ANTI-STEAP1 ANTIGEN-BINDING PROTEIN

TECHNICAL FIELD

[0001] The disclosure provides a novel antigen-binding protein that binds Six Transmembrane Epithelial Antigen of the Prostate 1 (STEAP1) and uses thereof.

CROSS-REFERENCE TO RELATED APPLICATIONS

[0002] This application claims priority to U.S. Provisional Patent Application No. 62/693,216, filed July 2, 2018, and U.S. Provisional Patent Application No. 62/800,259, filed February 1, 2019, the disclosures of which are hereby incorporated by reference in their entireties.

SEQUENCE LISTING

[0003] This application contains, as a separate part of the disclosure, a sequence listing in computer-readable form (Filename: 52601_Seqlisting.txt; Size: 298,914 Bytes; Created: June 27, 2019), which is incorporated by reference in its entirety.

BACKGROUND

[0004] Prostate cancer remains one of the most common cancers among men in the United States. U.S. Cancer Statistics Working Group. United States Cancer Statistics: 1999–2014 Incidence and Mortality Web-based Report. Atlanta (GA): Department of Health and Human Services, Centers for Disease Control and Prevention, and National Cancer Institute; 2017. While the survival rate for prostate cancer is relatively high compared to other cancer types, current treatment options are accompanied by risk and unwanted side effects. For example, surgery is accompanied by risk of nerve damage and impotence, and radiation therapy can increase the risk of development bladder or gastrointestinal cancers. Traditional chemotherapy is associated with a host of side effects that limit the patient's quality of life during treatment.

[0005] Antibody-based therapeutics have been successful in treating a variety of diseases, including cancer and autoimmune/inflammatory disorders. Prostate cancer is believed to be particularly amenable to antibody-based therapy due, at least in part, to the existence of prostate cancer-specific antigens. Despite recent progress in elucidating the underlying biological mechanism of carcinogenesis and potential biomarkers, there exists a need for alternative antibody-based therapeutic options for cancer, including prostate cancer.

SUMMARY

[0006] The disclosure provides an antigen-binding protein that binds STEAP1 of SEQ ID NO: 2 and comprises: (a) heavy chain CDRs comprising amino acid sequences that differ by no more than 3, 2, or 1 amino acid from i) vhCDR1 SEQ ID NO: 14, vhCDR2 SEQ ID NO:15 or vhCDR2 SEQ ID NO: 21, and vhCDR3 SEQ ID NO: 16, or ii) vhCDR1 SEQ ID NO: 33, vhCDR2 SEQ ID NO: 34, and vhCDR3 SEQ ID NO: 35; or (b) light chain CDRs comprising amino acid sequences that differ by no more than 3, 2, or 1 amino acid from i) vlCDR1 SEQ ID NO: 11, vlCDR2 SEQ ID NO: 12, and vlCDR3 SEQ ID NO: 13; or ii) vlCDR1 SEQ ID NO: 30, vlCDR2 SEQ ID NO: 31, and vlCDR3 SEQ ID NO: 32; or (c) a light chain variable domain comprising an amino acid sequence at least 90% identical to SEQ ID NO: 183 or SEQ ID NO: 186; or (d) a heavy chain variable domain comprising an amino acid sequence at least 90% identical to SEQ ID NO: 182, SEQ ID NO: 184, or SEQ ID NO: 185. In various aspects, the antigen-binding protein comprises a vhCDR1 comprising SEQ ID NO: 14, a vhCDR2 comprising SEQ ID NO: 15 or SEQ ID NO: 21, a vhCDR3 comprising SEQ ID NO: 16, a vlCDR1 comprising SEQ ID NO: 11, a vlCDR2 comprising SEQ ID NO: 12, and a vlCDR3 comprising SEQ ID NO: 13. Alternatively, the antigen-binding protein comprises a vhCDR1 comprising SEQ ID NO: 33, a vhCDR2 comprising SEQ ID NO: 34, a vhCDR3 comprising SEQ ID NO: 35, a vlCDR1 comprising SEQ ID NO: 30, a vlCDR2 comprising SEQ ID NO: 31, and a vlCDR3 comprising SEQ ID NO: 32. In various aspects, the antigen-binding protein comprises a variable heavy domain comprising SEQ ID NO: 182 or SEQ ID NO: 184 and a variable light domain comprising SEQ ID NO: 183; for example, the antigen-binding protein comprises a variable heavy domain comprising SEQ ID NO: 182 and a variable light domain comprising SEQ ID NO: 183, or variable heavy domain comprising SEQ ID NO: 184 and a variable light domain comprising SEQ ID NO: 183. Alternatively, the antigen-binding protein comprises a variable heavy domain comprising SEQ ID NO: 185 and a variable light domain comprising SEQ ID NO: 186. The disclosure further provides an antigen-binding protein comprising a heavy chain comprising SEQ ID NO: 201 and a light chain comprising SEQ ID NO: 200; or a heavy chain comprising SEQ ID NO: 203 and a light chain comprising SEQ ID NO: 200.

[0007] The disclosure further provides a heterodimeric antibody comprising a first monomer comprising a first heavy chain comprising: 1) a first variable heavy domain; 2) a first constant heavy chain comprising a first CH1 domain and a first Fc domain; and 3) a scFv that binds human CD3 and comprises a scFv variable light domain, an scFv linker, and a scFv

variable heavy domain; wherein said scFv is covalently attached between the C-terminus of said CH1 domain and the N-terminus of said first Fc domain using domain linker(s). The heterodimeric antibody further comprises a second monomer comprising a second heavy chain comprising a second variable heavy domain and a second constant heavy chain comprising a second Fc domain; and a common light chain comprising a variable light domain and a constant light domain. The first variable heavy domain and the variable light domain bind human STEAP1, the second variable heavy domain and the variable light domain bind human STEAP1, and wherein (i) the first variable heavy domain and the second variable heavy domain comprise heavy chain CDRs comprising amino acid sequences that differ by no more than 3, 2, or 1 amino acid from vhCDR1 SEQ ID NO: 14, vhCDR2 SEQ ID NO: 15 or vhCDR2 SEQ ID NO: 21, and vhCDR3 SEQ ID NO: 16, and the variable light domain comprises light chain CDRs comprising amino acid sequences that differ by no more than 3, 2, or 1 amino acid from vlCDR1 SEQ ID NO: 11, vlCDR2 SEQ ID NO: 12, and vlCDR3 SEQ ID NO: 13; or (ii) the first variable heavy domain and the second variable heavy domain comprise heavy chain CDRs comprising amino acid sequences that differ by no more than 3, 2, or 1 amino acid from vhCDR1 SEQ ID NO: 33, vhCDR2 SEQ ID NO: 34, and vhCDR3 SEQ ID NO: 35, and the variable light domain comprises light chain CDRs comprising amino acid sequences that differ by no more than 3, 2, or 1 amino acid from vlCDR1 SEQ ID NO: 30, vlCDR2 SEQ ID NO: 31, and vlCDR3 SEQ ID NO: 32; or (iii) the first variable heavy domain and the second variable heavy domain comprise an amino acid sequence at least 90% identical to SEQ ID NO: 182 or SEQ ID NO: 184 and the variable light domain comprises an amino acid sequence at least 90% identical to SEQ ID NO: 183; or (iv) the first variable heavy domain and the second variable heavy domain comprise an amino acid sequence at least 90% identical to SEQ ID NO: 185 and the variable light domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:186. In various aspects, the first variable heavy domain and the second variable heavy domain comprise CDR sequences: vhCDR1 comprising SEQ ID NO: 14, vhCDR2 comprising SEQ ID NO: 15 or SEQ ID NO: 21, and vhCDR3 comprising SEQ ID NO: 16; and the variable light domain comprises CDR sequences: vlCDR1 comprising SEQ ID NO: 11, vlCDR2 comprising SEQ ID NO: 12, and vlCDR3 comprising SEQ ID NO: 13. In various aspects, the first variable heavy domain and the second variable heavy domain comprise CDR sequences: vhCDR1 comprising SEQ ID NO: 33, vhCDR2 comprising SEQ ID NO: 34, and vhCDR3 comprising SEQ ID NO: 35; and the variable light domain comprises CDR sequences: vlCDR1 comprising SEQ ID NO: 30, vlCDR2 comprising SEQ ID NO: 31, and vlCDR3 comprising

SEQ ID NO: 32. In various aspects, the first variable heavy domain and the second variable heavy domain comprise SEQ ID NO: 182 or SEQ ID NO: 184 and the variable light domain comprises SEQ ID NO: 183 (e.g., SEQ ID NOs: 182 and 183 or SEQ ID NOs: 184 and 183), or the first variable heavy domain and the second variable heavy domain comprise SEQ ID NO: 185 and the variable light domain comprises SEQ ID NO: 186. The scFv comprises CDRs comprising: vhCDR1 comprising SEQ ID NO: 170, vhCDR2 comprising SEQ ID NO: 171, vhCDR3 comprising SEQ ID NO: 172, vlCDR1 comprising SEQ ID NO:174, vlCDR2 comprising SEQ ID NO: 175, and vlCDR3 comprising SEQ ID NO: 176; or a variable heavy region and a variable light region of SEQ ID NO:169 and SEQ ID NO:173.

[0008] Methods of treating cancer, such as prostate cancer, comprising administering to a subject in need thereof the antigen-binding protein described herein also are provided.

[0009] The use of section headings herein is merely for the convenience of reading, and not intended to be limiting per se. The entire document is intended to be viewed as a unified disclosure, and it should be understood that all combinations of features described herein are contemplated.

[0010] Unless otherwise defined herein, scientific and technical terms used in connection with the present application shall have the meanings that are commonly understood by those of ordinary skill in the art. Further, unless otherwise required by context, singular terms shall include pluralities and plural terms shall include the singular. The terms "comprising," "having," "including," and "containing" are to be construed as open-ended terms unless otherwise noted. If aspects of the invention are described as "comprising" a feature, embodiments also are contemplated "consisting of" or "consisting essentially of" the feature. The use of any and all examples, or exemplary language (e.g., "such as") provided herein, is intended merely to better illustrate the disclosure and does not pose a limitation on the scope of the disclosure unless otherwise claimed. No language in the specification should be construed as indicating any non-claimed element as essential to the practice of the disclosure. Other than in the operating examples, or where otherwise indicated, all numbers expressing quantities of ingredients or reaction conditions used herein should be understood as modified in all instances by the term "about" as that term would be interpreted by the person skilled in the relevant art.

[0011] Recitation of ranges of values herein are merely intended to serve as a shorthand method of referring individually to each separate value falling within the range and each

endpoint, unless otherwise indicated herein, and each separate value and endpoint is incorporated into the specification as if it were individually recited herein.

[0012] Generally, the terminology and techniques of cell and tissue culture, molecular biology, immunology, microbiology, genetics, protein and nucleic acid chemistry, manufacturing, formulation, pharmacology, and medicine described herein are those well known and commonly used in the art. The methods and techniques of the present application are generally performed according to conventional methods well known in the art and as described in various general and more specific references that are cited and discussed throughout the present specification unless otherwise indicated. See, e.g., Sambrook et al., Molecular Cloning: A Laboratory Manual, 3rd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (2001), Ausubel et al., Current Protocols in Molecular Biology, Greene Publishing Associates (1992), and Harlow and Lane Antibodies: A Laboratory Manual Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1990), which are incorporated herein by reference. Enzymatic reactions and purification techniques are performed according to manufacturer's specifications, as commonly accomplished in the art, or as described herein. The terminology used in connection with, and the laboratory procedures and techniques of, analytical chemistry, synthetic organic chemistry, and medicinal and pharmaceutical chemistry described herein are those well known and commonly used in the art. Standard techniques can be used for chemical syntheses, chemical analyses, pharmaceutical preparation, formulation, and delivery, and treatment of patients. Percent identity is calculated using methodology routinely used in the art, including the methodology described in, e.g., U.S. Patent Publication No. 2017/0342155, incorporated herein by reference in its entirety and particularly with respect to paragraphs [0075]-[0083].

BRIEF DESCRIPTION OF THE DRAWINGS

[0013] Figure 1 depicts a bispecific antibody of the disclosure.

[0014] Figure 2 depicts the sequence of human CD3 epsilon chain (SEQ ID NO: 1).

[0015] Figure 3 depicts the sequence of human STEAP1 (SEQ ID NO: 2). Sequences of extracellular loops are underlined.

[0016] Figures 4A-4E depict useful pairs of heterodimerization variant sets (including skew and pI variants).

[0017] Figure 5 depicts a list of isosteric variant antibody constant regions and their respective substitutions. pI_(-) indicates lower pI variants, while pI_(+) indicates higher pI variants. These can be optionally and independently combined with other heterodimerization variants of the disclosure (and other variant types as well, as outlined herein).

[0018] Figure 6 depicts useful ablation variants that ablate FcγR binding (sometimes referred to as "knock outs" or "KO" variants).

[0019] Figure 7 describes two embodiments of the disclosure.

[0020] Figures 8A and 8B depict useful linkers, including charged scFv linkers and domain linkers that can be used in the antigen binding proteins and heterodimeric antibody formats provided herein. Charged linkers, in various aspects of the disclosure, are useful for, e.g., increasing or decreasing the pI of heterodimeric antibodies that utilize one or more scFv as a component. A single prior art scFv linker with a single charge is referenced as "Whitlow," from Whitlow et al., Protein Engineering 6(8):989-995 (1993). This linker was used for reducing aggregation and enhancing proteolytic stability in scFvs.

[0021] Figure 9 depicts a list of engineered heterodimer-skewing Fc variants with heterodimer yields (determined by HPLC-CIEX) and thermal stabilities (determined by DSC). Not determined thermal stability is denoted by "n.d." Additional information is provided in U.S. Patent No. 9,822,186, incorporated by reference herein in its entirety.

[0022] Figures 10A and 10B depict stability-optimized, humanized anti-CD3 variant scFvs. Substitutions are given relative to the H1_L1.4 scFv sequence. Amino acid numbering is Kabat numbering. Specific variable light and variable heavy regions are noted; the substitutions listed may be employed for variable light and variable heavy regions other than those specifically listed. Additional information is provided in International Patent Publication No. 2017/091656, incorporated by reference herein in its entirety.

[0023] Figures 11A and 11B show specific detection of STEAP1 at the surface of C4-2B luc cells with murine STEAP1 antibody Ab-Am.

[0024] Figures 12A-12C shows specific detection of STEAP1 on C4-2B luc prostate cancer cells using murine STEAP1 antibody Ab-Am (Figure 12A); Ab-A1 XmAb (●) or Ab-A1 XmAb^{2+1} (■) for 1 hr at 4°C (Figure 12B) and antibody Ab-A1 XmAb^{2+1} (Figure 12C).

[0025] Figure 13 shows specific detection of STEAP1 on C4-2B luc prostate cancer cells with STEAP1 antibody Ab-Bx (Ab-B1 XmAb).

[0026] Figures 14A-14C show that STEAP1 antibody Ab-Ax (Figure 14A), STEAP1 antibody Ab-A1 Xmab^{2+1} (Figure 14B), and STEAP1 antibody Ab-A2(N67Q) Xmab^{2+1} (Figure 14C) mediated target cell lysis of human tumor cell line C4-2B luc by human T cells.

[0027] Figure 15 shows that STEAP1 antibody Ab-A1 Xmab^{2+1} and Ab-A2(N67Q) Xmab^{2+1} mediated dose-dependent target cell lysis of human tumor cell line C4-2B luc but not C4-2B luc STEAP1 KO by human T cells.

[0028] Figures 16A-16B show that murine STEAP1 antibody Ab-Am detected STEAP1 expressed by tested 293 T cells. Figure 16C shows that STEAP1 binder Ab-A2(N67Q) Xmab^{2+1} mediated dose-dependent target cell lysis of human cell line 293T stably transfected with human STEAP1 and not of parental human 293T cell line.

[0029] Figure 17A shows that Ab-Bx (Ab-B1-XmAb) and Ab-B1 Xmab^{2+1} mediated target cell lysis of C4-2B luc prostate cancer cells. Figure 17B shows that Xmab^{2+1} Ab-B1 variants (i.e., Ab-B1-G37A, Ab-B1-S39A, and Ab-B1-G37A/S39A) mediated target cell lysis of C4-2B luc prostate cancer cells. Figure 17C shows that Xmab^{2+1} Ab-B1 variants (i.e., Ab-B1-G37A, Ab-B1-S39A, and Ab-B1-G37A/S39A) did not mediate target cell lysis of C4-2B luc STEAP1 knockout prostate cancer cells.

[0030] Figures 18A-18I depict several formats of antigen-binding proteins: the "bottle opener" format, mAb-Fv, mAb-scFv, central-scFv, central-Fv, one armed central-scFv, one scFv-mAb, scFv-mAb and dual scFv. For all of the scFv domains depicted, they can be either N-to C-terminus variable heavy-(optional linker)-variable light, or the opposite. In addition, for the one armed scFv-mAb, the scFv can be attached either to the N-terminus of a heavy chain monomer or to the N-terminus of the light chain.

[0031] Figure 19 provides the sequences of CDRs, variable heavy domains, variable light domains, scFvs, linker sequences, and monomer sequences of the disclosure. Underlining in variable region sequences denotes CDR sequences.

[0032] Figures 20A and 20B illustrate the results of the T-cell dependent cytotoxicity assay described in Example 9. Figure 20A is a graph illustrating specific cytotoxicity (%) mediated by Ab-A2 (N67Q) XmAb^{2+1} alone (open circles) and Ab-A2 (N67Q) XmAb^{2+1} in combination with an anti-PD-1 antibody (closed circles) in one representative T-cell donor (y-axis=Log (pM)). Figure 20B illustrates the EC50 (pM) of Ab-A2 (N67Q) XmAb^{2+1} alone (left) and Ab-A2 (N67Q) XmAb^{2+1} in combination with an anti-PD-1 antibody (right) from four different T-cell donors.

[0033] Figures 21A-21C are line graphs illustrating PD-1 expression (% CD3+) in total T cells (Figure 21A), $CD8^+$ T cells (Figure 21B), and $CD4^+$ T cells (Figure 21C) exposed to varying amounts of Ab-A2 (N67Q) $XmAb^{2+1}$. Circles and squares in the graph denote different donors of the T cells. PD-1 expression increases in T cells exposed to a heterodimeric antibody of the disclosure.

[0034] Figure 22 is a line graph illustrating tumor volume (mm^3; y-axis) over time (days of study, x-axis). Human SK-N-MC cells (5 x 10^6 cells/mouse) were injected subcutaneously into the right dorsal flank of female, sub-lethally irradiated NOD/SCID mice on day 1. On day 8, human CD3+ T cells (2 x 10^7 cells/mouse) were injected into the peritoneal cavity of all animals, except of group 1. Vehicle (groups 1 and 2) or Ab-A2 (N67Q) $XmAb^{2+}$ at dose levels of 1.0, 0.1, or 0.01 mg/kg (groups 3, 4, 5, respectively) was administered by intravenous bolus injections on days 12, 19 and 26 (arrows at top of graph). Tumor volumes were determined three times/week using an electronic caliper. Group mean tumor volume [mm^3] +/- SEM are shown. Asterisks in the figure denote statistically significant differences (one-way ANOVA; * = $p < 0.05$; *** = $p < 0.001$) between vehicle (group 2) and Ab-A2(N67Q) $XmAb^{2+}$-treated groups.

[0035] Figure 23. Mean and Median SK-N-MC Human Neuroblastoma Tumor Volumes in Female NOD/SCID Mice.

DETAILED DESCRIPTION

[0036] STEAP1 is a 339 amino acid protein comprising six transmembrane domains, resulting in three extracellular loops and two intracellular loops. The amino acid sequence of human STEAP1 is set forth herein as SEQ ID NO: 2. The estimated positions of the extracellular loops are amino acids 92-118 (extracellular loop 1), amino acids 185-217 (extracellular loop 2), and amino acids 279-290 (extracellular loop 3). STEAP1 is differentially expressed in prostate cancer compared to normal tissues, and increased expression in bone and lymph node prostate cancer metastatic lesions was observed compared to primary prostate cancer samples. STEAP1 represents an ideal target for diagnostics and antibody-based therapeutics, such as a bispecific anti-STEAP1/anti-CD3 T cell recruiting antibody to, e.g., trigger T cell dependent cellular cytotoxicity or redirected lysis of prostate cancer cells. The disclosure provides antigen-binding proteins that bind STEAP1, as described further herein.

Antigen-Binding Protein

[0037] An "antigen-binding protein" is a protein comprising a portion that binds a specified target antigen (such as STEAP1). An antigen-binding protein comprises a scaffold or framework portion that allows the antigen-binding portion to adopt a conformation that promotes binding of the antigen-binding protein to the antigen. In exemplary aspects, the antigen-binding protein is an antibody or immunoglobulin (e.g., a heterodimeric and/or bispecific antibody), or an antigen-binding antibody fragment, or an antibody protein product.

[0038] The term "antibody" refers to an intact antigen-binding immunoglobulin. An "antibody" is a type of an antigen-binding protein. The antibody can be an IgA, IgD, IgE, IgG, or IgM antibody, including any one of IgG1, IgG2, IgG3 or IgG4. In various embodiments, an intact antibody comprises two full-length heavy chains and two full-length light chains. An antibody has a variable region and a constant region. In IgG formats, a variable region is generally about 100-110 or more amino acids, comprises three complementarity determining regions (CDRs), is primarily responsible for antigen recognition, and substantially varies among other antibodies that bind to different antigens. A variable region typically comprises at least three heavy or light chain CDRs (Kabat et al., 1991, Sequences of Proteins of Immunological Interest, Public Health Service N.I.H., Bethesda, Md.; see also Chothia and Lesk, 1987, J. Mol. Biol. 196:901-917; Chothia et al., 1989, Nature 342: 877-883), within a framework region (designated framework regions 1-4, FR1, FR2, FR3, and FR4, by Kabat et al., 1991; see also Chothia and Lesk, 1987, supra). The constant region allows the antibody to recruit cells and molecules of the immune system.

[0039] In various aspects, the antibody is a monoclonal antibody. In certain aspects, the antibody is a human antibody. In certain aspects, the antibody (or other antigen-binding protein) is chimeric or humanized. The term "chimeric" refers to an antibody containing domains from two or more different antibodies. A chimeric antibody can, for example, contain the constant domains from one species and the variable domains from a second, or more generally, can contain stretches of amino acid sequence from at least two species. Both "chimeric" and "humanized" often refer to antigen-binding proteins that combine regions from more than one species. A chimeric antibody also can contain domains of two or more different antibodies within the same species. In one embodiment, the chimeric antibody is a CDR grafted antibody.

[0040] The term "humanized" when used in relation to antigen-binding proteins refers to antigen-binding proteins (e.g., antibodies) having at least CDR region from a non-human

source and which are engineered to have a structure and immunological function more similar to true human antibodies than the original source antibodies. For example, humanizing can involve grafting a CDR from a non-human antibody, such as a mouse antibody, into a human framework region. Generally, in a humanized antibody, the entire antibody, except the CDRs, is encoded by a polynucleotide of human origin or is identical to such an antibody except within its CDRs. The CDRs, some or all of which are encoded by nucleic acids originating in a non-human organism, are grafted into the beta-sheet framework of a human antibody variable region to create an antibody, the specificity of which is determined by the engrafted CDRs. The creation of such antibodies is described in, e.g., International Patent Publication No. WO 92/11018; Jones, 1986, Nature 321:522-525; and Verhoeyen et al., 1988, Science 239:1534-1536, all entirely incorporated by reference. "Back mutation" of selected acceptor framework residues to the corresponding donor residues is often employed to regain affinity that is lost in the initial grafted construct (See, e.g., U.S. Patent Nos. 5530101; 5585089; 5693761; 5693762; 6180370; 5859205; 5821337; 6054297; and 6407213, all entirely incorporated by reference). The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region, typically that of a human immunoglobulin, and thus will typically comprise a human Fc region.

[0041] A variety of techniques and methods for generating chimeric antibodies, humanized antibodies, and reshaping non-human antibodies are well known in the art. See Tsurushita & Vasquez, 2004, Humanization of Monoclonal Antibodies, Molecular Biology of B Cells, 533-545, Elsevier Science (USA), and references cited therein; Jones et al., 1986, Nature 321:522-525; Riechmann et al.,1988; Nature 332:323-329; Verhoeyen et al., 1988, Science, 239:1534-1536; Queen et al., 1989, Proc Natl Acad Sci, USA 86:10029-33; He et al., 1998, J. Immunol. 160: 1029-1035; Carter et al., 1992, Proc Natl Acad Sci USA 89:4285-9, Presta et al., 1997, Cancer Res. 57(20):4593-9; Gorman et al., 1991, Proc. Natl. Acad. Sci. USA 88:4181-4185; O'Connor et al., 1998, Protein Eng 11:321-8, U.S. Patent Publication No. 20030039649; U.S. Patent Nos. 5,869,619, 5,225,539, 5,821,337, 5,859,205; Padlan et al., 1995, FASEB J. 9:133-39; and Tamura et al., 2000, J. Immunol. 164:1432-41, all entirely incorporated by reference. Humanization or other methods of reducing the immunogenicity of nonhuman antibody variable regions may include resurfacing methods, as described for example in Roguska et al., 1994, Proc. Natl. Acad. Sci. USA 91:969-973, entirely incorporated by reference. A parent antibody may be affinity matured, which is well understood in the art. Structure-based methods may be employed for humanization and

affinity maturation, for example as described in U.S. Patent Publication No. 20060008883. Selection based methods may be employed to humanize and/or affinity mature antibody variable regions, including but not limited to methods described in Wu et al., 1999, J. Mol. Biol. 294:151-162; Baca et al., 1997, J. Biol. Chem. 272(16):10678-10684; Rosok et al., 1996, J. Biol. Chem. 271(37): 22611-22618; Rader et al., 1998, Proc. Natl. Acad. Sci. USA 95: 8910-8915; Krauss et al., 2003, Protein Engineering 16(10):753-759, all entirely incorporated by reference. Humanizing also can involve select amino acid substitutions to make a non-human sequence more similar to a human sequence. Other humanization methods may involve the grafting of only parts of the CDRs, including but not limited to methods described in Tan et al., 2002, J. Immunol. 169:1119-1125; De Pascalis et al., 2002, J. Immunol. 169:3076-3084, all entirely incorporated by reference.

[0042] In other embodiments, the antigen-binding protein is an antigen-binding antibody fragment, i.e., a fragment of an antibody that lacks part or all of an antibody's light chains and/or part or all of an antibody's heavy chains. Antibody fragments can be recombinantly produced or can be prepared by cleaving an intact antibody using enzymes, such as, e.g., papain and pepsin. Papain cleaves an antibody to produce two Fab fragments and a single Fc fragment. Pepsin cleaves an antibody to produce a $F(ab')_2$ fragment and a pFc' fragment. In exemplary instances, the antigen-binding antibody fragment is a Fab fragment or a $F(ab')_2$ fragment. A Fab fragment is a monovalent fragment having the VL, VH, CL and CH1 domains. Fab may refer to this region in isolation, or this region in the context of a full length antibody, antibody fragment, etc. A $F(ab')_2$ fragment is a bivalent fragment having two Fab fragments linked by a disulfide bridge at the hinge region.

[0043] The architecture of antibodies has been exploited to create a growing range of alternative formats that span a molecular-weight range of at least about 12-150 kDa and has a valency (n) range from monomeric (n = 1), to dimeric (n = 2), to trimeric (n = 3), to tetrameric (n = 4), and potentially higher; such alternative formats are referred to herein as "antibody protein products" and are examples of antigen-binding proteins. Antibody protein products include those based on the full antibody structure and those that mimic antibody fragments which retain full antigen-binding capacity, e.g., scFvs and VHH/VH (discussed below). A single-chain antibody (scFv) is an antibody in which a VL and a VH region are joined via a linker (e.g., a synthetic sequence of amino acid residues usually about 15 amino acids in length) to form a continuous protein chain wherein the linker is long enough to allow the protein chain to fold back on itself and form a monovalent antigen-binding site (see, e.g.,

Bird et al., 1988, Science 242:423-26 and Huston et al., 1988, Proc. Natl. Acad. Sci. USA 85:5879-83).

