 heavy chain antibody variable domain amino acid sequences.

Clone ID #	SEQ_aa_FR1_FR4	SEQ ID NO:
335207	QLQLQESGPGLVKPSETLSLTCTVSGDSISSGDYYWGWIRQPPGKGLEWIG HIYYSGVTYYNPSLKSRVTISVDTSRNQFSLKLSSVTAADTAVYYCTREDSS NWRSRGQGTLVTVSS	24
335161	QLQLQESGPGLVKPSETLSLTCTVSGDSISSGDYYWGWIRQPPGKGLEWIG HIYYSGATYYNPSLENRVTISVDTSKNQFSLKLSSVTAADTAVYYCTRDDS SNWRSRGQGTLVTVSS	25
335254	QLQLQESGPGLVKPSETLSLTCTVSGDSISSGDYYWGWIRQPPGKGLEWIG HIYYSGVTYYNPSLKNRVTISVDTSKNQFSLKLSSVTAADTAVYYCTREDS SSWRSRGQGTLVTVSS	26
335260	QLQLQESGPGLVKPSETLSLTCTVSGDSISSGDYYWGWIRQPPGKGLEWIG HIYYSGVTYYNPSLKNRVTISVDTSRNQFSLNLSSVTAADTAVYYCTREDS SSWRSRGQGTLVTVSS	27
335151	QLQLQESGPGLVKPSETLSLTCTVSGDSISSGDYYWGWIRQPPGKGLEWIG HIYYSGATYYNPSLKNRVTISVDTSRNQFSLNLSSVTAADTAVYYCTRDDS SNWRSRGQGTLVTVSS	28
335170	QLQLQESGPGLVKPSETLSLTCTVSGDSISSGDYYWGWIRQPPGKGLEWIG HIYYSGATYYNPSLKNRVTISVDTSRNQFSLKLSSVTAADTAVYYCTRDDS SNWRSRGQGTLVTVSS	29
335176	QLQLQESGPGLVKPSETLSLTCTVSGDSISSGDYYWGWIRQPPGKGLEWIG HIYYSGATYYNPSLKNRVTISVDTSKNQFSLKLSSVTAADTAVYYCTRDDS SNWRSRGQGTLVTVSS	30
335181	QLQLQESGPGLVKPSETLSLTCTVSGDSISSGGYYWGWIRQPPGKGLEWIG HIYYSGATYYNPSLKNRVTISVDTSKNQFSLKLSSVTAADTAVYYCTRDDS SNWRSRGQGTLVTVSS	31

Clone ID #	SEQ_aa_FR1_FR4	SEQ ID NO:
335244	QLQLQESGPGLVKPSETLSLTCTVSGDSISSGDYYWGWIRQPPGKGLEWIG HIYYSGATYYNPSLKNRVTISVDTSRNQFSLNLSSVTAADTAVYYCTREDS SSWRSRGQGTLVTVSS	32
335154	QLQLQESGPGLVKPSETLSLTCTVSGDSISSGDYYWGWIRQPPGKGLEWIG HIYYSGVTYYNPSLKNRVTISVDTSKNQFSLKLSSVTAADTAVYYCTRDDS SNWRSRGQGTLVTVSS	33
335201	QLQLQESGPGLVKPSETLSLTCTVSGDSISSGDYYWGWIRQPPGKGLEWIG HIYYSGVTYYNPSLKNRVTISVDTSRNQFSLKLSSVTAADTAVYYCTREDS SNWRSRGQGTLVTVSS	34
335261	QLQLQESGPGLVKPSETLSLTCTVSGDSISSGDYYWGWIRQPPGKGLEWIG HIYYSGATYYNPSLENRVTISVDTSKNQFSLKLSSVTAADTAVYYCTREDS SSWRSRGQGTLVTVSS	35
335293	QLQLQESGPGLVKPSETLSLTCTVSGDSISSGDYYWGWIRQPPGKGLEWIG HIYYSGATYYNPSLKNRVTISVDTSRNQFSLKLSSVTAADTAVYYCTREDS SSWRSRGQGTLVTVSS	36
335203	QLQLQESGPGLVKPSETLSLTCTVSGDSISSGDYYWGWIRQPPGKGLEWIG HIYYSGVTYYNPSLKNRVTISVDTSKNQFSLKLSSVTAADTAVYYCTREDS SNWRSRGQGTLVTVSS	37
335185	QLQLQESGPGLVKPSETLSLTCTVSGDSISSGDYYWGWIRQPPGKGLEWIG HIYYSGATYYNPSLKNRVTISVDTSRNQFSLNLSSVTAADTAVYYCTREDS SNWRSRGQGTLVTVSS	38
335206	QLQLQESGPGLVKPSETLSLTCTVSGDSISSGDYYWGWIRQPPGKGLEWIG HIYYSGATYYNPSLKNRVTISVDTSKNQFSLKLSSVTAADTAVYYCTREDS SNWRSRGQGTLVTVSS	39
335245	QLQLQESGPGLVKPSETLSLTCTVSGDSISSGDYYWGWIRQPPGKGLEWIG HIYYSGATYYNPSLKNRVTISVDTSKNQFSLKLSSVTAADTAVYYCTREDS SSWRSRGQGTLVTVSS	40
335218	QLQLQESGPGLVKPSETLSLTCTVSGDSISSGDYYWGWIRQPPGKGLEWIG HIYYSGATYYNPSLKNRVTISVDTSRNQFSLKLSSVTAADTAVYYCTREDS SNWRSRGQGTLVTVSS	41
335160	QLQLQESGPGLVKPSETLSLTCTVSGDSISSGDYYWGWIRQPPGKGLEWIG SIYYSGATYYNPSLKNRVTISVDTSKNQFSLKLSSVTAADTAVYYCTRDDS SNWRSRGQGTLVTVSS	42
335158	QLQLQESGPGLVKPSETLSLTCTVSGGSISSGDYYWGWIRQPPGKGLEWIG HIYYSGATYYNPSLKNRVTISVDTSRNQFSLKLSSVTAADTAVYYCTRDDS SNWRSRGQGTLVTVSS	43
324508	QLQLQESGPGLVKPSETLSLTCTVSGGSISSGDYYWGWIRQPPGKGLEWIG HIYYSGATYYNPSLENRVTISVDTSKNQFSLKLSSVTAADTAVYYCTRDDS SNWRSRGQGTLVTVSS	44
335307	QLQLQESGPGLVKPSETLSLTCTVSGDSISSGDYYWGWIRQPPGKGLEWIG SIYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCTREDSS SWRSRGQGTLVTVSS	45
335301	QLQLQESGPGLVKPSETLSLTCTVSGDSISSGDYYWGWIRQPPGKGLEWIG NIYYSGATYYNPSLKNRVTISVDTSKNQFSLKLSSVTAADTAVYYCTREDS SSWRSRGQGTLVTVSS	46
335323	QLQLQESGPGLVKPSETLSLTCTVSGDSISSGGYYWGWIRQPPGKGLEWIG SIYYSGSTYYNPSLKNRVTISVDTSKNQFSLKLSSVTAADTAVYYCTREDSS SWRSRGQGTLVTVSS	47
335271	QLQLQESGPGLVKPSETLSLTCTVSGDSISSGDYYWGWIRHPPGKGLEWIG HIYYSGATYYNPSLKNRVTISVDTSKNQFSLKLSSVTAADTAVYYCTREDS SSWRSRGQGTLVTVSS	48
335234	QLQLQESGPGLVKPSETLSLTCTVSGDSISSGDYYWGWIRQPPGKGLEWIG NIYYSGATYYNPSLKNRVTISVDTSKNQFSLKLSSVTAADTAVYYCTREDS SNWRSRGQGTLVTVSS	49

Clone ID #	SEQ_aa_FR1_FR4	SEQ ID NO:
335182	QLQLQESGPGLVKPSETLSLTCTVSGDSISSGDYYWGWIRQPPGKGLEWIG NIYYSGATYYNPSLKNRVTISVDTSKNQFSLKLSSVTAADTAVYYCTRDDS SNWRSRGQGTLVTVSS	50
335186	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGS IYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCTRDDSSN WRSRGQGTLVTVSS	51
335233	QLQLQESGPGLVKPSETLSLTCTVSGDSISSGDYYWGWIRQPPGKGLEWIG SIYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCTREDSS NWRSRGQGTLVTVSS	52
335224	QLQLQESGPGLVKPSETLSLTCTVSGDSISSGDYYWGWIRQPPGKGLEWIG SIYYTGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCTREDSS NWRSRGQGTLVTVSS	53
335210	QLQLQESGPGLVKPSETLSLTCTVSGGSISSGDYYWGWIRQPPGKGLEWIG HIYYSGATYYNPSLKNRVTISVDTSRNQFSLKLSSVTAADTAVYYCTREDS SNWRSRGQGTLVTVSS	54
335311	QLQLQESGPGLVKPSETLSLTCAVYGGSFSGYYWGWIRQPPGKGLEWIGHI YYSGATYYNPSLKNRVTISVDTSRNQFSLNLSSVTAADTAVYYCTREDSSS WRSRGQGTLVTVSS	55
335159	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGH IYYSGVTYYNPSLKNRVTISVDTSKNQFSLKLSSVTAADTAAYYCTRDDSS NWRSRGQGTLVTVSS	56
335188	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGH IYYSGVTYYNPSLKNRVTISVDTSKNQFSLKLSSVTAADTAVYYCTRDDSS NWRSRGQGTLVTVSS	57
335274	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGS IYYSGSTYYNPSLKSRVTISVDTSRNQFSLNLSSVTAADTAVYYCTREDSSS WRSRGQGTLVTVSS	58
335226	QLQLQESGPGLVKPSETLSLTCTVSGDSISSSSYYWGWIRQPPGKGLEWIGS IYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCTREDSSN WRSRGQGTLVTVSS	59
335333	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGS IYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREDSSS WRSRGQGTLVTVSS	60
335283	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGS IYYSGATYYNPSLKNRVTISVDTSKNQFSLKLSSVTAADTAVYYCTREDSS SWRSRGQGTLVTVSS	61
335297	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGH IYYSGATYYNPSLKNRVTISVDTSRNQFSLNLSSVTAADTAVYYCTREDSSS WRSRGQGTLVTVSS	62
335273	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGS IYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCTREDSSS WRSRGQGTLVTVSS	63
335187	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGH IYYSGATYYNPSLKNRVTISVDTSKNQFSLKLSSVTAADTAVYYCTRDDSS NWRSRGQGTLVTVSS	64
335295	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGS IYYSGATYYNPSLKNRVTISVDTSRNQFSLNLSSVTAADTAVYYCTREDSSS WRSRGQGTLVTVSS	65
335220	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGS IYYSGSTYYNPSLKNRVTISVDTSKNQFSLKLSSVTAADTAVYYCTREDSS NWRSRGQGTLVTVSS	66
335173	QLQLQESGPGLVKPSETLSLTCTVSGGSITSSSYYWGWIRQPPGKGLEWIGS IYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCTRDDSSN WRSRGQGTLVTVSS	67

Clone ID #	SEQ_aa_FR1_FR4	SEQ ID NO:
335219	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGS IYYSGVTYYNPSLKNRVTISVDTSKNQFSLKLSSVTAADTAVYYCTREDSS NWRSRGQGTLVTVSS	68
335236	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGS IYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCTREDSSN WRSRGQGTLVTVSS	69
335266	QLQLQESGPGLVRPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGS IYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCTREDSSS WRSRGQGTLVTVSS	70
335208	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGS IYYSGATYYNPSLKNRVTISVDTSRNQFSLNLSSVTAADTAVYYCTREDSS NWRSRGQGTLVTVSS	71
335195	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGS IYYSGATYYNPSLKNRVTISVDTSRNQFSLNLSSVTAADTAMYYCTREDSS NWRSRGQGTLVTVSS	72
335285	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGS IYYSGVTYYNPSLKNRVTISVDTSKNQFSLKLSSVTAADTAVYYCTREDSS SWRSRGQGTLVTVSS	73
335150	QLQLQESGPGLVKPSETLSLTCTVSGDSISSGDYYWGWIRQSPEKGLEWIG HIYYSGVTYYNPSLKNRVTISVDTSKNQFSLKLSSVTAADTAVYYCKRDDS SNWRSRGQGTLVTVSS	74
335316	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGH IYYSGATYYNPSLKNRVTISVDTSKNQFSLKLSSVTAADTAVYYCTREDSS SWRSRGQGTLVTVSS	75
335189	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGS VYYTGATYYNPSLKNRVTISVDTSKNQFSLKLSSVTAADTAVYYCTRDDS SNWRSRGQGTLVTVSS	76
335179	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWFRHPPGKGLDWIG SIHYSGSTYYNPSLKSRVTISVDTSRNQFSLNLSSVTAADTAVYYCTRDDSS NWRSRGQGTLVTVSS	77
335230	QLQLQESDPGLVKPSETLSLTCTVSGGSISSSSHYWGWIRQPPGKGLEWIGH IYYSGATYYNPSLKNRVTISVDTSRNQFSLNLSSVTAADTAVYYCTREDSS NWRSRGQGTLVTVSS	78
335166	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGS IYYSGSTYYNPSLKNRVTISVDTSRNQFSLNLSSVTAADTAVYYCTRDDSS NWRSRGQGTLVTVSS	79
335242	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGH IYYSGATYYNPSLKNRVTISVDTSRNQFSLNLSSVTAADTAVYYCTREDSS NWRSRGQGTLVTVSS	80
335162	QLQLQESGPGLVKPSETLSLTCTVSGGSIISSSYYWGWIRQPPGKGLEWIGSI YYSGSAYYHPSLKSRVTISIDTSKNQFSLKLSSVTAADTAVYYCARDDSSN WRSRGQGTLVTVSS	81
335171	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGS IYYSGATYYNPSLKNRVTISVDTSRNQFSLNLSSVTAADTAVYYCTRDDSS NWRSRGQGTLVTVSS	82
335232	QLQLQESGPGLVKPSETLSLTCTVSGDSISSGDYYWGWIRQPPGKGLEWIG HIYYSGATYYNPSLKNRVTISVDTSRNQSSLNLSSVTAADTAVYYCTREDS SNWRSRGQGTLVTVSS	83
335263	QLQLQESGPGLVKPSETLSLTCTVSGGSINDNSHYWGWIRQPPGKGLEWIG HIYYSGATYYNPSLKNRVTISVDTSRNQFSLNLSSVTAADTAVYYCTREDS SSWRSRGQGTLVTVSS	84

[0127] A suitable antibody may be selected from those provided herein for development and therapeutic or other use, including, without limitation, use as a bispecific antibody, e.g., as shown in

FIG. 14A, or a tri-specific antibody, or part of a CAR-T structure (e.g., as shown in FIG. 14B). FIG. 14A is an illustration of a non-limiting example of an anti-CD3 x anti-CD22 multi-specific antibody, where the anti-CD22 domain is monovalent and monospecific. In some embodiments, the anti-CD3 domain contains a CH1 domain and pairs with a light chain, while the anti-CD22 domain(s) is derived from heavy chain-only antibodies and does not contain a CH1 domain or interact with a light chain. In some embodiments, the two heavy chains are pared using, e.g., knobs-into-holes technology.

[0128] Turning to the antibodies depicted in FIG. 15, FIG. 15A depicts an anti-CD3 x anti-CD22 bispecific antibody wherein the anti-CD22 binding arm is monovalent and monospecific, and the antigen-binding domain of the anti-CD22 arm is in a single configuration, meaning only one antigen-binding domain is present. FIG. 15B depicts an anti-CD3 x anti-CD22 bispecific antibody wherein the anti-CD22 binding arm is bivalent and monospecific, and the antigen-binding domain of the anti-CD22 arm is in a tandem configuration, meaning there are two identical antigen binding domains placed in tandem. FIG. 15C depicts an anti-CD3 x anti-CD22 bispecific antibody wherein the anti-CD22 binding arm is bivalent and biparatopic, and the antigen-binding domains of the anti-CD22 arm are in a tandem configuration.

[0129] Determination of affinity for a candidate protein can be performed using methods known in the art, such as Biacore measurements. Members of the antibody family may have an affinity for CD22 with a Kd of from about 10^{-6} to around about 10^{-11}, including without limitation: from about 10^{-6} to around about 10^{-10}; from about 10^{-6} to around about 10^{-9}; from about 10^{-6} to around about 10^{-8}; from about 10^{-8} to around about 10^{-11}; from about 10^{-8} to around about 10^{-10}; from about 10^{-8} to around about 10^{-9}; from about 10^{-9} to around about 10^{-11}; from about 10^{-9} to around about 10^{-10}; or any value within these ranges. The affinity selection may be confirmed with a biological assessment for modulating, e.g., blocking, a CD22 biological activity, including *in vitro* assays, pre-clinical models, and clinical trials, as well as assessment of potential toxicity.

[0130] Members of the antibody family herein are not cross-reactive with the CD22 protein of *Cynomolgus* macaque, but can be engineered to provide cross-reactivity with the CD22 protein of *Cynomolgus* macaque, or with the CD22 of any other animal species, if desired.

[0131] The family of CD22-specific antibodies herein comprises a VH domain, comprising CDR1, CDR2 and CDR3 sequences in a human VH framework. The CDR sequences may be situated, as an example, in the region of around amino acid residues 26-35; 53-59; and 98-117 for CDR1, CDR2 and CDR3, respectively, of the provided exemplary variable region sequences set forth in SEQ ID NOs: 24 to 84. It will be understood by one of ordinary skill in the art that the CDR sequences may be in different positions if a different framework sequence is selected, although generally the order of the sequences will remain the same.

[0132] The CDR1, CDR2, and CDR3 sequences of the anti-CD22 antibodies of the present invention may be encompassed by the following structural formulas, where an X indicates a variable amino acid, which may be specific amino acids as indicated below.

CDR1

$G\ X_1\ S\ I\ X_2\ X_3\ X_4\ X_5\ X_6\ Y$ (SEQ ID NO: 104)

where X_1 is D or G;
X_2 is S, T, I or N;
X_3 is S or D;
X_4 is G, S or N;
X_5 is D, G or S; and
X_6 is Y or H.

CDR2

$X_7\ X_8\ Y\ X_9\ G\ X_{10}\ X_{11}$ (SEQ ID NO: 105)

where X_7 is I or V;
X_8 is Y or H;
X_9 is S or T;
X_{10} is A, V or S; and
X_{11} is T or A.

CDR3

$X_{12}\ R\ X_{13}\ D\ S\ S\ X_{14}\ W\ R\ S$ (SEQ ID NO: 106)

where X_{12} is T, A or K;
X_{13} is D or E; and
X_{14} is N or S.

[0133] Representative CDR1, CDR2 and CDR3 sequences are shown in Tables 1 and 3.

Table 3: Anti-CD22 heavy chain antibody CDR1, CDR2 and CDR3 amino acid sequences.