[0044] An antigen-binding fragment that retains its complete antigen-binding site is the Fv fragment, which consists entirely of a variable (V) region (the VL and VH domain of a single antibody). A soluble, flexible amino acid peptide linker is often used to connect the V regions to a scFv (single chain fragment variable) fragment for stabilization of the molecule, or a constant (C) domain is added to the V regions to generate a Fab fragment (fragment, antigen-binding). scFv and Fab fragments can be easily produced in host cells, e.g., prokaryotic or eukaryotic host cells. Other antibody protein products include disulfide-bond stabilized scFv (ds-scFv), single chain Fab (scFab), single chain antibody (SCA), domain antibodies (dAbs) (e.g., peptides comprising VH domain, a VL domain, or an antigen-binding fragment of a VH or VL domain), peptides comprising an Fd fragment (comprising VH and CH1 domains), complementarity determining region (CDR) fragments, as well as di- and multimeric antibody formats like dia-, tria- and tetra-bodies, or minibodies (miniAbs) that comprise different formats consisting of scFvs linked to oligomerization domains. The smallest fragments are VHH/VH of camelid heavy chain Abs as well as single domain Abs (sdAb). A peptibody or peptide-Fc fusion is yet another antibody protein product. The structure of a peptibody consists of a biologically active peptide grafted onto an Fc domain. Peptibodies are further described in the art. See, e.g., Shimamoto et al., mAbs 4(5): 586-591 (2012).

[0045] Alternatively, an antibody protein product can comprise, for example, an alternative protein scaffold or artificial scaffold with grafted CDRs or CDR derivatives. Such scaffolds include, but are not limited to, antibody-derived scaffolds comprising mutations introduced to, for example, stabilize the three-dimensional structure of the antigen-binding protein as well as wholly synthetic scaffolds comprising, for example, a biocompatible polymer. See, for example, Korndorfer et al., 2003, Proteins: Structure, Function, and Bioinformatics, Volume 53, Issue 1:121-129; Roque et al., 2004, Biotechnol. Prog. 20:639-654. In addition, peptide antibody mimetics ("PAMs") can be used, as well as scaffolds based on antibody mimetics utilizing fibronectin components as a scaffold.

[0046] In various aspects, the antigen-binding protein comprises heavy chain CDRs comprising amino acid sequences that differ by no more than 3, 2, or 1 amino acid from i) vhCDR1 SEQ ID NO: 14, vhCDR2 SEQ ID NO: 15 or vhCDR2 SEQ ID NO: 21, and vhCDR3 SEQ ID NO: 16, or ii) vhCDR1 SEQ ID NO: 33, vhCDR2 SEQ ID NO: 34, and

vhCDR3 SEQ ID NO: 35; and/or light chain CDRs comprising amino acid sequences that differ by no more than 3, 2, or 1 amino acid from i) vlCDR1 SEQ ID NO: 11, vlCDR2 SEQ ID NO: 12, and vlCDR3 SEQ ID NO: 13; or ii) vlCDR1 SEQ ID NO: 30, vlCDR2 SEQ ID NO: 31, and vlCDR3 SEQ ID NO: 32. Each such sequence difference is independently either a deletion, insertion, or substitution, although substitutions (e.g., conservative substitutions) are preferred. Examples of conservative substitutions include, but are not limited to, exchanges within the following groups: small aliphatic, nonpolar or slightly polar residues, Ala, Ser, Thr, Pro, Gly; polar, negatively charged residues and their amides and esters, Asp, Asn, Glu, Gln, cysteic acid and homocysteic acid; polar, positively charged residues, His, Arg, Lys, Ornithine (Orn); large, aliphatic, nonpolar residues, Met, Leu, Ile, Val, Cys, Norleucine (Nle), homocysteine; and large, aromatic residues: Phe, Tyr, Trp, acetyl phenylalanine.

[0047] In various aspects, the antigen-binding protein comprises the following CDR sequences: a) vhCDR1 comprising SEQ ID NO: 14, vhCDR2 comprising SEQ ID NO:15 or SEQ ID NO: 21, and vhCDR3 comprising SEQ ID NO: 16; or b) vhCDR1 comprising SEQ ID NO: 33, vhCDR2 comprising SEQ ID NO: 34, and vhCDR3 comprising SEQ ID NO: 35. Alternatively or in addition, the antigen-binding protein comprises the following CDR sequences: a) vlCDR1 comprising SEQ ID NO: 11, vlCDR2 comprising SEQ ID NO: 12, and vlCDR3 comprising SEQ ID NO: 13; or b) vlCDR1 comprising SEQ ID NO: 30, vlCDR2 comprising SEQ ID NO: 32, and vlCDR3 comprising SEQ ID NO: 33.

[0048] Thus, in various aspects, the antigen-binding protein comprises vhCDR1 comprising SEQ ID NO: 14, vhCDR2 comprising SEQ ID NO: 15 or SEQ ID NO: 21, vhCDR3 comprising SEQ ID NO: 16, vlCDR1 comprising SEQ ID NO: 11, vlCDR2 comprising SEQ ID NO: 12, and vlCDR3 comprising SEQ ID NO: 13. In alternative aspects, the antigen-binding protein comprises vhCDR1 comprising SEQ ID NO: 33, vhCDR2 comprising SEQ ID NO: 34, vhCDR3 comprising SEQ ID NO: 35, vlCDR1 comprising SEQ ID NO: 30, vlCDR2 comprising SEQ ID NO: 31, and vlCDR3 comprising SEQ ID NO: 32.

[0049] In various embodiments, the antigen-binding protein comprises a light chain variable domain comprising an amino acid sequence at least 90% identical (e.g., at least 95% identical or 100% identical) to SEQ ID NO: 183 or SEQ ID NO:186; and/or a heavy chain variable domain comprising an amino acid sequence at least 90% identical (e.g., at least 95% identical or 100% identical) to SEQ ID NO: 182, SEQ ID NO: 184, or SEQ ID NO:185. For example, the antigen-binding protein can comprise (i) SEQ ID NO: 183 and SEQ ID NO:

182, (ii) SEQ ID NO: 184 and SEQ ID NO: 183, or (iii) SEQ ID NO: 185 and SEQ ID NO: 186. In various aspects, the antigen-binding protein comprises a light chain variable region and/or a heavy chain variable region comprising a sequence of amino acids that differs from the aforementioned amino acid sequences only at 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 residue(s), wherein each such sequence difference is independently either a deletion, insertion, or substitution (e.g., conservative substitution). In various aspects, the sequence difference(s) is located outside the CDR (e.g., within the framework region).

[0050] In various embodiments, the antigen-binding protein comprises a light chain comprising an amino acid sequence at least 90% identical (e.g., at least 95% identical or 100% identical) to SEQ ID NO: 17 or SEQ ID NO: 36; and/or a heavy chain comprising an amino acid sequence at least 90% identical (e.g., at least 95% identical or 100% identical) to SEQ ID NO: 18, SEQ ID NO: 199 or SEQ ID NO: 37. For example, the antigen-binding protein can comprise (i) SEQ ID NO: 17 and SEQ ID NO: 18; (ii) SEQ ID NO: 17 and SEQ ID NO: 199; or (iii) SEQ ID NO: 36 and SEQ ID NO: 37.

[0051] In various embodiments, the antigen-binding protein comprises a light chain comprising an amino acid sequence at least 90% identical (e.g., at least 95% identical or 100% identical) to SEQ ID NO: 200 or SEQ ID NO: 204; and/or a heavy chain comprising an amino acid sequence at least 90% identical (e.g., at least 95% identical or 100% identical) to SEQ ID NO: 201, SEQ ID NO: 203 or SEQ ID NO: 205. For example, the antigen-binding protein can comprise (i) SEQ ID NO: 200 and SEQ ID NO: 201; (ii) SEQ ID NO: 200 or SEQ ID NO: 203; (iii) SEQ ID NO: 204 and SEQ ID NO: 205.

Competition, Epitope, Binding Affinity

[0052] The antigen-binding protein binds STEAP1 of SEQ ID NO: 2. Specific binding (i.e., binding to STEAP1 that is measurably different from a non-specific interaction) can be determined, for example, by determining binding of a molecule compared to binding of a control molecule, which generally is a molecule of similar structure that does not have binding activity. For example, specific binding can be determined by competition with a control molecule that is similar to the target.

[0053] The binding affinity of the antigen-binding protein to STEAP1 may be described in terms of dissociation constant (Kd). In exemplary aspects, the Kd of the antigen-binding protein provided herein is micromolar, nanomolar, picomolar, or femtomolar. Typically, an antigen-binding protein that specifically binds an antigen will have a Kd that is 20-, 50-, 100-,

500-, 1000-, 5,000-, 10,000- or more times greater for a control molecule relative to the target antigen or epitope. Also, specific binding for a particular antigen can be exhibited, for example, by an antibody having a KA or Ka for an antigen or epitope of at least 20-, 50-, 100-, 500-, 1000-, 5,000-, 10,000- or more times greater for the epitope relative to a control, where KA or Ka refers to an association rate of a particular antibody-antigen interaction. In exemplary aspects, the KD of the antigen-binding protein provided herein for STEAP1 is less than or equal to 10^{-7} M, less than or equal to 10^{-8} M, less than or equal to 10^{-9} M, less than or equal to 10^{-10} M, less than or equal to 10^{-11} M, or less than or equal to 10^{-12} M. For example, the KD of the antigen-binding protein is optionally within a range of about 10^{-4} to 10^{-6} M, or about 10^{-7} to 10^{-9} M, or about 10^{-10} to 10^{-12} M, or about 10^{-7} to 10^{-12}, or about 10^{-9} to 10^{-12}, or about 10^{-13} to 10^{-15} M. Alternatively (or in addition), the antigen-binding protein has a low dissociation rate from STEAP1. In some embodiments, the antigen-binding protein has a K_{off} of $1x10^{-4}$ s^{-1} or lower. In another embodiment, the K_{off} is $5x10^{-5}$ s^{-1} or lower. In various aspects, the antigen-binding protein differentiates between target cells expressing a high level of STEAP1 and those off-target cells that display less STEAP1. For example, in various aspects, the antigen-binding protein preferentially binds cells comprising more than about 100,000 STEAP receptors per cell (e.g., about 200,000 STEAP1 receptors per cell) down to about 10,000 STEAP1 receptors per cell. It will be appreciated the disclosure regarding competition, binding affinity, and binding specificity relating to STEAP1 also applies to a multispecific antigen-binding protein's binding to a second or third antigen (e.g., CD3) or a different antibody which is used in conjunction with the anti-STEAP1 antigen-binding protein. For example, in exemplary aspects, the Kd of the antigen-binding protein provided herein for CD3 (or PD-1, as described below) is less than or equal to 10^{-7} M, less than or equal to 10^{-8} M, less than or equal to 10^{-9} M, less than or equal to 10^{-10} M, less than or equal to 10^{-11} M, or less than or equal to 10^{-12} M. For example, the Kd of the antigen-binding protein is optionally within a range of about 10^{-4} to 10^{-6} M, or about 10^{-7} to 10^{-9} M, or about 10^{-10} to 10^{-12} M, or about 10^{-7} to 10^{-12}, or about 10^{-9} to 10^{-12}, or about 10^{-13} to 10^{-15} M. Alternatively (or in addition), the antigen-binding protein has a low dissociation rate from CD3. In some embodiments, the antigen-binding protein has a K_{off} of $1x10^{-4}$ s^{-1} or lower. In another embodiment, the K_{off} is $5x10^{-5}$ s^{-1} or lower with respect to CD3.

[0054] The disclosure further provides an antigen-binding protein (e.g., an antibody) that competes for binding to STEAP1 with any of the antigen-binding proteins described herein (e.g., Ab-A, Ab-A1, Ab-A2, Ab-B, or Ab-B1, including in the $^{XmAb2+1}$ format as described

herein). Put another way, the disclosure provides an antigen-binding protein that cross-blocks the binding of a reference antigen-binding protein described herein to STEAP1 or is cross-blocked from binding to STEAP1 by the reference antigen-binding protein. By "compete" is meant that one antigen-binding protein prevents, reduces or inhibits binding of a reference antigen-binding protein to STEAP1. Numerous types of competitive binding assays can be used, for example, surface plasmon resonance, solid phase direct or indirect radioimmunoassay (RIA), solid phase direct or indirect enzyme immunoassay (EIA), sandwich competition assay (see, e.g., Stahli et al., 1983, Methods in Enzymology 9:242-253), solid phase direct biotin-avidin EIA (see, e.g., Kirkland et al., 1986, J. Immunol. 137:3614-3619), solid phase direct labeled assay, solid phase direct labeled sandwich assay (see, e.g., Harlow and Lane, 1988, Antibodies, A Laboratory Manual, Cold Spring Harbor Press), solid phase direct label RIA using 1-125 label (see, e.g., Morel et al., 1988, Molec. Immunol. 25:7-15), solid phase direct biotin-avidin EIA (see, e.g., Cheung, et al., 1990, Virology 176:546-552), and direct labeled RIA (Moldenhauer et al., 1990, Scand. J. Immunol. 32:77-82). Typically, such an assay involves the use of purified antigen bound to a solid surface or exposed on cells, an unlabeled test antigen-binding protein, and a labeled reference antigen-binding protein. Competitive inhibition is measured by determining the amount of label bound to the solid surface or cells in the presence of the test antigen-binding protein. Usually the test antigen-binding protein is present in excess. Antigen-binding proteins identified by competition assay (competing antigen-binding proteins) include antigen-binding proteins binding to the same epitope as the reference antigen-binding proteins, an epitope that overlaps the epitope recognized by the reference antigen-binding protein, and epitopes that do not overlap but that allow for steric hindrance to occur between the test and reference antigen-binding proteins. Usually, when a competing antigen-binding protein is present in excess, it will inhibit binding of a reference antigen-binding protein to a common antigen by at least 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, or 75%. In some instances, binding is inhibited by at least 80%, 85%, 90%, 95%, or 97% or more. In at least one aspect, the antigen-binding protein (e.g., antibody) competes with a reference antigen-binding protein (e.g., Ab-A, Ab-A1, Ab-A2, Ab-B, or Ab-B1 described herein, optionally in a bispecific antibody format, such as the bispecific antibody format described in the Examples (e.g., $XmAb^{2+1}$)) such that binding of the reference antigen-binding protein to STEAP1 is reduced by at least 80% or at least 90%.

[0055] The antigen-binding protein binds STEAP1 of SEQ ID NO: 2. A competing (or cross-blocking) antigen-binding protein may bind an epitope that overlaps the epitope recognized by the reference antigen-binding protein, or an epitope that does not overlap but that allows for steric hindrance to occur between the test and reference antigen-binding proteins. In various aspects, the antigen-binding protein binds to the same epitope as the reference antigen-binding protein, such as Ab-A, Ab-A1, Ab-A2 (N67Q), Ab-B, or Ab-B1 or bispecific or heterodimeric versions thereof (e.g., Ab-A1 XmAb^{2+1}, Ab-A2 (N67Q) XmAb^{2+1}, or Ab-B1 XmAb^{2+1}) described herein. For example, the antigen-binding protein of the disclosure optionally binds STEAP1 in a region outside of the second extracellular loop. The antigen-binding protein, in at least one embodiment, binds a region of STEAP1 within amino acids 92-118 (extracellular loop 1) and/or amino acids 279-290 (extracellular loop 3). In various aspects, the disclosure provides an antigen-binding protein binds a region of STEAP 1 within amino acids 92-118 and amino acids 279-290. Also optionally, the antigen-binding protein does not bind STEAP2 (UniProtKB No. Q8NFT2; SEQ ID NO: 177). If desired, the epitope of the reference antigen-binding protein and/or the tested antigen-binding protein can be determined by solving the X-ray crystal structure of the antigen-binding protein bound to STEAP1 or a portion thereof. In one such embodiment, the epitope is defined as those residues on extracellular portion of STEAP1 that show at least a 10% reduction in solvent accessibility when the antigen-binding protein (reference or tested) is bound to it as compared to when it is not.

Methods of Making Antigen-Binding Proteins

[0056] Suitable methods of making antigen-binding proteins (e.g., antibodies, antigen-binding antibody fragments, and antibody protein products) are known in the art. For instance, standard hybridoma methods for producing antibodies are described in, e.g., Harlow and Lane (eds.), Antibodies: A Laboratory Manual, CSH Press (1988), and CA. Janeway et al. (eds.), Immunobiology, 5th Ed., Garland Publishing, New York, NY (2001)). EBV-hybridoma methods and Bacteriophage vector expression systems are described in, e.g., Haskard and Archer, J. Immunol. Methods, 74(2), 361-67 (1984), Roder et al., Methods Enzymol., 121, 140-67 (1986), and Huse et al., Science, 246, 1275-81 (1989)). Methods of producing antibodies in non-human animals are described in, e.g., U.S. Patent Nos. 5,545,806, 5,569,825, 5,714,352, and 5,814,318; and U.S. Patent Application Publication No. 2002/0197266 (all incorporated herein by reference). In certain aspects, a recombinant antigen-binding protein that binds STEAP1 is provided. In this context, a "recombinant

protein" is a protein made using recombinant techniques, e.g., through the expression of a recombinant nucleic acid. Methods and techniques for the production of recombinant proteins are well known in the art.

[0057] Molecular evolution of the CDRs in the binding site also has been used to generate antigen-binding proteins (e.g., antibodies) with increased affinity, for example, antibodies having increased affinity for c-erbB-2, as described by Schier et al., 1996, J. Mol. Biol. 263:551. Such techniques are useful in preparing anti-STEAP1 antigen-binding proteins (or other antigen-binding proteins described herein).

[0058] Methods of testing antigen-binding proteins for the ability to bind to an antigen, such as STEAP1, are known in the art and include, e.g., radioimmunoassay (RIA), ELISA, Western blot, immunoprecipitation, surface plasmon resonance (e.g., BIAcore®), and competitive inhibition assays (see, e.g., Janeway et al., *infra*; U.S. Patent Publication No. 2002/0197266; and U.S. Patent No. 7,872,106, all of which are hereby incorporated by reference in their entirety and particularly with respect to disclosure of competition assays). Indeed, assays which test the ability of an antigen-binding protein to compete with a second antigen-binding proteins for binding to an antigen, or to an epitope thereof, are known in the art and can be used to test the ability of an antibody to bind to, e.g., STEAP1. See, e.g., U.S. Patent Application Publication No. 2014/0178905, Chand et al., Biologicals 46: 168-171 (2017); Liu et al., Anal Biochem 525: 89-91 (2017); and Goolia et al., J Vet Diagn Invest 29(2): 250-253 (2017). Surface plasmon resonance can be used to determine the binding constants of the antigen-binding protein and a second antigen-binding protein and the two binding constants can be compared.

Multi-specific Antigen-Binding Proteins

[0059] An ongoing problem in antibody technologies is the desire for bispecific (and/or multispecific) antibodies that bind to two (or more) different antigens simultaneously, in general allowing the different antigens to be brought into proximity and resulting in new functionalities and new therapies. The disclosure provides a novel multispecific antigen-binding protein that binds STEAP1 and one or more additional target antigens. In a preferred embodiment, the disclosure provides a novel bispecific antigen-binding protein (e.g., bispecific antibody) comprising an anti-STEAP1 binding domain as described above and a binding region that binds a second target antigen (which may be a different STEAP1 epitope, but which generally is a different antigen). In various aspects, the second antigen is cell surface molecule present on an effector cell, i.e., a leukocyte which expresses one or more

FcRs (e.g., FcγRIII) and performs one or more effector functions attributable to the Fc region of an antibody.

[0060] Examples of effector functions include, but are not limited to, Clq binding and complement dependent cytotoxicity (CDC), Fc receptor binding, antibody-dependent cell-mediated cytotoxicity (ADCC), phagocytosis, down regulation of cell surface receptors, and B cell activation. Examples of effector cells involved in ADCC include, but are not limited to, cytotoxic T cells, peripheral blood mononuclear cells (PBMC), natural killer (NK) cells, monocytes, and neutrophils. In various aspects, the disclosure provides a bispecific antigen-binding protein (e.g., bispecific antibody) that binds to both CD3 (e.g., SEQ ID NO: 1) and STEAP1 (SEQ ID NO: 2). In various aspects, the disclosure provides a bispecific antigen-binding protein (e.g., bispecific antibody) that binds to both CD3 and extracellular loops 1 and 3 of STEAP1.

[0061] In various aspects, the multispecific antigen-binding protein differentiates between target cells expressing a high level of STEAP1 and those off-target cells that display less STEAP1. In this regard, in some embodiments, a bispecific antigen-binding protein (e.g., heterodimeric antibody) of the disclosure is able to preferentially mediate T cell dependent killing of tumor cells, demonstrating reduced "off target" effects. For example, in some aspects, a bispecific antibody comprising the STEAP1 antigen-binding protein described herein alongside a CD3 antigen-binding region preferentially mediates T cell dependent killing of cells with a surface density of STEAP1 of greater than 10,000 (e.g., the EC90 is at least 10-fold less for cells with a surface density of STEAP1 of greater than 10,000 compared to cells having a surface density of STEAP1 less than 10,000).

[0062] The disclosure provides a bispecific antigen-binding protein comprising novel anti-CD3 sequences, including sets of CDRs and full variable light and heavy chains. In some aspects, the CD3 binding domain (optionally an scFv as discussed below) of the bispecific construct comprises a variable heavy domain comprising heavy chain CDRs comprising amino acid sequences that differ by no more than 3, 2, or 1 amino acid from vhCDR1 SEQ ID NO: 170, vhCDR2 SEQ ID NO: 171, and vhCDR3 SEQ ID NO: 172, and a variable light domain comprising light chain CDRs comprising amino acid sequences that differ by no more than 3, 2, or 1 amino acid from vlCDR1 SEQ ID NO: 174, vlCDR2 SEQ ID NO:175, and vlCDR3 SEQ ID NO: 176. For example, the disclosure provides a multispecific (e.g., bispecific) construct comprising a variable heavy domain comprising an amino acid sequence at least 90% identical (e.g., at least 95% identical or 100% identical) to SEQ ID NO:169 and

a variable light domain comprising an amino acid sequence at least 90% identical (e.g., at least 95% identical or 100% identical) to SEQ ID NO:173.

[0063] For example, the anti-CD3 portion optionally comprises the CDR sequences vhCDR1 comprising SEQ ID NO:170, vhCDR2 comprising SEQ ID NO: 171, vhCDR3 comprising SEQ ID NO: 172, vlCDR1 comprising SEQ ID NO: 174, vlCDR2 comprising SEQ ID NO: 175, and vlCDR3 comprising SEQ ID NO: 176. In this regard, the CD3 binding region optionally comprises a variable heavy region of SEQ ID NO:169 and a variable light region of SEQ ID NO:173.

[0064] Bispecific antigen-binding proteins may comprise two antigen-binding domains (e.g., each antigen is bound monovalently) or three (or more) antigen-binding domains (e.g., one antigen is bound bivalently and the other is bound monovalently), such as the STEAP1 and CD3 binding domains described herein. Bispecific antibodies in include, but are not limited to, traditional bispecific immunoglobulins (e.g., BsIgG), IgG comprising an appended antigen-binding domain (e.g., the amino or carboxy termini of light or heavy chains are connected to additional antigen-binding domains, such as single domain antibodies or paired antibody variable domains (e.g., Fv or scFv)), BsAb fragments (e.g., bispecific single chain antibodies), bispecific fusion proteins (e.g., antigen-binding domains fused to an effector moiety), and BsAb conjugates. See, e.g., Spiess et al., Molecular Immunology 67(2) Part A: 97-106 (2015), which describes various bispecific formats and is hereby incorporated by reference. Examples of bispecific constructs include, but are not limited to, diabodies, single chain diabodies, tandem scFvs, and Fab_2 bispecifics, as well as engineered constructs comprising full length antibodies. See, e.g., Chames & Baty, 2009, mAbs 1[6]:1-9; and Holliger & Hudson, 2005, Nature Biotechnology 23[9]:1126-1136; Wu et al., 2007, Nature Biotechnology 25[11]:1290-1297; Michaelson et al., 2009, mAbs 1[2]:128-141; International Patent Publication No. 2009032782 and 2006020258; Zuo et al., 2000, Protein Engineering 13[5]:361-367; U.S. Patent Application Publication No. 20020103345; Shen et al., 2006, J Biol Chem 281[16]:10706-10714; Lu et al., 2005, J Biol Chem 280[20]:19665-19672; and Kontermann, 2012 MAbs 4(2):182, all of which are expressly incorporated herein.

[0065] In various aspects, the bispecific antigen-binding protein is a bispecific single chain antibody (BiScFv). A light chain variable region and a heavy chain variable region are connected to one another as a single chain as a first antigen-binding domain, which is connected to a second antigen-binding domain of similar structure, optionally via a linker. In the event that a linker is used, the linker is preferably of a length and sequence sufficient to

ensure that each of the first and second antigen-binding domains can, independently from one another, retain their differential binding specificities. Bispecific single chain molecules are known in the art and are further described in U.S. Patent No. 7635472, International Patent Publication No. WO 99/54440; Mack, J. Immunol. (1997), 158, 3965-3970; Mack, PNAS, (1995), 92, 7021-7025; Kufer, Cancer Immunol. Immunother., (1997), 45, 193-197; Loffler, Blood, (2000), 95, 6, 2098-2103; Bruhl, Immunol., (2001), 166, 2420-2426; and Kipriyanov, J. Mol. Biol., (1999), 293,41-56, which are all incorporated by reference in their entireties.

[0066] Alternative bispecific antigen-binding formats are described in, e.g., U.S. Patent Application Publication No. 2011/0054151, incorporated by reference herein. For example, the bispecific antigen-binding protein may comprise a mAb-Fv format, wherein an IgG antibody is fused at the C-terminus with an Fv fragment. Alternatively, a mAb-Fab format may be used wherein an IgG antibody is fused at the C-terminus with a Fab. The mAb-Fab construct contains CH and CL constant domains C-terminal to the C-terminal Fv fusion, whereas mAb-Fv does not. See Figure 8 of U.S. Patent Application Publication No. 2011/0054151. Optionally, the N-terminal binding region of the mAb-Fv and mAb-Fab constructs lack a light chain and a CH1 domain (i.e., comprise a single domain VHH region). mAb-Fv and mAb-Fab constructs contain three variable regions, such that they bind a first antigen bivalently and a second antigen monovalently. Suitable bispecific antigen-binding formats also include Fab-Fv and Fab-Fab constructs described in U.S. Patent Application Publication No. 2011/0054151. The Fab-Fv and Fab-Fab immunoglobulins comprise an N-terminal Fab fragment that binds a first antigen and a C-terminal Fv or Fab fragment binds a second antigen.

[0067] In one aspect, the present disclosure is directed to the creation of heterodimeric antibodies that co-engage antigens and rely on amino acid variants in the constant regions that are different on each chain to promote heterodimeric formation and/or allow for ease of purification of heterodimers over the homodimers. In general, bispecific antibodies are made by including genes for each heavy and light chain into the host cells. This generally results in the formation of the desired heterodimer (A-B), as well as the two homodimers (A-A and B-B). However, a major obstacle in the formation of multispecific antibodies is the difficulty in purifying the heterodimeric antibodies away from the homodimeric antibodies and/or biasing the formation of the heterodimer over the formation of the homodimers.

[0068] The present disclosure provides heterodimeric antibody formats that overcome hurdles associated with previous technologies. Additionally, in the context of STEAP1/CD3

bispecific antigen-binding proteins, the heterodimeric antibody of the disclosure allows for monovalent binding of CD3. CD3 activation of T-cells occurs only when its associated T-cell receptor (TCR) engages antigen-loaded MHC on antigen presenting cells in a highly avid cell-to-cell synapse (Kuhns et al., 2006, Immunity 24:133-139). Nonspecific bivalent cross-linking of CD3 using an anti-CD3 antibody elicits a cytokine storm and toxicity (Perruche et al., 2009, J Immunol 183[2]:953-61; Chatenoud & Bluestone, 2007, Nature Reviews Immunology 7:622-632; expressly incorporated by reference). Thus for practical clinical use, a preferred mode of CD3 co-engagement for redirected killing of targets cells is monovalent binding that results in activation only upon engagement with the co-engaged target. Thus, in one embodiment, the heterodimeric antibody of the disclosure provides the advantage of monovalent binding to CD3 and bivalent binding to STEAP1 in a format that provides efficient antibody production.

[0069] An exemplary heterodimeric antibody format comprising one heavy chain having a single chain Fv (scFv) and a second heavy chain in a "regular" Fab format, i.e., comprising a variable heavy chain and a light chain. Put another way, the heterodimeric antibody comprises a) a first heavy chain comprising a first variable Fc domain and a single chain Fv region (scFv) that binds a first antigen (optionally CD3); b) a second heavy chain comprising a second variable Fc domain and a first variable heavy domain; and c) a first light chain comprising a first variable light domain and a first constant light domain, wherein the first variable heavy domain and the first variable light domain bind to a second antigen (optionally STEAP1). To illustrate, the construct comprises one monomer having scFv region-domain linker-Fc domain and a second monomer having a VH-CH1-hinge- CH2-CH3 plus associated light chain, optionally with heterodimerization variants, including steric and pI variants, Fc and FcRn variants, and additional antigen-binding domains (with optional linkers) included in these regions. In some embodiments, the linker is a hinge region or a fragment thereof. This structure is sometimes referred to herein as the XmAb format, the "triple F" format (scFv-FAb-Fc) or the "bottle-opener" format. The two chains are preferably brought together by the use of amino acid variants in the constant regions (e.g., the Fc domain and/or the hinge region) that promote the formation of heterodimeric antibodies as is described more fully below. Preferably, the scFv binds CD3, and optionally includes a positively charged scFv linker. Alternatively, the scFv binds STEAP1. The “triple F” format is further described in U.S. Patent No. 9,822,186, incorporated by reference herein in its entirety and particularly with respect to the disclosure of heterodimeric antibody structure.

[0070] In another aspect, the bispecific antigen-binding protein is a heterodimeric antibody comprising a first monomer comprising a first heavy chain comprising a first variable heavy domain, first constant heavy chain comprising a first CH1 domain and a first Fc domain, with a scFv comprising a scFv variable light domain, an scFv linker, and a scFv variable heavy domain. The scFv is covalently attached between the C-terminus of the CH1 domain of the heavy constant domain and the N-terminus of the first Fc domain using domain linker(s), and the scFv binds CD3. The heterodimeric antibody further comprises a second monomer comprising a second heavy chain comprising a second variable heavy domain and a second constant heavy chain comprising a second Fc domain. The heterodimeric antibody further utilizes a common light chain comprising a variable light domain and a constant light domain, that associates with the heavy chains to form two identical Fabs that bind STEAP1. This format is sometimes referred to herein as the "XmAb^{2+1}" format due to the bivalent binding to one target antigen. Thus, in one embodiment, the heterodimeric antibody of the disclosure provides the advantage of monovalent binding to CD3 and bivalent binding to STEAP1 in a format that provides efficient antibody production.

[0071] As described further below, the heterodimeric antibody may also include mutations to produce skew variants, pI variants, ablation variants, additional Fc variants, etc. For example, in various aspects, the first and said second Fc domains have a set of amino acid substitutions selected from the group consisting of S364K/E357Q:L368D/K370S; L368D/K370S:S364K; L368E/K370S:S364K; T411T/E360E/Q362E:D401K; L368D/K370S:S364K/E357L and K370S:S364K/E357Q.

[0072] An illustration of the XmAb^{2+1} heterodimeric antibody format of the instant disclosure is provided in Figure 1. The scFv domain and provision of two Fab portions form three antigen-binding domains, wherein the Fab portions of the two monomers bind STEAP1 and the scFv domain binds CD3. The scFv domain is inserted between the Fc domain and the CH1-Fv region of one of the monomers.

[0073] The heterodimeric antibody is preferably of the IgG class, which has several subclasses, including, but not limited to IgG1, IgG2, IgG3, and IgG4, although IgM, IgD, IgG, IgA, and IgE also are contemplated. It should be understood that antibodies can also comprise hybrids of isotypes and/or subclasses. For example, pI engineering of IgG1/G2 hybrids, as shown in U.S. Patent Publication No. 2009/0163699, incorporated by reference, is contemplated as part of the disclosure.

[0074] There are a number of mechanisms that can be used to generate the heterodimers of the present disclosure. In addition, as will be appreciated by those in the art and described more fully below, these mechanisms can be combined to ensure high heterodimerization.

[0075] One mechanism is generally referred to in the art as "knobs and holes" ("KIH"), referring to amino acid engineering that creates steric influences to favor heterodimeric formation and disfavor homodimeric formation can also optionally be used; this is sometimes referred to as "knobs and holes," as described in U.S. Patent Publication No. 20130205756, Ridgway et al., Protein Engineering 9(7):617 (1996); Atwell et al., J. Mol. Biol. 1997 270:26; and U.S. Patent No. 8,216,805, all of which are hereby incorporated by reference in their entirety, particularly with respect to the disclosure of heterodimeric antibody production. In addition, as described in Merchant et al., Nature Biotech. 16:677 (1998), these "knobs and hole" mutations can be combined with disulfide bonds to skew formation to heterodimerization. An example of mutations includes T366S/L368A/Y407V paired with T366W, as well as this variant with a bridging disulfide, T366S/L368A/Y407V/Y349C paired with T366W/S354C, particularly in combination with other heterodimerization variants including pi variants as outlined below.

[0076] An additional mechanism that finds use in the generation of heterodimers is sometimes referred to as "electrostatic steering" as described in Gunasekaran et al., J. Biol. Chem. 285(25):19637 (2010), hereby incorporated by reference in its entirety. This is sometimes referred to herein as "charge pairs." In this embodiment, electrostatics are used to skew the formation towards heterodimerization. As those in the art will appreciate, these may also have an effect on pI, and thus on purification, and thus could in some cases also be considered pI variants. However, as these were generated to force heterodimerization and were not used as purification tools, they are classified as "steric variants." These include, but are not limited to, D221E/P228E/L368E paired with D221R/P228R/K409R (i.e., these are monomer corresponding sets) and C220E/P228E/368E paired with C220R/E224R/P228R/K409R. In some embodiments of framework regions, a position 220 mutation removes a cysteine no longer needed for heavy and light chain disulfide formation. "Steric variants" are an optional embodiment of the disclosure.

[0077] There are several mechanisms that can lead to ease of purifying heterodimeric proteins; one relies on the use of pI variants, such that each monomer has a different pI, thus allowing the isoelectric purification of A-A, A-B and B-B dimeric proteins. Alternatively, separation may be performed on the basis of size. It is also possible to "skew" the formation

of heterodimers over homodimers, as is generally outlined below. Thus, a combination of steric heterodimerization variants and pI or charge pair variants may be used in the context of the disclosure. Additionally, the scFv can include a charged scFv linker (either positive or negative), that give a further pI boost for purification purposes. As will be appreciated by those in the art, some Triple F formats are useful with just charged scFv linkers and no additional pi adjustments, although the invention does provide the use of skew variants with charged scFv linkers as well (and combinations of Fc, FcRn and KO variants discussed herein).

[0078] In embodiments that utilize pI as a separation mechanism, amino acid variants can be introduced into one or both of the monomer polypeptides; that is, the pI of one of the monomers (referred to herein for simplicity as "monomer A") can be engineered away from monomer B, or both monomer A and B change be changed, with the pI of monomer A increasing and the pI of monomer B decreasing. The pI changes of either or both monomers can be done by removing or adding a charged residue (for example, a neutral amino acid is replaced by a positively or negatively charged amino acid residue, e.g., glycine to glutamic acid), changing a charged residue from positive or negative to the opposite charge (e.g., aspartic acid to lysine), or changing a charged residue to a neutral residue (e.g., loss of a charge; lysine to serine). In addition, suitable pI variants for use in the creation of heterodimeric antibodies herein are those that are isotypic, e.g., importing pI variants from different IgG isotypes such that pI is changed without introducing significant immunogenicity; see Figure 29 from U.S. Patent Publication No. 20140288275, hereby incorporated by reference in its entirety.

[0079] Accordingly, an embodiment provides for creating a sufficient change in pI in at least one of the monomers such that heterodimers can be separated from homodimers. This can be accomplished using a "wild type" heavy chain constant region and a variant region that has been engineered to either increase or decrease its pI (wt A-+B or wt A - -B), or by increasing one region and decreasing the other region (A+ -B- or A- B+). It should be noted that in this discussion it does not matter which monomer comprises the scFv and which the Fab. A schematic associated with the use of pI variants is set forth in Figure 34 of U.S. Patent No. 9,822,186 (incorporated herein by reference in its entirety, and particularly with respect to the discussion of heterodimeric antibody variants and anti-CD3 sequences). pI variants may be combined with skew variants in a "plug and play" format, in that the effects

of the variants transfer into different antibodies with different Fv regions easily and are very stable.

[0080] Thus, in general, an aspect of the disclosure includes amino acid variants in the constant regions of antibodies that are directed to altering the isoelectric point (pI) of at least one, if not both, of the monomers of the antibody to form "pI heterodimers" (i.e., "pI antibodies") by incorporating amino acid substitutions ("pI variants" or "pI substitutions") into one or both of the monomers. The separation of the heterodimers from the two homodimers can be accomplished if the pIs of the two monomers differ by as little as 0.1 pH unit, e.g., a difference of 0.2, 0.3, 0.4 and 0.5 pH or greater.

[0081] The number of pI variants to be included on each or both monomer(s) to achieve desired separation will depend, in part, on the starting pI of the scFv and Fab(s). That is, to determine which monomer to engineer or in which "direction" (e.g., more positive or more negative), the Fv sequences of the two target antigens are calculated and a decision is made from there. As is known in the art, different Fvs will have different starting pIs which are exploited. In general, the pIs are engineered to result in a total pI difference of each monomer of at least about 0.1 logs, with 0.2 to 0.5 being preferred.

[0082] Furthermore, in some cases (depending on the format) heterodimers can be separated from homodimers on the basis of size (e.g., molecular weight). For example, as shown in some embodiments of Figure 18A-I, some formats result in homodimers and heterodimers with different sizes (e.g., for bottle openers, one homodimer is a "dual scFv" format, one homodimer is a standard antibody, and the heterodimer has one Fab and one scFv). In addition, as depicted in Figure 18A-I, it is possible that some antigens are bound bivalently (e.g., two antigen-binding sites to a single antigen). As will be appreciated, any combination of Fab and scFvs can be utilized to achieve the desired result and combinations.

[0083] In the case where pI variants are used to achieve heterodimerization, by using the constant region(s) of the heavy chain(s), a more modular approach to designing and purifying multispecific proteins, including antibodies, is provided. Thus, in some embodiments, heterodimerization variants (including skew and purification heterodimerization variants) are not included in the variable regions, such that each individual antibody must be engineered. In addition, in some embodiments, the possibility of immunogenicity resulting from the pI variants is significantly reduced by importing pI variants from different IgG isotypes such that pI is changed without introducing significant immunogenicity. Thus, an additional

problem to be solved is the elucidation of low pI constant domains with high human sequence content, e.g., the minimization or avoidance of non-human residues at any particular position.

[0084] A side benefit that can occur with pI engineering is also the extension of serum half-life and increased FcRn binding. That is, as described in U.S. Patent Publication No. 20120028304 (incorporated by reference in its entirety), lowering the pI of antibody constant domains (including those found in antibodies and Fc fusions) can lead to longer serum retention *in vivo*. These pI variants for increased serum half life also facilitate pI changes for purification.

[0085] The heterodimeric fusion proteins of the disclosure can take on a variety of configurations, as are generally depicted in Figures 18A-I. Some figures depict "single ended" configurations, where there is one type of specificity on one "arm" of the molecule and a different specificity on the other "arm." Other figures depict "dual ended" configurations, where there is at least one type of specificity at the "top" of the molecule and one or more different specificities at the "bottom" of the molecule. One heterodimeric scaffold that finds use in the present disclosure is the "triple F" or "bottle opener" scaffold format as depicted in Figure 18A and described above. There are several distinct advantages to the "triple F" format. Antibody analogs relying on two scFv constructs often have stability and aggregation problems, which can be alleviated by the construct described herein by the addition of a "regular" heavy and light chain pairing. In addition, as opposed to formats that rely on two heavy chains and two light chains, there is no issue with the incorrect pairing of heavy and light chains (e.g., heavy 1 pairing with light 2, etc.). Additional useful antigen-binding protein formats are described below.

[0086] In various aspects, the scFv of the heterodimeric antibody comprises the anti-CD3 CDR sequences described herein. For example, in various aspects, the scFv comprises vhCDR1 comprising SEQ ID NO: 170, vhCDR2 comprising SEQ ID NO: 171, vhCDR3 comprising SEQ ID NO: 172, vlCDR1 comprising SEQ ID NO: 174, vlCDR2 comprising SEQ ID NO: 175, and vlCDR3 comprising SEQ ID NO: 176. For example, the scFv optionally comprises a variable heavy region of SEQ ID NO: 169 and a variable light region of SEQ ID NO: 173. In various aspects, the scFv comprises the sequence of SEQ ID NO: 44.

[0087] In some embodiments, the scFv comprises an amino acid sequence set forth in Figure 19, e.g., the amino acid sequence set forth in SEQ ID NO: 44. The sequences set forth in Figure 19 provide antigen-binding domains of differing affinities. In some indications,

stronger affinities may be preferred, while in others, lesser affinities can find use. Accordingly, in some embodiments the disclosure provides heterodimeric antibodies comprising anti-CD3 antigen-binding domains that are "strong" or "high affinity" binders to CD3 (e.g., one example are heavy and light variable domains depicted as H1.30_L1.47 (optionally including a charged linker as appropriate)). In other embodiments, the disclosure provides heterodimeric antibodies comprising anti-CD3 antigen-binding domains that are "lite" or "lower affinity" binders to CD3.

[0088] Typical scFv linkers are well known in the art and are generally 10 to 25 amino acids in length and include glycines and serines. By "charged scFv linker" is meant a scFv linker that utilizes charged amino acids for use in the creation and purification of heterodimeric antibodies that include at least one scFv. Suitable charged scFv linkers are shown in Figures 8A, 8B and 19, although others can be used. In general, the charged scFv linkers contemplated for use in the context of the disclosure have a charge change from 3 to 8 (3, 4, 5, 6, 7 or 8 all being possible) as compared to the standard uncharged scFv linkers such as $(GGGGS)_{3-5}$ (SEQ ID NO:179) sequences traditionally used (either negative or positive). The charged scFv optionally comprises an amino acid sequence selected from IRPRAIGGSKPRVA (SEQ ID NO: 145), GKGGSGKGGSGKGGS (SEQ ID NO: 146), GGKGSGGKGSGGKGS (SEQ ID NO: 147), GGGKSGGGKSGGGKS (SEQ ID NO: 148), GKGKSGKGKSGKGKS (SEQ ID NO: 149), GGGKSGGKGSGKGGS (SEQ ID NO: 150), GKPGSGKPGSGKPGS (SEQ ID NO: 151), GKPGSGKPGSGKPGSGKPGS (SEQ ID NO: 152), or GKGKSGKGKSGKGKSGKGKS (SEQ ID NO: 153). In various aspects, the scFv comprises the amino acid sequence GKPGSGKPGSGKPGSGKPGS (SEQ ID NO: 152).

[0089] In exemplary aspects, the scFv comprises CDR sequences, variable region sequences, a scFv linker sequence, or a scFv sequence having at least about 70%, at least about 80%, at least about 85%, at least about 90%, or has greater than about 90% (e.g., about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, or about 99%) sequence identity to any of the sequences provided herein (e.g., CDR sequences of any one or more of SEQ ID NOs: 4-6, 8-10, 11-17, 21, 23-25, 27-29, 30-35, 170-173, and 174-176, variable region sequences of any one or more of SEQ ID NOs: 3, 7, 22, 26, 41, 42, 45, 46, 49, 50, 53, 54, 57, 58, 61, 62, 65, 66, 69, 70, 73, 74, 77, 78, 81, 82, 85, 86, 89, 90, 93, 94, 97, 98, 101, 102, 105, 106, 109, 110, 113, 114, 117, 118, 121, 122, 125, 126, 129, 130, 133, 134, 137, 138, 141, 142, 169, 173, and 182-186; scFv linker sequence of any one of SEQ ID NOs: 143-168, and/or scFv sequence of any one of SEQ ID NO: 19, 20, 38, 40, 43,

44, 47, 48, 51, 52, 55, 56, 59, 60, 63, 64, 67, 68, 71, 72, 75, 76, 79, 80, 83, 84, 87, 88, 91, 92, 95, 96, 99, 100, 104, 104, 107, 108, 111, 112, 115, 116, 119, 120, 123, 124, 127, 128, 131, 132, 135, 136, 139, and 140). For example, the scFv may comprise CDR sequences as set forth in any one or more of SEQ ID NO: 4-6, 8-10, 11-17, 21, 23-25, 27-29, 30-35, 170-173, and 174-176 but comprising one or two amino acid substitutions. Alternatively, in various aspects, the scFv may comprise variable region sequences which are modified with respect to SEQ ID NO: 3, 7, 22, 26, 41, 42, 45, 46, 49, 50, 53, 54, 57, 58, 61, 62, 65, 66, 69, 70, 73, 74, 77, 78, 81, 82, 85, 86, 89, 90, 93, 94, 97, 98, 101, 102, 105, 106, 109, 110, 113, 114, 117, 118, 121, 122, 125, 126, 129, 130, 133, 134, 137, 138, 141, 142, 169, 173, or 182-186, wherein the modifications are outside the CDR sequences.

[0090] The first variable heavy domain and the second variable heavy domain of the heterodimeric antibody, in various aspects, comprises the anti-STEAP1 CDR or variable region sequences described herein. For example, in some embodiments, the first variable heavy domain and the second variable heavy domain of the heterodimeric antibody comprise vhCDR1 comprising SEQ ID NO: 14, vhCDR2 comprising SEQ ID NO: 15 or SEQ ID NO: 21, and vhCDR3 comprising SEQ ID NO: 16; and the variable light domain comprises vlCDR1 comprising SEQ ID NO: 11, vlCDR2 comprising SEQ ID NO: 12, and vlCDR3 comprising SEQ ID NO: 13. Alternatively, the first variable heavy domain and the second variable heavy domain comprise vhCDR1 comprising SEQ ID NO: 33, vhCDR2 comprising SEQ ID NO: 34, and vhCDR3 comprising SEQ ID NO: 35; and the variable light domain comprises vlCDR1 comprising SEQ ID NO: 30, vlCDR2 comprising SEQ ID NO: 31, and vlCDR3 comprising SEQ ID NO: 32. In preferred embodiments, the first variable heavy domain and the second variable heavy domain comprise SEQ ID NO: 182 or SEQ ID NO: 184 and the variable light domain comprises SEQ ID NO: 183. Alternatively, the first variable heavy domain and the second variable heavy domain comprise SEQ ID NO: 185 and the variable light domain comprises SEQ ID NO: 186.

[0091] In various aspects of the disclosure, the heterodimeric antibody comprises a) a first monomer comprising the sequence of SEQ ID NO: 19 or 20, a second monomer comprising the sequence of SEQ ID NO: 18, and a common light chain comprising the sequence of SEQ ID NO: 17; or b) a first monomer comprising the sequence of SEQ ID NO: 38, a second monomer comprising the sequence of SEQ ID NO: 37, and a common light chain comprising the sequence of SEQ ID NO: 36.

[0092] In various aspects of the disclosure, the heterodimeric antibody comprises a first monomer comprising the sequence of SEQ ID NO: 202 or 207, a second monomer comprising the sequence of SEQ ID NO: 201 or 203, and a common light chain comprising the sequence of SEQ ID NO: 200 (e.g., a first monomer comprising the sequence SEQ ID NO: 202, a second monomer comprising the sequence of SEQ ID NO: 201, and a light chain comprising the sequence of SEQ ID NO: 200; or a first monomer comprising the sequence SEQ ID NO: 207, a second monomer comprising the sequence of SEQ ID NO: 203, and a light chain comprising the sequence of SEQ ID NO: 200). Alternatively; the heterodimeric antibody may comprise a first monomer comprising the sequence of SEQ ID NO: 206, a second monomer comprising the sequence of SEQ ID NO: 205, and a common light chain comprising the sequence of SEQ ID NO: 204.

[0093] In exemplary aspects, the first and/or second variable heavy domain may comprise CDR sequences or variable region sequences having at least about 70%, at least about 80%, at least about 85%, at least about 90%, or has greater than about 90% (e.g., about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, or about 99%) sequence identity to any of the sequences provided herein (e.g., CDR sequences of any one or more of SEQ ID NO: 4-6, 14-17, 21, 23-25, 33-35, and 170-172 or variable region sequences of any one of SEQ ID NO: 3, 22, 41, 45, 49, 53, 57, 61, 65, 69, 73, 77, 81, 85, 89, 93, 97, 101, 105, 109, 113, 117, 121, 125, 129, 133, 137, 141, 169, 182, 184, and 185). For example, the first and/or second variable heavy domain may comprise CDR sequences as set forth in any one or more of SEQ ID NO: 4-6, 14-17, 21, 23-25, 33-35, and 170-172 but comprising one or two amino acid substitutions. Alternatively, in various aspects, the first and/or second variable heavy domain may comprise variable region sequences which are modified with respect to SEQ ID NO: 3, 22, 41, 45, 49, 53, 57, 61, 65, 69, 73, 77, 81, 85, 89, 93, 97, 101, 105, 109, 113, 117, 121, 125, 129, 133, 137, 141, 169 182, 184, or 185, wherein the modifications are outside the CDR sequences. Similarly, the variable light domain may comprise CDR sequences or variable region sequences having at least about 70%, at least about 80%, at least about 85%, at least about 90%, or has greater than about 90% (e.g., about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, or about 99%) sequence identity to any of the sequences provided herein (e.g., CDR sequences of any one or more of SEQ ID NO: 8-10, 11-13, 27-29, 30-32, and 174-176 or variable region sequences of any one of SEQ ID NO: 7, 26, 42, 46, 50, 54, 58, 62, 66, 70, 74, 78, 82, 86, 90, 94, 98, 102, 106, 110, 114, 118, 122, 126, 130, 134, 138, 142, 173, 183, and 186), in various

aspects. For example, the variable light domain may comprise CDR sequences as set forth in any one or more of SEQ ID NO: 8-10, 11-13, 27-29, 30-32, and 174-176, but comprising one or two amino acid substitutions. Alternatively, in various aspects, the variable light domain may comprise variable region sequences which are modified with respect to SEQ ID NO: 7, 26, 42, 46, 50, 54, 58, 62, 66, 70, 74, 78, 82, 86, 90, 94, 98, 102, 106, 110, 114, 118, 122, 126, 130, 134, 138, 142, 173, 183, or 186, wherein the modifications are outside the CDR sequences. If desired, the first monomer may comprise an amino acid sequence having at least about 70%, at least about 80%, at least about 85%, at least about 90%, or has greater than about 90% (e.g., about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, or about 99%) sequence identity to any of the sequences provided herein (SEQ ID NO: 19, 20, 38, 202, 206 or 207); the second monomer may comprise an amino acid sequence having at least about 70%, at least about 80%, at least about 85%, at least about 90%, or has greater than about 90% (e.g., about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, or about 99%) sequence identity to any of the sequences provided herein (SEQ ID NO: 18, 199 or 37; or SEQ ID NO: 202, 207 or 206); and/or the common light chain may comprise an amino acid sequence having at least about 70%, at least about 80%, at least about 85%, at least about 90%, or has greater than about 90% (e.g., about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, or about 99%) sequence identity to any of the sequences provided herein (SEQ ID NO: 17, 36, 200 or 204).

[0094] In some embodiments, a full length heterodimeric antibody is employed. By "full length" is meant the structure that constitutes the natural biological form of an antibody, including variable and constant regions, including one or more modifications as outlined herein. The heterodimeric antibody of the disclosure can be monoclonal, synthetic, chimeric, and/or humanized. Antigen-binding antibody fragments in the context of the heterodimeric antibody contain at least one constant domain which can be engineered to produce heterodimers, such as pI engineering. Other antibody fragments include those that contain one or more of the CH1, CH2, CH3, hinge and CL domains of the invention that have been pI engineered. For example, Fc fusions are fusions of the Fc region (CH2 and CH3, optionally with the hinge region) fused to another protein. A number of Fc fusions are known the art and can be improved by the addition of the heterodimerization variants of the invention. Antibody fusions can be made comprising CH1; CH1, CH2 and CH3; CH2; CH3; CH2 and

CH3; CH1 and CH3, any or all of which can be made optionally with the hinge region, utilizing any combination of heterodimerization variants described herein.

[0095] The antigen-binding proteins, including heterodimeric antibodies, of the disclosure are generally isolated or recombinant. Nucleic acids encoding all or part of the heterodimeric antibody described herein, vectors, and host cells are described herein and contemplated as part of the disclosure.

Antibody Structure/Fc Region Modifications

[0096] The disclosure includes antibodies with modified Fc variants having amino acid modifications relative to the wildtype antibody sequence. The variants are defined according to the amino acid modifications that compose them. Thus, for example, N434S or 434S is an Fc variant with the substitution serine at position 434 relative to the parent Fc polypeptide, wherein the numbering is according to the EU index. Likewise, M428L/N434S defines an Fc variant with the substitutions M428L and N434S relative to the parent Fc polypeptide. The identity of the wildtype amino acid may be unspecified, in which case the aforementioned variant is referred to as 428L/434S. The order in which substitutions are provided is arbitrary, i.e., for example, 428L/434S is the same Fc variant as M428L/N434S, and so on. The modification can be an addition, deletion, or substitution. Substitutions can include naturally occurring amino acids and, in some cases, synthetic amino acids. Examples include U.S. Patent No. 6,586,207; U.S. Publication No. 20040214988; International Patent Publication Nos. WO 98/48032, WO 03/073238, WO 05/35727A2, and WO 05/74524A2; J. W. Chin et al., (2002), Journal of the American Chemical Society 124:9026-9027; J. W. Chin, & P. G. Schultz, (2002), ChemBioChem 11:1135-1137; J. W. Chin, et al., (2002), PICAS United States of America 99:11020-11024; and, L. Wang, & P. G. Schultz, (2002), Chem. 1-10, all entirely incorporated by reference.

[0097] For all positions discussed in the disclosure that relate to antibodies and other antigen-binding proteins, unless otherwise noted, amino acid position numbering is according to the EU index. The EU index or EU index as in Kabat or EU numbering scheme refers to the numbering of the EU antibody (Edelman et al., 1969, Proc Natl Acad Sci USA 63:78-85, hereby entirely incorporated by reference.) For example, it is understood that each variable heavy region (VH) and variable light region (VL) is composed of three hypervariable regions ("complementary determining regions," "CDRs") and four FRs, arranged from amino-terminus to carboxy-terminus in the following order: FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4. The hypervariable region generally encompasses amino acid residues from about

amino acid residues 24-34 (LCDR1; "L" denotes light chain), 50-56 (LCDR2) and 89-97 (LCDR3) in the light chain variable region and around about 31-35B (HCDR1; "H" denotes heavy chain), 50-65 (HCDR2), and 95-102 (HCDR3) in the heavy chain variable region; 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 forming a hypervariable loop (e.g., residues 26-32 (LCDR1), 50-52 (LCDR2) and 91-96 (LCDR3) in the light chain variable region and 26-32 (HCDR1), 53-55 (HCDR2) and 96-101 (HCDR3) in the heavy chain variable region; Chothia and Lesk (1987) J. Mol. Biol. 196:901-917).

[0098] As will be appreciated by those in the art, the exact numbering and placement of the CDRs can be different among different numbering systems. However, it should be understood that the disclosure of a variable heavy and/or variable light sequence includes the disclosure of the associated (inherent) CDRs. Accordingly, the disclosure of each variable heavy region is a disclosure of the vhCDRs (e.g. vhCDRl, vhCDR2 and vhCDR3) and the disclosure of each variable light region is a disclosure of the vlCDRs (e.g. vlCDRl, vlCDR2 and vlCDR3). A useful comparison of CDR numbering is as below, see Lafranc et al, Dev. Comp. Immunol. 27(l):55-77 (2003):

	Kabat+ Chothia	IMGT	Kabat	AM	Chothia	Contact
vhCDR1	26-35	27-38	31-35	26-35	26-32	30-35
vhCDR2	50-65	56-65	50-65	50-58	52-56	47-58
vhCDR3	95-102	105-117	95-102	95-102	95-102	93-101
vlCDR1	24-34	27-38	24-34	24-34	24-34	30-36
vlCDR2	50-56	56-65	50-56	50-56	50-56	46-55
vlCDR3	89-97	105-117	89-97	89-97	89-97	89-96

[0099] Throughout the specification, the Kabat numbering system is generally used when referring to a residue in the variable domain (approximately, residues 1-107 of the light chain variable region and residues 1-113 of the heavy chain variable region) (e.g, Kabat et al., supra (1991)).

[00100] The carboxy-terminal portion of each chain defines a constant region primarily responsible for effector function. Kabat et al. collected numerous primary sequences of the variable regions of heavy chains and light chains. Based on the degree of conservation of the sequences, they classified individual primary sequences into the CDR and the framework and

made a list thereof (see SEQUENCES OF IMMUNOLOGICAL INTEREST, 5th edition, NIH publication, No. 91-3242, E.A. Kabat et al., entirely incorporated by reference).

[00101] In the IgG subclass of immunoglobulins, there are several immunoglobulin domains in the heavy chain. By "immunoglobulin (Ig) domain" herein is meant a region of an immunoglobulin having a distinct tertiary structure. Of interest are the heavy chain domains, including, the constant heavy (CH) domains and the hinge domains. In the context of IgG antibodies, the IgG isotypes each have three CH regions. Accordingly, "CH" domains in the context of IgG are as follows: "CH1" refers to positions 118-220 according to the EU index as in Kabat. "CH2" refers to positions 237-340 according to the EU index as in Kabat, and "CH3" refers to positions 341-447 according to the EU index as in Kabat. As shown herein and described below, the pI variants can be in one or more of the CH regions, as well as the hinge region, discussed below. In various aspects, the sequences depicted herein start at the CH1 region, position 118; the variable regions are not included except as noted.