Clone ID #	SEQ_aa_CDR1	SEQ_aa_CDR2	SEQ_aaCDR3
335207	GDSISSGDYY (SEQ ID NO: 1)	IYYSGVT (SEQ ID NO: 11)	TREDSSNWRS (SEQ ID NO: 18)

Clone ID #	SEQ_aa_CDR1	SEQ_aa_CDR2	SEQ_aaCDR3
335161	GDSISSGDYY (SEQ ID NO: 1)	IYYSGAT (SEQ ID NO: 12)	TRDDSSNWRS (SEQ ID NO: 19)
335254	GDSISSGDYY (SEQ ID NO: 1)	IYYSGVT (SEQ ID NO: 11)	TREDSSSWRS (SEQ ID NO: 20)
335260	GDSISSGDYY (SEQ ID NO: 1)	IYYSGVT (SEQ ID NO: 11)	TREDSSSWRS (SEQ ID NO: 20)
335151	GDSISSGDYY (SEQ ID NO: 1)	IYYSGAT (SEQ ID NO: 12)	TRDDSSNWRS (SEQ ID NO: 19)
335170	GDSISSGDYY (SEQ ID NO: 1)	IYYSGAT (SEQ ID NO: 12)	TRDDSSNWRS (SEQ ID NO: 19)
335176	GDSISSGDYY (SEQ ID NO: 1)	IYYSGAT (SEQ ID NO: 12)	TRDDSSNWRS (SEQ ID NO: 19)
335181	GDSISSGGYY (SEQ ID NO: 2)	IYYSGAT (SEQ ID NO: 12)	TRDDSSNWRS (SEQ ID NO: 19)
335244	GDSISSGDYY (SEQ ID NO: 1)	IYYSGAT (SEQ ID NO: 12)	TREDSSSWRS (SEQ ID NO: 20)
335154	GDSISSGDYY (SEQ ID NO: 1)	IYYSGVT (SEQ ID NO: 11)	TRDDSSNWRS (SEQ ID NO: 19)
335201	GDSISSGDYY (SEQ ID NO: 1)	IYYSGVT (SEQ ID NO: 11)	TREDSSNWRS (SEQ ID NO: 18)
335261	GDSISSGDYY (SEQ ID NO: 1)	IYYSGAT (SEQ ID NO: 12)	TREDSSSWRS (SEQ ID NO: 20)
335293	GDSISSGDYY (SEQ ID NO: 1)	IYYSGAT (SEQ ID NO: 12)	TREDSSSWRS (SEQ ID NO: 20)
335203	GDSISSGDYY (SEQ ID NO: 1)	IYYSGVT (SEQ ID NO: 11)	TREDSSNWRS (SEQ ID NO: 18)
335185	GDSISSGDYY (SEQ ID NO: 1)	IYYSGAT (SEQ ID NO: 12)	TREDSSNWRS (SEQ ID NO: 18)
335206	GDSISSGDYY (SEQ ID NO: 1)	IYYSGAT (SEQ ID NO: 12)	TREDSSNWRS (SEQ ID NO: 18)
335245	GDSISSGDYY (SEQ ID NO: 1)	IYYSGAT (SEQ ID NO: 12)	TREDSSSWRS (SEQ ID NO: 20)
335218	GDSISSGDYY (SEQ ID NO: 1)	IYYSGAT (SEQ ID NO: 12)	TREDSSNWRS (SEQ ID NO: 18)
335160	GDSISSGDYY (SEQ ID NO: 1)	IYYSGAT (SEQ ID NO: 12)	TRDDSSNWRS (SEQ ID NO: 19)
335158	GGSISSGDYY (SEQ ID NO: 3)	IYYSGAT (SEQ ID NO: 12)	TRDDSSNWRS (SEQ ID NO: 19)
324508	GGSISSGDYY (SEQ ID NO: 3)	IYYSGAT (SEQ ID NO: 12)	TRDDSSNWRS (SEQ ID NO: 19)
335307	GDSISSGDYY (SEQ ID NO: 1)	IYYSGST (SEQ ID NO: 13)	TREDSSSWRS (SEQ ID NO: 20)
335301	GDSISSGDYY (SEQ ID NO: 1)	IYYSGAT (SEQ ID NO: 12)	TREDSSSWRS (SEQ ID NO: 20)
335323	GDSISSGGYY (SEQ ID NO: 2)	IYYSGST (SEQ ID NO: 13)	TREDSSSWRS (SEQ ID NO: 20)
335271	GDSISSGDYY (SEQ ID NO: 1)	IYYSGAT (SEQ ID NO: 12)	TREDSSSWRS (SEQ ID NO: 20)
335234	GDSISSGDYY (SEQ ID NO: 1)	IYYSGAT (SEQ ID NO: 12)	TREDSSNWRS (SEQ ID NO: 18)
335182	GDSISSGDYY (SEQ ID NO: 1)	IYYSGAT (SEQ ID NO: 12)	TRDDSSNWRS (SEQ ID NO: 19)
335186	GGSISSSSYY (SEQ ID NO: 4)	IYYSGST (SEQ ID NO: 13)	TRDDSSNWRS (SEQ ID NO: 19)

Clone ID #	SEQ_aa_CDR1	SEQ_aa_CDR2	SEQ_aaCDR3
335233	GDSISSGDYY (SEQ ID NO: 1)	IYYSGST (SEQ ID NO: 13)	TREDSSNWRS (SEQ ID NO: 18)
335224	GDSISSGDYY (SEQ ID NO: 1)	IYYTGST (SEQ ID NO: 14)	TREDSSNWRS (SEQ ID NO: 18)
335210	GGSISSGDYY (SEQ ID NO: 3)	IYYSGAT (SEQ ID NO: 12)	TREDSSNWRS (SEQ ID NO: 18)
335311	GGSFSGYY (SEQ ID NO: 5)	IYYSGAT (SEQ ID NO: 12)	TREDSSSWRS (SEQ ID NO: 20)
335159	GGSISSSSYY (SEQ ID NO: 4)	IYYSGVT (SEQ ID NO: 11)	TRDDSSNWRS (SEQ ID NO: 19)
335188	GGSISSSSYY (SEQ ID NO: 4)	IYYSGVT (SEQ ID NO: 11)	TRDDSSNWRS (SEQ ID NO: 19)
335274	GGSISSSSYY (SEQ ID NO: 4)	IYYSGST (SEQ ID NO: 13)	TREDSSSWRS (SEQ ID NO: 20)
335226	GDSISSSSYY (SEQ ID NO: 6)	IYYSGST (SEQ ID NO: 13)	TREDSSNWRS (SEQ ID NO: 18)
335333	GGSISSSSYY (SEQ ID NO: 4)	IYYSGST (SEQ ID NO: 13)	AREDSSSWRS (SEQ ID NO: 21)
335283	GGSISSSSYY (SEQ ID NO: 4)	IYYSGAT (SEQ ID NO: 12)	TREDSSSWRS (SEQ ID NO: 20)
335297	GGSISSSSYY (SEQ ID NO: 4)	IYYSGAT (SEQ ID NO: 12)	TREDSSSWRS (SEQ ID NO: 20)
335273	GGSISSSSYY (SEQ ID NO: 4)	IYYSGST (SEQ ID NO: 13)	TREDSSSWRS (SEQ ID NO: 20)
335187	GGSISSSSYY (SEQ ID NO: 4)	IYYSGAT (SEQ ID NO: 12)	TRDDSSNWRS (SEQ ID NO: 19)
335295	GGSISSSSYY (SEQ ID NO: 4)	IYYSGAT (SEQ ID NO: 12)	TREDSSSWRS (SEQ ID NO: 20)
335220	GGSISSSSYY (SEQ ID NO: 4)	IYYSGST (SEQ ID NO: 13)	TREDSSNWRS (SEQ ID NO: 18)
335173	GGSITSSSYY (SEQ ID NO: 7)	IYYSGST (SEQ ID NO: 13)	TRDDSSNWRS (SEQ ID NO: 19)
335219	GGSISSSSYY (SEQ ID NO: 4)	IYYSGVT (SEQ ID NO: 11)	TREDSSNWRS (SEQ ID NO: 18)
335236	GGSISSSSYY (SEQ ID NO: 4)	IYYSGST (SEQ ID NO: 13)	TREDSSNWRS (SEQ ID NO: 18)
335266	GGSISSSSYY (SEQ ID NO: 4)	IYYSGST (SEQ ID NO: 13)	TREDSSSWRS (SEQ ID NO: 20)
335208	GGSISSSSYY (SEQ ID NO: 4)	IYYSGAT (SEQ ID NO: 12)	TREDSSNWRS (SEQ ID NO: 18)
335195	GGSISSSSYY (SEQ ID NO: 4)	IYYSGAT (SEQ ID NO: 12)	TREDSSNWRS (SEQ ID NO: 18)
335285	GGSISSSSYY (SEQ ID NO: 4)	IYYSGVT (SEQ ID NO: 11)	TREDSSSWRS (SEQ ID NO: 20)
335150	GDSISSGDYY (SEQ ID NO: 1)	IYYSGVT (SEQ ID NO: 11)	KRDDSSNWRS (SEQ ID NO: 22)
335316	GGSISSSSYY (SEQ ID NO: 4)	IYYSGAT (SEQ ID NO: 12)	TREDSSSWRS (SEQ ID NO: 20)
335189	GGSISSSSYY (SEQ ID NO: 4)	VYYTGAT (SEQ ID NO: 15)	TRDDSSNWRS (SEQ ID NO: 19)
335179	GGSISSSSYY (SEQ ID NO: 4)	IHYSGST (SEQ ID NO: 16)	TRDDSSNWRS (SEQ ID NO: 19)
335230	GGSISSSSHY (SEQ ID NO: 8)	IYYSGAT (SEQ ID NO: 12)	TREDSSNWRS (SEQ ID NO: 18)

Clone ID #	SEQ_aa_CDR1	SEQ_aa_CDR2	SEQ_aaCDR3
335166	GGSISSSSYY (SEQ ID NO: 4)	IYYSGST (SEQ ID NO: 13)	TRDDSSNWRS (SEQ ID NO: 19)
335242	GGSISSSSYY (SEQ ID NO: 4)	IYYSGAT (SEQ ID NO: 12)	TREDSSNWRS (SEQ ID NO: 18)
335162	GGSIISSSYY (SEQ ID NO: 9)	IYYSGSA (SEQ ID NO: 17)	ARDDSSNWRS (SEQ ID NO: 23)
335171	GGSISSSSYY (SEQ ID NO: 4)	IYYSGAT (SEQ ID NO: 12)	TRDDSSNWRS (SEQ ID NO: 19)
335232	GDSISSGDYY (SEQ ID NO: 1)	IYYSGAT (SEQ ID NO: 12)	TREDSSNWRS (SEQ ID NO: 18)
335263	GGSINDNSHY (SEQ ID NO: 10)	IYYSGAT (SEQ ID NO: 12)	TREDSSSWRS (SEQ ID NO: 20)

[0134] In some embodiments, an anti-CD22 heavy chain-only antibody of the invention comprises a CDR1 sequence of any one of SEQ ID NOs: 1-10. In a particular embodiment, the CDR1 sequence is SEQ ID NO: 1.

[0135] In some embodiments, an anti-CD22 heavy chain-only antibody of the invention comprises a CDR2 sequence of any one of SEQ ID NOs: 11-17. In a particular embodiment, the CDR2 sequence is SEQ ID NO: 11.

[0136] In some embodiments, an anti-CD22 heavy chain-only antibody of the invention comprises a CDR3 sequence of any one of SEQ ID NOs: 18-23. In a particular embodiment, the CDR2 sequence is SEQ ID NO: 18.

[0137] In a further embodiment, an anti-CD22 heavy chain-only antibody of the invention comprises the CDR1 sequence of SEQ ID NO:1; the CDR2 sequence of SEQ ID NO: 11; and the CDR3 sequence of SEQ ID NO: 18.

[0138] In further embodiments, an anti-CD22 heavy chain-only antibody of the invention comprises any of the heavy chain variable region amino acid sequences of SEQ ID NOs: 24 to 84 (Table 2).

[0139] In a still further embodiment, an anti-CD22 heavy chain-only antibody of the present invention comprises the heavy chain variable region sequence of SEQ ID NO: 24.

[0140] In some embodiments, a CDR sequence in an anti-CD22 heavy chain-only antibody of the invention comprises one or two amino acid substitutions relative to a CDR1, CDR2 and/or CDR3 sequence or set of CDR1, CDR2 and CDR3 sequences in any one of SEQ ID NOs:1 to 23 (FIG. 1). In some embodiments, said amino acid substitution(s) are one or two of amino acid positions 4-6 of CDR1, and/or one or two of the amino acid positions of 2, 4-7 of CDR2, and/or one or two of the amino acid positions 5 and 12 of CDR3, relative to the formulas provided above. In some embodiments, the heavy chain-only anti-CD22 antibodies herein can comprise a heavy chain variable region sequence with at least about 85% identity, at least 90% identity, at least 95% identity, at least 98% identify, or at least 99% identity to any one of the heavy chain variable region sequences of SEQ ID NOs: 24 to 84 (shown in Table 2).

[0141] In some embodiments, bispecific or multi-specific antibodies are provided, which may have any of the configurations discussed herein, including, without limitation, a bispecific three-chain antibody like molecule. In some embodiments, a multi-specific antibody can comprise at least one heavy chain variable region having binding specificity for CD22. In some embodiments, a multi-specific antibody can comprise a heavy chain variable region comprising at least two antigen-binding domains, wherein each of the antigen-binding domains has binding specificity for CD22. In some embodiments, a multi-specific antibody can comprise a heavy chain/light chain pair that has binding specificity for a first antigen (e.g., CD3), and a heavy chain from a heavy chain-only antibody. In certain embodiments, the heavy chain from the heavy chain only antibody comprises an Fc portion comprising CH2 and/or CH3 and/or CH4 domains, in the absence of a CH1 domain. In one particular embodiment, a bispecific antibody comprises a heavy chain/light chain pair that has binding specificity for an antigen on an effector cell (e.g., a CD3 protein on a T cell), and a heavy chain from a heavy chain-only antibody comprising an antigen-binding domain that has binding specificity for CD22.

[0142] In some embodiments, a multi-specific antibody comprises a CD3-binding VH domain that is paired with a light chain variable domain. In certain embodiments, the light chain is a fixed light chain. In some embodiments, the CD3-binding VH domain comprises a CDR1 sequence of SEQ ID NO: 85, a CDR2 sequence of SEQ ID NO: 86, and a CDR3 sequence of SEQ ID NO: 87, in a human VH framework. In some embodiments, the fixed light chain comprises a CDR1 sequence of SEQ ID NO: 88, a CDR2 sequence of SEQ ID NO: 89, and a CDR3 sequence of SEQ ID NO: 90, in a human VL framework. Together, the CD3-binding VH domain and the light chain variable domain have binding affinity for CD3. In some embodiments, a CD3-binding VH domain comprises a heavy chain variable region sequence of SEQ ID NO: 91. In some embodiments, a CD3-binding VH domain comprises a sequence having at least about 80%, at least about 85%, at least about 90%, at least about 95%, or at least about 99% percent identity to the heavy chain variable region sequence of SEQ ID NO: 91. In some embodiments, a fixed light chain comprises a light chain variable region sequence of SEQ ID NO: 92. In some embodiments, a fixed light chain comprises a sequence having at least about 80%, at least about 85%, at least about 90%, at least about 95%, or at least about 99% percent identity to the heavy chain variable region sequence of SEQ ID NO: 92.

[0143] Multi-specific antibodies comprising the above-described CD3-binding VH domain and light chain variable domain have advantageous properties, for example, as described in published PCT application publication number WO2018/052503, the disclosure of which is incorporated by reference herein in its entirety. Any of the multi-specific antibodies and antigen-binding domains described herein, having binding affinity to CD22, can be combined with the CD3-binding domains and fixed

light chain domains described herein to generate multi-specific antibodies having binding affinity to one or more CD22 epitopes as well as CD3.

Table 4. Anti-CD3 Heavy and Light Chain CDR1, CDR2, CDR3 amino acid sequences.

	SEQ_aa_CDR1	**SEQ_aa_CDR2**	**SEQ_aa_CDR3**
Heavy Chain	GFTFHNYA (SEQ ID NO: 85)	ISWNSGSI (SEQ ID NO: 86)	AKDSRGYGDYSLGGAY (SEQ ID NO: 87)
Light Chain	QSVSSN (SEQ ID NO: 88)	GAS (SEQ ID NO: 89)	QQYNNWPWT (SEQ ID NO: 90)

Table 5. Anti-CD3 heavy and light chain variable region amino acid sequences.

VH	EVQLVESGGGLVQPGRSLRLSCAASGFTFHNYAMHWVRQAPGKGLEWVSGISWNSGSIGY ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAKDSRGYGDYSLGGAYWGQGTLV TVSSDYRLGGAYWGQGTLVTVSS (SEQ ID NO: 91)
VL	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYG ASTRATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPWTFGQ GTKVEIK (SEQ ID NO: 92)

Table 6: Human IgG1 and IgG4 Fc region sequences.

Human IgG1 (UniProt No. P01857)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT QKSLSLSPGK (SEQ ID NO: 93)
Human IgG4 (UniProt No. P01861)	ASTKGPSVFP LAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKT YTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVD GVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPS SIEKTISKAKGQPREPQVYTLPPSQEEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS DGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKS LSLSLGK (SEQ ID NO: 94)

Human IgG1 with silencing mutation (Fc region)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK KVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCV VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 95)
Human IgG4 with silencing mutation (Fc region)	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDK RVESKYGPPCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY SRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK (SEQ ID NO: 96)

Table 7: additional sequences.

Anti-CD3 light chain constant region sequence (kappa light chain)	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLI YGASTRATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWPW TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAK VQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKV YACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 97)
Anti-CD3 heavy chain sequence (with wt IgG1 Fc)	EVQLVESGGGLVQPGRSLRLSCAASGFTFHNYAMHWVRQAPGKGLE WVSGISWNSGSIGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAL YYCAKDSRGYGDYSLGGAYWGQGTLVTVSSASTKGPSVFPLAPSSKS TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 98)
Anti-CD3 heavy chain constant region sequence (with silenced IgG1 Fc)	EVQLVESGGGLVQPGRSLRLSCAASGFTFHNYAMHWVRQAPGKGLE WVSGISWNSGSIGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAL YYCAKDSRGYGDYSLGGAYWGQGTLVTVSSASTKGPSVFPLAPSSKS TSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC PAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 99)

Anti-CD3 heavy chain constant region sequence (with wt IgG4 Fc)	EVQLVESGGGLVQPGRSLRLSCAASGFTFHNYAMHWVRQAPGKGLE WVSGISWNSGSIGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAL YYCAKDSRGYGDYSLGGAYWGQGTLVTVSSASTKGPSVFPLAPCSRS TSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPE FLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKG LPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSD IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVF SCSVMHEALHNHYTQKSLSLSLGK (SEQ ID NO: 100)
Anti-CD3 heavy chain constant region sequence (with silenced IgG4 Fc)	EVQLVESGGGLVQPGRSLRLSCAASGFTFHNYAMHWVRQAPGKGLE WVSGISWNSGSIGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAL YYCAKDSRGYGDYSLGGAYWGQGTLVTVSSASTKGPSVFPLAPCSRS TSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPE AAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVD GVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK GLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNV FSCSVMHEALHNHYTQKSLSLSLGK (SEQ ID NO: 101)

[0144] In some embodiments, bispecific or multi-specific antibodies are provided, which may have any of the configurations discussed herein, including, without limitation, a bispecific three-chain antibody like molecule. In some embodiments, a bispecific antibody can comprise at least one heavy chain variable region having binding specificity for CD22, and at least one heavy chain variable region having binding specificity for a protein other than CD22. In some embodiments, a bispecific antibody can comprise a heavy chain/light chain pair that has binding specificity for a first antigen, and a heavy chain from a heavy chain-only antibody, comprising an Fc portion comprising CH2 and/or CH3 and/or CH4 domains, in the absence of a CH1 domain, and an antigen binding domain that binds an epitope of a second antigen or a different epitope of the first antigen. In one particular embodiment, a bispecific antibody comprises a heavy chain/light chain pair that has binding specificity for an antigen on an effector cell (e.g., a CD3 protein on a T cell), and a heavy chain from a heavy chain-only antibody comprising an antigen-binding domain that has binding specificity for CD22.

[0145] In some embodiments, where a binding compound of the invention is a bispecific antibody, one arm of the antibody (one binding moiety, or one binding unit) is specific for human CD22, while the other arm may be specific for target cells, tumor-associated antigens, targeting antigens, e.g., integrins, etc., pathogen antigens, checkpoint proteins, and the like. Target cells specifically include cancer cells, including, without limitation, cells from hematologic tumors, e.g. B-cell tumors, as discussed below. In some embodiments, one arm of the antibody (one binding moiety, or one binding unit) is specific for human CD22, while the other arm is specific for CD3.