[00102] Another type of Ig domain of the heavy chain is the hinge region. By "hinge" or "hinge region" or "antibody hinge region" or "immunoglobulin hinge region" herein is meant the flexible polypeptide comprising the amino acids between the first and second constant domains of an antibody. Structurally, the IgG CH1 domain ends at EU position 220, and the IgG CH2 domain begins at residue EU position 237. Thus for IgG the antibody hinge is herein defined to include positions 221 (D221 in IgG1) to 236 (G236 in IgG1), wherein the numbering is according to the EU index as in Kabat. In some embodiments, for example in the context of an Fc region, the lower hinge is included, with the "lower hinge" generally referring to positions 226 or 230. As noted herein, pI variants can be made in the hinge region as well.

[00103] By "Fc" or "Fc region" or "Fc domain" as used herein is meant the polypeptide comprising the constant region of an antibody excluding the first constant region immunoglobulin domain and in some cases, part of the hinge. Thus Fc refers to the last two constant region immunoglobulin domains of IgA, IgD, and IgG, the last three constant region immunoglobulin domains of IgE and IgM, and the flexible hinge N-terminal to these domains. For IgA and IgM, Fc may include the J chain. For IgG, the Fc domain comprises immunoglobulin domains Cγ2 and Cγ3 (Cγ2 and Cγ3) and the lower hinge region between Cγ1 (Cγ1) and Cγ2 (Cγ2). Although the boundaries of the Fc region may vary, the human IgG heavy chain Fc region is usually defined to include residues C226 or P230 to its carboxyl-terminus, wherein the numbering is according to the EU index as in Kabat.

[00104] Amino acid variants may be introduced into the antigen-binding protein (e.g., bispecific antibody) of the disclosure to add additional functionalities. For example, amino acid changes within the Fc region can be added (either to one monomer or both) to facilitate increased ADCC or CDC (e.g., altered binding to Fcγ receptors), to allow or increase yield of the addition of toxins and drugs (e.g., for ADC), as well as to increase binding to FcRn and/or increase serum half-life of the resulting molecules. Effector functions that may be adjusted by varying the amino acid sequence include, but are not limited to, ADCC, ADCP, and CDC. Any and all of the variants outlined herein can be optionally and independently combined with other variants.

[00105] By "FcRn" or "neonatal Fc Receptor" is meant a protein that binds the IgG antibody Fc region and is encoded at least in part by an FcRn gene. The FcRn may be from any organism, including but not limited to humans, mice, rats, rabbits, and monkeys. As is known in the art, the functional FcRn protein comprises two polypeptides, often referred to as the heavy chain and light chain. The light chain is beta-2-microglobulin and the heavy chain is encoded by the FcRn gene. Unless otherwise noted herein, FcRn or an FcRn protein refers to the complex of FcRn heavy chain with beta-2-microglobulin. A variety of FcRn variants used to increase binding to the FcRn receptor, and in some cases, to increase serum half-life. Fc variants conferring increased binding to the FcRn receptor and corresponding increases in serum half life include, but are not limited to, 434A, 434S, 428L, 308F, 259I, 428L/434S, 259I/308F, 436I/428L, 436I or V/434S, 436V/428L, 252Y, 252Y/254T/256E and 259I/308F/428L. For clarity, as each heavy chain is different, FcRn variants (as well as the Fc variants) can reside on one or both monomers.

[00106] Another category of functional variants are "Fcγ ablation variants" or "Fc knock out (FcKO or KO) variants." In these embodiments, for some therapeutic applications, it is desirable to reduce or remove the normal binding of the Fc domain to one or more or all of the Fcγ receptors (e.g. FcγR1, FcγRIIa, FcγRIIb, FcγRIIIa, etc.) to avoid additional mechanisms of action. By "Fc gamma receptor," "FcγR" or "FcgammaR" is meant any member of the family of proteins that bind the IgG antibody Fc region and is encoded by an FcγR gene. In humans this family includes but is not limited to FcγRI (CD64), including isoforms FcγRIa, FcγRIb, and FcγRIc; FcγRII (CD32), including isoforms FcγRIIa (including allotypes H131 and R131), FcγRIIb (including FcγRIIb-1 and FcγRIIb-2), and FcγRIIc; and FcγRIII (CD16), including isoforms FcγRIIIa (including allotypes V158 and F158) and FcγRIIIb (including allotypes FcγRIIb-NA1 and FcγRIIb-NA2) (Jefferis et al.,

2002, Immunol Lett 82:57-65, entirely incorporated by reference). An FcγR may be from any organism, including but not limited to humans, mice, rats, rabbits, and monkeys. Mouse FcγRs include but are not limited to FcγRI (CD64), FcγRII (CD32), FcγRIII (CD16), and FcγRIII-2 (CD16-2). In many embodiments, it is generally desirable to ablate FcγRIIIa binding to eliminate or significantly reduce ADCC activity. Figure 36 of U.S. Patent No. 9,822,186 depicts the use of an Fc knock-out (or ablation variant) that retains wild type stability but removes all FcγR binding.

[0100] Representative ablation variants include those selected from the group consisting of G236R/L328R, E233P/L234V/L235A/G236del/S239K, E233P/L234V/L235A/G236del/S267K, E233P/L234V/L235A/G236del/S239K/A327G, E233P/L234V/L235A/G236del/S267K/A327G, and E233P/L234V/L235A/G236del. It should be noted that the ablation variants referenced herein ablate FcyR binding but generally not FcRn binding.

[0101] As is known in the art, the Fc domain of human IgGl has the highest binding to the Fγ receptors, and thus ablation variants can be used when the constant domain (or Fc domain) in the backbone of the heterodimeric antibody is IgG1. Alternatively, or in addition to ablation variants in an IgGl background, mutations at the glycosylation position 297 (generally to A or S) can significantly ablate binding to FcγRIIIa, for example. Human IgG2 and IgG4 have naturally reduced binding to the Fcγ receptors, and thus those backbones can be used with or without the ablation variants.

[0102] Deamidation can severely impact antibody activity and stability. In various aspects, the heterodimeric antibody comprises one or more substitutions to remove deamidation sites. In this regard, the heterodimeric antibody optionally comprises a substitution at position N67, such as the substitution N67Q.

Heterodimeric Heavy Chain Constant Regions

[0103] The disclosure provides heterodimeric antibodies based on the use of monomers containing variant heavy chain constant regions as a first domain. By "monomer" herein is meant one half of the heterodimeric protein. It should be noted that traditional antibodies are actually tetrameric (two heavy chains and two light chains). For ease of reference, in the context of the present disclosure, a pair comprising a heavy chain and a light chain is considered a "monomer." A heavy chain region comprising the scFv (and, in some instances a Fab) is considered a monomer. Essentially, each monomer comprises sufficient heavy

chain constant region to allow heterodimerization engineering, whether that be the entire constant region, e.g., CH1-hinge-CH2-CH3, the Fc region (CH2-CH3), or just the CH3 domain.

[0104] The variant heavy chain constant regions can comprise all or part of the heavy chain constant region, including the full length construct, CH1-hinge-CH2-CH3, or portions thereof, including for example CH2-CH3 or CH3 alone. In addition, the heavy chain region of each monomer can be the same backbone (CH1-hinge-CH2-CH3 or CH2-CH3) or different. N- and C-terminal truncations and additions are also included within the definition; for example, some pI variants include the addition of charged amino acids to the C-terminus of the heavy chain domain.

[0105] In addition to the heterodimerization variants (e.g., steric and pI variants) outlined herein, the heavy chain regions may also contain additional amino acid substitutions, including changes for altering FcγR and FcRn binding.

[0106] The heterodimerization variants include a number of different types of variants, including, but not limited to, steric variants (including charge variants) and pI variants, that can be optionally and independently combined with any other variants. In these embodiments, it is important to match "monomer A" with "monomer B," that is, if a heterodimeric protein relies on both steric variants and pI variants, these need to be correctly matched to each monomer, e.g., the set of steric variants that work (1 set on monomer A, 1 set on monomer B) is combined with pI variant sets (1 set on monomer A, 1 set on monomer B), such that the variants on each monomer are designed to achieve the desired function. In the case for example where steric variants may also change the charge, the correct sets have to be matched to the correct monomer.

[0107] The heterodimerization variants outlined herein (for example, including but not limited to those variants shown in the Figures), can be optionally and independently combined with any other variants, and on any other monomer. What is important for the heterodimerization is that there are "sets" of variants, one set for one monomer and one set for the other. Whether these are combined 1 to 1 (e.g., monomer 1 listings can go together) or switched (monomer 1 pI variants with monomer 2 steric variants) is irrelevant. However, "strandedness" should be preserved when combinations are made as outlined above such that heterodimerization is favored; e.g., charge variants that increase pI should be used with increased pI variants and/or an scFv linker with increase pI, etc. By "strandedness" in the

context of the monomers of the heterodimeric proteins is meant that, similar to the two strands of DNA that "match," heterodimerization variants are incorporated into each monomer so as to preserve the ability to "match" to form heterodimers. For example, if some pI variants are engineered into monomer A (e.g., making the pI higher) then steric variants that are "charge pairs" that can be utilized as well do not interfere with the pI variants, e.g., the charge variants that make a pI higher are put on the same "strand" or "monomer" to preserve both functionalities. Furthermore, for the additional Fc variants (such as for FcγR binding, FcRn binding, ablation variants etc.), either monomer, or both monomers, can include any of the listed variants, independently and optionally. In some cases, both monomers have the additional variants, and in some only one monomer has the additional variants, or they can be combined.

Steric Variants

[0108] In some embodiments, the formation of heterodimers is facilitated by the addition of steric variants. That is, by changing amino acids in each heavy chain, different heavy chains are more likely to associate to form the heterodimeric structure than to form homodimers with the same Fc amino acid sequences. Representative suitable steric variants are shown in the Figures.

[0109] One mechanism for producing steric variants is the “knobs and holes” mechanism described above. An additional mechanism that finds use in the generation of heterodimers is sometimes referred to as “electrostatic steering” as described in Gunasekaran et al., J. Biol. Chem. 285(25):19637 (2010), hereby incorporated by reference in its entirety. This is sometimes referred to herein as “charge pairs.” In this embodiment, electrostatics are used to skew the formation towards heterodimerization. These may also have an effect on pI, and thus on purification, and thus could, in some cases, also be considered pI variants. However, as these were generated to force heterodimerization and were not used as purification tools, they are classified as “steric variants.” These include, but are not limited to, variants resulting in greater than 75% heterodimerization such as D221E/P228E/L368E paired with D221R/P228R/K409R (e.g., these are “monomer corresponding sets”) and C220E/P228E/368E paired with C220R/E224R/P228R/K409R.

[0110] In some embodiments, the skew variants advantageously and simultaneously favor heterodimerization based on both the “knobs and holes” mechanism as well as the “electrostatic steering” mechanism. These variants come in “pairs” of “sets.” That is, one set

of the pair is incorporated into the first monomer and the other set of the pair is incorporated into the second monomer. It should be noted that these sets do not necessarily behave as "knobs in holes" variants, with a one-to-one correspondence between a residue on one monomer and a residue on the other. That is, these pairs of sets may instead form an interface between the two monomers that encourages heterodimer formation and discourages homodimer formation, allowing the percentage of heterodimers that spontaneously form under biological conditions to be over 90%, rather than the expected 50% (25 % homodimer A/A:50% heterodimer A/B:25% homodimer B/B). Exemplary heterodimerization "skew" variants are depicted in Figure 4. Examples of such skew variants include pairs of sets of mutations including, but not limited to, S364K/E357Q : L368D/K370S; L368D/K370S : S364K; L368E/K370S : S364K; T411T/E360E/Q362E : D401K; L368D/K370S : S364K/E357L, K370S : S364K/E357Q; and T366S/L368A/Y407V : T366W (optionally including a bridging disulfide, T366S/L368A/Y407V/Y349C : T366W/S354C).

[0111] Additional monomer A and monomer B variants that can be combined with other variants, optionally and independently in any amount, such as pI variants outlined herein or other steric variants that are shown in Figure 37 of U.S. Publication No. 2012/0149876, the figure and legend of which are incorporated expressly by reference herein.

[0112] In some embodiments, the steric variants outlined herein can be optionally and independently incorporated with any heterodimerization variants including pI variants (or other variants such as Fc variants, FcRn variants, ablation variants, etc.) into one or both monomers.

pI (Isoelectric point) Variants for Heterodimers

[0113] In general, there are two categories of pI variants: those that increase the pI of the protein (basic changes) and those that decrease the pI of the protein (acidic changes). As described herein, all combinations of these variants can be performed: one monomer may be wild type, or a variant that does not display a significantly different pI from wild-type, and the other can be either more basic or more acidic. Alternatively, each monomer is changed, one to more basic and one to more acidic. Exemplary combinations of pI variants are shown in the Figures.

[0114] In various embodiments, for example in the Figure 18A, E, F, G, H and I formats, a preferred combination of pI variants has one monomer (the negative Fab side) comprising 208D/295E/384D/418E/421D variants (N208D/Q295E/N384D/Q418E/N421D when relative

to human IgGl) and a second monomer (the positive scFv side) comprising a positively charged scFv linker, including $(GKPGS)_4$. However, as will be appreciated by those in the art, the first monomer includes a CH1 domain, including position 208. Accordingly, in constructs that do not include a CH1 domain (for example for antibodies that do not utilize a CH1 domain on one of the domains, for example in a dual scFv format or a "one armed" format such as those depicted in Figure 18B, C or D), a preferred negative pI variant Fc set includes 295E/384D/418E/421D variants (Q295E/N384D/Q418E/N421D when relative to human IgGl).

Acidic pI Changes

[0115] When one monomer comprising a variant heavy chain constant domain is to be made more positive (e.g., lower the pI), one or more of the following modifications (e.g., substitutions) are suitable in the context of the disclosure: S119E, K133E, K133Q, T164E, K205E, K205Q, N208D, K210E, K210Q, K274E, K320E, K322E, K326E, K334E, R355E, K392E, a deletion of K447, adding peptide DEDE at the C-terminus, G137E, N203D, K274Q, R355Q, K392N, and Q419E. These changes are described relative to IgG1, but all isotypes can be altered this way, as well as isotype hybrids. In the case where the heavy chain constant domain is from IgG2-4, R133E and R133Q can also be used.

Basic pI changes

[0116] When one monomer comprising a variant heavy chain constant domain is to be made more negative (e.g., increase the pI), one or more of the following exemplary substitutions are suitable in the context of the disclosure: Q196K, P217R, P228R, N276K, and H435R. These changes are described relative to IgG1, but all isotypes can be altered this way, as well as isotype hybrids.

Heterodimeric Antibody Light Chain Variants

[0117] pI variants can also be made in an antibody light chain. Amino acid modifications for lowering the pI of the light chain include, but are not limited to, K126E, K126Q, K145E, K145Q, N152D, S156E, K169E, S202E, K207E, and adding peptide DEDE at the C-terminus of the light chain. Changes in this category based on the constant lambda light chain include but are not limited to one or more substitutions at R108Q, Q124E, K126Q, N138D, K145T, and Q199E. In addition, increasing the pI of the light chain also is possible and contemplated in various aspects of the disclosure.

Isotypic Variants

[0118] In addition, various embodiments of the disclosure entail the "importation" of pI amino acids at particular positions from one IgG isotype into another, thus reducing or eliminating the possibility of unwanted immunogenicity being introduced into the variants. A number of these are shown in Figure 21 of U.S. Patent Publication No. 2014/0370013, hereby incorporated by reference. That is, IgG1 is a common isotype for therapeutic antibodies for a variety of reasons, including high effector function. However, the heavy constant region of IgG1 has a higher pI than that of IgG2 (8.10 versus 7.31). By introducing IgG2 residues at particular positions into the IgG1 backbone, the pI of the resulting monomer is lowered (or increased) and additionally exhibits longer serum half-life. For example, IgG1 has a glycine (pI 5.97) at position 137, and IgG2 has a glutamic acid (pI 3.22); importing the glutamic acid will affect the pI of the resulting protein. A number of amino acid substitutions are generally required to significant affect the pI of the variant antibody. However, it should be noted as discussed below that even changes in IgG2 molecules allow for increased serum half-life.

[0119] In other embodiments, non-isotypic amino acid changes are made, either to reduce the overall charge state of the resulting protein (e.g., by changing a higher pI amino acid to a lower pI amino acid) or to allow accommodations in structure for stability, etc.

[0120] In addition, by pI engineering both the heavy and light constant domains, significant changes in each monomer of the heterodimer can be observed. As discussed herein, having the pIs of the two monomers differ by at least 0.5 can allow separation by ion exchange chromatography or isoelectric focusing, or other methods sensitive to isoelectric point.

[0121] In addition, pI variants that are isosteric, e.g., charge variants that are roughly the same size as the parent amino acid, can be generated and are contemplated herein.

Calculating pI

[0122] The pI of each monomer can depend on the pI of the variant heavy chain constant domain and the pI of the total monomer, including the variant heavy chain constant domain and the fusion partner. Thus, in some embodiments, the change in pI is calculated on the basis of the variant heavy chain constant domain. Alternatively, the pI of each monomer can be compared. Similarly, the pIs of the "starting" variable regions (e.g., either scFv or Fab) are calculated to inform which monomer will be engineered in which direction.

pI Variants Conferring Better FcRn Binding *In Vivo*

[0123] pI variants decreasing the pI of the monomer may display the added benefit of improving serum retention *in vivo*.

[0124] Fc regions are believed to have longer half-lives *in vivo* because binding to FcRn at pH 6 in an endosome sequesters the Fc (Ghetie and Ward, 1997 Immunol Today. 18(12): 592-598, hereby incorporated by reference). The endosomal compartment then recycles the Fc to the cell surface. Once the compartment opens to the extracellular space, the higher pH, ~7.4, induces the release of Fc back into the blood. The increased affinity of Fc for FcRn at pH 7.4 is thought to forbid the release of the Fc back into the blood. Therefore, the Fc mutations that will increase Fc's half-life *in vivo* will ideally increase FcRn binding at the lower pH while still allowing release of Fc at higher pH. The amino acid histidine changes its charge state in the pH range of 6.0 to 7.4. Therefore, it is not surprising to find His residues at important positions in the Fc/FcRn complex.

[0125] Recently it has been suggested that antibodies with variable regions that have lower isoelectric points may also have longer serum half-lives (Igawa et al., 2010 PEDS. 23(5): 385-392, entirely incorporated by reference). Constant region variants with reduced pI and extended half-life provide a more modular approach to improving the pharmacokinetic properties of antibodies.

[0126] pI variants that find use in this embodiment, as well as their use for purification optimization, are disclosed in the Figures.

Combination of Variants

[0127] As will be appreciated by those in the art, all of the recited heterodimerization variants can be optionally and independently combined in any way, as long as they retain their "strandedness" or "monomer partition." In addition, all of these variants can be combined into any of the heterodimerization formats. In the case of pI variants, while exemplary embodiments are shown in the Figures, other combinations can be generated, following the basic rule of altering the pI difference between two monomers to facilitate purification.

Antigen-Binding Protein (e.g., Antibody) Formats

[0128] One heterodimeric scaffold that finds use in the context of the present disclosure is the "triple F" or "bottle opener" scaffold format described above and set forth in Figure 18. In this embodiment, one heavy chain of the antibody contains a single chain Fv ("scFv", as

defined below) and the other heavy chain is a "regular" Fab format, comprising a variable heavy chain and a light chain. Many of the embodiments outlined herein rely in general on the bottle opener format that comprises a first monomer comprising an scFv, comprising a variable heavy and a variable light domain, covalently attached using an scFv linker (charged in many, but not all, instances), where the scFv is covalently attached to the N-terminus of a first Fc domain usually through a domain linker (which, as outlined herein can either be un-charged or charged and can be exogeneous or endogeneous (e.g. all or part of the native hinge domain)). The second monomer of the bottle opener format is a heavy chain, and the composition further comprises a light chain.

[0129] In addition, the Fc domains of the bottle opener format generally comprise skew variants (e.g., selected from the group consisting of S364K/E357Q : L368D/K370S; L368D/K370S : S364K; L368E/K370S : S364K; T411T/E360E/Q362E : D401K; L368D/K370S : S364K/E357L, K370S : S364K/E357Q, T366S/L368A/Y407V : T366W; and T366S/L368A/Y407V/Y349C : T366W/S354C), optionally ablation variants, optionally charged scFv linkers, and the heavy chain comprises pI variants. In some embodiments, the bottle opener format includes skew variants, pI variants, and ablation variants. Accordingly, some embodiments include bottle opener formats that comprise: a) a first monomer (the "scFv monomer") that comprises a charged scFv linker, the skew variants S364K/E357Q, the ablation variants E233P/L234V/L235A/G236del/S267K, and an Fv; b) a second monomer (the "Fab monomer") that comprises the skew variants L368D/K370S, the pI variants N208D/Q295E/N384D/Q418E/N421D, the ablation variants E233P/L234V/L235A/G236del/S267K, and a variable heavy domain that, with the variable light domain, makes up an Fv that binds to a second antigen; and c) a light chain.

[0130] In some embodiments, the bottle opener format includes skew variants, pI variants, ablation variants and FcRn variants. Accordingly, some embodiments include bottle opener formats that comprise: a) a first monomer (the "scFv monomer") that comprises a charged scFv linker, the skew variants S364K/E357Q, the ablation variants E233P/L234V/L235A/G236del/S267K, the FcRn variants M428L/N434S and an Fv that binds to a first antigen; b) a second monomer (the "Fab monomer") that comprises the skew variants L368D/K370S, the pI variants N208D/Q295E/N384D/ Q418E/N421D, the ablation variants E233P/L234V/L235A/G236del/S267K, the FcRn variants M428L/N434S and a variable heavy domain that, with the variable light domain, makes up an Fv that binds to a second antigen; and c) a light chain.

[0131] Another heterodimeric scaffold that finds use in the present disclosure is the mAb-Fv format shown in Figure 18H. In this embodiment, the format relies on the use of a C-terminal attachment of an "extra" variable heavy domain to one monomer and the C-terminal attachment of an "extra" variable light domain to the other monomer, thus forming a third antigen-binding domain, wherein the Fab portions of the two monomers bind one antigen and the "extra" scFv domain binds a different antigen.

[0132] In this embodiment, the first monomer comprises a first heavy chain, comprising a first variable heavy domain and a first constant heavy domain comprising a first Fc domain, with a first variable light domain covalently attached to the C-terminus of the first Fc domain using a domain linker (vhl-CHl-[domain linker (e.g., hinge)]-CH2-CH3-[optional domain linker]-vl2). The second monomer comprises a second variable heavy domain of the second constant heavy domain comprising a second Fc domain, and a third variable heavy domain covalently attached to the C-terminus of the second Fc domain using a domain linker (vhl-CHl- domain linker (e.g., hinge)-CH2-CH3-[optional domain linker]-vh2). The two C-terminally attached variable domains make up a scFv. This embodiment further utilizes a common light chain comprising a variable light domain and a constant light domain, which associates with the heavy chains to form two identical Fabs. As for many of the embodiments herein, these constructs include skew variants, pI variants, ablation variants, additional Fc variants, etc. as desired and described herein.

[0133] Optionally, the Fc domains of the mAb-Fv format comprise skew variants (e.g., selected from the group consisting of S364K/E357Q : L368D/K370S; L368D/K370S : S364K; L368E/K370S : S364K; T411T/E360E/Q362E : D401K; L368D/K370S : S364K/E357L, K370S : S364K/E357Q, T366S/L368A/Y407V : T366W; and T366S/L368A/Y407V/Y349C : T366W/S354C), optionally ablation variants, optionally charged scFv linkers, and the heavy chain comprises pI variants. In some embodiments, the mAb-Fv format includes skew variants, pI variants, and ablation variants. Accordingly, some embodiments include bottle opener formats that comprise: a) a first monomer that comprises the skew variants S364K/E357Q, the ablation variants 233P/L234V/L235A/G236del/S267K, and a first variable heavy domain that, with the first variable light domain of the light chain, makes up an Fv that binds to an antigen, and a second variable heavy domain; b) a second monomer that comprises the skew variants L368D/K370S, the pI variants N208D/Q295E/N384D/Q418E/N421D, the ablation variants E233P/L234V/L235A/G236del/S267K, and a first variable heavy domain that, with the first

variable light domain, makes up the Fv that binds to the first antigen, and a second variable light chain, that together with the second variable heavy chain forms an Fv that binds a second antigen; and c) a light chain comprising a first variable light domain and a constant light domain.

[0134] Yet another heterodimeric scaffold that finds use in the present disclosure is the mAb-scFv format shown in Figure 18I. In this embodiment, the format relies on the use of a C-terminal attachment of an scFv to one of the monomers, thus forming a third antigen-binding domain, wherein the Fab portions of the two monomers bind one antigen and the "extra" scFv domain binds a different antigen. In this embodiment, the first monomer comprises a first heavy chain (comprising a variable heavy domain and a constant domain), with a C-terminally covalently attached scFv comprising a scFv variable light domain, an scFv linker and a scFv variable heavy domain in either orientation (vhl-CHl-domain linker-CH2-CH3-[optional domain linker] -vh2-scFv linker-vl2 or vhl-CHl-domain linker-CH2-CH3-[optional domain linker] -vl2-scFv linker-vh2). This embodiment further utilizes a common light chain comprising a variable light domain and a constant light domain, which associates with the heavy chains to form two identical Fabs that bind one of the target antigens. As for many of the embodiments herein, these constructs include skew variants, pI variants, ablation variants, additional Fc variants, etc., as desired and described herein.

[0135] In addition, the Fc domains of the mAb-scFv format optionally comprise skew variants (e.g., selected from the group consisting of S364K/E357Q : L368D/K370S; L368D/K370S : S364K; L368E/K370S : S364K; T411T/E360E/Q362E : D401K; L368D/K370S : S364K/E357L, K370S : S364K/E357Q, T366S/L368A/Y407V : T366W; and T366S/L368A/Y407V/Y349C : T366W/S354C), optionally ablation variants, optionally charged scFv linkers, and the heavy chain comprises pI variants. In some embodiments, the mAb-scFv format includes skew variants, pI variants, and ablation variants. Accordingly, some embodiments include formats that comprise: a) a first monomer that comprises the skew variants S364K/E357Q, the ablation variants E233P/L234V/L235A/G236del/S267K, and a first variable heavy domain that, with the first variable light domain of the light chain, makes up an Fv that binds to a first antigen, and a second variable heavy domain; b) a second monomer that comprises the skew variants L368D/K370S, the pI variants N208D/Q295E/N384D/Q418E/N421D, the ablation variants E233P/L234V/L235A/G236del/S267K, and a first variable heavy domain that, with the first variable light domain, makes up the Fv that binds to the first antigen, and a second variable

light chain, that together with the second variable heavy chain forms an Fv that binds a second antigen; and c) a light chain comprising a first variable light domain and a constant light domain.

[0136] Yet another heterodimeric scaffold that finds use in the present disclosure is the central-scFv or "XmAb^{2+1}" format shown in Figure 18F. The format relies on the use of an inserted scFv domain thus forming a third antigen-binding domain, wherein the Fab portions of the two monomers bind one target and the "extra" scFv domain binds another. The scFv domain is inserted between the Fc domain and the CH1-Fv region of one of the monomers, thus providing a third antigen-binding domain. In this embodiment, one monomer comprises a first heavy chain comprising a first variable heavy domain, a CH1 domain (and optional linker/hinge) and Fc domain, with a scFv comprising a scFv variable light domain, an scFv linker and a scFv variable heavy domain. The scFv is covalently attached between the C-terminus of the CH1 domain of the heavy constant domain and the N-terminus of the first Fc domain using optional domain linkers (VHl-CHl-[optional domain linker] -VH2-scFv linker-VL2-[optional domain linker including the hinge]-CH2-CH3, or the opposite orientation for the scFv, VHl –CH1 -[optional domain linker] -VL2-scFv linker-VH2-[optional domain linker including the hinge] -CH2-CH3). In some embodiments, the first monomer is VH1-CH1-domain linker-VH2-scFv linker-VL2-domain linker-CH2-CH3. The other monomer is a standard Fab side (i.e., VH1-CH1-domain linker (e.g., hinge)-CH2-CH3). This embodiment further utilizes a common light chain comprising a variable light domain and a constant light domain, which associates with the heavy chains to form two identical Fabs that bind a target. As for many of the embodiments herein, these constructs include skew variants, pI variants, ablation variants, additional Fc variants, etc. as desired and described herein.