[0146] In some embodiments, a binding compound comprises an anti-CD3 light chain polypeptide comprising the sequence of SEQ ID NO: 92 linked to the sequence of SEQ ID NO: 97, an anti-CD3 heavy chain polypeptide comprising the sequence of any one of SEQ ID NOs: 98, 99, 100 or 101, and an anti-CD22 heavy chain polypeptide comprising the sequence of any one of SEQ ID NOs: 24-84 linked to the sequence of any one of SEQ ID NOs: 93, 94, 95 or 96. These sequences can be combined in various ways to produce a bispecific antibody of a desired IgG subclass, e.g., IgG1, IgG4, silenced IgG1, silenced IgG4.

[0147] Various formats of bispecific antibodies are within the ambit of the invention, including, without limitation, single chain polypeptides, two chain polypeptides, three chain polypeptides, four chain polypeptides, and multiples thereof. The multi-specific antibodies herein specifically include T cell multi-specific (e.g., bispecific) antibodies binding to CD22 (anti-CD22 x anti-CD3 antibodies), which is selectively expressed on mature B-cells, and CD3. Such antibodies induce potent T cell mediated killing of cells expressing CD22.

Preparation of antibodies

[0148] The multispecific binding compounds of the present invention can be prepared by methods known in the art. In a preferred embodiment, the heavy chain antibodies herein are produced by transgenic animals, including transgenic mice and rats, preferably rats, in which the endogenous immunoglobulin genes are knocked out or disabled. In a preferred embodiment, the heavy chain antibodies herein are produced in UniRat™. UniRat™ have their endogenous immunoglobulin genes silenced and use a human immunoglobulin heavy-chain translocus to express a diverse, naturally optimized repertoire of fully human HCAbs. While endogenous immunoglobulin loci in rats can be knocked out or silenced using a variety of technologies, in UniRat™ the zinc-finger (endo)nuclease (ZNF) technology was used to inactivate the endogenous rat heavy chain J-locus, light chain Cκ locus and light chain Cλ locus. ZNF constructs for microinjection into oocytes can produce IgH and IgL knock out (KO) lines. For details see, e.g., Geurts et al., 2009, Science 325:433. Characterization of Ig heavy chain knockout rats has been reported by Menoret et al., 2010, Eur. J. Immunol. 40:2932-2941. Advantages of the ZNF technology are that non-homologous end joining to silence a gene or locus via deletions up to several kb can also provide a target site for homologous integration (Cui et al., 2011, Nat Biotechnol 29:64-67). Human heavy chain antibodies produced in UniRat™ are called UniAbs™ and can bind epitopes that cannot be attacked with conventional antibodies. Their high specificity, affinity, and small size make them ideal for mono- and poly-specific applications.

[0149] In addition to UniAbs™, specifically included herein are heavy chain-only antibodies lacking the camelid VHH framework and mutations, and their functional VH regions. Such heavy chain-only

antibodies can, for example, be produced in transgenic rats or mice which comprise fully human heavy chain-only gene loci as described, e.g., in WO2006/008548, but other transgenic mammals, such as rabbit, guinea pig, rat can also be used, rats and mice being preferred. Heavy chain-only antibodies, including their VHH or VH functional fragments, can also be produced by recombinant DNA technology, by expression of the encoding nucleic acid in a suitable eukaryotic or prokaryotic host, including, for example, mammalian cells (e.g., CHO cells), E. coli or yeast.

[0150] Domains of heavy chain-only antibodies combine advantages of antibodies and small molecule drugs: can be mono- or multi-valent; have low toxicity; and are cost-effective to manufacture. Due to their small size, these domains are easy to administer, including oral or topical administration, are characterized by high stability, including gastrointestinal stability; and their half-life can be tailored to the desired use or indication. In addition, VH and VHH domains of HCAbs can be manufactured in a cost effective manner.

[0151] In a particular embodiment, the heavy chain antibodies of the present invention, including UniAbs™, have the native amino acid residue at the first position of the FR4 region (amino acid position 101 according to the Kabat numbering system), substituted by another amino acid residue, which is capable of disrupting a surface-exposed hydrophobic patch comprising or associated with the native amino acid residue at that position. Such hydrophobic patches are normally buried in the interface with the antibody light chain constant region but become surface exposed in HCAbs and are, at least partially, for the unwanted aggregation and light chain association of HCAbs. The substituted amino acid residue preferably is charged, and more preferably is positively charged, such as lysine (Lys, K), arginine (Arg, R) or histidine (His, H), preferably arginine (R). In a preferred embodiment the heavy chain-only antibodies derived from the transgenic animals contain a Trp to Arg mutation at position 101. The resultant HCAbs preferably have high antigen-binding affinity and solubility under physiological conditions in the absence of aggregation.

[0152] As part of the present invention, human anti-CD22 heavy chain antibodies with unique sequences from UniRat™ animals (UniAb™) were identified that bind human CD22 in ELISA protein and cell-binding assays. The identified heavy chain variable region (VH) sequences (see, e.g., Table 2) are positive for human CD22 protein binding and/or for binding to CD22+ cells, and are all negative for binding to cells that do not express CD22.

[0153] Heavy chain antibodies binding to non-overlapping epitopes on a CD22 protein, e.g., UniAbs™ can be identified by competition binding assays, such as enzyme-linked immunoassays (ELISA assays) or flow cytometric competitive binding assays. For example, one can use competition between known antibodies binding to the target antigen and the antibody of interest. By using this approach, one can divide a set of antibodies into those that compete with the reference antibody and those that do not. The non-competing antibodies are identified as binding to a distinct epitope that

does not overlap with the epitope bound by the reference antibody. Often, one antibody is immobilized, the antigen is bound, and a second, labeled (e.g., biotinylated) antibody is tested in an ELISA assay for ability to bind the captured antigen. This can be performed also by using surface plasmon resonance (SPR) platforms, including ProteOn XPR36 (BioRad, Inc), Biacore 2000 and Biacore T200 (GE Healthcare Life Sciences), and MX96 SPR imager (Ibis technologies B.V.), as well as on biolayer interferometry platforms, such as Octet Red384 and Octet HTX (ForteBio, Pall Inc). For further details see the examples herein.

[0154] Typically, an antibody "competes" with a reference antibody if it causes about 15-100% reduction in the binding of the reference antibody to the target antigen, as determined by standard techniques, such as by the competition binding assays described above. In various embodiments, the relative inhibition is at least about 15%, at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50% at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95% or higher.

Pharmaceutical Compositions, Uses and Methods of Treatment

[0155] It is another aspect of the present invention to provide pharmaceutical compositions comprising one or more multispecific binding compounds of the present invention in admixture with a suitable pharmaceutically acceptable carrier. Pharmaceutically acceptable carriers as used herein are exemplified, but not limited to, adjuvants, solid carriers, water, buffers, or other carriers used in the art to hold therapeutic components, or combinations thereof.

[0156] In one embodiment, a pharmaceutical composition comprises a heavy chain antibody (e.g., UniAb™) that binds to CD22. In another embodiment, a pharmaceutical composition comprises a multi-specific (including bispecific) heavy chain antibody (e.g., UniAb™) with binding specificity for two or more non-overlapping epitopes on a CD22 protein. In a preferred embodiment, a pharmaceutical composition comprises a multi-specific (including bispecific) heavy chain antibody (e.g., UniAb™) with binding specificity to CD22 and with binding specificity to a binding target on an effector cell (e.g., a binding target on a T cell, such as, e.g., a CD3 protein on a T cell).

[0157] Pharmaceutical compositions of the antibodies used in accordance with the present invention are prepared for storage by mixing proteins having the desired degree of purity with optional pharmaceutically acceptable carriers, excipients or stabilizers (see, e.g. Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980)), such as in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients, or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid and methionine; preservatives (such as

octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride, benzethonium chloride; phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal complexes (e.g. Zn-protein complexes); and/or non-ionic surfactants such as TWEEN™, PLURONICS™ or polyethylene glycol (PEG).

[0158] Pharmaceutical compositions for parenteral administration are preferably sterile and substantially isotonic and manufactured under Good Manufacturing Practice (GMP) conditions. Pharmaceutical compositions can be provided in unit dosage form (i.e., the dosage for a single administration). The formulation depends on the route of administration chosen. The antibodies herein can be administered by intravenous injection or infusion or subcutaneously. For injection administration, the antibodies herein can be formulated in aqueous solutions, preferably in physiologically-compatible buffers to reduce discomfort at the site of injection. The solution can contain carriers, excipients, or stabilizers as discussed above. Alternatively, antibodies can be in lyophilized form for constitution with a suitable vehicle, e.g., sterile pyrogen-free water, before use.

[0159] Antibody formulations are disclosed, for example, in U.S. Patent No. 9,034,324. Similar formulations can be used for the heavy chain antibodies, including UniAbs™, of the present invention. Subcutaneous antibody formulations are described, for example, in US20160355591 and US20160166689.

Methods of Use

[0160] The heavy chain-only anti-CD22 antibodies, multi-specific antibodies, and pharmaceutical compositions described herein can be used for the treatment of diseases and conditions characterized by the expression of CD22, including, without limitation, the conditions and diseases described further herein.

[0161] CD22 is a 135-kDa type I transmembrane protein that is expressed at low levels on pre- and immature B cells, maximally on mature B cells, and ultimately downregulated on plasma cells. (*E.g.*, Walker et al., Immunology, 2008 Mar; 123(3) 314-25). CD22 is strongly expressed in follicular (primary and secondary B cell zones), mantle, and marginal zone B cells, and has been reported to be present in 60% to 80% of samples from patients with B cell malignancies (Alderson et al., Clin.

Cancer Res 2009;15(3) February 11, 2009). Due to its observed expression in a number of hematological malignancies, CD22 is a promising target for antibody-based therapeutics.

[0162] In one aspect, the CD22 heavy chain antibodies (e.g., UniAbs™) and pharmaceutical compositions herein can be used to treat hematological malignancies characterized by the expression of CD22, including, without limitation, diffuse large B cell lymphoma (DLBCL), non-Hodgkin's lymphoma, B-cell chronic lymphocylic leukemia (CLL), and B-cell acute lymphoblastic leukemia (ALL).

[0163] Diffuse large B cell lymphoma (DLBCL or DLBL) is the most common form of non-Hodgkin's lymphoma among adults (Blood 1997 89 (11): 3909-18), with an estimated annual incidence of 7 to 8 cases per 100,000 people per year in the US and the UK. It is characterized as an aggressive cancer that can arise in virtually any part of the body. The causes of DLBCL are not well understood, and it can arise from normal B cells as well as malignant transformation of other types of lymphoma or leukemia cells. Treatment approaches generally involve chemotherapy and radiation, and have resulted in an overall five-year survival rate average of approximately 58% for adults. Although some monoclonal antibodies have shown promise for treating DLBCL, consistent clinical efficacy has not yet been conclusively demonstrated. There is therefore a great need for new therapies, including immunotherapies, for DLBCL.

[0164] In another aspect, the CD22 heavy chain antibodies (e.g., UniAbs™) and pharmaceutical compositions herein can be used to treat autoimmune disorders characterized by pathogenic B-cells that express CD22, including, without limitation, systemic lupus erythematosus (SLE), rheumatoid arthritis (RA), and multiple sclerosis (MS).

[0165] Effective doses of the compositions of the present invention for the treatment of disease vary depending upon many different factors, including means of administration, target site, physiological state of the patient, whether the patient is human or an animal, other medications administered, and whether treatment is prophylactic or therapeutic. Usually, the patient is a human, but nonhuman mammals may also be treated, e.g., companion animals such as dogs, cats, horses, etc., laboratory mammals such as rabbits, mice, rats, etc., and the like. Treatment dosages can be titrated to optimize safety and efficacy.

[0166] Dosage levels can be readily determined by the ordinarily skilled clinician, and can be modified as required, e.g., as required to modify a subject's response to therapy. The amount of active ingredient that can be combined with the carrier materials to produce a single dosage form varies depending upon the host treated and the particular mode of administration. Dosage unit forms generally contain between from about 1 mg to about 500 mg of an active ingredient.

[0167] In some embodiments, the therapeutic dosage the agent may range from about 0.0001 to 100 mg/kg, and more usually 0.01 to 5 mg/kg, of the host body weight. For example dosages can be 1

mg/kg body weight or 10 mg/kg body weight or within the range of 1-10 mg/kg. An exemplary treatment regime entails administration once every two weeks or once a month or once every 3 to 6 months. Therapeutic entities of the present invention are usually administered on multiple occasions. Intervals between single dosages can be weekly, monthly or yearly. Intervals can also be irregular as indicated by measuring blood levels of the therapeutic entity in the patient. Alternatively, therapeutic entities of the present invention can be administered as a sustained release formulation, in which case less frequent administration is required. Dosage and frequency vary depending on the half-life of the polypeptide in the patient.

[0168] Typically, compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection can also be prepared. The pharmaceutical compositions herein are suitable for intravenous or subcutaneous administration, directly or after reconstitution of solid (e.g., lyophilized) compositions. The preparation also can be emulsified or encapsulated in liposomes or micro particles such as polylactide, polyglycolide, or copolymer for enhanced adjuvant effect, as discussed above. Langer, Science 249: 1527, 1990 and Hanes, Advanced Drug Delivery Reviews 28: 97-119, 1997. The agents of this invention can be administered in the form of a depot injection or implant preparation which can be formulated in such a manner as to permit a sustained or pulsatile release of the active ingredient. The pharmaceutical compositions are generally formulated as sterile, substantially isotonic and in full compliance with all Good Manufacturing Practice (GMP) regulations of the U.S. Food and Drug Administration.

[0169] Toxicity of the antibodies and antibody structures described herein can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., by determining the LD50 (the dose lethal to 50% of the population) or the LD100 (the dose lethal to 100% of the population). The dose ratio between toxic and therapeutic effect is the therapeutic index. The data obtained from these cell culture assays and animal studies can be used in formulating a dosage range that is not toxic for use in humans. The dosage of the antibodies described herein lies preferably within a range of circulating concentrations that include the effective dose with little or no toxicity. The dosage can vary within this range depending upon the dosage form employed and the route of administration utilized. The exact formulation, route of administration and dosage can be chosen by the individual physician in view of the patient's condition.

[0170] The compositions for administration will commonly comprise an antibody or other agent (e.g., another ablative agent) dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically

acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., Remington's Pharmaceutical Science (15th ed., 1980) and Goodman & Gillman, The Pharmacological Basis of Therapeutics (Hardman et al., eds., 1996)).

[0171] Also within the scope of the invention are kits comprising the active agents and formulations thereof, of the invention and instructions for use. The kit can further contain a least one additional reagent, e.g., a chemotherapeutic drug, etc. Kits typically include a label indicating the intended use of the contents of the kit. The term "label" as used herein includes any writing, or recorded material supplied on or with a kit, or which otherwise accompanies a kit.

[0172] The invention now being fully described, it will be apparent to one of ordinary skill in the art that various changes and modifications can be made without departing from the spirit or scope of the invention.

EXAMPLES

Materials and Methods

CD22 Protein Binding

[0173] The kinetic binding experiments to determine the antigen-antibody affinities were performed on the Octet QK-384 system (ForteBio) using bilayer interferometry. Anti-human IgG Fc Capture (AHC) biosensors (Forte Bio, Part No: 18-5064) were hydrated in assay buffer (1x PBS, 0.1% BSA, 0.02% Tween-20, pH 7.2) and preconditioned in 100mM Glycine pH 1.5. A baseline was established in the assay buffer for 120 seconds. AHC biosensors were then immobilized with UniAbs™ at a concentration of 5 μg/mL for 120 seconds. Another baseline (120 seconds) was established in the assay buffer. Next, they were then dipped into a 7-point, 1:2 dilution series of the human CD22 protein in the assay buffer, starting from 250 nM. The last well of the analyte column contained only assay buffer to test for non-specific binding between the buffer and the loaded biosensors, and was used as a reference well. Association was observed for 600 seconds, followed by dissociation for 900 seconds. Data analysis was performed using Octet Data Analysis v9.0 (ForteBio). Binding kinetics were analyzed using a standard 1:1 binding model.

CD22 Cell Binding

[0174] Binding to CD22 positive cells was assessed by flow cytometry (Guava easyCyte 8HT, EMD Millipore) using the Daudi cell line (ATCC). Briefly, 100,000 target cells were stained with a dilution series of purified UniAbs™ for 30 minutes at 4°C. Following incubation, the cells were washed twice with flow cytometry buffer (1X PBS, 1% BSA, 0.1% NaN_3) and stained with goat $F(ab')_2$ anti-human IgG conjugated to R-phycoerythrin (PE) (Southern Biotech, cat. #2042-09) to detect cell-bound antibodies. After a 20-minute incubation at 4°C, the cells were washed twice with flow cytometry buffer and then mean fluorescence intensity (MFI) was measured by flow cytometry. EC50 values were calculated using GraphPad Prism 7. Binding to cynomolgus CD22 positive cells was determined using the same protocol with the following modifications: the target cells were from CHO cells stably transfected to express the extracellular domain of cynomolgus CD22 and each antibody was tested at a single concentration (~1.7 µg/mL) so EC50 values were not calculated.

Example 1: Genetically Engineered Rats Expressing Heavy Chain-Only Antibodies

[0175] A 'human – rat' IgH locus was constructed and assembled in several parts. This involved the modification and joining of rat C region genes downstream of human J_Hs and subsequently, the upstream addition of the human V_H6 –D-segment region. Two BACs with separate clusters of human V_H genes [BAC6 and BAC3] were then co-injected with the BAC termed Georg, encoding the assembled and modified region comprising human V_H6 , all Ds, all J_Hs , and modified rat Cγ2a/1/2b (ΔC_H1).

[0176] Transgenic rats carrying artificial heavy chain immunoglobulin loci in unrearranged configuration were generated. The IgG2a(ΔC_H1)., IgG1(ΔC_H1)., IgG2b(ΔC_H1) genes lacked the C_H1 segment. The constant region genes IgE, IgA and 3' enhancer were included in Georg BAC. RT-PCR and serum analysis (ELISA) of transgenic rats revealed productive rearrangement of transgenic immunoglobulin loci and expression of heavy chain-only antibodies of various isotypes in serum. Transgenic rats were cross-bred with rats with mutated endogenous heavy chain and light chain loci previously described in US patent publication 2009/0098134 A1. Analysis of such animals demonstrated inactivation of rat immunoglobulin heavy and light chain expression and high level expression of heavy chain antibodies with variable regions encoded by human V, D, and J genes. Immunization of transgenic rats resulted in production of high titer serum responses of antigen-specific heavy chain antibodies. These transgenic rats expressing heavy chain antibodies with a human VDJ region were called UniRats™.

Example 2: Immunization

Immunization with recombinant extracellular domain of CD22.

[0177] Twelve UniRat animals (6 HC27, 6 HC28) were immunized with recombinant human CD22 protein. The animals were immunized according to standard protocol using a Titermax/Alhydrogel

adjuvant. Recombinant extracellular domain of CD22 was purchased from R&D Systems and was diluted with sterile saline and combined with adjuvant. The immunogen was combined with Titermax and Alhydrogel adjuvants. The first immunization (priming) with immunogen in Titermax was administered in the left and right legs. Subsequent boosting immunizations were done in the presence of Alhydrogel and three days before harvest boosts were performed with immunogens in PBS. Serum was collected from rats at the final bleed to determine serum titers.

Serum titer results

[0178] Serum titer summary information is shown in FIG 17. In the graphs depicted in FIG. 17, each line represents an individual animal. The legends of the graphs show the ID number of each individual animal. Binding activity for an 8-point dilution series of serum was tested by ELISA against a huCD22+Fc protein, huCD22+His tag, rhesus CD22+His tag protein protein, and a His tag off-target protein. Among this group of animals, a range of serum reactivity levels to both human and rhesus CD22 protein was observed. A serum response to the His protein tag was also observed.

Example 3: Binding to CD22-expressing cell lines

[0179] FIG. 16 summarizes target binding activity of the anti-CD22 heavy chain-only antibodies described herein. Column 1 indicates the Clone ID number of the anti-CD22 heavy chain-only antibody. Column 2 indicates the binding affinity to protein (KD) measured in molarity. Column 3 indicates the dissociation constant of binding to protein (K-off rate) measured in seconds. Column 4 indicates binding to Daudi cells measured as fold over background MFI signal. Column 5 indicates binding to CHO cells stably expressing cyno CD22 measured as fold over background MFI signal. Column 6 indicates binding to CHO cells that do not express CD22 protein measured as fold over background MFI signal.

Example 4: T cell mediated cytotoxicity of CD22 positive cells using resting human pan T cells

[0180] Unstimulated human T cells were incubated with CD22 positive cells (Daudi) and different concentrations of bispecific antibodies. After 48 hours, flow cytometry was performed on the cells to measure cytotoxicity. Supernatants from the cell culture were used to measure release of the cytokine IL-2. POS CTRL antibody refers to an antibody which comprises the same anti-CD22 arm, but a stronger affinity anti-CD3 arm. Results are provided in FIG. 1A and FIG. 1B.

[0181] Unstimulated human T cells were incubated with CD22 positive cells (SUDHL10) and different concentrations of bispecific antibodies. After 72 hours, flow cytometry was performed on the cells to measure cytotoxicity. Supernatants from the cell culture were used to measure release of the cytokine IL-2. POS CTRL antibody refers to an antibody which comprises the same anti-CD22 arm, but a stronger affinity anti-CD3 arm. Results are provided in FIG. 2A and FIG. 2B.

[0182] Unstimulated human T cells were incubated with CD22 positive DL-BCL cell line (RI-1) and different concentrations of bispecific antibodies with varying effector:target (E:T) cell ratios of 10:1, 5:1 or 1:1. After 72 hours, flow cytometry was performed on the cells to measure cytotoxicity. Supernatants from the cell culture were used to measure release of the cytokine IL-2. POS CTRL antibody refers to an antibody which comprises the same anti-CD22 arm, but a stronger affinity anti-CD3 arm. Data shows that the % cytotoxicity is dependent of E:T ratio. Results are provided in FIG. 3A and FIG. 3B.

Example 5: T cell mediated cytotoxicity of CD22 positive cells using activated human pan T cells

[0183] Activated human T cells were incubated with CD22 positive cells (Daudi and RI-1) or a CD22 negative cell line (K562) and different concentrations of bispecific antibodies. Cell lysis was measured using a calcein-based fluorescence readout. The bispecific CD22xCD3_F2F binding compound specifically caused lysis of CD22+ cells, but not CD22- K562 cells. POS CTRL antibody refers to an antibody which comprises the same anti-CD22 arm, but a stronger affinity anti-CD3 arm. NEG CTRL refers to an antibody with a non-specific tumor arm and the same anti-CD3 arm as anti-CD3_F2F. Results are provided in FIG. 4.

Example 6: Cell binding of bispecific antibodies against CD22 and CD3

[0184] CD22 positive cells Daudi, Raji, Ramos and CD22 negative cells K562 were incubated with bispecific antibodies. Cell binding was measured by flow cytometry using an anti-human IgG secondary antibody reagent. Data shows that the bispecific antibodies bind to CD22+ cells, but not CD22- cells. POS CTRL antibody refers to an antibody which comprises the same anti-CD22 arm, but a stronger affinity anti-CD3 arm. NEG CTRL refers to an antibody with a non-specific tumor arm and the same anti-CD3 arm as anti-CD3_F2F. Results are provided in FIG. 5.

Example 7: *In vivo* efficacy study with CD22-1 x CD3_F2F in Daudi xenografts

[0185] To test the *in vivo* efficacy of CD22-1 x CD3_F2F, varying doses of CD22-1 x CD3_F2F were administered to female NSG mice implanted with Daudi cells (5e6 cells/mouse) as shown in FIG. 6. The treatment schedule is shown below in Table 7. Mean tumor volume, body weight, percent body weight change, and individual tumor volume were used to assess efficacy of treatment.

Table 7: Sample treatment schedule

Group	Treatment	Dose	Route	n	Schedule
1	PBS	---	ip	10	
2	CD22-1 x CD3_F2F	0.05 (1µg/mouse)	ip	10	2x/wk (q3-4d) x 4
3	CD22-1 x CD3_F2F	0.5 (10 µg/mouse)	ip	10	2x/wk (q3-4d) x 4
4	CD22-1 x CD3_F2F	2.5 (50 µg/mouse)	ip	10	2x/wk (q3-4d) x 4
5	CD19 x CD3 BiTe	0.05 (1 µg/mouse)	ip	10	qd x10
6	Rituximab	15 (300 µg/mouse)	ip	10	2x/wk (q3-4d) x 4

[0186] The data from CD22-1 x CD3_F2F are shown in FIGS. 7-13, compared to a negative control and Rituximab, and demonstrate the efficacy of CD22-1 x CD3_F2F.

[0187] While preferred embodiments of the present invention have been shown and described herein, it will be obvious to those skilled in the art that such embodiments are provided by way of example only. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the invention. It should be understood that various alternatives to the embodiments of the invention described herein may be employed in practicing the invention. It is intended that the following claims define the scope of the invention and that methods and structures within the scope of these claims and their equivalents be covered thereby.

CLAIMS:

1. A multi-specific binding compound that binds to CD3, comprising:
a heavy chain variable region comprising:
(a) a CDR1 sequence having two or fewer substitutions in SEQ ID NO: 85; and/or
(b) a CDR2 sequence having two or fewer substitutions in SEQ ID NO: 86; and/or
(c) a CDR3 sequence having two or fewer substitutions in SEQ ID NO: 87; and
a light chain variable region.

2. The multi-specific binding compound of claim 1, wherein said heavy chain CDR1, CDR2 and CDR3 sequences are present in a human VH framework.

3. The multi-specific binding compound of claim 1, comprising a heavy chain variable region comprising heavy chain CDR1, CDR2 and CDR3 sequences in a human VH framework, wherein each CDR sequence comprises a sequence with at least 85% identity to any one of SEQ ID NOs:85-87; and
a light chain variable region.

4. The multi-specific binding compound of claim 1, comprising:
a heavy chain variable region comprising:
(a) a CDR1 sequence having two or fewer substitutions in SEQ ID NO: 85; and
(b) a CDR2 sequence having two or fewer substitutions in SEQ ID NO: 86; and
(c) a CDR3 sequence having two or fewer substitutions in SEQ ID NO: 87; and
a light chain variable region.

5. The multi-specific binding compound of claim 4, comprising:
a heavy chain variable region comprising a CDR1 sequence of SEQ ID NO: 85, a CDR2 sequence of SEQ ID NO: 86, and a CDR3 sequence of SEQ ID NO: 87; and
a light chain variable region.

6. The multi-specific binding compound of any one of claims 1-5, wherein the light chain variable region comprises a CDR1, CDR2 and CDR3 sequence in a human VL framework, wherein each CDR sequence comprises a sequence with 3 or fewer amino acid substitutions relative to a CDR sequence or set of CDR sequences in SEQ ID NO:92; or wherein the CDR sequences comprise a sequence with at least 85% identity to a CDR sequence or set of CDR sequences in SEQ ID NO:92.

7. The multi-specific binding compound of any one of claims 1-6, wherein the light chain variable region comprises a CDR1 sequence of SEQ ID NO: 88, a CDR2 sequence of SEQ ID NO: 89, and a CDR3 sequence of SEQ ID NO: 90.

8. The multi-specific binding compound of any one of claims 1-7, wherein the heavy chain variable region comprises an amino acid sequence having at least 95% identity to SEQ ID NO: 91.

9. The multi-specific binding compound of any one of claims 1-7, wherein the heavy chain variable region comprises an amino acid sequence set forth in SEQ ID NO: 91.

10. The multi-specific binding compound of any one of claims 1-9, wherein the light chain variable region comprises an amino acid sequence having at least 95% identity to SEQ ID NO: 92.

11. The multi-specific binding compound of any one of claims 1-9, wherein the light chain variable region comprises an amino acid sequence of SEQ ID NO: 92.

12. A multi-specific binding compound comprising a first binding unit having binding affinity to CD22 and a second binding unit having binding affinity to CD3, wherein the first binding unit comprises:

(a) a CDR1 having two or fewer substitutions in any of the amino acid sequences of SEQ ID NOs: 1 to 10; and/or

(b) a CDR2 having two or fewer substitutions in any of the amino acid sequences of SEQ ID NOs: 11 to 17; and/or

(c) a CDR3 having two or fewer substitutions in any of the amino acid sequences of SEQ ID NOs: 18 to 23.

13. The multi-specific binding compound of claim 12, wherein said CDR1, CDR2, and CDR3 sequences of the first binding unit are present in a human framework.

14. The multi-specific binding compound of any one of claims 12-13, wherein the first binding unit further comprises a heavy chain constant region sequence in the absence of a CH1 sequence.

15. The multi-specific binding compound of any one of claims 12 to 14, wherein the first binding unit comprises a heavy chain variable region comprising:

(a) a CDR1 sequence selected from the group consisting of SEQ ID NOs: 1 to 10; and/or

(b) a CDR2 sequence selected from the group consisting of SEQ ID NOs: 11 to 17; and/or

(c) a CDR3 sequence selected from the group consisting of SEQ ID NOs: 18 to 23.

16. The multi-specific binding compound of any one of claim 15, comprising:

(a) a CDR1 sequence selected from the group consisting of SEQ ID NOs: 1 to 10; and

(b) a CDR2 sequence selected from the group consisting of SEQ ID NOs: 11 to 17; and

(c) a CDR3 sequence selected from the group consisting of SEQ ID NOs: 18 to 23.

17. The multi-specific binding compound of any one of claims 12 to 16, comprising:

(a) a CDR1 sequence of SEQ ID NO: 1, a CDR2 sequence of SEQ ID NO: 11, and a CDR3 sequence of SEQ ID NO: 18;

(b) a CDR1 sequence of SEQ ID NO: 1, a CDR2 sequence of SEQ ID NO: 12, and a CDR3 sequence of SEQ ID NO: 19; or

(c) a CDR1 sequence of SEQ ID NO: 1, a CDR2 sequence of SEQ ID NO: 12, and a CDR3 sequence of SEQ ID NO: 20.

18. The multi-specific binding compound of claim 12, comprising a heavy chain variable region having at least 95% sequence identity to any one of the sequences of SEQ ID NOs: 24 to 84.

19. The multi-specific binding compound of claim 18, comprising a heavy chain variable region sequence selected from the group consisting of SEQ ID NOs: 24 to 84.

20. The multi-specific binding compound of claim 19, comprising a heavy chain variable region sequence of SEQ ID NO: 24.

21. A multi-specific binding compound comprising a first binding unit having binding affinity to CD22 and a second binding unit having binding affinity to CD3, wherein the first binding unit comprises

a heavy chain variable region comprising:

(a) a CDR1 sequence of the formula:

G X_1 S I X_2 X_3 X_4 X_5 X_6 Y (SEQ ID NO: 104)

where X_1 is D or G;

X_2 is S, T, I or N;

X_3 is S or D;

X_4 is G, S or N;

X_5 is D, G or S; and

X_6 is Y or H; and

(b) a CDR2 sequence of the formula:

X_7 X_8 Y X_9 G X_{10} X_{11} (SEQ ID NO: 105)

where X_7 is I or V;

X_8 is Y or H;

X_9 is S or T;

X_{10} is A, V or S; and

X_{11} is T or A; and

(c) a CDR3 sequence of the formula:

X_{12} R X_{13} D S S X_{14} W R S (SEQ ID NO: 106)

where X_{12} is T, A or K;

X_{13} is D or E; and

X_{14} is N or S.

22. A multi-specific binding compound comprising a first binding unit having binding affinity to CD22 and a second binding unit having binding affinity to CD3, wherein the first binding unit comprises

a heavy chain variable region comprising CDR1, CDR2 and CDR3 sequences in a human VH framework, wherein the CDR sequences comprise a sequence having two or fewer substitutions in a CDR sequence selected from the group consisting of SEQ ID NOs: 1-23.

23. A multi-specific binding compound comprising a first binding unit having binding affinity to CD22 and a second binding unit having binding affinity to CD3, wherein the first binding unit comprises

a heavy chain variable region comprising CDR1, CDR2 and CDR3 sequences in a human VH framework, wherein the CDR sequences are selected from the group consisting of SEQ ID NOs: 1-23.

24. A multi-specific binding compound comprising a first binding unit having binding affinity to CD22 and a second binding unit having binding affinity to CD3, wherein the first binding unit comprises

a heavy chain variable region comprising:

(a) a CDR1 sequence of SEQ ID NO: 1, a CDR2 sequence of SEQ ID NO: 11, and a CDR3 sequence of SEQ ID NO: 18; or

(b) a CDR1 sequence of SEQ ID NO: 1, a CDR2 sequence of SEQ ID NO: 12, and a CDR3 sequence of SEQ ID NO: 19; or

(c) a CDR1 sequence of SEQ ID NO: 1, a CDR2 sequence of SEQ ID NO: 12, and a CDR3 sequence of SEQ ID NO: 20,

in a human VH framework.

25. The multi-specific binding compound of claim 24, which is bispecific.

26. The multi-specific binding compound of any one of the preceding claims, which is in a CAR-T format.

27. A multi-specific binding compound comprising:

(i) a heavy chain variable region having binding affinity to CD3, comprising a CDR1 sequence of SEQ ID NO: 85, a CDR2 sequence of SEQ ID NO: 86, and CDR3 sequence of SEQ ID NO: 87, in a human VH framework;

(ii) a light chain variable region comprising a CDR1 sequence of SEQ ID NO: 88, a CDR2 sequence of SEQ ID NO: 89, and CDR3 sequences of SEQ ID NO: 90, in a human VL framework; and

(iii) an antigen-binding domain of an anti-CD22 heavy chain antibody, comprising a CDR1 sequence of SEQ ID NO: 1, a CDR2 sequence of SEQ ID NO: 11, and a CDR3 sequence of SEQ ID NO: 18, in a human VH framework.

28. A multi-specific binding compound comprising:

(i) a heavy chain variable region having binding affinity to CD3, comprising a CDR1 sequence of SEQ ID NO: 85, a CDR2 sequence of SEQ ID NO: 86, and CDR3 sequence of SEQ ID NO: 87, in a human VH framework;

(ii) a light chain variable region comprising a CDR1 sequence of SEQ ID NO: 88, a CDR2 sequence of SEQ ID NO: 89, and CDR3 sequences of SEQ ID NO: 90, in a human VL framework; and

(iii) an antigen-binding domain of an anti-CD22 heavy chain antibody, comprising a CDR1 sequence of SEQ ID NO: 1, a CDR2 sequence of SEQ ID NO: 12, and a CDR3 sequence of SEQ ID NO: 19, in a human VH framework.

29. A multi-specific binding compound comprising:

(i) a heavy chain variable region having binding affinity to CD3, comprising a CDR1 sequence of SEQ ID NO: 85, a CDR2 sequence of SEQ ID NO: 86, and CDR3 sequence of SEQ ID NO: 87, in a human VH framework;

(ii) a light chain variable region comprising a CDR1 sequence of SEQ ID NO: 88, a CDR2 sequence of SEQ ID NO: 89, and CDR3 sequences of SEQ ID NO: 90, in a human VL framework; and

(iii) an antigen-binding domain of an anti-CD22 heavy chain antibody, comprising a CDR1 sequence of SEQ ID NO: 1, a CDR2 sequence of SEQ ID NO: 12, and a CDR3 sequence of SEQ ID NO: 20, in a human VH framework.

30. The multispecific binding compound of any one of claims 1-29, comprising a human IgG1 Fc region.

31. The multispecific binding compound of claim 30, wherein the human IgG1 Fc region is a silenced human IgG1 Fc region.

32. The multispecific binding compound of any one of claims 1-29, comprising a human IgG4 Fc region.

33. The multispecific binding compound of claim 32, wherein the human IgG4 Fc region is a silenced human IgG4 Fc region.

34. A pharmaceutical composition comprising a multi-specific binding compound of any one of claims 1 to 33.

35. A method for the treatment of a B-cell disorder characterized by expression of CD22, comprising administering to a subject with said disorder a multi-specific binding compound of any one of claims 1 to 33, or the pharmaceutical composition of claim 34.

36. Use of a multi-specific binding compound of any one of claims 1 to 33, in the preparation of a medicament for the treatment of a B-cell disorder characterized by expression of CD22.

37. A multi-specific binding compound of any one of claims 1 to 33 for use in the treatment of a B-cell disorder characterized by expression of CD22.

38. The method, use or multi-specific binding compound of any one of claims 35-37, wherein the disorder is diffuse large B cell lymphoma (DLBCL).

39. The method, use or multi-specific binding compound of any one of claims 35-37, wherein the disorder is non-Hodgkin's lymphoma (NHL).

40. The method, use or multi-specific binding compound of any one of claims 35-37, wherein the disorder is systemic lupus erythematosus (SLE).

41. The method, use or multi-specific binding compound of any one of claims 35-37, wherein the disorder is rheumatoid arthritis (RA).

42. The method, use or multi-specific binding compound of any one of claims 35-37, wherein the disorder is multiple sclerosis (MS).

43. A polynucleotide encoding a multi-specific binding compound of any of claims 1 to 33.

44. A vector comprising the polynucleotide of claim 43.

45. A cell comprising the vector of claim 44.

46. A method of producing a multi-specific binding compound of any of claims 1 to 33, comprising growing a cell according to claim 45 under conditions permissive for expression of the binding compound, and isolating the binding compound from the cell.

47. A method of making a multi-specific binding compound of any one of claims 1 to 33, comprising immunizing a UniRat animal with CD22 and identifying CD22-binding heavy chain sequences.

48. A method of treatment, comprising administering to an individual an effective dose of the multi-specific binding compound of any one of claims 1 to 33, or the pharmaceutical composition of claim 34.