[0137] In various aspects, the antigen-binding protein comprises a first heavy chain comprising VHl-CHl-[domain linker] -VH2-scFv linker-VL2-[domain linker (optionally including the hinge)]-CH2-CH3; a second heavy chain comprising a VH1-CH1-domain linker-CH2-CH3; and a common light chain comprising a VL1; wherein VH1 and VL1 bind STEAP 1 and VH2 and VL2 bind CD3. In this format, VH2 optionally comprises CDR sequences of SEQ ID NO: 170 (CDR1), SEQ ID NO: 171 (CDR2), and SEQ ID NO: 172 (CDR3), while VL2 comprises CDR sequences of SEQ ID NO: 174 (CDR1), SEQ ID NO: 175 (CDR2), and SEQ ID NO:176 (CDR3). VH1 comprises CDR sequences of SEQ ID NO: 14 (CDR1), SEQ ID NO: 15 or 21 (CDR2), and SEQ ID NO: 16 (CDR3); and VL1 comprises CDR sequences of SEQ ID NO: 11 (CDR1), SEQ ID NO: 12 (CDR2), and SEQ

ID NO: 13 (CDR3). Alternatively, VH1 comprises CDR sequences of SEQ ID NO: 33 (CDR1), SEQ ID NO: 34 (CDR2), and SEQ ID NO: 35 (CDR3); and VL1 comprises CDR sequences of SEQ ID NO: 30 (CDR1), SEQ ID NO: 31 (CDR2), and SEQ ID NO: 32 (CDR3). Optionally, the antigen-binding protein comprises modifications in the first heavy chain including, but not limited to, E233P, delL234, L235V, G236A, S267K, r292c, n297g, v302c, E357Q, and S364K (EU numbering, lower case letters referencing SEFL2 substitutions described further herein), and the second heavy chain comprises modifications including, but not limited to, N208D, E233P, delL234, L235V, G236A, S267K, r292c Q295E, n297g, v302c, L368D, K370S, N384D, Q418E, and N421D (EU numbering, lower case letters referencing SEFL2 substitutions described further herein). A linker for use in the context of this embodiment is optionally GKPGSGKPGSGKPGSGKPGS (SEQ ID NO: 152).

[0138] The Fc domains of the central scFv format optionally comprise skew variants (e.g., selected from the group consisting of S364K/E357Q : L368D/K370S; L368D/K370S : S364K; L368E/K370S : S364K; T411T/E360E/Q362E : D401K; L368D/K370S : S364K/E357L, K370S : S364K/E357Q, T366S/L368A/Y407V : T366W and T366S/L368A/Y407V/Y349C : T366W/S354C), optionally ablation variants, optionally charged scFv linkers, and the heavy chain comprises pI variants. In some embodiments, the central scFv format includes skew variants, pI variants, and ablation variants. Accordingly, some embodiments include formats that comprise: a) a first monomer that comprises the skew variants S364K/E357Q, the ablation variants E233P/L234V/L235A/G236del/S267K, and a first variable heavy domain that, with the first variable light domain of the light chain, makes up an Fv that binds to a first target, and a second variable heavy domain; b) a second monomer that comprises the skew variants L368D/K370S, the pI variants N208D/Q295E/N384D/Q418E/N421D, the ablation variants E233P/L234V/L235A/G236del/S267K, and a first variable heavy domain that, with the first variable light domain, makes up the Fv that binds to the first target, and a second variable light chain, that together with the second variable heavy chain forms an Fv that binds a second target; and c) a light chain comprising a first variable light domain and a constant light domain.

[0139] Another heterodimeric scaffold that finds particular use in the disclosure is the central-Fv format shown in Figure l8G. The format relies on the use of an inserted scFv domain thus forming a third antigen-binding domain, wherein the Fab portions of the two

monomers bind one target and the "extra" scFv domain binds another. The scFv domain is inserted between the Fc domain and the CHl-Fv region of the monomers, thus providing a third antigen-binding domain, wherein each monomer contains a component of the scFv (e.g., one monomer comprises a variable heavy domain and the other a variable light domain). In this embodiment, one monomer comprises a first heavy chain comprising a first variable heavy domain, a CH1 domain, and Fc domain and an additional variable light domain. The light domain is covalently attached between the C-terminus of the CH1 domain of the heavy constant domain and the N-terminus of the first Fc domain using domain linkers (vhl -CHI -[optional domain linker]-vl2-hinge-CH2-CH3). The other monomer comprises a first heavy chain comprising a first variable heavy domain, a CH1 domain and Fc domain and an additional variable heavy domain (vhl -CHI -[optional domain linker] -vh2-hinge-CH2-CH3). The light domain is covalently attached between the C-terminus of the CH1 domain of the heavy constant domain and the N-terminus of the first Fc domain using domain linkers. This embodiment further utilizes a common light chain comprising a variable light domain and a constant light domain, that associates with the heavy chains to form two identical Fabs that bind a target. As for many of the embodiments herein, these constructs include skew variants, pI variants, ablation variants, additional Fc variants, etc. as desired and described herein.

[0140] A further heterodimeric scaffold that finds use in the context of the disclosure is the one armed central-scFv format shown in Figure 18C. In this embodiment, one monomer comprises just an Fc domain, while the other monomer uses an inserted scFv domain thus forming the second antigen-binding domain. In this format, the Fab portion binds one target and the scFv binds another. The scFv domain is inserted between the Fc domain and the CHl-Fv region of one of the monomers. In this embodiment, one monomer comprises a first heavy chain comprising a first variable heavy domain, a CH1 domain and Fc domain, with a scFv comprising a scFv variable light domain, an scFv linker and a scFv variable heavy domain. The scFv is covalently attached between the C-terminus of the CH1 domain of the heavy constant domain and the N-terminus of the first Fc domain using domain linkers. The second monomer comprises an Fc domain. This embodiment further utilizes a light chain comprising a variable light domain and a constant light domain, that associates with the heavy chain to form a Fab. As for many of the embodiments herein, these constructs include skew variants, pI variants, ablation variants, additional Fc variants, etc. as desired and described herein.

[0141] In addition, the Fc domains of the one armed central-scFv format optionally comprise skew variants (e.g., selected from the group consisting of S364K/E357Q : L368D/K370S; L368D/K370S : S364K; L368E/K370S : S364K; T411T/E360E/Q362E : D401K; L368D/K370S : S364K/E357L, K370S : S364K/E357Q, T366S/L368A/Y407V : T366W and T366S/L368A/Y407V Y349C : T366W/S354C), optionally ablation variants, optionally charged scFv linkers, and the heavy chain comprises pI variants. In some embodiments, the one armed central-scFv format includes skew variants, pI variants, and ablation variants. Accordingly, some embodiments include bottle opener formats that comprise: a) a first monomer that comprises the skew variants S364K/E357Q, the ablation variants E233P/L234V/L235A/G236del/S267K, and a first variable heavy domain that, with the first variable light domain of the light chain, makes up an Fv that binds to a first target, and a second variable heavy domain; b) a second monomer that comprises the skew variants L368D/K370S, the pI variants N208D/Q295E/N384D/Q418E/N421D, the ablation variants E233P/L234V/L235A/ G236del/S267K, and a first variable heavy domain that, with the first variable light domain, makes up the Fv that binds to the first target, and a second variable light chain, that together with the second variable heavy chain forms an Fv that binds a second target; and c) a light chain comprising a first variable light domain and a constant light domain. In some embodiments, the one armed central-scFv format includes skew variants, pi variants, ablation variants and FcRn variants. Accordingly, some embodiments include formats that comprise: a) a first monomer that comprises the skew variants S364K/E357Q, the ablation variants E233P/L234V/L235A/G236del/S267K, the FcRn variants M428L/N434S and a first variable heavy domain that, with the first variable light domain of the light chain, makes up an Fv that binds to a first target, and a second variable heavy domain; b) a second monomer that comprises the skew variants L368D/K370S, the pi variants N208D/Q295E/N384D/Q418E/N421D, the ablation variants E233P/L234V/L235A/G236del/S267K, the FcRn variants M428L/N434S and a first variable heavy domain that, with the first variable light domain, makes up the Fv that binds to the first target as outlined herein, and a second variable light chain, that together with the second variable heavy chain forms an Fv that binds a second target; and c) a light chain comprising a first variable light domain and a constant light domain.

[0142] A further heterodimeric scaffold that finds use in the disclosure is the one armed scFv-mAb format shown in Figure 18D. In this embodiment, one monomer comprises just an Fc domain, while the other monomer uses a scFv domain attached at the N-terminus of the

heavy chain, generally through the use of a linker: vh-scFv linker-vl-[optional domain linker] -CHl-hinge-CH2-CH3 or (in the opposite orientation) vl-scFv linker- vh-[optional domain linker] -CHl-hinge-CH2-CH3. In this format, the Fab portion binds one target and the scFv binds another. This embodiment further utilizes a light chain comprising a variable light domain and a constant light domain, that associates with the heavy chain to form a Fab. As for many of the embodiments herein, these constructs include skew variants, pI variants, ablation variants, additional Fc variants, etc. as desired and described herein.

[0143] The Fc domains of the one armed scFv-mAb comprise skew variants (e.g., selected from the group consisting of S364K/E357Q : L368D/K370S; L368D/K370S : S364K; L368E/K370S : S364K; T411T/E360E/Q362E : D401K; L368D/K370S : S364K/E357L, K370S : S364K/E357Q, T366S/L368A/Y407V : T366W; and T366S/L368A/Y407V/Y349C : T366W/S354C), optionally ablation variants, optionally charged scFv linkers, and the heavy chain comprises pi variants. In some embodiments, the one armed scFv-mAb format includes skew variants, pi variants, and ablation variants. Accordingly, some embodiments include bottle opener formats that comprise: a) a first monomer that comprises the skew variants S364K/E357Q, the ablation variants E233P/L234V/L235A/G236del/S267K, and a first variable heavy domain that, with the first variable light domain of the light chain, makes up an Fv that binds to a first target, and a second variable heavy domain; b) a second monomer that comprises the skew variants L368D/K370S, the pI variants N208D/Q295E/N384D/Q418E/N421D, the ablation variants E233P/L234V/L235A/ G236del/S267K, and a first variable heavy domain that, with the first variable light domain, makes up the Fv that binds to the first target as outlined herein, and a second variable light chain, that together with the second variable heavy chain forms an Fv that binds a second target; and c) a light chain comprising a first variable light domain and a constant light domain. In some embodiments, the one armed scFv-mAb format includes skew variants, pI variants, ablation variants and FcRn variants. Accordingly, some embodiments include bottle opener formats that comprise: a) a first monomer that comprises the skew variants S364K/E357Q, the ablation variants E233P/L234V/L235A/G236del/S267K, the FcRn variants M428L/N434S and a first variable heavy domain that, with the first variable light domain of the light chain, makes up an Fv that binds to a first target, and a second variable heavy domain; b) a second monomer that comprises the skew variants L368D/K370S, the pi variants N208D/Q295E/N384D/Q418E/N421D, the ablation variants E233P/L234V/L235A/G236del/S267K, the FcRn variants M428L/N434S and a first variable

heavy domain that, with the first variable light domain, makes up the Fv that binds to the first target as outlined herein, and a second variable light chain, that together with the second variable heavy chain forms an Fv that binds a second target; and c) a light chain comprising a first variable light domain and a constant light domain.

[0144] Another heterodimeric scaffold that finds use in the disclosure is the mAb-scFv format shown in Figure 18E. In this embodiment, the format relies on the use of an N-terminal attachment of a scFv to one of the monomers, thus forming a third antigen-binding domain, wherein the Fab portions of the two monomers bind one target and the "extra" scFv domain binds a different target. In this embodiment, the first monomer comprises a first heavy chain (comprising a variable heavy domain and a constant domain), with a N-terminally covalently attached scFv comprising a scFv variable light domain, an scFv linker and a scFv variable heavy domain in either orientation ((vhl-scFv linker-vll -[optional domain linker]- vh2-CHl-hinge-CH2-CH3) or (with the scFv in the opposite orientation) (vll-scFv linker-vhl-[optional domain linker]-vh2-CHl-hinge-CH2-CH3)). This embodiment further utilizes a common light chain comprising a variable light domain and a constant light domain, that associates with the heavy chains to form two identical Fabs that bind one of the target antigens. As for many of the embodiments herein, these constructs include skew variants, pi variants, ablation variants, additional Fc variants, etc. as desired and described herein.

[0145] The Fc domains of the scFv-mAb format optionally comprise skew variants (e.g., being selected from the group consisting of S364K/E357Q : L368D/K370S; L368D/K370S : S364K; L368E/K370S : S364K; T411T/E360E/Q362E : D401K; L368D/K370S : S364K/E357L, K370S : S364K/E357Q, T366S/L368A/Y407V : T366W; and T366S/L368A/Y407V/Y349C : T366W/S354C), optionally ablation variants, optionally charged scFv linkers, and the heavy chain comprises pI variants. In some embodiments, the mAb-scFv format includes skew variants, pI variants, and ablation variants. Accordingly, some embodiments include bottle opener formats that comprise: a) a first monomer that comprises the skew variants S364K/E357Q, the ablation variants E233P/L234V/L235A/G236del/S267K, and a first variable heavy domain that, with the first variable light domain of the light chain, makes up an Fv that binds to a first target, and a second variable heavy domain; b) a second monomer that comprises the skew variants L368D/K370S, the pi variants N208D/Q295E/N384D/Q418E/N421D, the ablation variants E233P/L234V/L235A/G236del/S267K, and a first variable heavy domain that, with the first

variable light domain, makes up the Fv that binds to the first target as outlined herein, and a second variable light chain, that together with the second variable heavy chain forms an Fv that binds a second target; and c) a light chain comprising a first variable light domain and a constant light domain. In some embodiments, the mAb-scFv format includes skew variants, pI variants, ablation variants and FcRn variants. Accordingly, some embodiments include bottle opener formats that comprise: a) a first monomer that comprises the skew variants S364K/E357Q, the ablation variants E233P/L234V/L235A/G236del/S267K, the FcRn variants M428L/N434S and a first variable heavy domain that, with the first variable light domain of the light chain, makes up an Fv that binds to a first target, and a second variable heavy domain; b) a second monomer that comprises the skew variants L368D/K370S, the pI variants N208D/Q295E/N384D/Q418E/N421D, the ablation variants E233P/L234V/L235A/G236del/S267K, the FcRn variants M428L/N434S and a first variable heavy domain that, with the first variable light domain, makes up the Fv that binds to the first target, and a second variable light chain, that together with the second variable heavy chain forms an Fv that binds a second target; and c) a light chain comprising a first variable light domain and a constant light domain.

[0146] The disclosure also provides dual scFv formats, such as that depicted in Figure 18B. In this embodiment, the heterodimeric antigen-binding protein is made up of two scFv-Fc monomers (both in either (vh-scFv linker-vl-[optional domain linker] -CH2-CH3) format or (vl-scFv linker- vh- [optional domain linker]-CH2-CH3) format, or with one monomer in one orientation and the other in the other orientation). The Fc domains of the dual scFv format optionally comprise skew variants (e.g., selected from the group consisting of S364K/E357Q : L368D/K370S; L368D/K370S : S364K; L368E/K370S : S364K; T411T/E360E/Q362E : D401K; L368D/K370S : S364K/E357L, K370S : S364K/E357Q, T366S/L368A/Y407V : T366W; and T366S/L368A/Y407V/Y349C : T366W/S354C), optionally ablation variants, optionally charged scFv linkers, and the heavy chain comprises pI variants.

[0147] In some embodiments, the dual scFv format includes skew variants, pI variants, and ablation variants. Accordingly, some embodiments include formats that comprise: a) a first monomer that comprises the skew variants S364K/E357Q, the ablation variants E233P/L234V/L235A/G236del/S267K, and a first variable heavy domain that, with the first variable light domain of the light chain, makes up an Fv that binds to a first target, and a second variable heavy domain; b) a second monomer that comprises the skew variants

L368D/K370S, the pi variants N208D/Q295E/N384D/Q418E/N421D, the ablation variants E233P/L234V/L235A/G236del/S267K, and a first variable heavy domain that, with the first variable light domain, makes up the Fv that binds to the first target as outlined herein, and a second variable light chain, that together with the second variable heavy chain forms an Fv that binds a second target; and c) a light chain comprising a first variable light domain and a constant light domain. In some embodiments, the dual scFv format includes skew variants, pI variants, ablation variants and FcRn variants. Accordingly, some embodiments include bottle opener formats that comprise: a) a first monomer that comprises the skew variants S364K/E357Q, the ablation variants E233P/L234V/L235A/G236del/S267K, the FcRn variants M428L/N434S and a first variable heavy domain that, with the first variable light domain of the light chain, makes up an Fv that binds to a first target, and a second variable heavy domain; b) a second monomer that comprises the skew variants L368D/K370S, the pi variants N208D/Q295E/N384D/Q418E/N421D, the ablation variants E233P/L234V/L235A/G236del/S267K, the FcRn variants M428L/N434S and a first variable heavy domain that, with the first variable light domain, makes up the Fv that binds to the first target, and a second variable light chain, that together with the second variable heavy chain forms an Fv that binds a second target; and c) a light chain comprising a first variable light domain and a constant light domain.

[0148] Additional description of antibody formats is provided in International Patent Publication No. WO 2017/218707, hereby incorporated by reference.

Antibody Binding

[0149] The bispecific antigen-binding protein (e.g., heterodimeric antibody) of the disclosure, in various aspects, binds CD3 and STEAP1. The different binding regions independently display a KD for their respective antigen of less than or equal to 10^{-4} M, less than or equal to 10^{-5} M, less than or equal to 10^{-6} M, less than or equal to 10^{-7} M, less than or equal to 10^{-8} M, less than or equal to 10^{-9} M, less than or equal to 10^{-10} M, less than or equal to 10^{-11} M, or less than or equal to 10^{-12} M, where KD refers to a dissociation rate of a particular antibody-antigen interaction. Binding affinity is further described above. The STEAP1 binding region need not bind STEAP1 with the same affinity as, e.g., the CD3 binding region binds CD3. Binding affinity disclosed in the context of bispecific antigen-binding protein also applies to any of the monospecific constructs described herein, including constructs that bind PD-1.

Additional Antibody Modifications

[0150] In addition to the modifications outlined above, other modifications can be made. For example, the molecules may be stabilized by the incorporation of disulphide bridges linking the VH and VL domains (Reiter et al., 1996, Nature Biotech. 14:1239-1245, entirely incorporated by reference). In addition, there are a variety of covalent modifications of antibodies that can be made as outlined below.

[0151] Covalent modifications of antibodies are included within the scope of this disclosure, and are generally, but not always, done post-translationally. For example, several types of covalent modifications of the antibody are introduced into the molecule by reacting specific amino acid residues of the antibody with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C-terminal residues.

[0152] Cysteinyl residues most commonly are reacted with α-haloacetates (and corresponding amines), such as chloroacetic acid or chloroacetamide, to give carboxymethyl or carboxyamidomethyl derivatives. Cysteinyl residues may also be derivatized by reaction with bromotrifluoroacetone, α-bromo-β-(5-imidozoyl)propionic acid, chloroacetyl phosphate, N-alkylmaleimides, 3-nitro-2-pyridyl disulfide, methyl 2-pyridyl disulfide, p-chloromercuribenzoate, 2-chloromercuri-4-nitrophenol, or chloro-7-nitrobenzo-2-oxa-1,3-diazole and the like.

[0153] In addition, modifications at cysteines are particularly useful in antibody-drug conjugate (ADC) applications, further described below. In some embodiments, the constant region of the antibodies can be engineered to contain one or more cysteines that are particularly "thiol reactive," so as to allow more specific and controlled placement of the drug moiety. See for example U.S. Patent No. 7,521,541, incorporated by reference in its entirety herein.

[0154] Histidyl residues are derivatized by reaction with diethylpyrocarbonate at pH 5.5-7.0 because this agent is relatively specific for the histidyl side chain. Para-bromophenacyl bromide also is useful; the reaction is preferably performed in 0.1M sodium cacodylate at pH 6.0.

[0155] Lysinyl and amino terminal residues are reacted with succinic or other carboxylic acid anhydrides. Derivatization with these agents reverses the charge of the lysinyl residues. Other suitable reagents for derivatizing alpha-amino-containing residues include imidoesters such as methyl picolinimidate; pyridoxal phosphate; pyridoxal; chloroborohydride;

trinitrobenzenesulfonic acid; O-methylisourea; 2,4-pentanedione; and transaminase-catalyzed reaction with glyoxylate.

[0156] Arginyl residues are modified by reaction with one or several conventional reagents, among them phenylglyoxal, 2,3-butanedione, 1,2-cyclohexanedione, and ninhydrin. Derivatization of arginine residues requires that the reaction be performed in alkaline conditions because of the high pKa of the guanidine functional group. Furthermore, these reagents may react with the groups of lysine as well as the arginine epsilon-amino group.

[0157] The specific modification of tyrosyl residues may be made, with particular interest in introducing spectral labels into tyrosyl residues by reaction with aromatic diazonium compounds or tetranitromethane. Most commonly, N-acetylimidizole and tetranitromethane are used to form O-acetyl tyrosyl species and 3-nitro derivatives, respectively. Tyrosyl residues are iodinated using 125I or 131I to prepare labeled proteins for use in radioimmunoassay, the chloramine T method described above being suitable.

[0158] Carboxyl side groups (aspartyl or glutamyl) are selectively modified by reaction with carbodiimides (R'—N=C=N--R'), where R and R' are optionally different alkyl groups, such as 1-cyclohexyl-3-(2-morpholinyl-4-ethyl) carbodiimide or 1-ethyl-3-(4-azonia-4,4-dimethylpentyl) carbodiimide. Furthermore, aspartyl and glutamyl residues are converted to asparaginyl and glutaminyl residues by reaction with ammonium ions.

[0159] Derivatization with bifunctional agents is useful for crosslinking antibodies to a water-insoluble support matrix or surface for use in a variety of methods. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis (succinimidylpropionate), and bifunctional maleimides such as bis-N-maleimido-1,8-octane. Derivatizing agents such as methyl-3-[(p-azidophenyl)dithio]propioimidate yield photoactivatable intermediates that are capable of forming crosslinks in the presence of light. Alternatively, reactive water-insoluble matrices such as cyanogen bromide-activated carbohydrates and the reactive substrates described in U.S. Patent Nos. 3,969,287; 3,691,016; 4,195,128; 4,247,642; 4,229,537; and 4,330,440, all entirely incorporated by reference, are employed for protein immobilization.

[0160] Glutaminyl and asparaginyl residues are frequently deamidated to the corresponding glutamyl and aspartyl residues, respectively. Alternatively, these residues are

deamidated under mildly acidic conditions. Either form of these residues falls within the scope of this disclosure.

[0161] Other modifications include hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α-amino groups of lysine, arginine, and histidine side chains (T. E. Creighton, Proteins: Structure and Molecular Properties, W. H. Freeman & Co., San Francisco, pp. 79-86 [1983], entirely incorporated by reference), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

[0162] In addition, as will be appreciated by those in the art, labels (including fluorescent, enzymatic, magnetic, radioactive, etc.) can be added to any of the antigen-binding proteins described herein (as well as the other compositions of the disclosure).

Glycosylation

[0163] Another type of covalent modification is alteration in glycosylation. In another embodiment, the antibodies (or other types of antigen-binding protein) disclosed herein can be modified to include one or more engineered glycoforms. By "engineered glycoform" as used herein is meant a carbohydrate composition that is covalently attached to the antibody, wherein said carbohydrate composition differs chemically from that of a parent antibody. Engineered glycoforms may be useful for a variety of purposes, including but not limited to enhancing or reducing effector function. A preferred form of engineered glycoform is afucosylation, which has been shown to be correlated to an increase in ADCC function, presumably through tighter binding to the FcγRIIIa receptor. In this context, "afucosylation" means that the majority of the antibody produced in the host cells is substantially devoid of fucose, e.g., 90%, 95%, or 98% of the generated antibodies do not have appreciable fucose as a component of the carbohydrate moiety of the antibody (generally attached at N297 in the Fc region). Defined functionally, afucosylated antibodies generally exhibit at least a 50% or higher affinity to the FcγRIIIa receptor.

[0164] Optionally, the heterodimeric antibody comprises a sequence modification that removes one more glycosylation sites, e.g., at one or more of positions 292, 297, or 302. One non-limiting example comprises introduction of one or more stable effector functionless (SEFL2) mutations (e.g., in an IgG1 backbone), which are further described in, e.g., U.S. Patent No. 9,546,203, incorporated by reference herein in its entirety and particularly with respect to the description of SEFL2 mutations. This modification may be used in additional

to any other modification disclosed herein, e.g., the N67Q modification to decrease deamidation.

[0165] Engineered glycoforms may be generated by a variety of methods known in the art. See, e.g., Umaña et al., 1999, Nat Biotechnol 17:176-180; Davies et al., 2001, Biotechnol Bioeng 74:288-294; Shields et al., 2002, J Biol Chem 277:26733-26740; Shinkawa et al., 2003, J Biol Chem 278:3466-3473; U.S. Patent No. 6,602,684; U.S. Publication Nos. 2003/0157108 and 2003;0003097; and International Patent Publication Nos. WO 00/61739A1, WO 01/29246A1, WO 02/31140A1, and WO 02/30954A1, all entirely incorporated by reference, as well as Potelligent® technology [Biowa, Inc., Princeton, NJ] and GlycoMAb® glycosylation engineering technology [Glycart Biotechnology AG, Zürich, Switzerland]. Many of these techniques are based on controlling the level of fucosylated and/or bisecting oligosaccharides that are covalently attached to the Fc region, for example by expressing an IgG in various organisms or cell lines, engineered or otherwise (for example, Lec-13 CHO cells or rat hybridoma YB2/0 cells), by regulating enzymes involved in the glycosylation pathway (for example FUT8 [α1,6-fucosyltranserase] and/or β1-4- N-acetylglucosaminyltransferase III [GnTIII])), or by modifying carbohydrate(s) after the IgG has been expressed. For example, the "sugar engineered antibody technology" functions by adding modified saccharides that inhibit fucosylation during production; see for example U.S. Publication No. 20090317869, hereby incorporated by reference in its entirety. Engineered glycoform typically refers to the different carbohydrate or oligosaccharide; thus an antibody can include an engineered glycoform.

[0166] Alternatively, engineered glycoform may refer to the IgG variant that comprises the different carbohydrate or oligosaccharide. As is known in the art, glycosylation patterns can depend on both the sequence of the protein (e.g., the presence or absence of particular glycosylation amino acid residues, discussed below), or the host cell or organism in which the protein is produced. Particular expression systems are discussed below.

[0167] Glycosylation of polypeptides is typically either N-linked or O-linked. N-linked refers to the attachment of the carbohydrate moiety to the side chain of an asparagine residue. The tri-peptide sequences asparagine-X-serine and asparagine-X-threonine, where X is any amino acid except proline, are the recognition sequences for enzymatic attachment of the carbohydrate moiety to the asparagine side chain. Thus, the presence of either of these tri-peptide sequences in a polypeptide creates a potential glycosylation site. O-linked glycosylation refers to the attachment of one of the sugars N-acetylgalactosamine, galactose,

or xylose, to a hydroxyamino acid, most commonly serine or threonine, although 5-hydroxyproline or 5-hydroxylysine may also be used.

[0168] Addition of glycosylation sites to the antibody is conveniently accomplished by altering the amino acid sequence such that it contains one or more of the above-described tri-peptide sequences (for N-linked glycosylation sites). The alteration may also be made by the addition of, or substitution by, one or more serine or threonine residues to the starting sequence (for O-linked glycosylation sites). For ease, the antibody amino acid sequence is preferably altered through changes at the DNA level, particularly by mutating the DNA encoding the target polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

[0169] Another means of increasing the number of carbohydrate moieties on the antigen-binding protein (e.g., antibody) is by chemical or enzymatic coupling of glycosides to the protein. These procedures are advantageous in that they do not require production of the protein in a host cell that has glycosylation capabilities for N- and O-linked glycosylation. Depending on the coupling mode used, the sugar(s) may be attached to (a) arginine and histidine, (b) free carboxyl groups, (c) free sulfhydryl groups such as those of cysteine, (d) free hydroxyl groups such as those of serine, threonine, or hydroxyproline, (e) aromatic residues such as those of phenylalanine, tyrosine, or tryptophan, or (f) the amide group of glutamine. These methods are described in International Patent Publication No. WO 87/05330 and in Aplin and Wriston, 1981, CRC Crit. Rev. Biochem., pp. 259-306, both entirely incorporated by reference.

[0170] Removal of carbohydrate moieties present on the starting antibody (e.g., post-translationally) may be accomplished chemically or enzymatically. Chemical deglycosylation requires exposure of the protein to the compound trifluoromethanesulfonic acid, or an equivalent compound. This treatment results in the cleavage of most or all sugars except the linking sugar (N-acetylglucosamine or N-acetylgalactosamine), while leaving the polypeptide intact. Chemical deglycosylation is described by Hakimuddin et al., 1987, Arch. Biochem. Biophys. 259:52 and by Edge et al., 1981, Anal. Biochem. 118:131, both entirely incorporated by reference. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., 1987, Meth. Enzymol. 138:350, entirely incorporated by reference. Glycosylation at potential glycosylation sites may be prevented by the use of the compound tunicamycin as

described by Duskin et al., 1982, J. Biol. Chem. 257:3105, entirely incorporated by reference. Tunicamycin blocks the formation of protein-N-glycoside linkages.