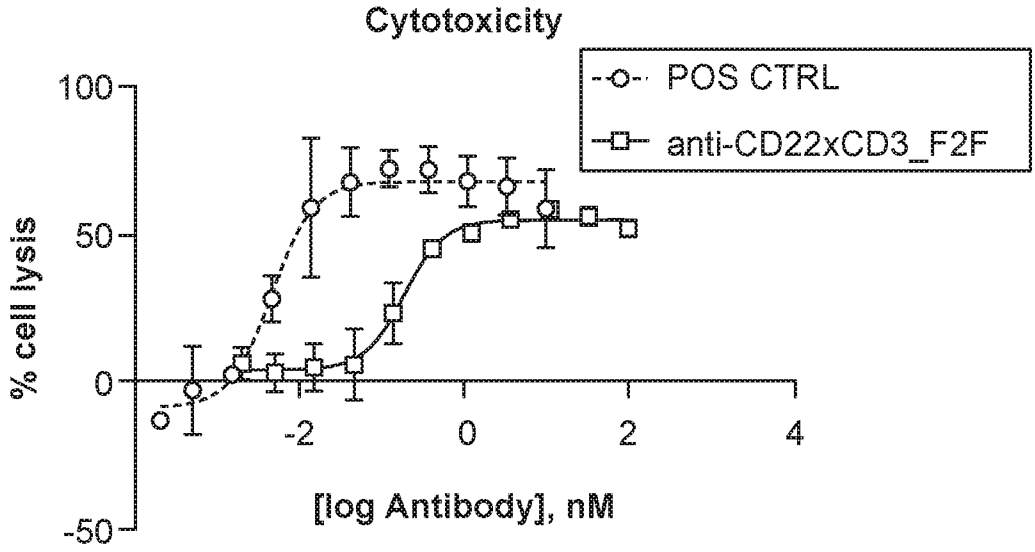

Cytotoxicity
POS CTRL
anti-CD22xCD3_F2F
% cell lysis
100
50
0
-50
-2
0
2
4
[log Antibody], nM

FIG. 1A

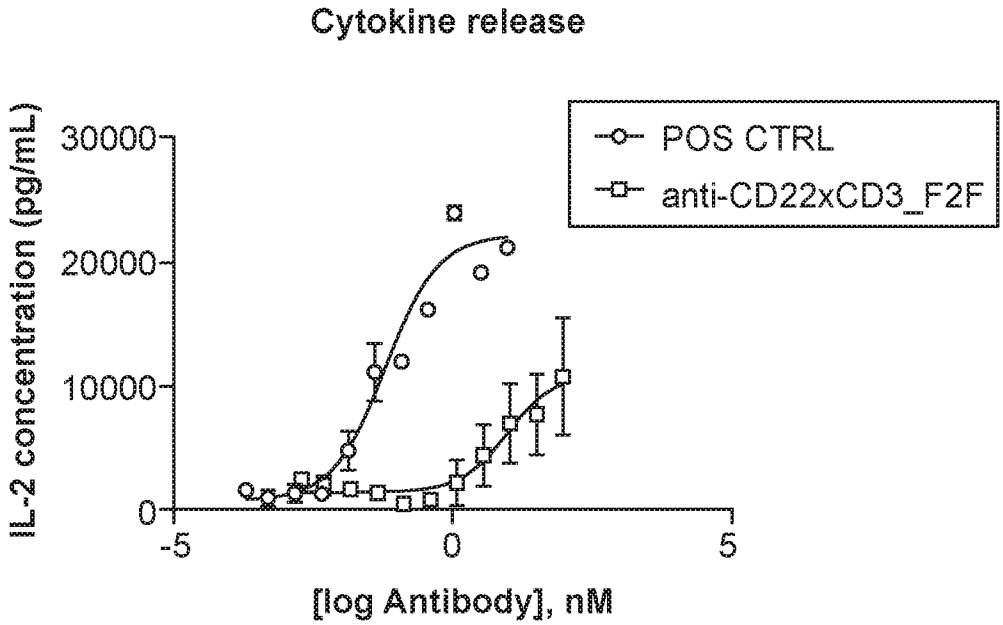

Cytokine release
POS CTRL
anti-CD22xCD3_F2F
IL-2 concentration (pg/mL)
30000
20000
10000
0
-5
0
5
[log Antibody], nM

FIG. 1B

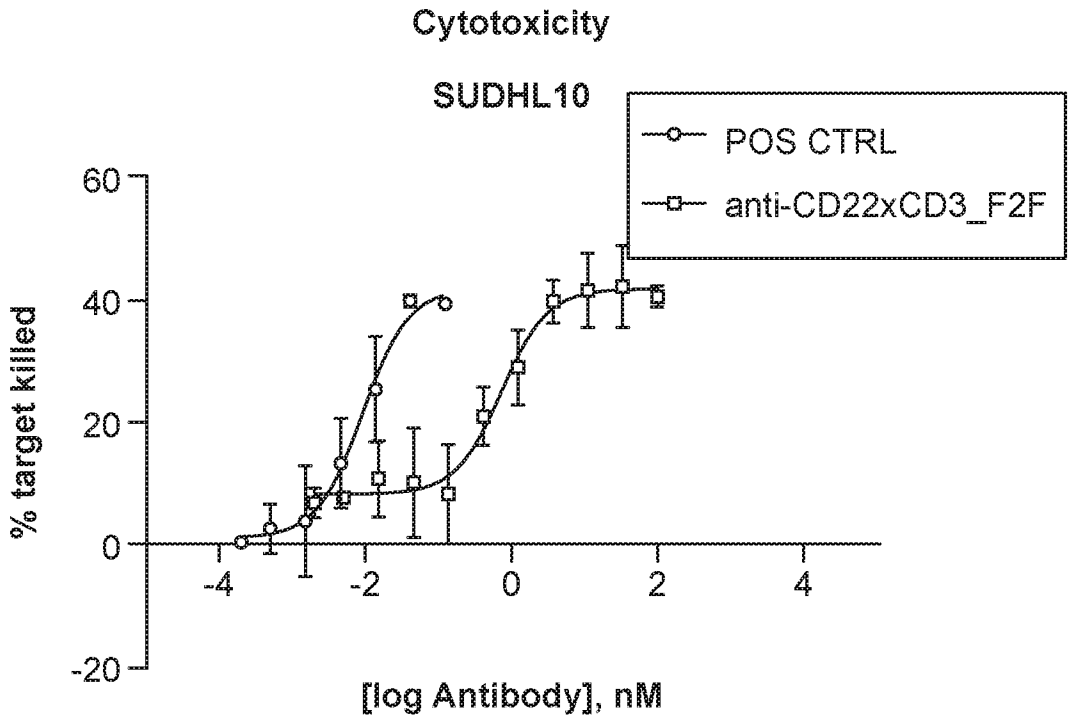

Cytotoxicity
SUDHL10
POS CTRL
anti-CD22xCD3_F2F
% target killed
60
40
20
0
-20
-4
-2
0
2
4
[log Antibody], nM

FIG. 2A

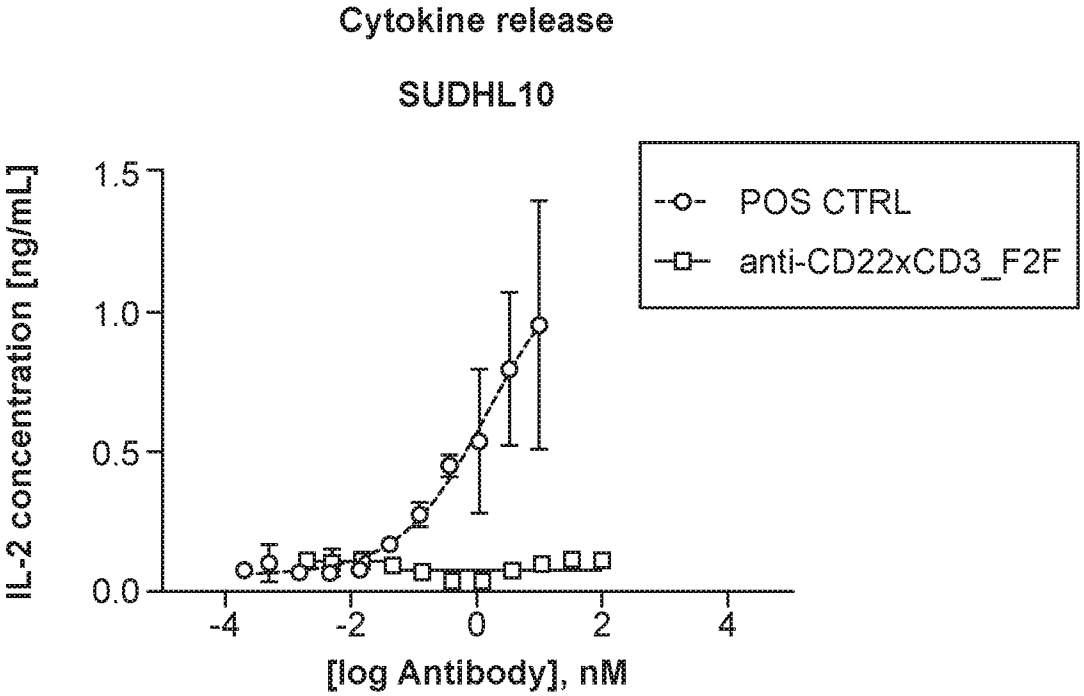

Cytokine release
SUDHL10
POS CTRL
anti-CD22xCD3_F2F
IL-2 concentration [ng/mL]
1.5
1.0
0.5
0.0
-4
-2
0
2
4
[log Antibody], nM

FIG. 2B

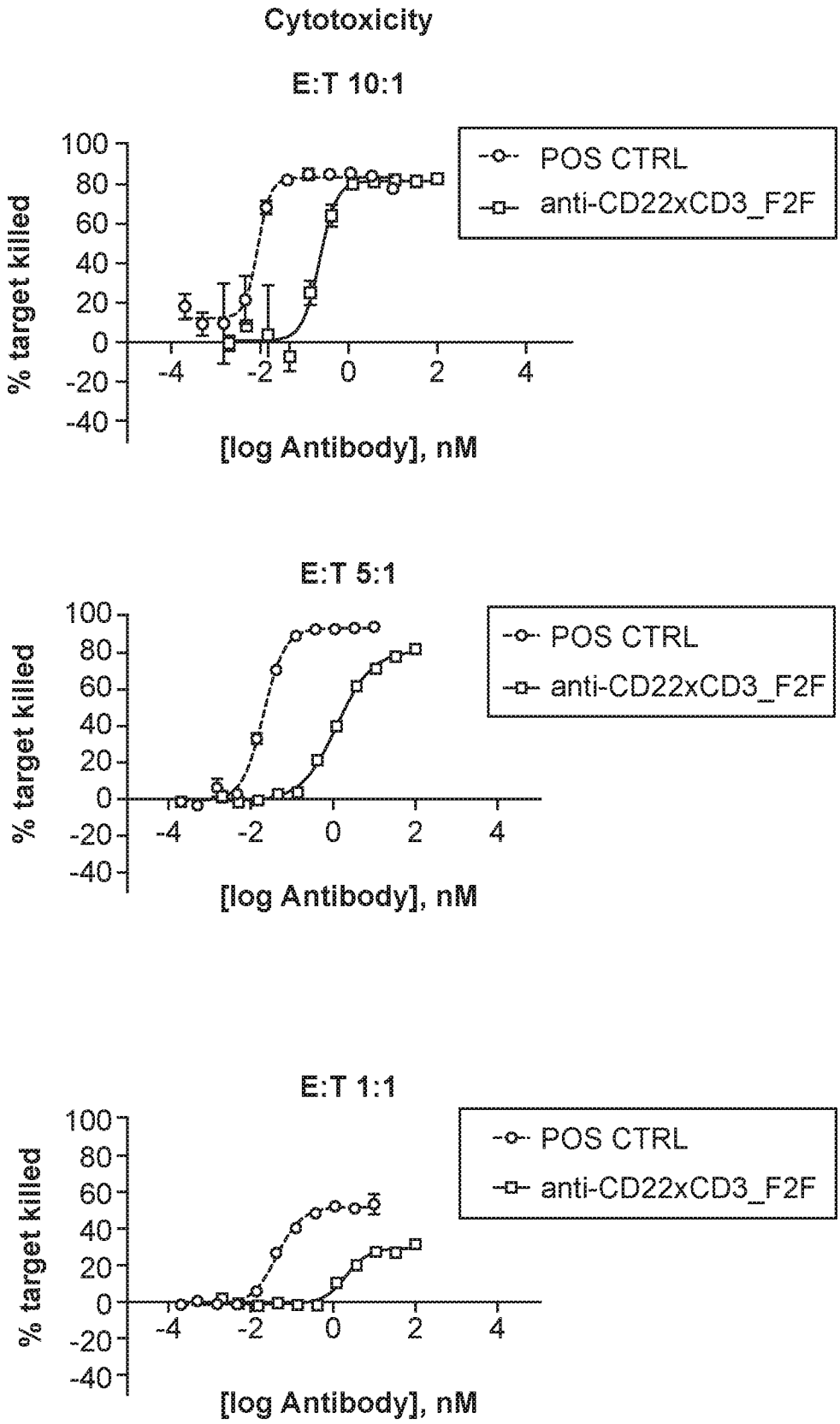

Cytotoxicity
E:T 10:1
% target killed
100
80
60
40
20
0
-20
-40
-4
-2
0
2
4
[log Antibody], nM
POS CTRL
anti-CD22xCD3_F2F
E:T 5:1
% target killed
[log Antibody], nM
POS CTRL
anti-CD22xCD3_F2F
E:T 1:1
% target killed
[log Antibody], nM
POS CTRL
anti-CD22xCD3_F2F

FIG. 3A

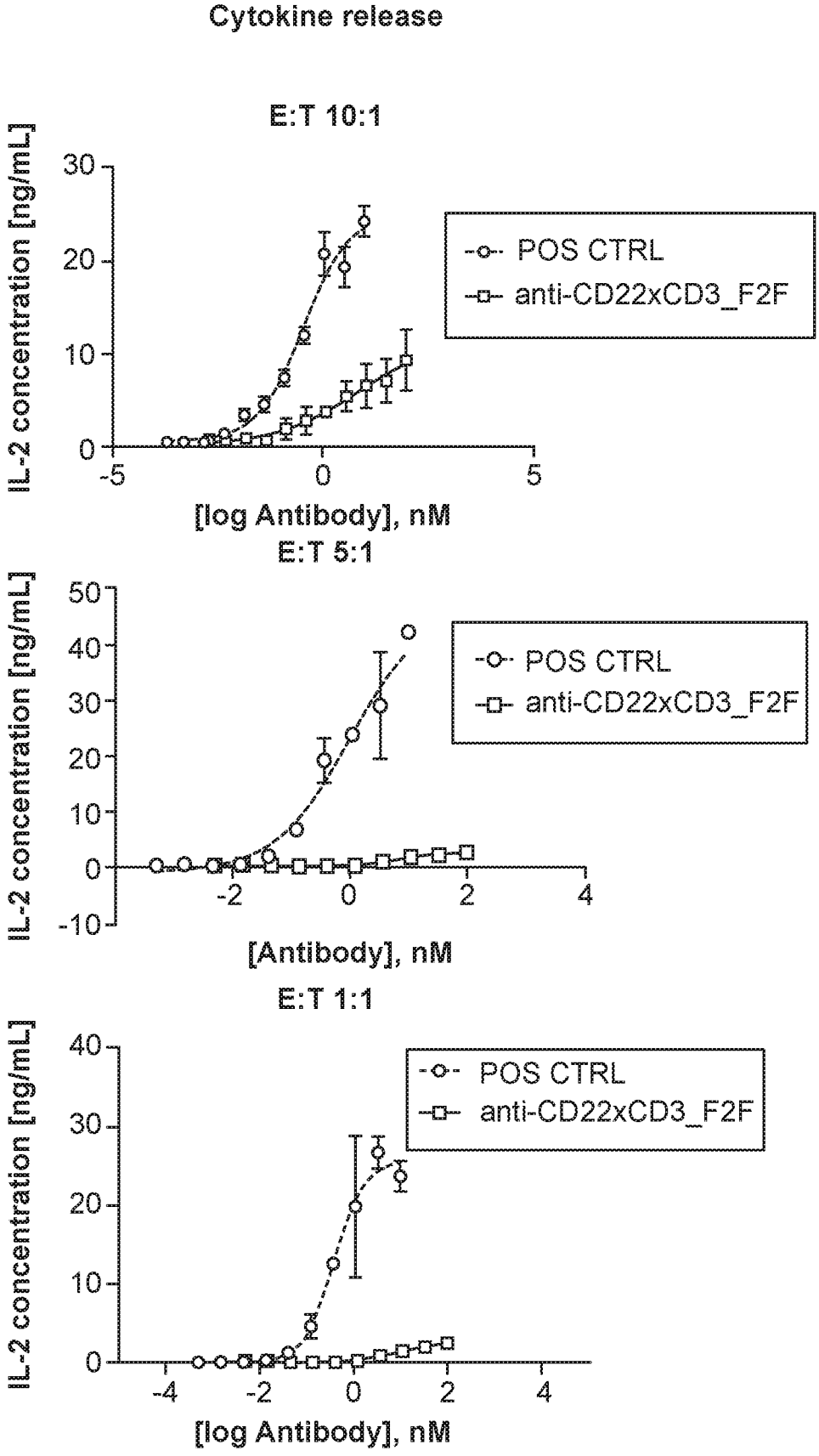

Cytokine release
E:T 10:1
IL-2 concentration [ng/mL]
30
20
10
0
-5
0
5
[log Antibody], nM
POS CTRL
anti-CD22xCD3_F2F
E:T 5:1
IL-2 concentration [ng/mL]
50
40
30
20
10
0
-10
-2
0
2
4
[Antibody], nM
POS CTRL
anti-CD22xCD3_F2F
E:T 1:1
IL-2 concentration [ng/mL]
40
30
20
10
0
-4
-2
0
2
4
[log Antibody], nM
POS CTRL
anti-CD22xCD3_F2F

FIG. 3B

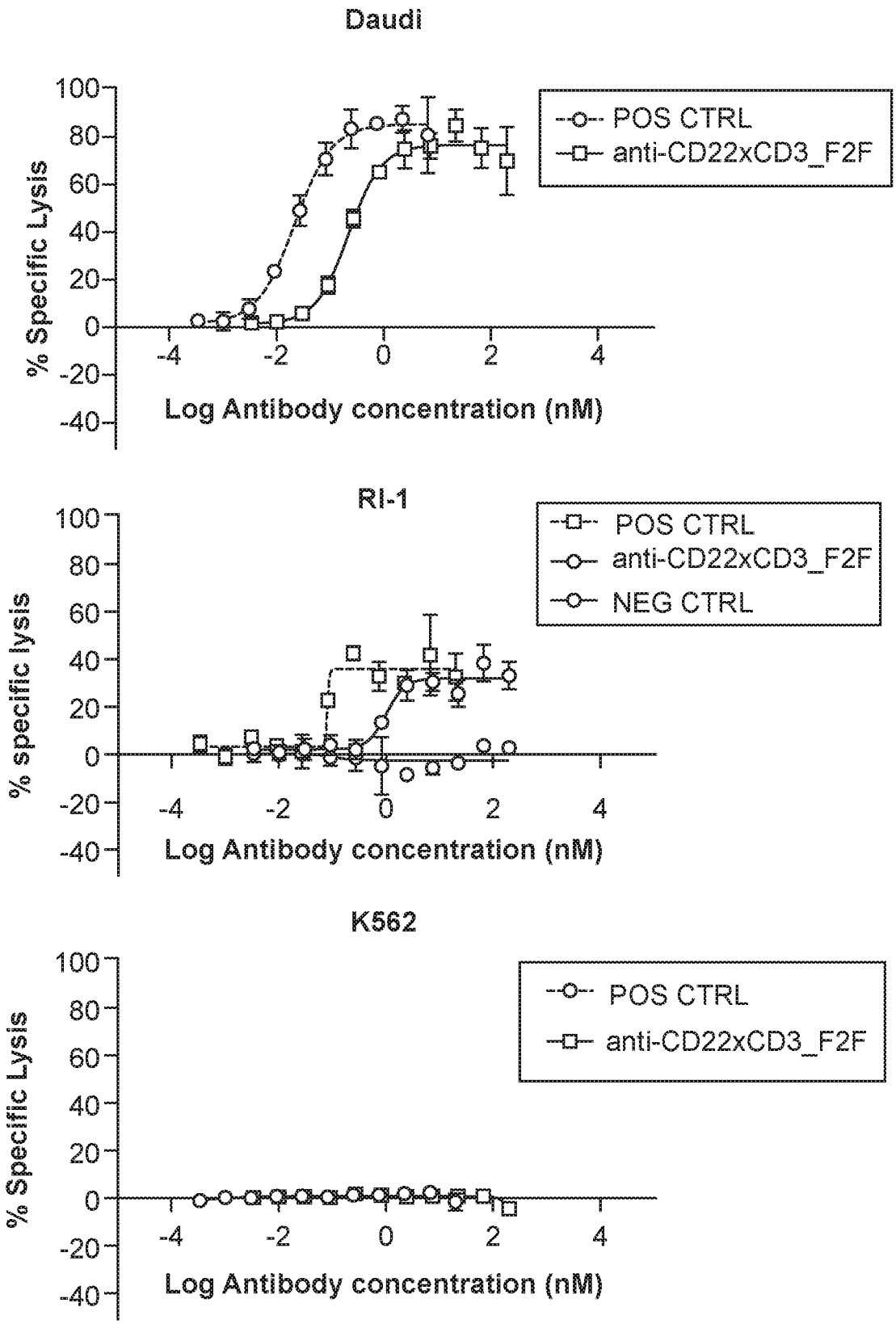

Daudi
% Specific Lysis
Log Antibody concentration (nM)
POS CTRL
anti-CD22xCD3_F2F
RI-1
% specific lysis
Log Antibody concentration (nM)
POS CTRL
anti-CD22xCD3_F2F
NEG CTRL
K562
% Specific Lysis
Log Antibody concentration (nM)
POS CTRL
anti-CD22xCD3_F2F

FIG. 4

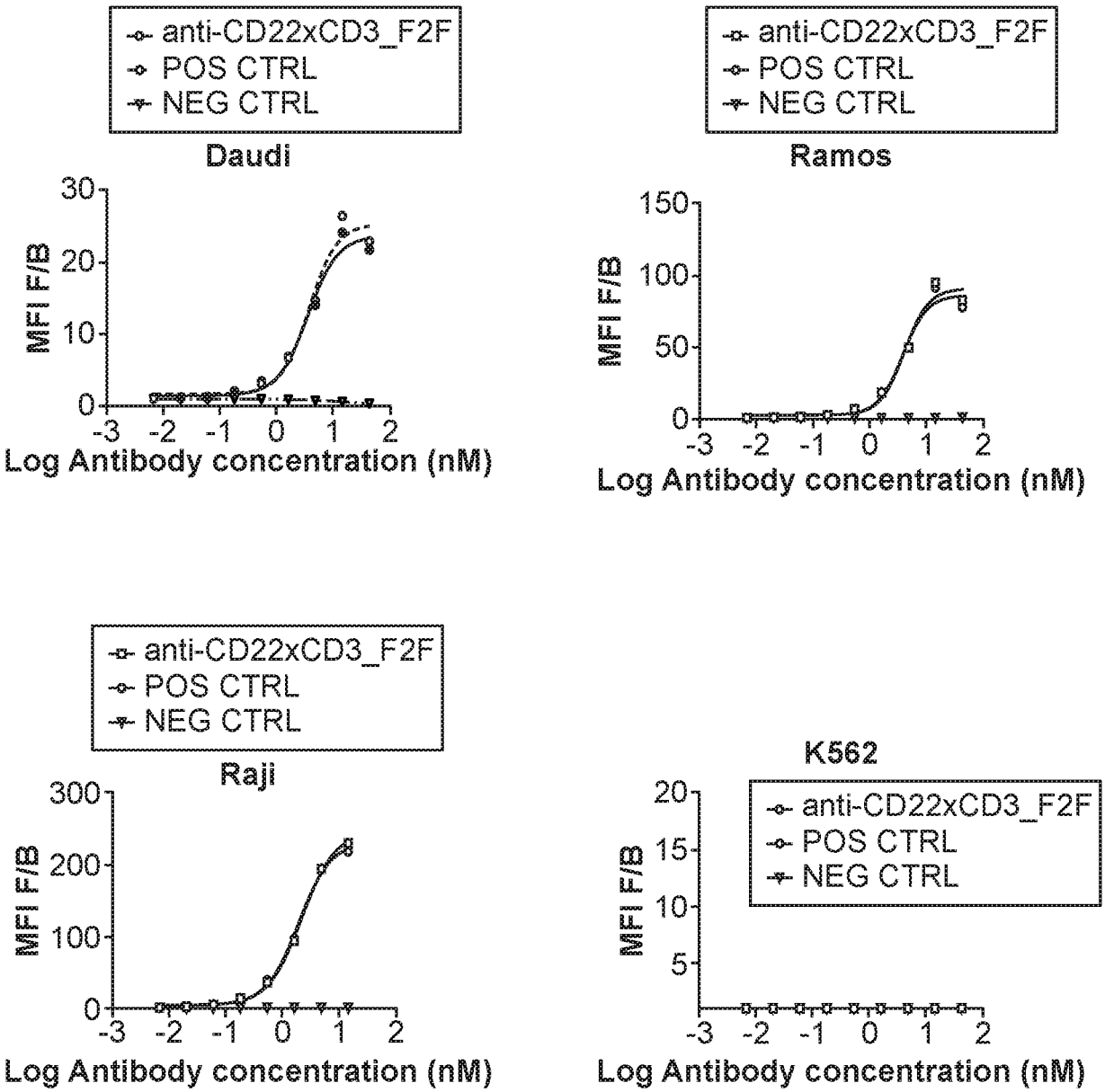

anti-CD22xCD3_F2F
POS CTRL
NEG CTRL
Daudi
MFI F/B
30
20
10
0
-3 -2 -1 0 1 2
Log Antibody concentration (nM)
anti-CD22xCD3_F2F
POS CTRL
NEG CTRL
Ramos
MFI F/B
150
100
50
0
-3 -2 -1 0 1 2
Log Antibody concentration (nM)
anti-CD22xCD3_F2F
POS CTRL
NEG CTRL
Raji
MFI F/B
300
200
100
0
-3 -2 -1 0 1 2
Log Antibody concentration (nM)
K562
anti-CD22xCD3_F2F
POS CTRL
NEG CTRL
MFI F/B
20
15
10
5
-3 -2 -1 0 1 2
Log Antibody concentration (nM)

FIG. 5

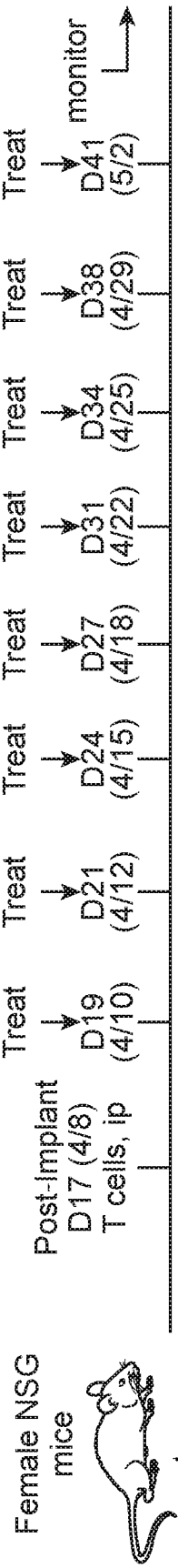

Female NSG mice
Implant Daudi cells sc (5e6 cells/mouse) Day 0, 3/22
Post-Implant D17 (4/8) T cells, ip
establish to ~ 100 mm3
Treat
D19 (4/10)
1 st
Treat
D21 (4/12)
2 nd
Treat
D24 (4/15)
3 rd
Treat
D27 (4/18)
4 th
Treat
D31 (4/22)
5 th
Treat
D34 (4/25)
6 th
Treat
D38 (4/29)
7 th
Treat
D41 (5/2)
8 th
monitor

FIG. 6

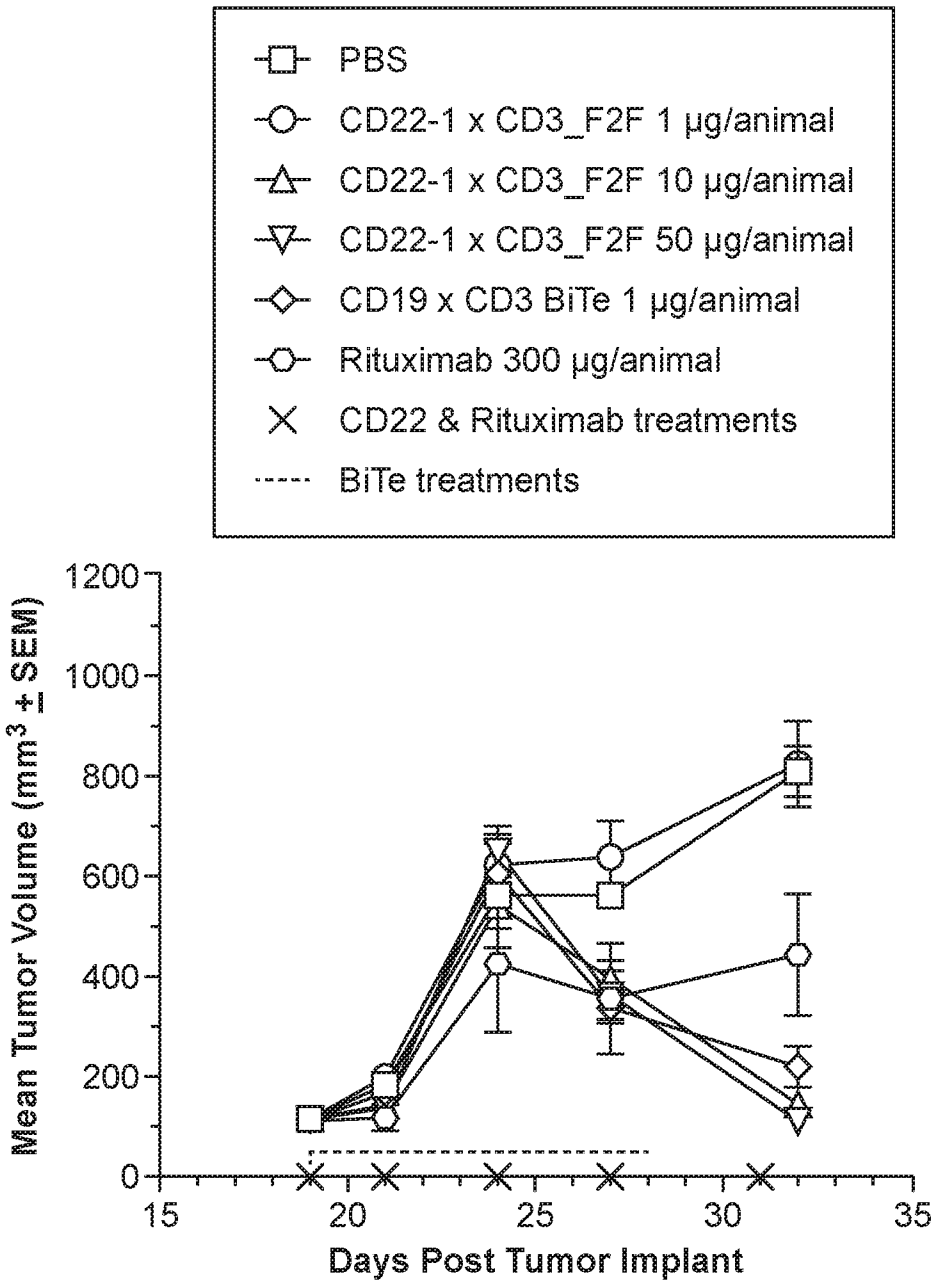

PBS
CD22-1 x CD3_F2F 1 µg/animal
CD22-1 x CD3_F2F 10 µg/animal
CD22-1 x CD3_F2F 50 µg/animal
CD19 x CD3 BiTe 1 µg/animal
Rituximab 300 µg/animal
CD22 & Rituximab treatments
BiTe treatments
Mean Tumor Volume (mm3 ± SEM)
1200
1000
800
600
400
200
0
15
20
25
30
35
Days Post Tumor Implant

FIG. 7

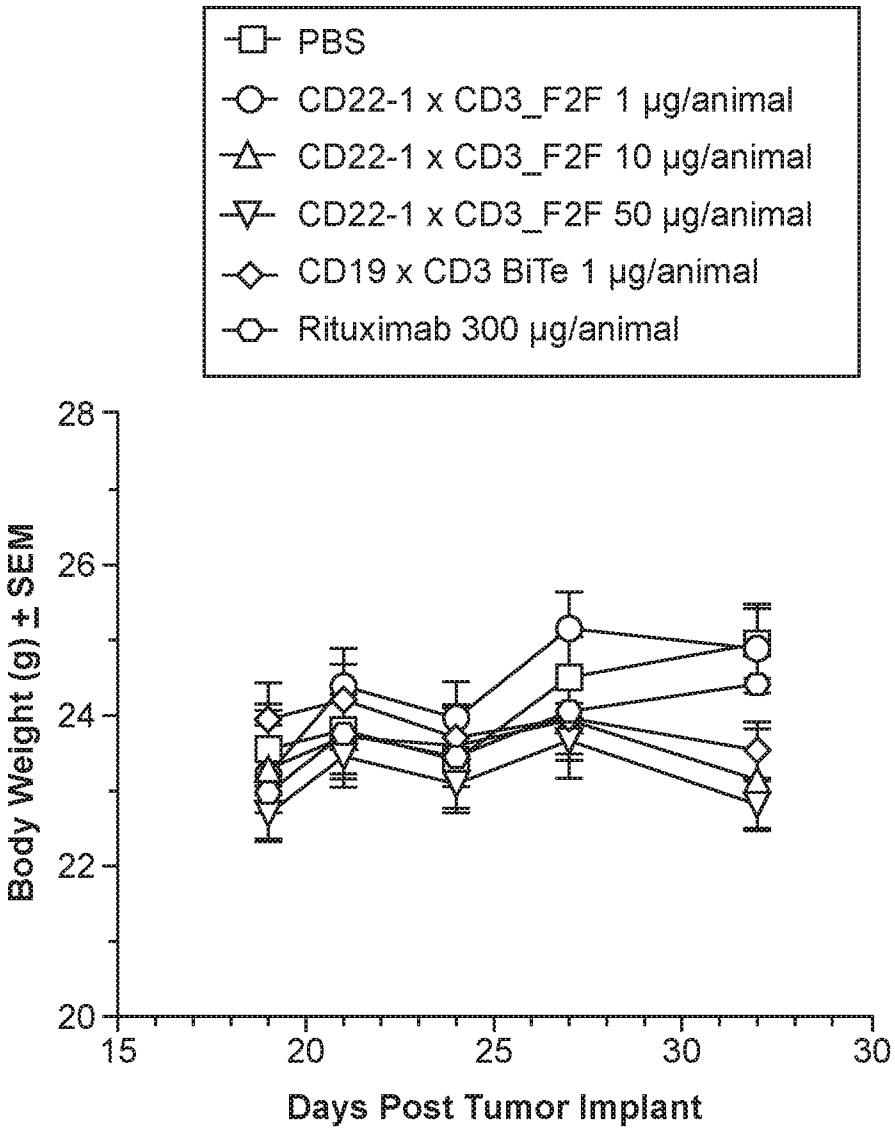

PBS
CD22-1 x CD3_F2F 1 µg/animal
CD22-1 x CD3_F2F 10 µg/animal
CD22-1 x CD3_F2F 50 µg/animal
CD19 x CD3 BiTe 1 µg/animal
Rituximab 300 µg/animal
Body Weight (g) ± SEM
28
26
24
22
20
15
20
25
30
30
Days Post Tumor Implant

FIG. 8

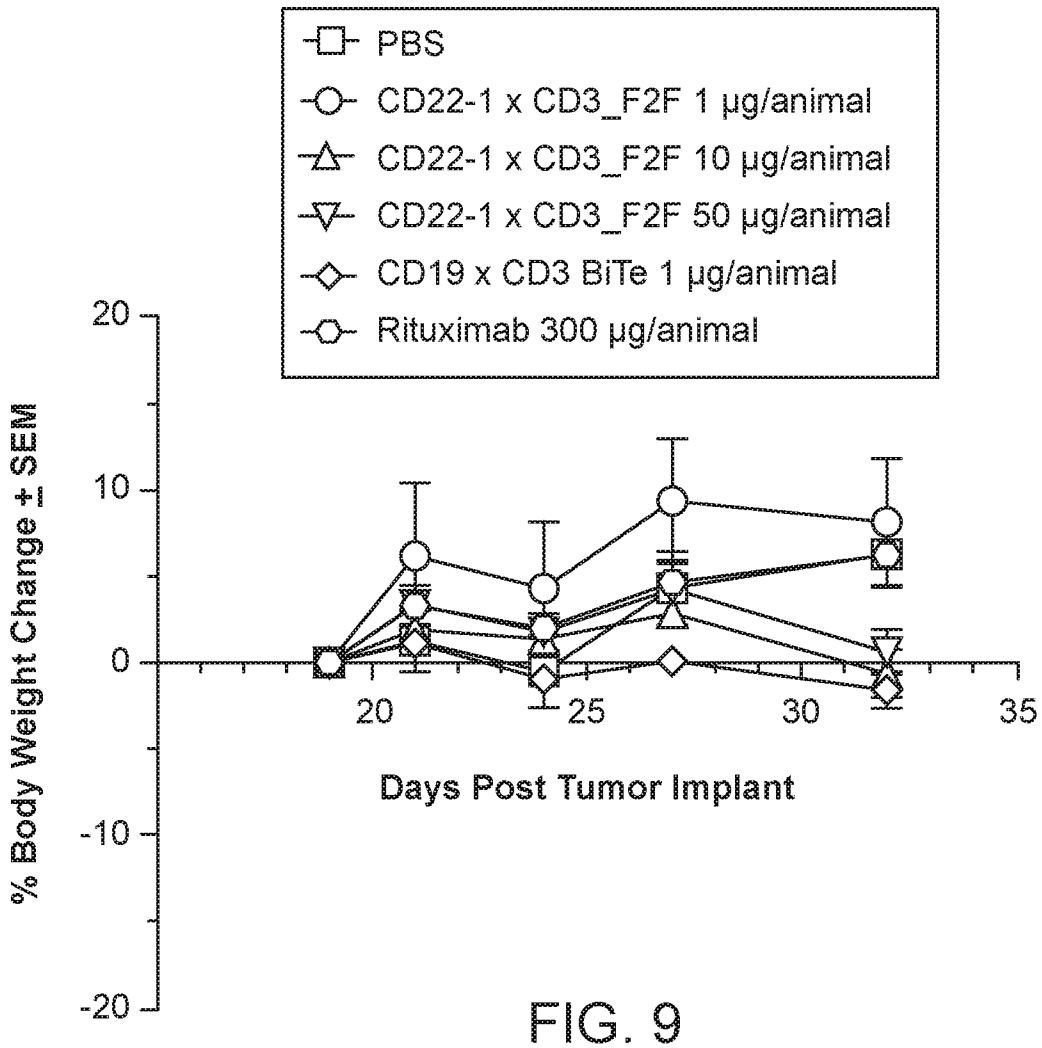

PBS
CD22-1 x CD3_F2F 1 µg/animal
CD22-1 x CD3_F2F 10 µg/animal
CD22-1 x CD3_F2F 50 µg/animal
CD19 x CD3 BiTe 1 µg/animal
Rituximab 300 µg/animal
% Body Weight Change ± SEM
20
10
0
-10
-20
20
25
30
35
Days Post Tumor Implant