[0171] Another type of covalent modification of the antibody comprises linking the antibody to various nonproteinaceous polymers, including, but not limited to, various polyols such as polyethylene glycol, polypropylene glycol or polyoxyalkylenes, in the manner set forth in, for example, 2005-2006 PEG Catalog from Nektar Therapeutics (available at the Nektar website), or U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192; or 4,179,337, all entirely incorporated by reference. In addition, as is known in the art, amino acid substitutions may be made in various positions within the antibody to facilitate the addition of polymers such as PEG. See for example, U.S. Publication No. 2005/0114037A1, entirely incorporated by reference.

Additional Fc Variants for Additional Functionality

[0172] In addition to pI amino acid variants and other variants described above, there are a number of useful Fc amino acid modifications that can be made for a variety of reasons, including, but not limited to, altering binding to one or more FcγR receptors, altered binding to FcRn receptors, etc. The following modifications may be employed in addition or in the alternative to any of the modifications described above.

FcγR Variants

[0173] There are a number of useful Fc substitutions that can be made to alter binding to one or more of the FcγR receptors. Substitutions that result in increased binding as well as decreased binding can be useful. For example, it is known that increased binding to FcγRIIIa generally results in increased ADCC (antibody dependent cell-mediated cytotoxicity; the cell-mediated reaction wherein nonspecific cytotoxic cells that express FcγRs recognize bound antibody on a target cell and subsequently cause lysis of the target cell). Similarly, decreased binding to FcγRIIb (an inhibitory receptor) can be beneficial as well in some circumstances. Amino acid substitutions that find use in the present disclosure include those listed in U.S. Patent Publication Nos. 2006/0024298 (particularly Figure 41), 2006/0121032, 2006/0235208, 2007/0148170, all of which are expressly incorporated herein by reference in their entirety and specifically for the variants disclosed therein. Particular variants that find use include, but are not limited to, 236A, 239D, 239E, 332E, 332D, 239D/332E, 267D, 267E, 328F, 267E/328F, 236A/332E, 239D/332E/330Y, 239D, 332E/330L, and 299T.

[0174] In addition, there are additional Fc substitutions that find use in increased binding to the FcRn receptor and increased serum half life, as specifically disclosed in U.S. Patent Publication No. 2009/0163699, hereby incorporated by reference in its entirety, including, but not limited to, 434S, 428L, 308F, 259I, 428L/434S, 259I/308F, 436I/428L, 436I or V/434S, 436V/428L and 259I/308F/428L.

Fc Ablation Variants

[0175] Additional variants which find use in the context of the present disclosure are those that ablate (e.g., reduce or eliminate) binding to Fcγ receptors. This can be desirable to reduce the potential mechanisms of action (e.g., reduce ADCC activity) of the heterodimeric antibody. A number of suitable Fc ablation variants are depicted in Figure 6, and can be optionally and independently included or excluded in combination with any other heterodimerization variants, including pI and steric variants.

[0176] Of particular use in some embodiments are a first monomer (the "negative side") that contains the pI variants N208D/Q295E/N384D/Q418E/N421D, skew variants 368D/370S, and ablation variants E233P/L234V/L235A/G236del/S267K, paired with a positive side comprising no pI variants, skew variants S364K/E357Q and ablation variants E233P/L234V/L235A/G236del/S267K (optionally both monomers containing FcRn variants 428L/434S), where the positive side is the monomer comprising the scFv and contains a charged scFv linker. A second embodiment utilizes a first negative side monomer comprising I199T/N203D/K274Q/R355Q/Q419E/K447del, skew variants S364K/E357Q and ablation variants E233P/L234V/L235A/G236del/S267K (optionally both monomers containing FcRn variants 428L/434S), paired with a positive side comprising pI variants Q196K/I199T/P271R/P228R/N276K, skew variants S364K/E357Q and ablation variants E233P/L234V/L235A/G236del/S267K (optionally both monomers containing FcRn variants 428L/434S), where the positive side is the monomer comprising the scFv and contains a charged scFv linker. A third embodiment utilizes a first negative side monomer comprising I199T/N203D/K274Q/R355Q/N384S/K392N/V397M/Q419E/K447del, skew variants S364K/E357Q and ablation variants E233P/L234V/L235A/G236del/S267K (optionally both monomers containing FcRn variants 428L/434S), paired with a positive side monomer with no pI variants, skew variants S364K/E357Q and ablation variants E233P/L234V/L235A/G236del/S267K (optionally both monomers containing FcRn variants 428L/434S), where the positive side is the monomer comprising the scFv and contains a charged scFv linker. A fourth embodiment utilizes a first monomer (the "negative side") that

contains the pI variants N208D/Q295E/N384D/Q418E/N421D, skew variants 368D/370S, and ablation variants E233P/L234V/L235A/G236del/S239K, paired with a positive side comprising no pI variants, skew variants S364K/E357Q and ablation variants E233P/L234V/L235A/G236del/S239K (optionally both monomers containing FcRn variants 428L/434S). A fifth embodiment utilizes a first negative side monomer comprising I199T/N203D/K274Q/R355Q/Q419E/K447del, skew variants S364K/E357Q and ablation variants E233P/L234V/L235A/G236del/S239K (optionally both monomers containing FcRn variants 428L/434S), paired with a positive side comprising pI variants Q196K/I199T/P271R/P228R/N276K, skew variants S364K/E357Q and ablation variants E233P/L234V/L235A/G236del/S239K (optionally both monomers containing FcRn variants 428L/434S). A sixth embodiment utilizes a first negative side monomer comprising I199T/N203D/K274Q/R355Q/N384S/K392N/V397M/Q419E/K447del, skew variants S364K/E357Q and ablation variants E233P/L234V/L235A/G236del/S267K (optionally both monomers containing FcRn variants 428L/434S), paired with a positive side monomer skew variants S364K/E357Q and ablation variants E233P/L234V/L235A/G236del/S239K (optionally both monomers containing FcRn variants 428L/434S), where the positive side is the scFv monomer and contains a charged scFv linker (particularly when the scFv is anti-CD3). A seventh embodiment utilizes a first monomer (the "negative side") that contains the pI variants N208D/Q295E/N384D/Q418E/N421D, skew variants 368D/370S, and ablation variants S239K/S267K, paired with a positive side comprising no pI variants, skew variants S364K/E357Q and ablation variants S239K/S267K (optionally both monomers containing FcRn variants 428L/434S), where the positive side is the scFv monomer and contains a charged scFv linker. An eighth embodiment utilizes a first negative side monomer comprising I199T/N203D/K274Q/R355Q/Q419E/K447del, skew variants S364K/E357Q and ablation variants S239K/S267K, (optionally both monomers containing FcRn variants 428L/434S), paired with a positive side comprising pI variants Q196K/I199T/P271R/P228R/N276K, skew variants S364K/E357Q and ablation variants S239K/S267K (optionally both monomers containing FcRn variants 428L/434S), where the positive side is the scFv monomer and contains a charged scFv linker. A ninth embodiment utilizes a first negative side monomer comprising I199T/N203D/K274Q/R355Q/N384S/K392N/V397M/Q419E/K447del, skew variants S364K/E357Q and ablation variants S239K/S267K (optionally both monomers containing FcRn variants 428L/434S), paired with a positive side monomer with no pI variants, skew variants S364K/E357Q and ablation variants S239K/S267K (optionally both monomers

containing FcRn variants 428L/434S), where the positive side is the scFv monomer and contains a charged scFv linker. A tenth embodiment utilizes a first monomer (the "negative side") that contains the pI variants N208D/Q295E/N384D/Q418E/N421D, skew variants 368D/370S, and ablation variants S267K/P329K, paired with a positive side comprising no pI variants, skew variants S364K/E357Q and ablation variants S267K/P329K (optionally both monomers containing FcRn variants 428L/434S), where the positive side is the scFv monomer and contains a charged scFv linker. An eleventh embodiment utilizes a first negative side monomer comprising I199T/N203D/K274Q/R355Q/Q419E/K447del, skew variants S364K/E357Q and ablation variants S267K/P329K (optionally both monomers containing FcRn variants 428L/434S), paired with a positive side comprising pI variants Q196K/I199T/P271R/P228R/N276K, skew variants S364K/E357Q and ablation variants S267K/P329K (optionally both monomers containing FcRn variants 428L/434S), where the positive side is the scFv monomer and contains a charged scFv linker. A 12th embodiment utilizes a first negative side monomer comprising I199T/N203D/K274Q/R355Q/N384S/K392N/V397M/Q419E/K447del, skew variants S364K/E357Q and ablation variants S267K/P329K (optionally both monomers containing FcRn variants 428L/434S), paired with a positive side monomer with no pI variants, skew variants S364K/E357Q and ablation variants S267K/P329K (optionally both monomers containing FcRn variants 428L/434S), where the positive side is the scFv monomer and contains a charged scFv linker.

[0177] In various aspects, the first monomer comprising a first heavy chain comprising a first variable heavy domain, a first constant heavy chain comprising a first CH1 domain and a first Fc domain, a scFv that binds human CD3 and comprises a scFv variable light domain, an scFv linker and a scFv variable heavy domain (i.e., the "Fab-scFv-Fc" heavy chain) comprises a deletion in the upper hinge and CH2 and CH3 substitutions are introduced. The substitutions include, for example, one or more (e.g., all) of E233P, delL234, L235V, G236A, S267K, r292c, n297g, v302c, E357Q, and S364K (EU numbering, lower case letters referencing SEFL2 substitutions). The second monomer comprising a second heavy chain comprising a second variable heavy domain and a second constant heavy chain comprising a second Fc domain optionally comprises one or more (e.g., all) of the following mutations: N208D, E233P, delL234, L235V, G236A, S267K, r292c, Q295E, n297g, v302c, L368D, K370S, N384D, Q418E, and N421D (EU numbering, lower case letters referencing SEFL2 substitutions).

Linkers

[0178] "Linker" herein is also referred to as "linker sequence" or "spacer" or grammatical equivalent. Homo- or hetero-bifunctional linkers as are well known (see, 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200, incorporated entirely by reference). (Note the distinction between generic "linkers" and "scFv linkers and "charged scFv linkers.") A number of strategies may be used to covalently link molecules together. These include, but are not limited to polypeptide linkages between N- and C-termini of proteins or protein domains, linkage via disulfide bonds, and linkage via chemical cross-linking reagents. In one aspect of this embodiment, the linker is a peptide bond, generated by recombinant techniques or peptide synthesis. The linker peptide may predominantly include the following amino acid residues: Gly, Ser, Ala, or Thr. The linker peptide should have a length that is adequate to link two molecules in such a way that they assume the correct conformation relative to one another so that they retain the desired activity. In one embodiment, the linker is from about 1 to 50 amino acids in length, preferably about 1 to 30 amino acids in length. In one embodiment, linkers of 1 to 20 amino acids in length may be used. Useful linkers include glycine-serine polymers, including for example (GS)n, (GSGGS)n (SEQ ID NO: 178), (GGGGS)n (SEQ ID NO: 179), and (GGGS)n (SEQ ID NO: 180), where n is an integer of at least one; glycine-alanine polymers; alanine-serine polymers; and other flexible linkers. Alternatively, a variety of nonproteinaceous polymers, including but not limited to polyethylene glycol (PEG), polypropylene glycol, polyoxyalkylenes, or copolymers of polyethylene glycol and polypropylene glycol, may find use as linkers, that is may find use as linkers.

[0179] Other linker sequences may include any sequence of any length of CL/CH1 domain but not all residues of CL/CH1 domain; for example the first 5-12 amino acid residues of the CL/CH1 domains. Linkers can be derived from immunoglobulin light chain, for example Cκ or Cλ. Linkers can be derived from immunoglobulin heavy chains of any isotype, including for example Cγ1, Cγ2, Cγ3, Cγ4, Cα1, Cα2, Cδ, Cε, and Cμ. Linker sequences may also be derived from other proteins such as Ig-like proteins (e.g., TCR, FcR, KIR), hinge region-derived sequences, and other natural sequences from other proteins.

[0180] In some embodiments, the linker is a "domain linker," used to link any two domains as outlined herein together. For example, in Figure 18F, there may be a domain linker that attaches the C-terminus of the CH1 domain of the Fab to the N-terminus of the scFv, with another optional domain linker attaching the C-terminus of the scFv to the CH2 domain

(although in many embodiments the hinge is used as this domain linker). In some embodiments, the linker is a hinge region or a fragment thereof.

Antibody-Drug Conjugates

[0181] The antigen-binding protein (e.g., antibody or heterodimeric antibody) of the disclosure is optionally conjugated with drugs to form antibody-drug conjugates (ADCs). In general, ADCs are used in a variety of contexts, including oncology applications, where the use of antibody-drug conjugates for the local delivery of cytotoxic or cytostatic agents allows for the targeted delivery of the drug moiety to tumors, which can allow higher efficacy, lower toxicity, etc. An overview of this technology is provided in Ducry et al., Bioconjugate Chem., 21:5-13 (2010); Carter et al., Cancer J. 14(3):154 (2008); and Senter, Current Opin. Chem. Biol. 13:235-244 (2009), all of which are hereby incorporated by reference in their entirety.

[0182] Generally, conjugation is performed by covalent attachment to an antibody, as further described below, and generally relies on a linker, often a peptide linkage (which, as described herein, may be designed to be sensitive to cleavage by proteases at the target site or not). In addition, linkage of the linker-drug unit (LU-D) can be achieved by attachment to cysteines within the antibody. The number of drug moieties per antibody can change, depending on the conditions of the reaction, and can vary from 1:1 to 10:1 drug:antibody. As will be appreciated by those in the art, the actual number is an average.

[0183] The drug of the ADC can be selected from any of a number of agents, including but not limited to cytotoxic agents such as chemotherapeutic agents, growth inhibitory agents, toxins (for example, an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (that is, a radioconjugate). The disclosure further provides methods of using the ADCs.

[0184] Drugs for use in the context of the disclosure include cytotoxic drugs, particularly those which are used for cancer therapy. Such drugs include, in general, DNA damaging agents, anti-metabolites, natural products and their analogs. Exemplary classes of cytotoxic agents include the enzyme inhibitors such as dihydrofolate reductase inhibitors, and thymidylate synthase inhibitors, DNA intercalators, DNA cleavers, topoisomerase inhibitors, the anthracycline family of drugs, vinca drugs, mitomycins, bleomycins, cytotoxic nucleosides, the pteridine family of drugs, diynenes, podophyllotoxins, dolastatins, maytansinoids, differentiation inducers, and taxols.

[0185] Members of these classes include, for example, methotrexate, methopterin, dichloromethotrexate, 5-fluorouracil, 6-mercaptopurine, cytosine arabinoside, melphalan, leurosine, leurosideine, actinomycin, daunorubicin, doxorubicin, mitomycin C, mitomycin A, caminomycin, aminopterin, tallysomycin, podophyllotoxin and podophyllotoxin derivatives such as etoposide or etoposide phosphate, vinblastine, vincristine, vindesine, taxanes including taxol, taxotere retinoic acid, butyric acid, N8-acetyl spermidine, camptothecin, calicheamicin, esperamicin, ene-diynes, duocarmycin A, duocarmycin SA, calicheamicin, camptothecin, maytansinoids (including DM1), monomethylauristatin E (MMAE), monomethylauristatin F (MMAF), and maytansinoids (DM4) and their analogues.

[0186] Toxins may be used as antibody-toxin conjugates and include bacterial toxins such as diphtheria toxin, plant toxins such as ricin, small molecule toxins such as geldanamycin (Mandler et al (2000) J. Nat. Cancer Inst. 92(19):1573-1581; Mandler et al (2000) Bioorganic & Med. Chem. Letters 10:1025-1028; Mandler et al (2002) Bioconjugate Chem. 13:786-791), maytansinoids (EP 1391213; Liu et al., (1996) Proc. Natl. Acad. Sci. USA 93:8618-8623), and calicheamicin (Lode et al (1998) Cancer Res. 58:2928; Hinman et al (1993) Cancer Res. 53:3336-3342). Toxins may exert their cytotoxic and cytostatic effects by mechanisms including tubulin binding, DNA binding, or topoisomerase inhibition.

[0187] Conjugates of an antibody (or other antigen-binding protein) and one or more small molecule toxins, such as a maytansinoids, dolastatins, auristatins, a trichothecene, calicheamicin, and CC1065, and the derivatives of these toxins that have toxin activity, are contemplated.

[0188] Maytansine compounds suitable for use as maytansinoid drug moieties are well known in the art, and can be isolated from natural sources according to known methods, produced using genetic engineering techniques (see Yu et al (2002) PNAS 99:7968-7973), or maytansinol and maytansinol analogues prepared synthetically according to known methods. As described below, drugs may be modified by the incorporation of a functionally active group such as a thiol or amine group for conjugation to the antibody.

[0189] Exemplary maytansinoid drug moieties include those having a modified aromatic ring, such as: C-19-dechloro (U.S. Patent No. 4,256,746) (prepared by lithium aluminum hydride reduction of ansamytocin P2); C-20-hydroxy (or C-20-demethyl) +/-C-19-dechloro (U.S. Pat. Nos. 4,361,650 and 4,307,016) (prepared by demethylation using Streptomyces or Actinomyces or dechlorination using LAH); and C-20-demethoxy, C-20-acyloxy (--OCOR),

+/-dechloro (U.S. Patent No. 4,294,757) (prepared by acylation using acyl chlorides) and those having modifications at other positions

[0190] Exemplary maytansinoid drug moieties also include those having modifications such as: C-9-SH (U.S. Patent No. 4,424,219) (prepared by the reaction of maytansinol with H2S or P2S5); C-14-alkoxymethyl(demethoxy/CH2OR) (U.S. Patent No. 4,331,598); C-14-hydroxymethyl or acyloxymethyl (CH2OH or CH2OAc) (U.S. Patent No. 4,450,254) (prepared from Nocardia); C-15-hydroxy/acyloxy (U.S. Pat. No. 4,364,866) (prepared by the conversion of maytansinol by Streptomyces); C-15-methoxy (U.S. Patent Nos. 4,313,946 and 4,315,929) (isolated from Trewia nudlflora); C-18-N-demethyl (U.S. Patent Nos. 4,362,663 and 4,322,348) (prepared by the demethylation of maytansinol by *Streptomyces*); and 4,5-deoxy (U.S. Patent No. 4,371,533) (prepared by the titanium trichloride/LAH reduction of maytansinol).

[0191] Of particular use are DM1 (disclosed in U.S. Patent No. 5,208,020, incorporated by reference) and DM4 (disclosed in U.S. Patent No. 7,276,497, incorporated by reference). See also a number of additional maytansinoid derivatives and methods in U.S. Patent Nos. 5,416,064; 6,441,163; 7,303,749; 7,368,565; and 7,601,354; International Publication Nos. WO/01/24763, WO02/098883, WO02/16368 and WO04/1033272; and USSN 12/631,508, all of which are expressly incorporated by reference in their entirety.

[0192] ADCs containing maytansinoids, methods of making same, and their therapeutic use are disclosed, for example, in U.S. Patent Nos. 5,208,020; 5,416,064; 6,441,163 and European Patent EP 0 425 235 B1, the disclosures of which are hereby expressly incorporated by reference. Liu et al., Proc. Natl. Acad. Sci. USA 93:8618-8623 (1996) described ADCs comprising a maytansinoid designated DM1 linked to the monoclonal antibody C242 directed against human colorectal cancer.

[0193] Chari et al., Cancer Research 52:127-131 (1992) describe ADCs in which a maytansinoid was conjugated via a disulfide linker to the murine antibody A7 binding to an antigen on human colon cancer cell lines, or to another murine monoclonal antibody TA.1 that binds the HER-2/neu oncogene. The drug conjugate achieved a degree of cytotoxicity similar to the free maytansinoid drug, which could be increased by increasing the number of maytansinoid molecules per antibody molecule.

[0194] In some embodiments, the ADC comprises a dolastatin or dolostatin peptidic analog or derivative, or an auristatin (U.S. Patent Nos. 5,635,483 and 5,780,588). Dolastatins

and auristatins have been shown to interfere with microtubule dynamics, GTP hydrolysis, and nuclear and cellular division (Woyke et al (2001) Antimicrob. Agents and Chemother. 45(12):3580-3584) and have anticancer (U.S. Patent No. 5,663,149) and antifungal activity (Pettit et al (1998) Antimicrob. Agents Chemother. 42:2961-2965). The dolastatin or auristatin drug moiety may be attached to the antibody through the N (amino) terminus or the C (carboxyl) terminus of the peptidic drug moiety (International Patent Publication No. WO 02/088172). In various aspects, the heterodimeric antibody is part of a treatment plan that also includes administration of eribulin.

[0195] Exemplary auristatin embodiments include the N-terminus linked monomethylauristatin drug moieties DE and DF, disclosed in "Senter et al, Proceedings of the American Association for Cancer Research, Volume 45, Abstract Number 623, presented Mar. 28, 2004 and described in United States Patent Publication No. 2005/0238648, the disclosure of which is expressly incorporated by reference in its entirety. An exemplary auristatin embodiment is MMAE (see U.S. Patent No. 6,884,869 expressly incorporated by reference in its entirety). Another exemplary auristatin embodiment is MMAF (see U.S. Publication No 2005/0238649 and U.S. Patent Nos. 5,767,237 and 6,124,431, expressly incorporated by reference in their entirety).

[0196] Typically, peptide-based drug moieties can be prepared by forming a peptide bond between two or more amino acids and/or peptide fragments. Such peptide bonds can be prepared, for example, according to the liquid phase synthesis method (see E. Schroder and K. Lubke, "The Peptides", volume 1, pp 76-136, 1965, Academic Press) that is well known in the field of peptide chemistry. The auristatin/dolastatin drug moieties may be prepared according to the methods of: U.S. Patent Nos. 5,635,483 and 5,780,588; Pettit et al (1989) J. Am. Chem. Soc. 111:5463-5465; Pettit et al (1998) Anti-Cancer Drug Design 13:243-277; Pettit, G. R., et al. Synthesis, 1996, 719-725; Pettit et al (1996) J. Chem. Soc. Perkin Trans. 1 5:859-863; and Doronina (2003) Nat Biotechnol 21(7):778-784.

[0197] In other embodiments, the ADC comprises one or more calicheamicin molecules. For example, Mylotarg is the first commercial ADC drug and utilizes calicheamicin $\gamma 1$ as the payload (see U.S. Patent No. 4,970,198, incorporated by reference in its entirety). Additional calicheamicin derivatives are described in U.S. Patent Nos. 5,264,586, 5,384,412, 5,550,246, 5,739,116, 5,773,001, 5,767,285 and 5,877,296, all expressly incorporated by reference. The calicheamicin family of antibiotics is capable of producing double-stranded DNA breaks at sub-picomolar concentrations. For the preparation of conjugates of the calicheamicin family,

see U.S. Patent Nos. 5,712,374, 5,714,586, 5,739,116, 5,767,285, 5,770,701, 5,770,710, 5,773,001, 5,877,296 (all to American Cyanamid Company). Structural analogues of calicheamicin which may be used include, but are not limited to, γ1I, α2I, α2I, N-acetyl- γ1I, PSAG and θI1 (Hinman et al., Cancer Research 53:3336-3342 (1993), Lode et al., Cancer Research 58:2925-2928 (1998), and the aforementioned U.S. patents to American Cyanamid). Another anti-tumor drug that the antibody can be conjugated is QFA which is an antifolate. Both calicheamicin and QFA have intracellular sites of action and do not readily cross the plasma membrane. Therefore, cellular uptake of these agents through antibody mediated internalization greatly enhances their cytotoxic effects.

[0198] CC-1065 (see U.S. Patent No. 4,169,888, incorporated by reference) and duocarmycins are members of a family of antitumor antibiotics utilized in ADCs. These antibiotics appear to work through sequence-selectively alkylating DNA at the N3 of adenine in the minor groove, which initiates a cascade of events that result in apoptosis. Important members of the duocarmycins include duocarmycin A (U.S. Patent No. 4,923,990, incorporated by reference) and duocarmycin SA (U.S. Patent No. 5,101,038, incorporated by reference), and a large number of analogues as described in U.S. Patent Nos. 7,517,903, 7,691,962, 5,101,038; 5,641,780; 5,187,186; 5,070,092; 5,070,092; 5,641,780; 5,101,038; 5,084,468; 5,475,092; 5,585,499; 5,703,080; 6,989,452; 7,087,600; 7,129,261; 7,498,302; 7,507,420; and 5,846,545; and International Patent Publication Nos. WO2007/089149 and WO2009/017394A1, all of which are expressly incorporated by reference.

Other Cytotoxic Agents

[0199] Other antitumor agents that can be conjugated to an antigen-binding protein include BCNU, streptozoicin, vincristine and 5-fluorouracil, the family of agents known collectively LL-E33288 complex described in U.S. Patent Nos. 5,053,394 and 5,770,710, as well as esperamicins (U.S. Patent No. 5,877,296).

[0200] Enzymatically active toxins and fragments thereof which can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin and the tricothecenes. See, for example, International Patent Publication No. WO 93/21232.

[0201] The disclosure further contemplates an ADC formed between an antigen-binding protein and a compound with nucleolytic activity (e.g., a ribonuclease or a DNA endonuclease such as a deoxyribonuclease; DNase).

[0202] For selective destruction of the tumor, the antigen-binding protein (e.g., antibody or heterodimeric antibody) may comprise a highly radioactive atom. A variety of radioactive isotopes are available for the production of radioconjugates. Examples include At211, I131, I125, Y90, Re186, Re188, Sm153, Bi212, P32, Pb212 and radioactive isotopes of Lu.

[0203] The radio- or other labels may be incorporated in the conjugate in known ways. For example, the peptide may be biosynthesized or may be synthesized by chemical amino acid synthesis using suitable amino acid precursors involving, for example, fluorine-19 in place of hydrogen. Labels such as Tc99m or I123, Re186, Re188, and In111 can be attached via a cysteine residue in the peptide. Yttrium-90 can be attached via a lysine residue. The IODOGEN method (Fraker et al (1978) Biochem. Biophys. Res. Commun. 80: 49-57 can be used to incorporate Iodine-123. "Monoclonal Antibodies in Immunoscintigraphy" (Chatal, CRC Press 1989) describes other methods in detail.

[0204] In some instances, separation, purification, and characterization of homogeneous ADCs where p is a certain value from ADCs with other drug loadings may be achieved by means such as reverse phase HPLC or electrophoresis. In exemplary embodiments, p is 2, 3, 4, 5, 6, 7, or 8 or a fraction thereof.

[0205] It will be understood that chemical modifications may also be made to the desired compound in order to make reactions of that compound more convenient for purposes of preparing conjugates of the invention. For example a functional group e.g., amine, hydroxyl, or sulfhydryl, may be appended to the drug at a position which has minimal or an acceptable effect on the activity or other properties of the drug

Linker Units

[0206] Typically, the antigen-binding protein -drug conjugate comprises a linker unit between the drug unit and the antigen-binding protein unit. In some embodiments, the linker is cleavable under intracellular or extracellular conditions, such that cleavage of the linker releases the drug unit from the antigen-binding protein in the appropriate environment. For example, solid tumors that secrete certain proteases may serve as the target of the cleavable linker; in other embodiments, it is the intracellular proteases that are utilized. In yet other

embodiments, the linker unit is not cleavable and the drug is released, for example, by antibody degradation in lysosomes.

[0207] In some embodiments, the linker is cleavable by a cleaving agent that is present in the intracellular environment (for example, within a lysosome or endosome or caveolea). The linker can be, for example, a peptidyl linker that is cleaved by an intracellular peptidase or protease enzyme, including, but not limited to, a lysosomal or endosomal protease. In some embodiments, the peptidyl linker is at least two amino acids long or at least three amino acids long or more.

[0208] Cleaving agents can include, without limitation, cathepsins B and D and plasmin, all of which are known to hydrolyze dipeptide drug derivatives resulting in the release of active drug inside target cells (see, e.g., Dubowchik and Walker, 1999, Pharm. Therapeutics 83:67-123). Peptidyl linkers that are cleavable by enzymes that are present in CD38-expressing cells. For example, a peptidyl linker that is cleavable by the thiol-dependent protease cathepsin-B, which is highly expressed in cancerous tissue, can be used (e.g., a Phe-Leu or a Gly-Phe-Leu-Gly linker (SEQ ID NO: 181)). Other examples of such linkers are described, e.g., in U.S. Patent No. 6,214,345, incorporated herein by reference in its entirety.

[0209] In some embodiments, the peptidyl linker cleavable by an intracellular protease is a Val-Cit linker or a Phe-Lys linker (see, e.g., U.S. Patent No. 6,214,345, which describes the synthesis of doxorubicin with the val-cit linker).