FIG. 9

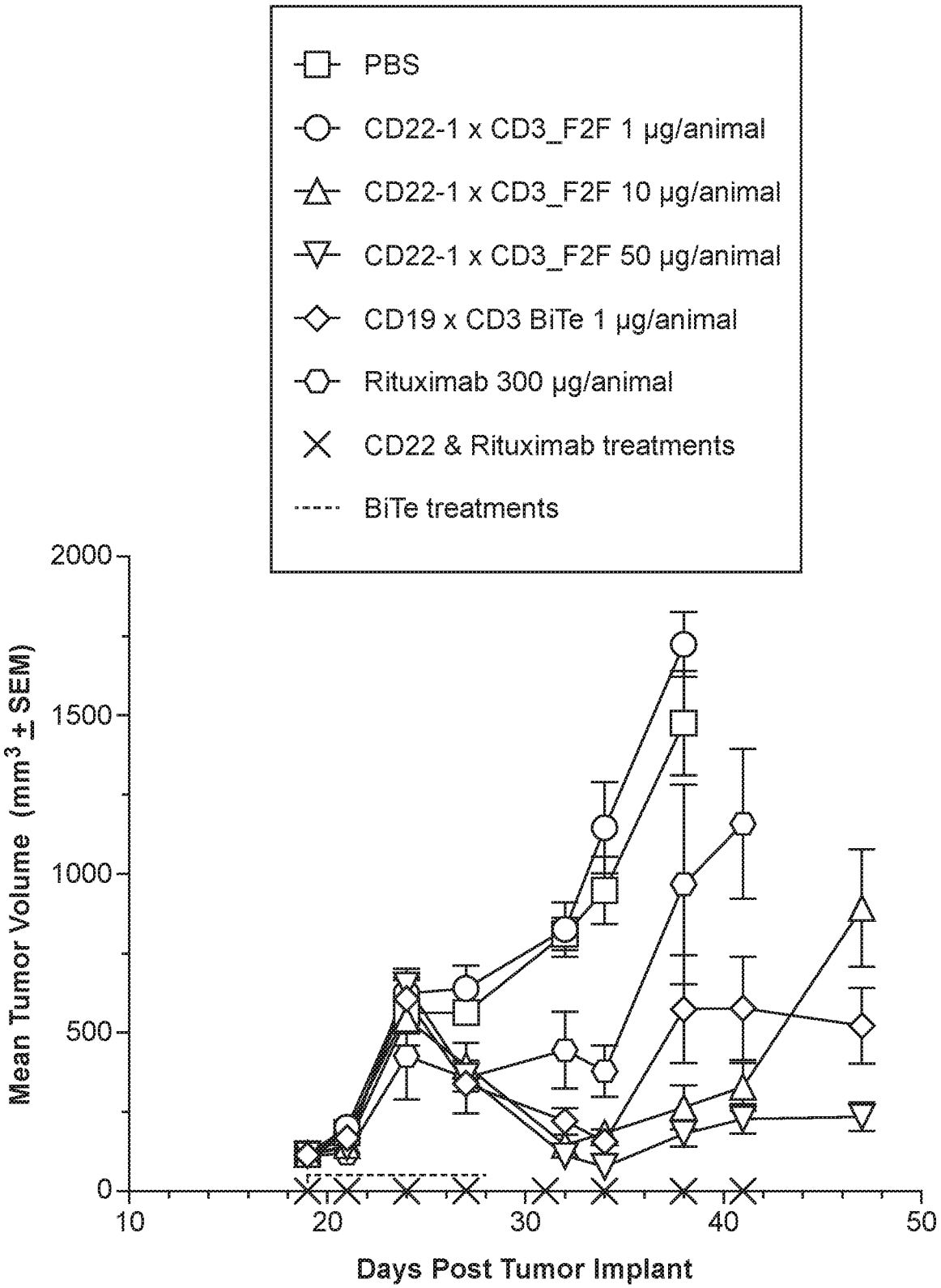

PBS
CD22-1 x CD3_F2F 1 µg/animal
CD22-1 x CD3_F2F 10 µg/animal
CD22-1 x CD3_F2F 50 µg/animal
CD19 x CD3 BiTe 1 µg/animal
Rituximab 300 µg/animal
CD22 & Rituximab treatments
BiTe treatments
Mean Tumor Volume (mm3 ± SEM)
2000
1500
1000
500
0
10
20
30
40
50
Days Post Tumor Implant

FIG. 10

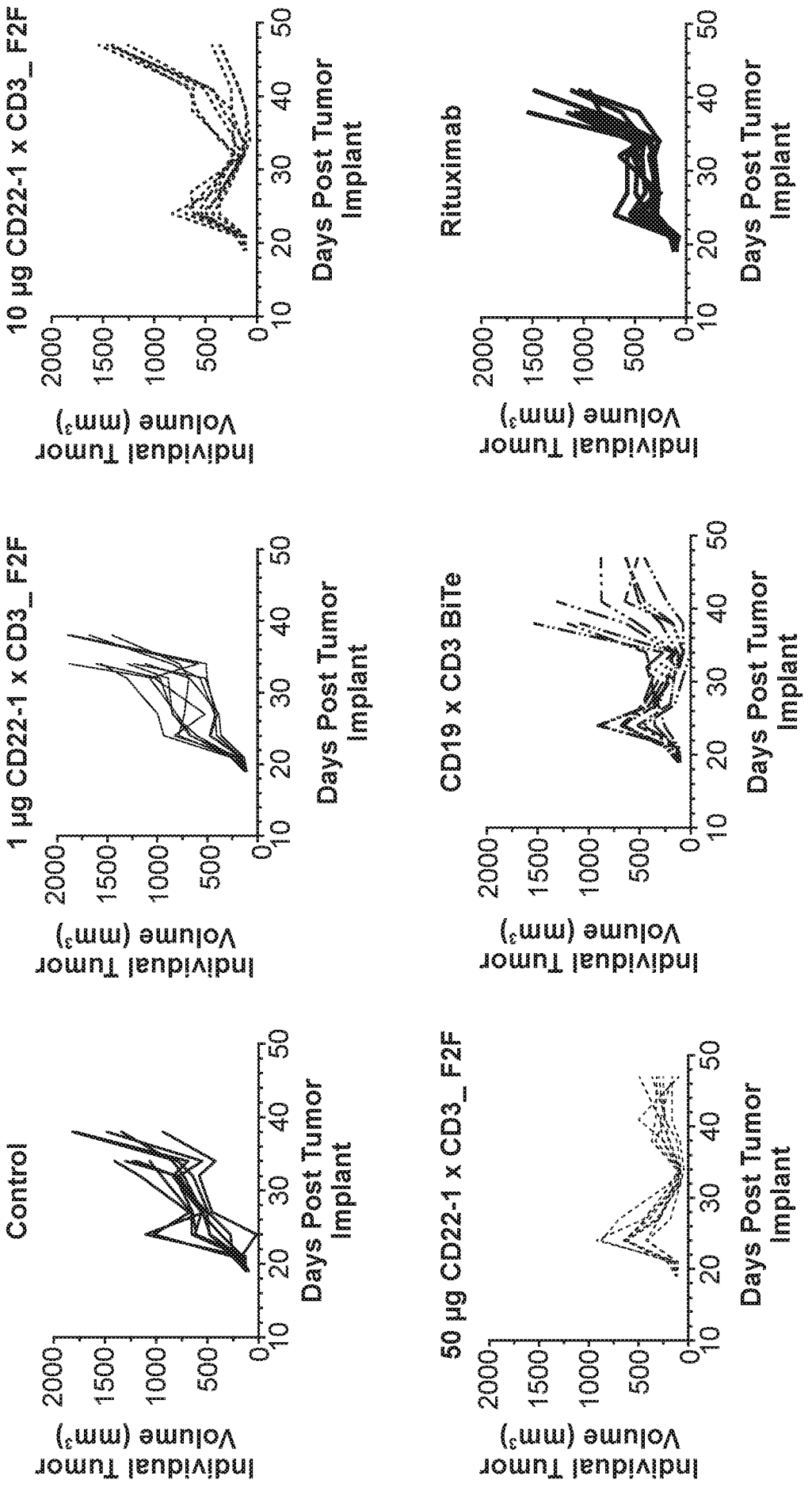

Control
1 µg CD22-1 x CD3_ F2F
10 µg CD22-1 x CD3_ F2F
50 µg CD22-1 x CD3_ F2F
CD19 x CD3 BiTe
Rituximab
Individual Tumor Volume (mm³)
Days Post Tumor Implant
0
500
1000
1500
2000
10
20
30
40
50

FIG. 11

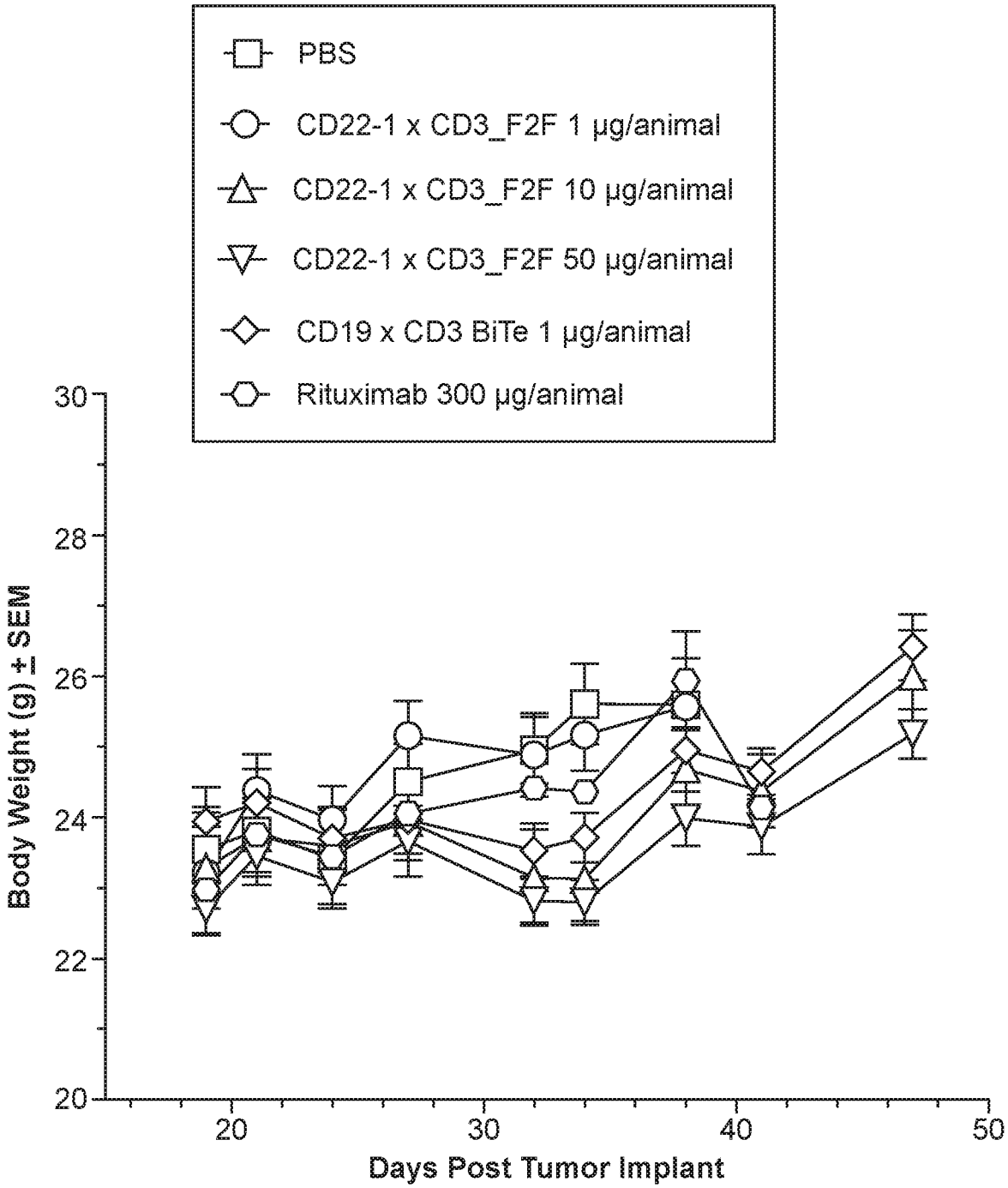

PBS
CD22-1 x CD3_F2F 1 µg/animal
CD22-1 x CD3_F2F 10 µg/animal
CD22-1 x CD3_F2F 50 µg/animal
CD19 x CD3 BiTe 1 µg/animal
Rituximab 300 µg/animal
Body Weight (g) ± SEM
30
28
26
24
22
20
20
30
40
50
Days Post Tumor Implant

FIG. 12

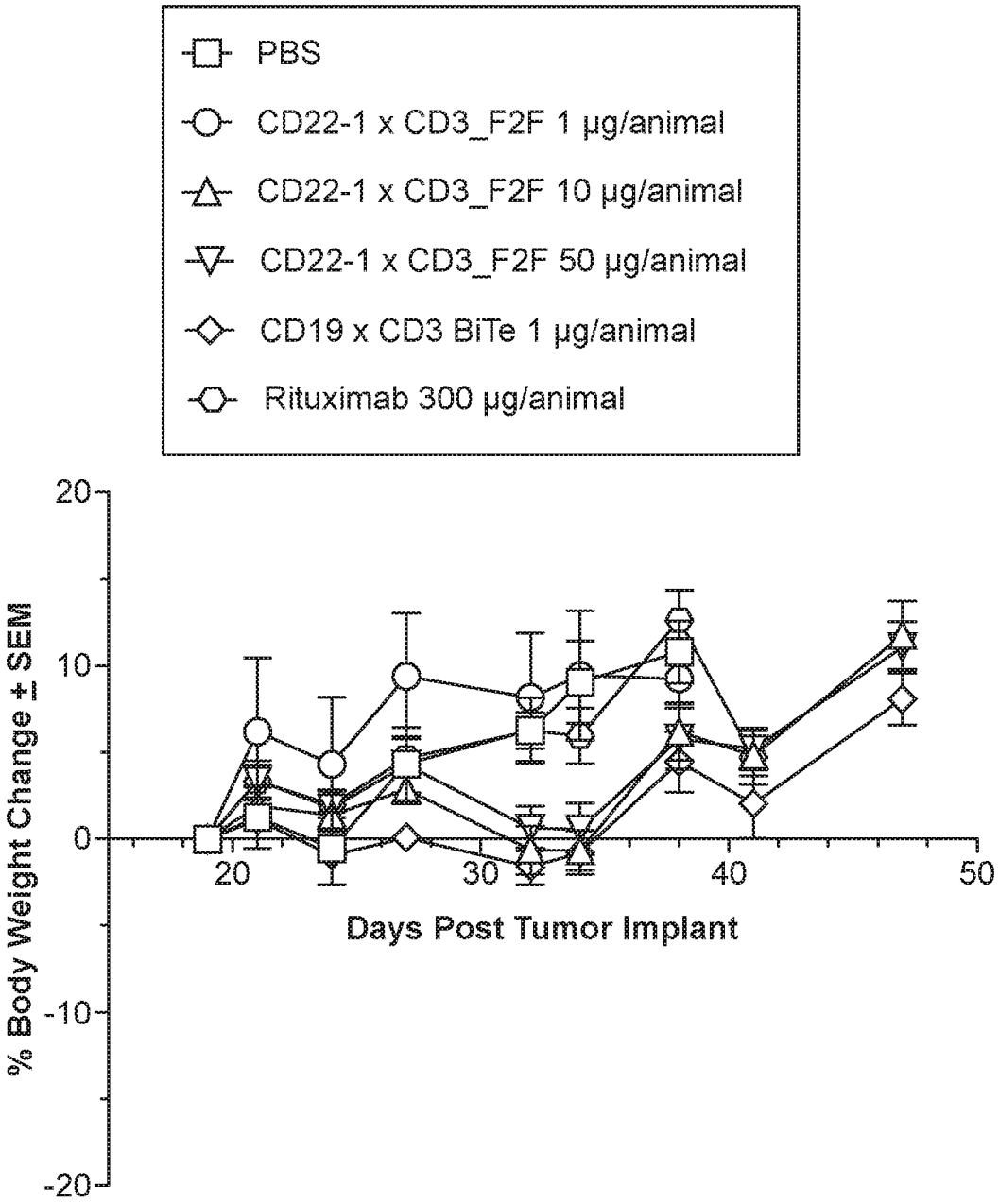

PBS
CD22-1 x CD3_F2F 1 µg/animal
CD22-1 x CD3_F2F 10 µg/animal
CD22-1 x CD3_F2F 50 µg/animal
CD19 x CD3 BiTe 1 µg/animal
Rituximab 300 µg/animal
20
10
0
-10
-20
% Body Weight Change ± SEM
20
30
40
50
Days Post Tumor Implant

FIG. 13

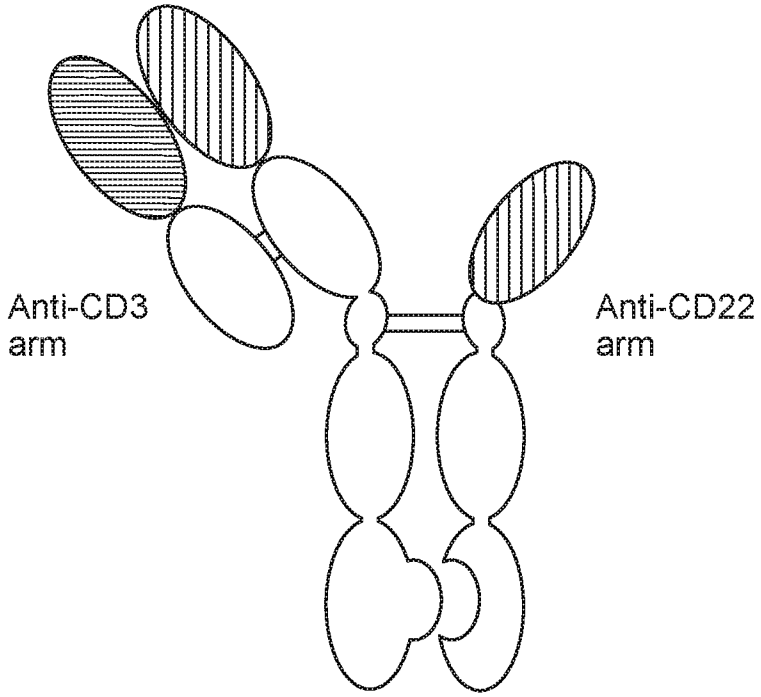


FIG. 14A

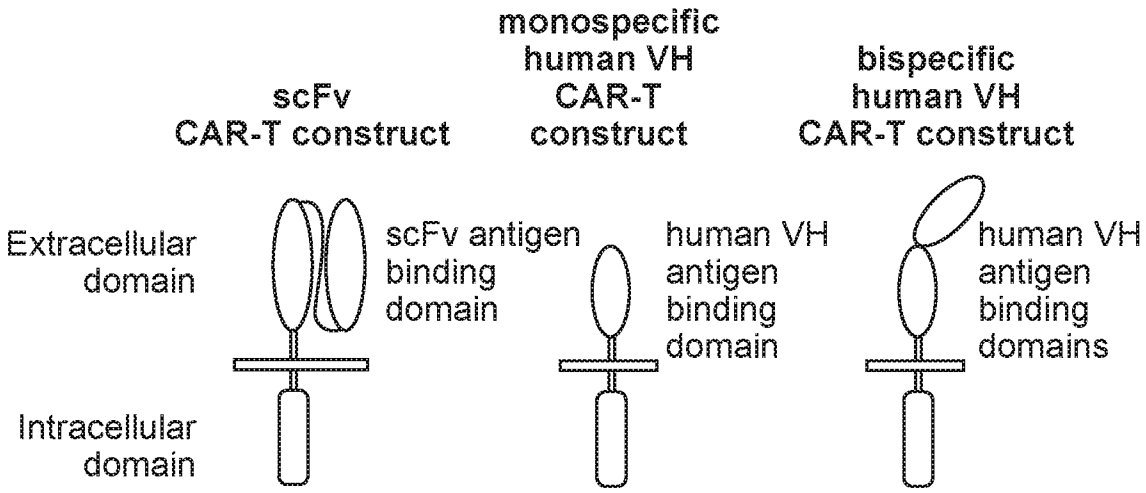
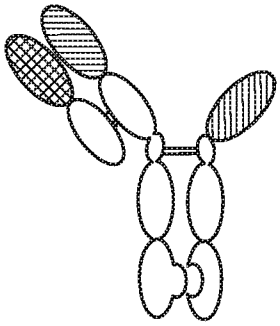
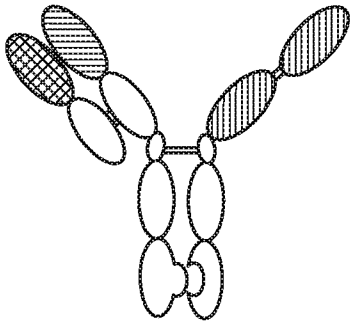


FIG. 14B



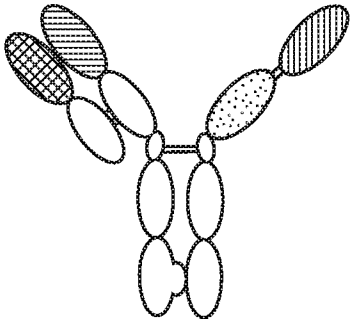
Anti-CD3 x monovalent, monospecific anti-CD22