[0210] In other embodiments, the cleavable linker is pH-sensitive, that is, sensitive to hydrolysis at certain pH values. Typically, the pH-sensitive linker hydrolyzable under acidic conditions. For example, an acid-labile linker that is hydrolyzable in the lysosome (for example, a hydrazone, semicarbazone, thiosemicarbazone, cis-aconitic amide, orthoester, acetal, ketal, or the like) may be used. (See, e.g., U.S. Patent Nos. 5,122,368; 5,824,805; and 5,622,929; Dubowchik and Walker, 1999, Pharm. Therapeutics 83:67-123; Neville et al., 1989, Biol. Chem. 264:14653-14661.) Such linkers are relatively stable under neutral pH conditions, such as those in the blood, but are unstable at below pH 5.5 or 5.0, the approximate pH of the lysosome. In certain embodiments, the hydrolyzable linker is a thioether linker (such as, e.g., a thioether attached to the therapeutic agent via an acylhydrazone bond (see, e.g., U.S. Patent No. 5,622,929)).

[0211] In yet other embodiments, the linker is cleavable under reducing conditions (for example, a disulfide linker). A variety of disulfide linkers are known in the art, including, for

example, those that can be formed using SATA (N-succinimidyl-5-acetylthioacetate), SPDP (N-succinimidyl-3-(2-pyridyldithio)propionate), SPDB (N-succinimidyl-3-(2-pyridyldithio)butyrate) and SMPT (N-succinimidyl-oxycarbonyl-alpha-methyl-alpha-(2-pyridyl-dithio)toluene)- , and SPDB and SMPT. See, e.g., Thorpe et al., 1987, Cancer Res. 47:5924-5931; Wawrzynczak et al., In Immunoconjugates: Antibody Conjugates in Radioimagery and Therapy of Cancer (C. W. Vogel ed., Oxford U. Press, 1987). See also U.S. Pat. No. 4,880,935.

[0212] In other embodiments, the linker is a malonate linker (Johnson et al., 1995, Anticancer Res. 15:1387-93), a maleimidobenzoyl linker (Lau et al., 1995, Bioorg-Med-Chem. 3(10):1299-1304), or a 3'-N-amide analog (Lau et al., 1995, Bioorg-Med-Chem. 3(10):1305-12).

[0213] In yet other embodiments, the linker unit is not cleavable and the drug is released by antibody degradation. See, e.g., U.S. Patent Publication No. 2005/0238649 incorporated by reference herein in its entirety.

[0214] In many embodiments, the linker is self-immolative. As used herein, the term "self-immolative Spacer" refers to a bifunctional chemical moiety that is capable of covalently linking together two spaced chemical moieties into a stable tripartite molecule. It will spontaneously separate from the second chemical moiety if its bond to the first moiety is cleaved. See, for example, International Patent Publication Nos. WO 2007059404A2, WO06110476A2, WO05112919A2, WO2010/062171, WO09/017394, WO07/089149, WO 07/018431, WO04/043493, and WO02/083180, which are directed to drug-cleavable substrate conjugates where the drug and cleavable substrate are optionally linked through a self-immolative linker and which are all expressly incorporated by reference.

[0215] Often the linker is not substantially sensitive to the extracellular environment, i.e., no more than about 20%, 15%, 10%, 5%, 3%, or no more than about 1% of the linkers, in a sample of antigen-binding protein -drug conjugate, are cleaved when the antigen-binding protein -drug conjugate presents in an extracellular environment (for example, in plasma). Whether a linker is not substantially sensitive to the extracellular environment can be determined, for example, by incubating with plasma the antigen-binding protein -drug conjugate compound for a predetermined time period (for example, 2, 4, 8, 16, or 24 hours) and then quantitating the amount of free drug present in the plasma.

[0216] In other, non-mutually exclusive embodiments, the linker promotes cellular internalization. In certain embodiments, the linker promotes cellular internalization when conjugated to the therapeutic agent (that is, in the milieu of the linker-therapeutic agent moiety of the ADC as described herein). In yet other embodiments, the linker promotes cellular internalization when conjugated to both the auristatin compound and the antigen-binding protein of the disclosure.

[0217] A variety of exemplary linkers that can be used with the present compositions and methods are described in International Patent Publication No. WO 2004-010957 and U.S. Publication Nos. 2006/0074008, 20050238649, and 2006/0024317 (each of which is incorporated by reference herein in its entirety).

[0218] It will be appreciated that the therapeutics described above may be administered separately, i.e., not conjugated to the antigen-binding protein, in various embodiments.

Drug Loading

[0219] Drug loading is represented by p and is the average number of drug moieties per antigen-binding protein in a molecule. Drug loading ("p") may be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more moieties (D) per antigen-binding protein, although frequently the average number is a fraction or a decimal. Generally, drug loading of from 1 to 4 is frequently useful, and from 1 to 2 is also useful. ADCs of the disclosure include collections of antigen-binding protein conjugated with a range of drug moieties, from 1 to 20. The average number of drug moieties per antigen-binding protein in preparations of ADC from conjugation reactions may be characterized by conventional means such as mass spectroscopy and, ELISA assay.

[0220] The quantitative distribution of ADC in terms of p may also be determined. In some instances, separation, purification, and characterization of homogeneous ADC where p is a certain value from ADC with other drug loadings may be achieved by means such as electrophoresis.

[0221] For some ADCs, p may be limited by the number of attachment sites on the antigen-binding protein. For example, where the attachment is a cysteine thiol, as in the exemplary embodiments above, an antigen-binding protein may have only one or several cysteine thiol groups, or may have only one or several sufficiently reactive thiol groups through which a linker may be attached. In certain embodiments, higher drug loading, e.g. p>5, may cause aggregation, insolubility, toxicity, or loss of cellular permeability of certain

antibody-drug conjugates. In certain embodiments, the drug loading for an ADC of the disclosure ranges from 1 to about 8; from about 2 to about 6; from about 3 to about 5; from about 3 to about 4; from about 3.1 to about 3.9; from about 3.2 to about 3.8; from about 3.2 to about 3.7; from about 3.2 to about 3.6; from about 3.3 to about 3.8; or from about 3.3 to about 3.7. Indeed, it has been shown that for certain ADCs, the optimal ratio of drug moieties per antigen-binding protein may be less than 8, and may be about 2 to about 5. See U.S. Publication No. 2005/0238649 A1 (herein incorporated by reference in its entirety).

[0222] In certain embodiments, fewer than the theoretical maximum of drug moieties are conjugated to an antigen-binding protein during a conjugation reaction. An antigen-binding protein may contain, for example, lysine residues that do not react with the drug-linker intermediate or linker reagent, as discussed below. Generally, antibodies do not contain many free and reactive cysteine thiol groups which may be linked to a drug moiety; indeed most cysteine thiol residues in antibodies exist as disulfide bridges. In certain embodiments, an antibody may be reduced with a reducing agent such as dithiothreitol (DTT) or tricarbonylethylphosphine (TCEP), under partial or total reducing conditions, to generate reactive cysteine thiol groups. In certain embodiments, an antibody is subjected to denaturing conditions to reveal reactive nucleophilic groups such as lysine or cysteine.

[0223] The loading (drug/ antigen-binding protein ratio) of an ADC may be controlled in different ways, e.g., by: (i) limiting the molar excess of drug-linker intermediate or linker reagent relative to antibody, (ii) limiting the conjugation reaction time or temperature, (iii) partial or limiting reductive conditions for cysteine thiol modification, (iv) engineering by recombinant techniques the amino acid sequence of the antigen-binding protein such that the number and position of cysteine residues is modified for control of the number and/or position of linker-drug attachments (such as thioMab or thioFab prepared as disclosed in, e.g., International Patent Publication No. WO2006/034488 (herein incorporated by reference in its entirety)).

[0224] It is to be understood that where more than one nucleophilic group reacts with a drug-linker intermediate or linker reagent followed by drug moiety reagent, then the resulting product is a mixture of ADC compounds with a distribution of one or more drug moieties attached to an antigen-binding protein. The average number of drugs per antigen-binding protein may be calculated from the mixture by a dual ELISA antibody assay, which is specific for antigen-binding protein and specific for the drug. Individual ADC molecules may

be identified in the mixture by mass spectroscopy and separated by HPLC, e.g., hydrophobic interaction chromatography.

[0225] In some embodiments, a homogeneous ADC with a single loading value may be isolated from the conjugation mixture by electrophoresis or chromatography.

Compositions

[0226] Formulations for use in accordance with the present disclosure are prepared for storage by mixing an antigen-binding protein having the desired degree of purity with optional pharmaceutically acceptable carriers, excipients or stabilizers (Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. [1980]), in the form of lyophilized formulations or aqueous solutions. The compositions of the disclosure are preferably sterile. 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).

[0227] The formulation may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. For example, it may be desirable to provide antigen-binding proteins with other specificities. Alternatively, or in addition, the composition may comprise a cytotoxic agent, cytokine, growth inhibitory agent and/or small molecule antagonist, such as any of the drugs mentioned herein. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

[0228] The active ingredients may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example,

hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles and nanocapsules) or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980).

[0229] Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antigen-binding protein, which matrices are in the form of shaped articles, e.g., film or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and γ-ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT™ (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods.

[0230] When encapsulated antibodies remain in the body for a long time, they may denature or aggregate as a result of exposure to moisture at 37°C, resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered to be intermolecular S--S bond formation through thio-disulfide interchange, stabilization may be achieved by modifying sulfhydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

Administrative Modalities

[0231] The antigen-binding protein and, optionally, a co-therapy, such as chemotherapeutic agent(s) or another antibody therapeutic (e.g., anti-PD-1 antibody) are administered to a subject in accordance with clinically-acceptable methods, such as intravenous, intramuscular, intraperitoneal, subcutaneous, intra-articular, intralesional, intrasynovial, intrathecal, oral, topical, intratumoral, via an afferent lymph vessel, or inhalation routes. Intravenous or subcutaneous administration of the antigen-binding protein is preferred. Bolus injection and continuous infusion are contemplated, as is localized

administration, e.g., at a site of disease or injury. Use of the antigen-binding protein (optionally with another therapeutic agent) in *ex vivo* procedures also is contemplated. For example, a patient's blood or other bodily fluid may be contacted with the antigen-binding protein *ex vivo*, and optionally administered. The antigen-binding protein may be bound to a suitable insoluble matrix or solid support material.

Methods of Use

[0232] The disclosure provides a method of treating a subject in need thereof, the method comprising administering to the subject the antigen-binding protein (e.g., antibody or heterodimeric antibody) described herein. In various embodiments, the disclosure provides a method of treating cancer (such as prostate cancer or Ewing sarcoma) in a subject in need thereof, the method comprising administering to the subject the antigen-binding protein (e.g., antibody or heterodimeric antibody) described herein. The disclosure further provides use of the antigen-binding protein (e.g., antibody or heterodimeric antibody) of the disclosure for treating a subject in need thereof, such as use for the treatment of cancer (e.g., prostate cancer or Ewing sarcoma) in a subject. The cancer is preferably a cancer associated with increased expression of STEAP1 (e.g., greater than 10,000 STEAP1/cell). Examples of cancer include, but are not limited to, cancers of the prostate, breast, pancreas, bladder, gastrointestinal tract, testis, ovary, cervix, as well as sarcoma (Ewing sarcoma) and melanoma.

[0233] The methods of treating a subject described herein are intended to provide an improvement in a disease or condition, and/or an improvement in the symptoms associated with the disease or condition. For example, a therapeutic response would refer to one or more of the following improvements in the disease: (1) a reduction in the number of neoplastic cells; (2) an increase in neoplastic cell death; (3) inhibition of neoplastic cell survival; (5) inhibition (i.e., slowing to some extent, preferably halting) of tumor growth or appearance of new lesions; (6) an increased patient survival rate; and/or (7) some relief from one or more symptoms associated with the disease or condition (e.g., in the context of prostate cancer, frequent urination, nocturia, hematuria, dysuria, or bone pain; in the context of Ewing sarcoma, pain, swelling, or tenderness in affected area).

[0234] Therapeutic responses in any given disease or condition can be determined by standardized response criteria specific to that disease or condition. Tumor response can be assessed using screening techniques such as magnetic resonance imaging (MRI) scan, x-radiographic imaging, computed tomographic (CT) scan, positron emission tomography

(PET) scan, bone scan, ultrasound, tumor biopsy sampling, counting of tumor cells in circulation, and/or measurement of tumor antigen (e.g., prostate specific antigen (PSA) and/or alphafeltoprotein (AFP)). In addition to these therapeutic responses, the subject undergoing therapy may experience the beneficial effect of an improvement in the symptoms associated with the disease.

[0235] The subject is a mammal, preferably a human, optionally a human male. In the context of cancer, the subject may be diagnosed with any stage of the disease (i.e., stage I, stage II, stage III, or stage IV prostate cancer), or may be at risk of developing cancer which has not yet been clinically confirmed.

[0236] For prostate cancer, the subject may experience a decrease in prostate cancer-related symptoms (such as those described herein), decrease in tumor size, decrease in levels of prostate cancer markers, decrease in the rate of appearance of new lesions, and the like. In various aspects, the methods of the disclosure further comprise monitoring treatment in the subject. Any improvement in the subject's well being is contemplated (e.g., absence of clinically detectable disease, any decrease (such as at least about a 50% decrease) in measurable tumor burden (i.e., the number of malignant cells present in the subject or the measured bulk of tumor masses) in the absence of new lesions, reduction in pain, improvement in urination).

[0237] Treatment according to the present disclosure includes a "therapeutically effective amount" of the medicaments used. A "therapeutically effective amount" refers to an amount effective, at dosages and for periods of time necessary, to achieve a desired therapeutic result. A therapeutically effective amount may vary according to factors such as the disease state, age, sex, and weight of the individual, and the ability of the medicaments to elicit a desired response in the individual. A therapeutically effective amount is also one in which any toxic or detrimental effects are outweighed by the therapeutically beneficial effects. A "therapeutically effective amount" for tumor therapy may also be measured by its ability to stabilize the progression of disease. An exemplary, non-limiting range for a therapeutically effective amount of an antigen-binding protein of the present disclosure is about 0.1-100 mg/kg. Parenteral compositions may be formulated in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subjects to be treated; each unit contains a predetermined quantity of therapeutic calculated to produce the desired biological effect in association with the required pharmaceutical carrier.

[0238] In some embodiments the antigen-binding protein (e.g., a monospecific antibody or heterodimeric antibody) is used in combination with one or more additional therapeutic agents, e.g., a chemotherapeutic agent or immunotherapy agent. The additional therapeutic agent(s) may be administered serially (within minutes, hours, days, or weeks of each other) or in parallel; they also may be administered to the patient in a pre-mixed single composition.

[0239] Non-limiting examples of DNA damaging chemotherapeutic agents include topoisomerase I inhibitors (e.g., irinotecan, topotecan, camptothecin and analogs or metabolites thereof, and doxorubicin); topoisomerase II inhibitors (e.g., etoposide, teniposide, and daunorubicin); alkylating agents (e.g., melphalan, chlorambucil, busulfan, thiotepa, ifosfamide, carmustine, lomustine, semustine, streptozocin, decarbazine, methotrexate, mitomycin C, and cyclophosphamide); DNA intercalators (e.g., cisplatin, oxaliplatin, epirubicin, and carboplatin); DNA intercalators and free radical generators such as bleomycin; and nucleoside mimetics (e.g., 5-fluorouracil, capecitibine, gemcitabine, fludarabine, cytarabine, mercaptopurine, thioguanine, pentostatin, and hydroxyurea).

[0240] Chemotherapeutic agents that disrupt cell replication include, but are not limited to, paclitaxel, docetaxel, and related analogs; cabzitaxel; vincristine, vinblastin, and related analogs; thalidomide, lenalidomide, and related analogs (e.g., CC-5013 and CC-4047); protein tyrosine kinase inhibitors (e.g., imatinib mesylate and gefitinib); proteasome inhibitors (e.g., bortezomib); NF-κB inhibitors, including inhibitors of IκB kinase; antibodies which bind to proteins overexpressed in cancers and thereby downregulate cell replication (e.g., trastuzumab, rituximab, cetuximab, and bevacizumab); and other inhibitors of proteins or enzymes known to be upregulated, over-expressed or activated in cancers, the inhibition of which downregulates cell replication.

[0241] In some embodiments, the antigen-binding protein (e.g., a monospecific antibody or heterodimeric antibody) of the disclosure can be used prior to, concurrent with, or after treatment with docetaxol. In various aspects, the antigen-binding protein (e.g., monospecific antibody or heterodimeric antibody) is administered as part of a treatment plan that includes surgery and/or radiation (e.g., external beam or brachytherapy).

[0242] In various aspects, the antigen-binding protein (e.g., a monospecific antibody or heterodimeric antibody) is provided as part of a treatment plan that also includes administration of hormone therapy (e.g., androgen-deprivation therapy, such as agents that block the release or production of luteinizing-hormone releasing hormone (e.g., leuprolide,

goserelin, triptorelin, or degarelix), anti-androgens (e.g., bicalutamide, flutamide, or nilutamide), ketoconazole, abiraterone acetate, enzalutamide)),

[0243] In various aspects, the antigen-binding protein (e.g., a monospecific antibody or heterodimeric antibody) is provided as part of a treatment plan that also includes administration of another immunotherapy (e.g., sipuleucel-T, bevacizumab, atezolizumab, avelumab, ipilimumab, tremelimumab, AM-224, MDX-1105, eftilagimod alpha (IMP321), or enoblituzumab (MGA271)). In this regard, the method optionally comprises administration of another antigen-binding protein that targets a different antigen, such as a cancer-related antigen or an antigen associated with an immune response. For example, in various embodiments, the anti-STEAP1 antigen-binding protein is administered to a subject alongside a PD-1 targeting antigen-binding protein (e.g., antibody) that decreases, blocks, inhibits, abrogates, or interferes with signal transduction resulting from the interaction of PD-1 with one or more of its binding partners, such as PD-L1 or PD-L2. In a specific aspect, the PD-1 antigen-binding protein inhibits the binding of PD-1 to PD-L1 and/or PD-L2. In one embodiment, a PD-1 antigen-binding protein reduces the negative co-stimulatory signal mediated by or through cell surface proteins expressed on T lymphocytes mediated signaling through PD-1 so as render a dysfunctional T-cell less dysfunctional (e.g., enhancing effector responses to antigen recognition). Examples of anti-PD-1 antibodies include nivolumab (BMS-936558), pembrolizumab (MK-3475), BMS 936558, BMS- 936559, TSR-042 (Tesaro), ePDR001 (Novartis), and pidilizumab (CT-011). While the disclosure references PD-1 antigen-binding proteins, the disclosure also contemplates use of other PD-1 binding antagonists that decrease, block, inhibit, abrogate, or interfere with signal transduction resulting from the interaction of PD-1 with one or more of its binding partners, such as PD-L1 or PD-L2.

[0244] The disclosure provided herein with respect to anti-STEAP1 antigen-binding proteins also applies to anti-PD-1 antigen-binding proteins. For example, in various instances, the anti-PD-1 antigen-binding protein is an antibody, such as a monoclonal IgG. The anti-PD-1 antibody, antigen-binding antibody fragment thereof, or anti-PD-1 antibody protein product is a monovalent or bivalent. In exemplary aspects, the anti-PD-1 antibody, antigen-binding antibody fragment thereof, or anti-PD-1 antibody protein product binds to human PD-1, which has the amino acid sequence of SEQ ID NO: 187. In exemplary aspects, the anti-PD-1 antibody, antigen-binding antibody fragment thereof, or anti-PD-1 antibody protein product binds to cynomolgus PD-1, which has the amino acid sequence of SEQ ID

NO: 188. In exemplary instances, the anti-PD-1 antibody, antigen-binding antibody fragment thereof, or anti-PD-1 antibody protein product binds to both human PD-1 and cynomolgus PD-1.

[0245] In exemplary embodiments, the binding strength of the anti-PD-1 antibody, antigen-binding antibody fragment thereof, or anti-PD-1 antibody protein product to PD-1 may be described in terms of KD. In exemplary aspects, the KD of the anti-PD-1 antibody, antigen-binding antibody fragment thereof, or anti-PD-1 antibody protein product provided herein is about 10^{-1} M, about 10^{-2} M, about 10^{-3} M, about 10^{-4} M, about 10^{-5} M, about 10^{-6} M, about 10^{-7} M, about 10^{-8} M, about 10^{-9} M, or less. In exemplary aspects, the KD of the anti-PD-1 antibody, antigen-binding antibody fragment thereof, or anti-PD-1 antibody protein product provided herein is micromolar, nanomolar, picomolar, or femtomolar. In exemplary aspects, the KD of the anti-PD-1 antibody, antigen-binding antibody fragment thereof, or anti-PD-1 antibody protein product provided herein is within a range of about 10^{-4} to 10^{-6} M, or 10^{-7} to 10^{-9} M, or 10^{-10} to 10^{-12} M, or 10^{-13} to 10^{-15} M. In exemplary aspects, the anti-PD-1 antibody, antigen-binding antibody fragment thereof, or anti-PD-1 antibody protein product has high affinity for human PD-1, cynomolgus PD-1, or both. In exemplary aspects, the anti-PD-1 antibody, antigen-binding antibody fragment thereof, or anti-PD-1 antibody protein product has a KD for human PD-1 of less than 100 pM, optionally, about 1 pM to about 50 pM. In exemplary aspects, the anti-PD-1 antibody, antigen-binding antibody fragment thereof, or anti-PD-1 antibody protein product has a KD for human PD-1 within about 1 pM to about 20 pM or less than about 10 pM. In exemplary aspects, the anti-PD-1 antibody, an antigen-binding antibody fragment thereof, or anti-PD-1 antibody protein product has a KD for cynomolgus PD-1 of less than 100 pM, optionally, about 1 pM to about 75 pM. In exemplary aspects, the anti-PD-1 antibody, antigen-binding antibody fragment thereof, or anti-PD-1 antibody protein product has a KD for cynomolgus PD-1 within about 1 pM to about 20 pM or less than 10 pM.

[0246] In exemplary aspects, the anti-PD-1 antibody, antigen-binding antibody fragment thereof, or anti-PD-1 antibody protein product inhibits at least 50% of the binding interactions between PD-1 and PD-L1 or PD-L2. In exemplary aspects, the anti-PD-1 antibody, antigen-binding antibody fragment thereof, or anti-PD-1 antibody protein product exhibits at least about 50%, at least about 60%, or at least about 70% inhibition of the binding interaction between PD-1 and PD-L1 or PD-L2.

[0247] In exemplary instances, the anti-PD-1 antibody, antigen-binding antibody fragment thereof, or anti-PD-1 antibody protein product inhibits PD-1-mediated production of IL-2 by T cells in a mixed lymphocyte reaction (MLR). In exemplary aspects, the IC50 of the anti-PD-1 antibody, antigen-binding antibody fragment thereof, or anti-PD-1 antibody protein product in the MLR is within about 0.1 nM to about 5 nM. In exemplary aspects, the IC50 of the anti-PD-1 antibody, antigen-binding antibody fragment thereof, or anti-PD-1 antibody protein product in the MLR is less than 2 nM or less than 1 nM. In exemplary aspects, the IC50 of the anti-PD-1 antibody, antigen-binding antibody fragment thereof, or anti-PD-1 antibody protein product in the MLR is about 0.5 nM to about 2 nM.

[0248] Methods of testing antibodies for the ability to bind to PD-1 are known in the art and include any suitable antibody-antigen binding assay, such as, for example, radioimmunoassay (RIA), ELISA, Western blot, immunoprecipitation, SPR, and competitive inhibition assays (see, e.g., Janeway et al., infra, and U.S. Patent Application Publication No. 2002/0197266, and the above section relating to competition assays). Other binding assays, e.g., competitive binding assays or competition assays, which test the ability of an antibody to compete with a second antibody for binding to an antigen or to an epitope thereof can be used to test the ability of an antibody to bind to PD-1. See, e.g., U.S. Patent Application Publication No. 2014/0178905; Chand et al., Biologicals 46: 168-171 (2017); Liu et al., Anal Biochem 525: 89-91 (2017); and Goolia et al., J Vet Diagn Invest 29(2): 250-253 (2017). Also, other methods of comparing two antibodies are known in the art, and include, for example, surface plasmon resonance (SPR). SPR can be used to determine the binding constants of the antibody and second antibody and the two binding constants can be compared. The disclosure contemplates use of an anti-PD1 antigen-binding protein that competes with, or cross-blocks, the binding of any of the anti-PD-1 antibodies described herein to the PD-1 protein in the context of the disclosed method.

[0249] A representative method for characterizing human and cynomolgus monkey PD-1 binding affinity is as follows. Antibodies are incubated in wells containing a 3-fold serial dilution of soluble, recombinant receptors human PD-1(1-170)-FLAG-His or cynomolgus monkey PD-1(1-167)-FLAG-His. In both cases, a top PD-1 concentration of 30 nM may be selected. Association for 300 seconds and dissociation for 500 seconds may be used, as these parameters typically produce enough curvature for accurate kinetic fits. Human/cynomolgus monkey PD-1 binding affinities may be quantitated with ForteBio Octet HTX and RED384 instruments. Standard Octet sample buffer may be used for sample dilution and binding

baseline, association, and dissociation steps (e.g., 10 mM Tris, pH 7.5, 150 mM NaCl, 1 mM CaCl2, 0.10 mg.ml BSA, 0.13% (v/v) Triton X-100). ForteBio raw data may be processed in the following manner using the standard instrument data analysis software (v9 and v10): (a) two reference curves which have immobilized target but no interaction (i.e., buffer only) are averaged and subtracted from the remaining sample curves in the same column; (b) the association and dissociation curves are isolated and aligned to the Y axis; (c) the association and dissociation interstep are aligned; (d) Savitzky-Golay filtering is implemented to reduce the signal noise and (e) the resulting set of association and dissociation curves for each sample-target interaction are globally fit with a single 1:1 binding model to determine the measured values of the association rate constant ka and the dissociation rates constants kd; the equilibrium dissociation constant KD is calculated as a ratio of the dissociation and association rates constants (= kd/ka).

[0250] In exemplary instances, the anti-PD-1 antibody (or antigen-binding antibody fragment thereof or antibody protein product) comprises the heavy chain (HC) complementarity-determining region 1 (vhCDR1) amino acid sequence set forth in SEQ ID NO: 189, the HC CDR2 (vhCDR2) amino acid sequence set forth in SEQ ID NO: 190, the HC CDR3 (vhCDR3) amino acid sequence set forth in SEQ ID NO: 191, the light chain (LC) CDR1 (vlCDR1) amino acid sequence set forth in SEQ ID NO: 192, the LC CDR2 (vlCDR2) amino acid sequence set forth in SEQ ID NO: 193, and the LC CDR3 (vlCDR3) amino acid sequence set forth in SEQ ID NO: 194. In exemplary embodiments, the anti-PD-1 antibody (or antigen-binding antibody fragment thereof or antibody protein product) comprises a heavy chain variable region (vh) comprising an amino acid sequence that is at least 90% identical (e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical) to the amino acid sequence of SEQ ID NO: 195 and/or a light chain variable region (vl) comprising an amino acid sequence that is at least 90% identical (e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical) to the amino acid sequence of SEQ ID NO: 196. In exemplary embodiments, the anti-PD-1 antibody (or antigen-binding antibody fragment thereof or antibody protein product) comprises a heavy chain comprising an amino acid sequence that is at least 90% identical (e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical) to the amino acid sequence of SEQ ID NO: 197 and/or a light chain comprising an amino acid sequence that is at least 90% identical (e.g., 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical) to the amino acid sequence of SEQ ID NO: 198.