FIG. 15A



Anti-CD3 x bivalent, monospecific anti-CD22

FIG. 15B



Anti-CD3 x bivalent, biparatopic anti-CD22

FIG. 15C

Clone ID #	KD (M)	Kdis (1/s)	Daudi binding	CHO_cyCD22	CHO_cyOFFtgt
335161	2.66E-09	2.40E-04	811.0	208.0	5.2
335254	2.83E-09	2.45E-04	733.0	194.0	5.1
335260	3.17E-09	2.75E-04	725.0	185.0	5.1
335207	3.24E-09	2.94E-04	776.0	209.0	5.3
335151	3.77E-09	3.21E-04	861.0	222.0	5.3
335170	6.50E-09	3.40E-04	791.0	181.0	5.3
335176	4.62E-09	3.79E-04	848.0	212.0	5.3
335181	9.44E-09	4.43E-04	809.0	234.0	5.4
335244	5.07E-09	4.45E-04	752.0	198.0	5.2
335154	5.41E-09	4.46E-04	837.0	232.0	5.3
335201	5.19E-09	4.67E-04	761.0	199.0	5.5
335261	5.27E-09	5.10E-04	748.0	181.0	5.1
324510	6.42E-09	5.54E-04	690.0	172.0	5.2
335293	7.41E-09	5.57E-04	742.0	179.0	5.3
335203	6.80E-09	6.41E-04	729.0	194.0	5.3
335185	8.43E-09	6.47E-04	754.0	220.0	5.5
324317	8.48E-09	6.58E-04	709.0	173.0	5.2
335206	7.53E-09	6.90E-04	735.0	189.0	5.3
335245	7.44E-09	7.02E-04	742.0	192.0	5.4
335218	8.91E-09	7.05E-04	711.0	204.0	5.1
335160	8.51E-09	7.24E-04	750.0	218.0	5.2
335158	4.23E-08	8.01E-41	883.0	193.0	5.4
324508	1.25E-08	8.28E-04	839.0	162.0	5.2
335307	1.03E-08	1.02E-03	737.0	176.0	5.0
335301	1.26E-08	1.29E-03	716.0	166.0	5.0
335323	1.41E-08	1.30E-03	720.0	169.0	5.3
335271	2.16E-08	1.31E-03	711.0	147.0	5.2
335234	1.24E-08	1.37E-03	734.0	161.0	5.2
335182	2.24E-08	1.58E-03	750.0	192.0	5.3

FIG. 16

Clone ID #	KD (M)	Kdis (1/s)	Daudi binding	CHO_cyCD22	CHO_cyOFFtgt
335186	1.76E-08	1.72E-03	402.0	33.5	5.5
335233	1.90E-08	2.01E-03	697.0	166.0	5.3
335224	2.34E-08	2.07E-03	689.0	173.0	5.4
335210	6.25E-08	2.28E-03	735.0	159.0	5.2
335311	2.66E-09	2.77E-03	151.0	11.7	5.1
335159	1.61E-08	3.58E-03	532.0	61.7	5.4
335188	5.30E-08	4.12E-03	663.0	113.0	5.3
335274	2.36E-08	4.30E-03	414.0	26.0	5.1
335226	2.55E-08	4.37E-03	221.0	12.0	5.2
335333	2.24E-08	4.37E-03	372.0	21.2	5.0
335283	3.69E-08	4.57E-03	513.0	42.4	5.2
335297	2.88E-08	4.80E-03	107.0	12.3	5.2
335273	4.22E-08	4.87E-03	385.0	23.1	5.2
335187	1.28E-07	5.12E-03	531.0	60.7	6.0
335295	3.16E-08	5.21E-03	491.0	43.8	5.1
335220	4.82E-08	5.31E-03	322.0	18.4	5.4
335173	3.05E-08	5.43E-03	393.0	26.7	5.5
335219	9.06E-08	5.50E-03	590.0	76.2	5.2
335236	2.73E-08	5.62E-03	338.0	18.4	5.3
335266	3.85E-08	5.79E-03	411.0	29.2	5.1
335208	5.84E-08	5.93E-03	452.0	34.0	5.4
335195	1.50E-07	5.99E-03	420.0	33.0	5.4
335285	1.14E-07	6.07E-03	620.0	94.7	5.1
335150	1.41E-08	6.08E-03	86.3	8.8	5.2
335316	2.35E-08	6.62E-03	103.0	9.6	5.1
335189	3.60E-08	6.92E-03	410.0	28.6	5.3
335179	1.48E-07	8.91E-03	88.8	10.5	5.5
335230	7.52E-08	8.92E-03	47.1	7.8	5.3
335166	3.30E-08	9.15E-03	422.0	35.5	5.2
335242	7.97E-08	9.30E-03	136.0	11.3	5.2
335162	9.96E-08	9.41E-03	23.3	9.1	5.2

FIG. 16 (Cont. 1)

Clone ID #	KD (M)	Kdis (1/s)	Daudi binding	CHO_cyCD22	CHO_cyOFFtgt
335171	8.45E-08	1.24E-02	471.0	39.0	5.4
335232	2.46E-08	1.83E-02	288.0	42.5	5.3
335263	2.58E-06	3.85E-02	30.0	8.2	5.2

FIG. 16 (Cont. 2)

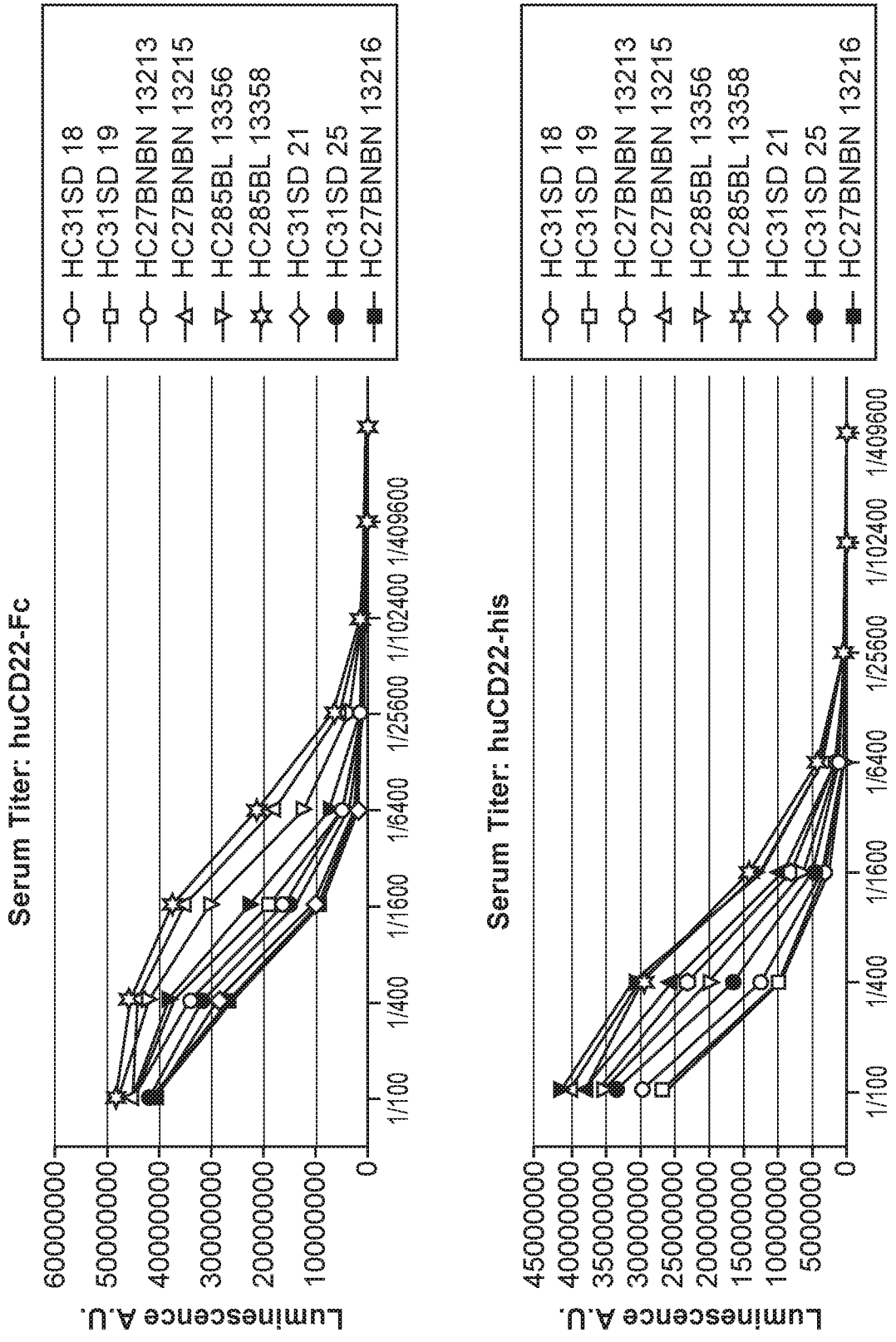

Serum Titer: huCD22-Fc
Luminescence A.U.
60000000
50000000
40000000
30000000
20000000
10000000
0
1/100
1/400
1/1600
1/6400
1/25600
1/102400
1/409600
HC31SD 18
HC31SD 19
HC27BNBN 13213
HC27BNBN 13215
HC285BL 13356
HC285BL 13358
HC31SD 21
HC31SD 25
HC27BNBN 13216
Serum Titer: huCD22-his
Luminescence A.U.
45000000
40000000
35000000
30000000
25000000
20000000
15000000
10000000
5000000
0
1/100
1/400
1/1600
1/6400
1/25600
1/102400
1/409600
HC31SD 18
HC31SD 19
HC27BNBN 13213
HC27BNBN 13215
HC285BL 13356
HC285BL 13358
HC31SD 21
HC31SD 25
HC27BNBN 13216

FIG. 17

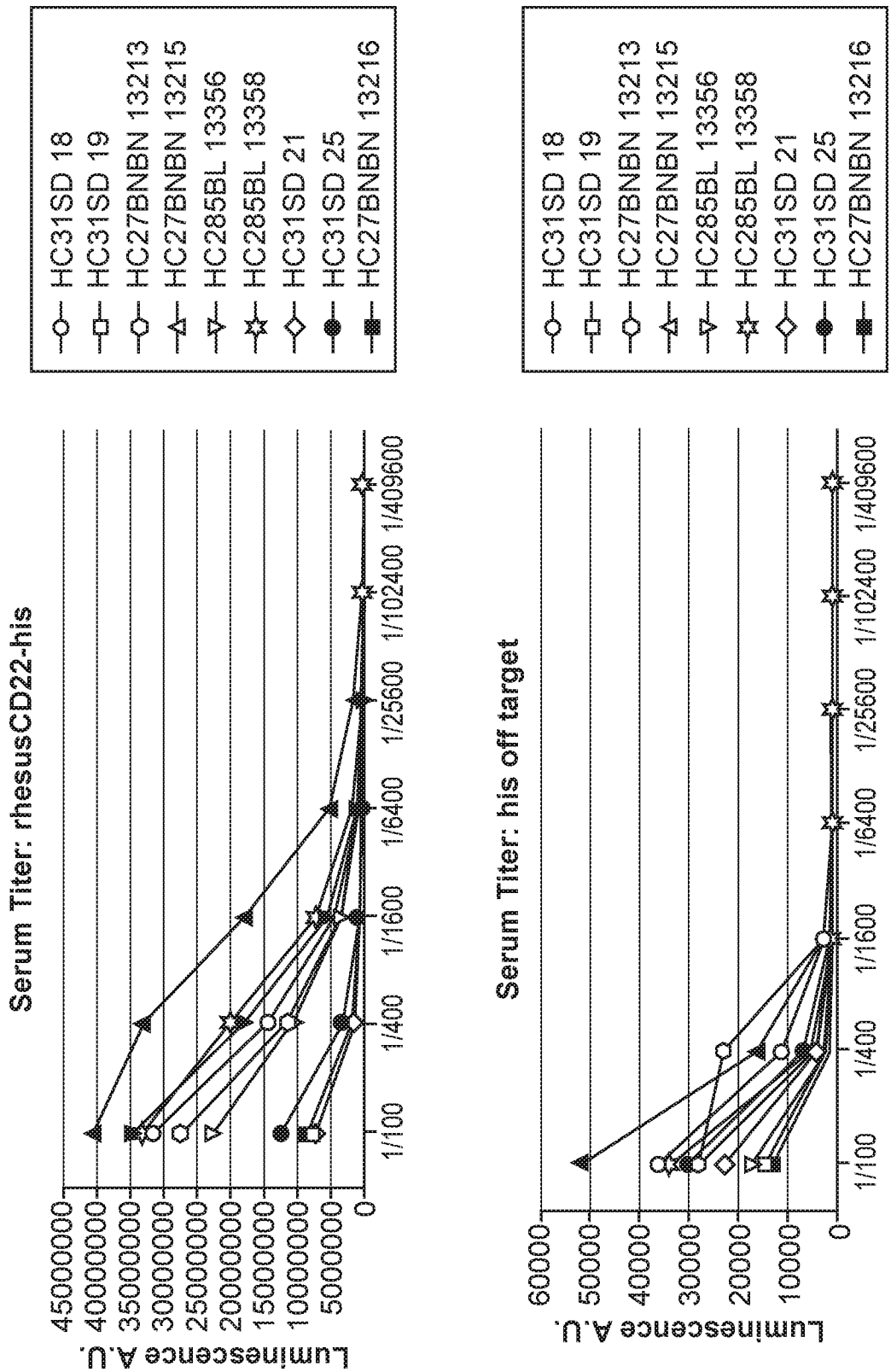

Serum Titer: rhesusCD22-his
Luminescence A.U.
45000000
40000000
35000000
30000000
25000000
20000000
15000000
10000000
5000000
0
1/100
1/400
1/1600
1/6400
1/25600
1/102400
1/409600
HC31SD 18
HC31SD 19
HC27BNBN 13213
HC27BNBN 13215
HC285BL 13356
HC285BL 13358
HC31SD 21
HC31SD 25
HC27BNBN 13216
Serum Titer: his off target
Luminescence A.U.
60000
50000
40000
30000
20000
10000
0
1/100
1/400
1/1600
1/6400
1/25600
1/102400
1/409600
HC31SD 18
HC31SD 19
HC27BNBN 13213
HC27BNBN 13215
HC285BL 13356
HC285BL 13358
HC31SD 21
HC31SD 25
HC27BNBN 13216

FIG. 17 (Cont.)

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2020/037566

A. CLASSIFICATION OF SUBJECT MATTER
INV. C07K16/28 A61P35/00
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C07K A61K A61P

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EPO-Internal, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2018/052503 A1 (TENEOBIO INC [US]) 22 March 2018 (2018-03-22) cited in the application the whole document, in particular paragraphs 16-20,23,65 examples 1-6; figures 1-4; sequences 13,19 -----	1-11, 30-48
X	UDAYA RANGASWAMY ET AL: "A novel T-cell bispecific antibody platform for efficient T-cell mediated killing of tumor cells with minimal cytokine release.", JOURNAL OF CLINICAL ONCOLOGY, vol. 36, no. 5_suppl, 26 February 2018 (2018-02-26), XP055727126, DOI: 10.1200/JCO.2018.36.5_suppl.209 the whole document -----	1-11, 30-48
	-/--	

[X] Further documents are listed in the continuation of Box C.

[X] See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
3 September 2020	11/11/2020

Name and mailing address of the ISA/	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Stein, Annette

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	NATHAN D. TRINKLEIN ET AL: "Efficient tumor killing and minimal cytokine release with novel T-cell agonist bispecific antibodies", MABS, vol. 11, no. 4, 19 May 2019 (2019-05-19), pages 639-652, XP055690535, US ISSN: 1942-0862, DOI: 10.1080/19420862.2019.1574521 the whole document, in particular figure 3	1-11, 30-48
A	MATHIEU DONDELINGER ET AL: "Understanding the Significance and Implications of Antibody Numbering and Antigen-Binding Surface/Residue Definition", FRONTIERS IN IMMUNOLOGY, vol. 9, 16 October 2018 (2018-10-16), pages 1-15, XP055572450, DOI: 10.3389/fimmu.2018.02278 the whole document, in particular page 9, left-hand column-right-hand column, bridging paragraph	1-11

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2020/037566

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-11(completely); 30-48(partially)

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 1-11(completely); 30-48(partially)

A multi-specific binding compound that binds to CD3, comprising:
a heavy chain variable region comprising:
a) a CDR1 sequence having two or fewer substitutions in SEQ ID NO: 85; and/or
b) a CDR2 sequence having two or fewer substitutions in SEQ ID NO: 86; and/or
(c) a CDR3 sequence having two or fewer substitutions in SEQ ID NO: 87; and
a light chain variable region, and related subject-matter.

2-62. claims: 12-26(completely); 30-48(partially)

A multi-specific binding compound comprising a first binding unit having binding affinity to CD22 and a second binding unit having binding affinity to CD3, wherein the first binding unit comprises the CDR sequences of one of the anti-CD22 antibodies disclosed in table 3 of the present application, wherein each of these antibodies defines an independent invention.

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63. claims: 27(completely); 30-48(partially)

A multi-specific binding compound comprising:
(i) a heavy chain variable region having binding affinity to CD3, comprising a CDR1 sequence of SEQ ID NO: 85, a CDR2 sequence of SEQ ID NO: 86, and CDR3 sequence of SEQ ID NO: 87, in a human VH framework;
(ii) a light chain variable region comprising a CDR1 sequence of SEQ ID NO: 88, a CDR2 sequence of SEQ ID NO: 89, and CDR3 sequences of SEQ ID NO: 90, in a human VL framework; and
(iii) an antigen-binding domain of an anti-CD22 heavy chain antibody, comprising a CDR1sequence of SEQ ID NO: 1, a CDR2 sequence of SEQ ID NO: 11, and a CDR3 sequence of SEQ ID NO: 18, in a human VH framework.

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64. claims: 28(completely); 30-48(partially)

A multi-specific binding compound comprising:
(i) a heavy chain variable region having binding affinity to CD3, comprising a CDR1 sequence of SEQ ID NO: 85, a CDR2 sequence of SEQ ID NO: 86, and CDR3 sequence of SEQ ID NO: 87, in a human VH framework;
(ii) a light chain variable region comprising a CDR1 sequence of SEQ ID NO: 88, a CDR2 sequence of SEQ ID NO: 89, and CDR3 sequences of SEQ ID NO: 90, in a human VL

framework; and
(iii) an antigen-binding domain of an anti-CD22 heavy chain antibody, comprising a CDR1sequence of SEQ ID NO: 1, a CDR2 sequence of SEQ ID NO: 12, and a CDR3 sequence of SEQ ID NO: 19, in a human VH framework.

---

65. claims: 29(completely); 30-48(partially)

A multi-specific binding compound comprising:
i) a heavy chain variable region having binding affinity to CD3, comprising a CDR1 sequence of SEQ ID NO: 85, a CDR2 sequence of SEQ ID NO: 86, and CDR3 sequence of SEQ ID NO: 87, in a human VH framework;
(ii) a light chain variable region comprising a CDR1 sequence of SEQ ID NO: 88, a CDR2 sequence of SEQ ID NO: 89, and CDR3 sequences of SEQ ID NO: 90, in a human VL framework; and
(iii) an antigen-binding domain of an anti-CD22 heavy chain antibody, comprising a CDR1sequence of SEQ ID NO: 1, a CDR2 sequence of SEQ ID NO: 12, and a CDR3 sequence of SEQ ID NO: 20, in a human VH framework.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/US2020/037566

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 2018052503 A1	22-03-2018	AU 2017327723 A1	02-05-2019
		BR 112019004873 A2	11-06-2019
		CA 3036550 A1	22-03-2018
		CL 2019000643 A1	09-08-2019
		CN 109843325 A	04-06-2019
		CO 2019003706 A2	28-06-2019
		CR 20190198 A	11-10-2019
		DO P2019000059 A	16-06-2019
		EC SP19026304 A	30-06-2019
		EP 3512549 A1	24-07-2019
		JP 2019536430 A	19-12-2019
		KR 20190052048 A	15-05-2019
		PE 20190976 A1	09-07-2019
		PH 12019500545 A1	29-07-2019
		RU 2019111037 A	15-10-2020
		US 2020048348 A1	13-02-2020
		WO 2018052503 A1	22-03-2018