[0251] In exemplary aspects, the anti-STEAP1 construct described herein is part of a treatment regimen that includes administration of a cytokine, lymphokine, growth factor, or hematopoietic factor effective in inhibiting tumor metastasis and/or having an antiproliferative effect on at least one cell population. Such cytokines, lymphokines, growth factors, or other hematopoietic factors include, but are not limited to: M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IL-16, IL-17, IL-18, IFN, TNFα, TNF1, TNF2, G-CSF, Meg-CSF, GM-CSF, thrombopoietin, stem cell factor, and erythropoietin. Additional growth factors include, e.g., angiogenin, bone morphogenic protein-1, bone morphogenic protein-2, bone morphogenic protein-3, bone morphogenic protein-4, bone morphogenic protein-5, bone morphogenic protein-6, bone morphogenic protein-7, bone morphogenic protein-8, bone morphogenic protein-9, bone morphogenic protein-10, bone morphogenic protein-11, bone morphogenic protein-12, bone morphogenic protein-13, bone morphogenic protein-14, bone morphogenic protein-15, bone morphogenic protein receptor IA, bone morphogenic protein receptor IB, brain derived neurotrophic factor, ciliary neutrophic factor, ciliary neutrophic factor receptor α, cytokine-induced neutrophil chemotactic factor 1, cytokine-induced neutrophil, chemotactic factor 2 α, cytokine-induced neutrophil chemotactic factor 2 β, β endothelial cell growth factor, endothelin 1, epithelial-derived neutrophil attractant, glial cell line-derived neutrophic factor receptor α 1, glial cell line-derived neutrophic factor receptor α 2, growth related protein, growth related protein α, growth related protein β, growth related protein γ, heparin binding epidermal growth factor, hepatocyte growth factor, hepatocyte growth factor receptor, insulin-like growth factor I, insulin-like growth factor receptor, insulin-like growth factor II, insulin-like growth factor binding protein, keratinocyte growth factor, leukemia inhibitory factor, leukemia inhibitory factor receptor α, nerve growth factor, nerve growth factor receptor, neurotrophin-3, neurotrophin-4, pre-B cell growth stimulating factor, stem cell factor, stem cell factor receptor, transforming growth factor α, transforming growth factor β, transforming growth factor β1, transforming growth factor β1.2, transforming growth factor β2, transforming growth factor β3, transforming growth factor β5, latent transforming growth factor β1, transforming growth factor β binding protein I, transforming growth factor β binding protein II, transforming growth factor β binding protein III, tumor necrosis factor receptor type I, tumor necrosis factor receptor type II, urokinase-type plasminogen activator receptor, and chimeric proteins and biologically or immunologically active fragments thereof. In exemplary embodiments, the anti-STEAP1 construct is

administered as part of a therapeutic regimen involving administration of an antibody specific for any one of the aforementioned cytokines, lymphokines, growth factors, or other hematopoietic factors.

[0252] The disclosure contemplates use of the anti-STEAP1 antigen-binding protein or a heterodimeric antibody in the preparation of a medicament for treating cancer in a subject in need thereof. Optionally, the medicament is for administering an effective amount of the anti-STEAP1 antigen-binding protein or heterodimeric antibody in association with an effective amount of anti-PD-1 antigen-binding protein (e.g., any of the anti-PD-1 antigen-binding proteins described herein).

[0253] The disclosure further contemplates the anti-STEAP1 antigen-binding protein or heterodimeric antibody described herein for use in treating cancer in a subject in need thereof (i.e., in a method of treating cancer, such as prostate cancer or Ewing sarcoma, in a subject in need thereof). Optionally, the anti-STEAP1 antigen-binding protein or heterodimeric antibody is administered with an anti-PD1 antigen-binding protein. By "administer with" is meant that the anti-STEAP1 antigen-binding protein or heterodimeric antibody is part of a therapeutic regimen that includes administration of an anti-PD1 antigen-binding protein. Indeed, the anti-STEAP1 antigen-binding protein (e.g., heterodimeric antibody) can be used prior to, concurrent with, or after treatment with an anti-PD1 antigen-binding protein. The administration of the anti-STEAP1 antigen-binding protein or heterodimeric antibody and the anti-PD1 antigen-binding protein need not occur simultaneously, although the disclosure contemplates embodiments wherein the components are included in the same pharmaceutical composition and administered together. The disclosure also provides a method of treatment wherein the anti-STEAP1 antigen-binding protein or heterodimeric antibody and the anti-PD1 antigen-binding protein are present in separate pharmaceutical compositions which are administered in parallel or administered near in time. The anti-STEAP1 antigen-binding protein or heterodimeric antibody and the anti-PD1 antigen-binding protein may be administered serially (e.g., within minutes, hours, days, or weeks within each other), in any order. Administration modalities are described above.

[0254] The anti-STEAP1 antigen-binding protein described herein also can be used, for example, in assays to detect the presence of STEAP1, either *in vitro* or *in vivo*. The antigen-binding protein also may be employed to purify STEAP1 by, e.g., immunoaffinity chromatography.

Nucleic Acids, Vectors, Host Cells

[0255] The disclosure further provides nucleic acid compositions encoding the antigen-binding protein (e.g., monospecific antibody or heterodimeric antibody) described herein. The nucleic acids encoding the components of the antigen-binding protein of the disclosure can be incorporated into expression vectors as is known in the art and depending on the host cells used to produce the antigen-binding protein. Examples of expression vectors include, but are not limited to, plasmids, viral vectors, non-episomal mammalian vectors and other expression vectors. Generally, the nucleic acid sequence encoding a desired polypeptide is operably linked to any number of regulatory elements (promoters, origin of replication, selectable markers, ribosomal binding sites, inducers, etc.). The expression vectors can be extra-chromosomal or integrating vectors.

[0256] The nucleic acids and/or expression vectors of the disclosure are optionally introduced into any number of different types of host cells as is well known in the art, including mammalian, bacterial, yeast, insect and/or fungal cells, with mammalian cells (e.g., CHO cells) finding use in many embodiments. In another aspect, the disclosure provides such host cells into which an expression vector encoding an antigen-binding protein has been introduced. Examples of suitable mammalian host cell lines include the COS-7 line of monkey kidney cells (ATCC CRL 1651) (Gluzman et al., 1981, Cell 23:175), L cells, human embryonic kidney 293 cells or derivatives thereof (e.g., HEK293T, HEK293-EBNA), C127 cells, mouse embryo fibroblast cells (3T3 cells) (ATCC CCL 163), Chinese hamster ovary (CHO) cells and derivatives thereof (e.g., CHO-K1, CHO pro-3), mouse myeloma cells (e.g., NS0, GS-NS0, Sp2/0), human cervical cancer cells (HeLa cells), baby hamster kidney (BHK) cells (ATCC CRL 10) cell lines, human bone osteosarcoma epithelial cells U2-OS, adenocarcinomic human alveolar basal epithelial cells (A549), human fibrosarcoma cells (HT1080), mouse brain tumor cells (CAD), embryonic carcinoma cells (P19), mouse neuroblastoma cells (N2a), human breast cancer cells (MCF-7), retinoblastoma cells (Y79), human retinoblastoma cells (SO-Rb50), human liver cancer cells (Hep G2), mouse B myeloma cells (J558L), and African green monkey kidney cells (e.g., COS cells, VERO cells and derivatives thereof (including the CVI/EBNA cell line derived from the African green monkey kidney cell line CVI (ATCC CCL 70) as described by McMahan et al., 1991, EMBO J. 10: 2821)). The transformed cells can be cultured under conditions that promote expression of the antigen-binding protein, and the protein recovered by conventional protein purification procedures. One such purification procedure includes the use of affinity

chromatography, e.g., over a matrix having all or a portion (e.g., one or more extracellular loops) of STEAP1 bound thereto. Antigen-binding proteins contemplated for use herein include substantially homogeneous recombinant antigen-binding proteins substantially free of contaminating endogenous materials.

[0257] With respect to heterodimeric antibodies, in various aspects, a composition is provided which comprises a nucleic acid encoding the first monomer, a nucleic acid encoding the second monomer, and a nucleic acid encoding the common light chain. The disclosure also provides nucleic acid constructs encoding portions of the monomers and common light chain, e.g., the anti-STEAP1 Fab or antibody fragments comprising six CDRs disclosed herein which bind STEAP1, the anti-CD3 scFv, the variable light and/or variable heavy domains that bind STEAP1 and/or CD3, and the like.

[0258] In some embodiments, nucleic acids encoding each monomer and, optionally, the nucleic acid encoding the common light chain, are each contained within a single expression vector, generally under different or the same promoter controls. In various embodiments, each of these two or three nucleic acids are contained on a different expression vector. As described in U.S. Patent Publication No. 2016/0215063 (hereby incorporated by reference in its entirety and particularly with respect to the discussion of recombinant antibody production), different vector ratios can be used to drive heterodimer formation. Surprisingly, in instances where antibody constructs comprise first monomer:second monomer:light chains in a 1:1:2 ratio, these are not necessarily the ratios that give the best results. See Figure 65 of U.S. Patent Publication No. 2016/0215063, incorporated herein by reference. In various aspects, the disclosure provides a nucleic acid composition comprising: a) a first expression vector comprising a first nucleic acid encoding the first monomer; b) a second expression vector comprising a second nucleic acid encoding the second monomer; and c) a third expression vector comprising a third nucleic acid encoding the common light chain. In alternative embodiments, the third nucleic acid encoding the common light chain is present on the same expression vector as the first or second nucleic acid.

[0259] The heterodimeric antibodies are optionally made by culturing host cells comprising the expression vector(s). Once produced, antibody purification steps are performed, typically including an ion exchange chromatography step. As discussed herein, having the pIs of the two monomers differ by at least 0.5 can allow separation by ion exchange chromatography or isoelectric focusing, or other methods sensitive to isoelectric point. That is, the inclusion of pI substitutions that alter the isoelectric point (pI) of each

monomer so that such that each monomer has a different pI and the heterodimer also has a distinct pI, thus facilitating isoelectric purification heterodimer (e.g., anionic exchange columns, cationic exchange columns). These substitutions also aid in the determination and monitoring of any contaminating mAb homodimers post-purification (e.g., IEF gels, cIEF, and analytical IEX columns).

Kits

[0260] In some embodiments, the antigen-binding protein of the present disclosure is provided in a kit. In exemplary aspects, the kit comprises the antigen-binding protein as a unit dose (i.e., a discrete amount dispersed in a suitable carrier). In exemplary aspects, the kit comprises several unit doses, e.g., a week or month supply of unit doses, optionally, each of which is individually packaged or otherwise separated from other unit doses. In some embodiments, the components of the kit/unit dose are packaged with instructions for administration to a patient. In some embodiments, the kit comprises one or more devices for administration to a patient, e.g., a needle and delivery device (such as a syringe), and the like. In some aspects, the antigen-binding protein is pre-packaged in a ready to use form, e.g., a syringe, an intravenous bag, etc., although it is also contemplated that the antigen-binding protein may be provided in lyophilized form requiring reconstitution. In some aspects, the kit further comprises other therapeutic or diagnostic agents or pharmaceutically acceptable carriers (e.g., solvents, buffers, diluents, etc.), including any of those described herein.

[0261] All references, including publications, patent applications, and patents, cited herein are hereby incorporated by reference to the same extent as if each reference were individually and specifically indicated to be incorporated by reference and were set forth in its entirety herein.

[0262] The following examples are given merely to illustrate the present disclosure and not in any way to limit its scope.

EXAMPLES

Example 1

[0263] This Example describes detection of STEAP1 at the surface of prostate cancer cells using a monospecific antibody as described above.

[0264] Prostate cancer cells (C4-2B luc cells (Figure 11A) or C4-2B luc $^{STEAP1\ KO}$ cells (Figure 11B)) that were engineered to have lost STEAP1 expression using a CRISPR

construct directed against STEAP1 were incubated with an isotype control antibody or the anti-STEAP1 mouse monoclonal antibody (Ab-Am) at a concentration of 10 μg/mL for 1 h at 4°C. Cell-bound Ab-Am was detected by flow cytometry after incubation with a FITC-conjugated (Figure 11A) or an APC-conjugated anti-mouse IgG secondary antibody (Figure 11B). FITC or APC fluorescence, identifying a STEAP1-dependent signal, were plotted in histograms (solid gray histograms) and compared to the isotype control (white histograms). Results are shown in Figures 11A and 11B.

Example 2

[0265] This Example describes the characterization of anti-STEAP1 antibodies.

[0266] A panel of 22 anti-human STEAP1 mouse monoclonal antibodies was generated. Antibody A demonstrated improved flow cytometry binding properties (parental mAb binding LnCAP(+)/DU145(-) FACS shift (fold)) compared to others tested: Ab-A (60.1), Ab-B (3.6), Ab-C (2.4), and Ab-D (4.3).

[0267] To determine the region of STEAP1 recognized by an antibody of the disclosure, chimeric constructs were generated wherein each of three extracellular loops of STEAP1 was replaced with the corresponding region of STEAP2 and expressed in 293 cells. Ab-A binds STEAP1 and does not bind STEAP2. Replacing extracellular loops 1 and 3 of STEAP1 with the corresponding loops from STEAP2 abrogated binding, while Ab-A binding to STEAP1 was not destroyed when extracellular loop 2 was replaced with the STEAP2 counterpart. Ab-A appears to bind to STEAP1 outside of extracellular loop 2.

[0268] Heterodimeric antibodies comprising the STEAP-1 binding arm of Ab-A1, Ab-A2 (N67Q), and Ab-B1 and an anti-CD3 binding arm were prepared in the "XmAb" format as described in, e.g., U.S. Patent Publication No. 2016/0215063. These heterodimeric antibodies displayed TDCC activity (pM): Ab-A1x (273.8), Ab-A2x (387.9), and Ab-B1x (128.7).

Example 3

[0269] This Example compares binding (characterized by EC50) of an anti-STEAP1/anti-CD3 bispecific antibody (XmAb) with a different scaffold with the heterodimeric anti-STEAP1/anti-CD3 of the disclosure ($Xmab^{2+1}$) to C4-2B cells.

[0270] Three anti-STEAP1 humanized antibodies (Ab-A1, Ab-A2(N67Q) and Ab-B1) in the "XmAb" format were generated as described in, e.g., U.S. Patent Publication No. 2016/0215063 (incorporated by reference herein, particularly with respect to the discussion of

"bottle opener" formats). The XmAb format entails a first heavy chain comprising a Fc domain attached to an anti-CD3 scFv; a second heavy chain comprising an Fc domain and a first variable heavy domain; and a light chain comprising a variable light domain and a constant light domain. The variable heavy domain and said variable light domain bind to STEAP1. Two anti-STEAP1 humanized antibodies were generated in the heterodimeric XmAb^{2+1} format (Ab-A1 XmAb^{2+1} and Ab-B1 XmAb^{2+1}). The CDR sequences of Ab-A1 XmAb^{2+1} and Ab-B1 XmAb^{2+1} are set forth in SEQ ID NOs: 11-16 (Ab-A1 XmAb^{2+1}) and SEQ ID NOs: 30-35 (Ab-B1 XmAb^{2+1}). A variant of Ab-A1 XmAb^{2+1} having a N67Q modification, designated herein as Ab-A2(N67Q) XmAb^{2+1} was also generated. The CDR sequences of Ab-A2(N67Q) XmAb^{2+1} are set forth in SEQ ID NOs: 11-13, 14, 16 and 21. The antibody designations Ab-A2 and Ab-A2(N67Q) XmAb^{2+1} are used interchangeably herein. The ability of the heterodimeric bispecific antibodies to bind to STEAP1 expressed on the surface of C4-2B prostate cancer cells was assessed, alongside three mouse anti-STEAP1 antibodies in the XmAb format (Ab-Mx1, Ab-Mx2, and Ab-Mx3) that had not been humanized.

[0271] C4-2B-Luc cells were incubated with increasing concentrations of Ab-A1 XmAb^{2+1}, Ab-A1 Xmab, Ab-B1 Xmab, Ab-Mx1, Ab-Mx2 and Ab-Mx3 up to 5 μM, for 1 hour at 4°C. Cell-bound antibodies were detected by flow cytometry after incubation with an APC-conjugated anti-human IgG secondary antibody and mean fluorescence intensity (MFI) of the APC channel at increasing concentrations of respective antibodies tested. As shown in Table 3, Ab-A1 Xmab^{2+1} demonstrated cell binding that was 65-fold lower than the binding EC50 of the same binder in the XmAb format (i.e., Ab-A1 Xmab), demonstrating very strong avidity beyond that of the corresponding XmAb. The XmAb^{2+1} format considerably improved binding of the Ab-A binder to STEAP1 expressed on prostate cancer cells.

Table 3. Binding EC50 of anti-STEAP XmAb and anti-STEAP Xmab $^{2+1}$ to C4-2B cells

Antibody molecule	EC50 (nM)
Ab-A1 Xmab	144.0
Ab-B1 Xmab	798.1
Ab-Mx1	1226
Ab-Mx2	1252
Ab-Mx3	5005
Ab-A1 XmAb^{2+1}	2.203

[0272] The experiment was repeated with Ab-A in various formats (Ab-A (traditional, monospecific antibody, not humanized), Ab-A1 XmAb format, Ab-A1 Xmab $^{2+1}$ format, and Ab-A2(N67Q) Xmab $^{2+1}$ format (with N67Q modification)) and Ab-B XmAb format. C4-2B-Luc cells were incubated with increasing concentrations of anti-STEAPI XmAb or XmAb^{2+1} molecules up to 5 μM, for one hour at 4°C. Cell-bound XmAb were detected by flow cytometry after incubation with an APC-conjugated anti-human IgG secondary antibody and mean fluorescence intensity (MFI) of the APC channel at increasing concentrations of respective anti-STEAPI XmAb molecules were displayed. Results are shown in Figures 12A-12C and Figure 13 and Table 4 below.

Table 4. Binding EC50 to C4-2B luc cells

Format	STEAP1 Binder	Binder Species	EC_{50} (nM)
mAb	Ab-A	Mouse	1.2
XmAb	Ab-A1 Xmab	Humanized	144
XmAb^{2+1}	Ab-A1 XmAb^{2+1}	Humanized	2.2
XmAb^{2+1}	AbA2-(N67Q) XmAb^{2+1}	Humanized	1.2
XmAb	Ab-B1 XmAb	Humanized	48.9

[0273] The antibodies all bound STEAP1 regardless of heterodimeric format. The XmAb^{2+1} format demonstrated improved binding to STEAP1 compared to other antibody formats.

[0274] TDCC activity also was evaluated using methods similar to those described above. All tested antibodies displayed TDCC activity, with antibodies in the XmAb^{2+1} demonstrating better activity than Xmab antibodies: Ab-A XmAb (EC50=274 pM, EC90=438 pM), Ab-A1 Xmab (EC50=388 pM, EC90=722 pM), Ab-B1 Xmab (EC50=129 pM, EC90=265 pM), Ab-A1 Xmab $^{2+1}$ (EC50=6 pM, EC90=11 pM), and Ab-B1 Xmab $^{2+1}$ (EC50=19 pM, EC90=43 pM).

Example 5

[0275] This Example characterizes lysis of human tumor cell line C4-2B luc by human T cells mediated by anti-STEAP1 XmAb and XmAb^{2+1}.

[0276] C4-2B luc prostate cancer cells were co-cultivated with human pan-T cells at an E:T cell ratio of 10 to 1 and increasing concentrations of (Figure 14A) Ab-A1 XmAb, (Figure 14B) Ab-A1 XmAb^{2+1}, or (Figure 14C) Ab-A2(N67Q) XmAb^{2+1} format (with N67Q

substitution) for 48 hours. Target cell lysis was monitored by luciferase activity measurement and the specific cytotoxicity was plotted at each concentration in comparison with no XmAb control conditions. As shown in Figures 14A-14C, Ab-A1 Xmab, Ab-A1 $XmAb^{2+1}$, and Ab-A2(N67Q) $XmAb^{2+1}$ were successful in mediating target cell lysis.

Example 6

[0277] This Example demonstrates the ability of a heterodimeric antibody of the disclosure to distinguish between STEAP1-expressing cells and cells which do not express STEAP.

[0278] STEAP1-positive C4-2B luc prostate cancer cells (●) and STEAP1-negative C4-2B $luc^{STEAP1\ KO}$ cells (■) were co-cultivated with human pan-T cells at an E:T cell ratio of 10 to 1 and increasing concentrations of Ab-A1 $XmAb^{2+1}$ for 48 hours. Target cell lysis was monitored by luciferase activity measurement, and the specific cytotoxicity was plotted at each concentration in comparison with control conditions (lacking XmAb). The results are shown in Figure 15 and Table 5 below. Ab-A1 $XmAb^{2+1}$ dose-dependently mediated target cell lysis of human tumor cell line C4-2B luc, but not C4-2B luc cells modified to knock out STEAP1 expression.

Table 5. T cell dependent cellular cytotoxicity (TDCC) EC50 against C4-2B luc and C4-2B $luc^{STEAP1KO}$ with anti-STEAP1 XmAb (Ab-A1 XmAb) and $XmAb^{2+1}$ (Ab-A1 and Ab-A2(N67Q)) variants

Format	**STEAP1 Binder**	**Binder Species**	**Target Cell Line**	**TDCC EC_{50} (pM)**
XmAb	Ab-A1	Humanized	C4-2B luc	324.9
$XmAb^{2+1}$	Ab-A1	Humanized		6.3
$XmAb^{2+1}$	Ab-A2(N67Q)	Humanized		5.4
$XmAb^{2+1}$	Ab-A1	Humanized	C4-2B $luc^{STEAP1KO}$	> 10,000

[0279] Additionally, 293T cells stably transfected with human STEAP1(Figure 16A) or parental 293T cells (Figure 16B) were incubated with an isotype control antibody or the anti-STEAP1 Ab-A mouse monoclonal antibody (Ab-Am; no bispecific format) at a concentration of 10 μg/mL for 1 h at 4°C. Cell-bound Ab-Am was detected by flow cytometry after incubation with a FITC-conjugated anti-mouse IgG secondary antibody (Figure 16A). FITC

fluorescence, identifying a STEAP1-dependent signal, was plotted in histograms (solid gray histograms) and compared to the isotype control (white histograms). As shown in Figures 16A and 16B, Ab-Am detected STEAP-1 expressed in both cell populations tested.

[0280] Figure 16C illustrates the results of co-cultivating STEAP1-stable 293T cells (●) and STEAP1-negative parental 293T cells (■) with human pan-T cells at an E:T cell ratio of 10 to 1 and increasing concentrations of Ab-A2(N67Q) $XmAb^{2+1}$ for 48 hours. Target cell lysis was monitored by luciferase activity measurement, and the specific cytotoxicity was plotted at each concentration in comparison with no XmAb control conditions. Results are shown in Figures 16A-16C and Table 6 below. The anti-STEAP1/anti-CD3 heterodimeric antibody selectively mediated cell lysis of STEAP1-expressing cells.

Table 6. T cell dependent cellular cytotoxicity (TDCC) EC50 against 293T cells stably transfected with human STEAP1 and parental 293T cells with Ab-A2-N67Q $XmAb^{2+1}$

Molecule Format	**STEAP1 Binder**	**Binder Species**	**Target Cell Line**	**TDCC EC_{50} (pM)**
$XmAb^{2+1}$	Ab-A2(N67Q)	Humanized	293T / STEAP1	0.1
$XmAb^{2+1}$	Ab-A2(N67Q)	Humanized	293T / Parental	> 10,000

[0281] STEAP1-positive C4-2B luc prostate cancer cells also were co-cultivated with human pan-T cells at an E:T cell ratio of 10 to 1 and increasing concentrations of Ab-B1 Xmab (●) or Ab-B1 $XmAb^{2+1}$ (■) for 48 hours. As shown in Figure 17A, Ab-B1 Xmab and Ab-B1 $XmAb^{2+1}$ mediated target cell lysis of C4-2B luc prostate cancer cells.

[0282] C4-2B luc prostate cancer cells were co-cultivated with human pan-T cells at an E:T cell ratio of 10 to 1 and increasing concentrations of $XmAb^{2+1}$ Ab-B1-G37A ($XmAb^{2+1}$ with G37A substitution) (■), $XmAb^{2+1}$ Ab-B1-S39A ($XmAb^{2+1}$ format with S39A substitution) (▲), or $XmAb^{2+1}$ Ab-B1-G37A/S39A ($XmAb^{2+1}$ format with both G37A and S39A substitutions) (▼) for 48 hours. As shown in Figure 17B, Ab-B1 variants (i.e., Ab-B1-G37A, Ab-B1-S39A, and Ab-B1-G37A/S39A) mediated target cell lysis of C4-2B luc prostate cancer cells. See also Table 7 below. Similarly, STEAP1-negative C4-2B $luc^{STEAP1\ KO}$ cancer cells were co-cultivated with human pan-T cells at an E:T cell ratio of 10 to 1 and increasing concentrations of Ab-B1 $XmAb^{2+1}$ (●), Ab-B1-G37A (■), Ab-B1-S39A (▲), or Ab-B1-G37A/S39A (▼) for 48 hours. Target cell lysis was monitored by luciferase activity measurement and the specific cytotoxicity was plotted at each concentration in comparison

with no XmAb control conditions. Results are shown in Figure 17C and Table 7 below. The anti-STEAP1/anti-CD3 heterodimeric antibody selectively mediated cell lysis of STEAP1-expressing cells, and the XmAb^{2+1} format of the disclosure outperformed other formats.

Table 7. T cell dependent cellular cytotoxicity (TDCC) EC50 against C4-2B luc and C4-2B luc^{STEAP1KO} with Ab-B1 variants

Molecule Format	**STEAP1 Binder**	**Target Cell line**	**TDCC EC_{50} (pM)**
XmAb	Ab-B1	C4-2B luc	326.2
XmAb^{2+1}	Ab-B1		111.9
XmAb^{2+1}	Ab-B1-G37A		42.5
XmAb^{2+1}	Ab-B1-S39A		34.9
XmAb^{2+1}	Ab-B1-G37A/S39A		184.8
XmAb^{2+1}	Ab-B1	C4-2B luc$^{STEAP1\ KO}$	>10,000
XmAb^{2+1}	Ab-B1-G37A		>10,000
XmAb^{2+1}	Ab-B1-S39A		>10,000
XmAb^{2+1}	Ab-B1-G37A/S39A		>10,000

Example 7

[0283] This Example characterizes the equilibrium binding constant (KD) of a heterodimeric antibody of the disclosure, Ab-A2(N67Q) XmAb^{2+1}, for human and cynomolgus CD3ε.

[0284] The affinity Ab-A2(N67Q) XmAb^{2+1} for recombinant human or cynomolgus CD3ε was measured using surface plasmon resonance (SPR - Pioneer FE). Recombinant human CD3ε-Fc and cynomolgus CD3ε-Fc were immobilized on a CM5 chip surface using standard amine coupling procedure at ~ 60 RU. Ab-A2(N67Q) XmAb^{2+1} was injected concentrations of 100, 33.3, 11.1 and 3.7 nM. The association and dissociation rates of Ab-A2(N67Q) XmAb^{2+1} interaction to the ligands were recorded for 120 sec and 300 sec, respectively, as set forth below in Table 8. The equilibrium dissociation constant (K_D) values were derived as a ratio of the dissociation rate constant and the association rate constant (k_{off}/k_{on}).

Table 8. Association and dissociation rates of Ab-A2-N67Q XmAb^{2+}interaction with human and cynomolgus CD3. "a" denotes data generated using BIAcore® and "b" denotes data generated using Octet

Molecule Format	STEAP1 Binder	Measurement Method	K_D to human CD3ε (nM)	K_D to cynomolgus CD3ε (nM)
XmAb^{2+1}	Ab-A2(N67Q)	SPR	16.3^{a} to 27.6^{b}	15.1^{a} to 25.8^{b}

Example 8

[0285] This Example demonstrates that a heterodimeric antibody of the disclosure (Ab-A2(N67Q) XmAb^{2+1}) mediates lysis of target cells displaying a range of STEAP1 surface densities.

[0286] STEAP-1 density at the surface of various target cell lines (SNU-5, C4-2B, Sk-N-MC, LOX-IMVI, VCaP, IM-95, TYKNU, 22RV-1, HBSCM, HUCCT1, PC3, HCT116 and NCIH1869) was evaluated. See Table 9 below, which identifies the STEAP1 density (number of STEAP I antibody binding sites per cell) in column 3 as measured using the Dako Qifikit method.

Table 9. STEAP1 surface density and T cell dependent cellular cytotoxicity (TDCC) EC50 and EC90

Cell Line	Tissue of Origin	STEAP1 (Qifikit)	EC50 (pM)	EC90 (pM)
SNU5	Stomach	220,612	6.2	13.7
C4-2B	Prostate	150,072	6.8	16.1
SK-N-MC	Neuroblastoma	19,057	10.4	33.9
LOX-IMVI	Skin	9,765	36.6	112
VCaP	Prostate	8,148	722	9,904
IM-95	Stomach	7,824	344.7	1,643
TYKNU	Ovary	6,293	1,716	>10,000
22RV-1	Prostate	5,671	257.3	1,604
HBSMC	Smooth Muscle	~5,000	1,517.5	>10,000
HUCCT1	Biliary Tract	4,295	>10,000	>10,000
PC3	Prostate	~4,000	>10,000	>10,000
HCT116	Colon	3,785	336	1,796
NCIH1869	Lung	1,915	>10,000	>10,000

[0287] In a separate study, STEAP-1 density at the surface of OE33, EBC1, and A673 cell lines was evaluated. See Table 10 below, which identifies the STEAP1 density (number of STEAP I antibody binding sites per cell) in column 3 as measured using the Dako Qifikit method.

Cell Line	Tissue of Origin	STEAP1 (Qifikit)	EC50 (pM)	EC90 (pM)
OE33	Esophagus	83,303	145	3,022
EBC1	Lung	32,718	162	2,741
A673	Bone	25,241	122	1,587

[0288]

[0289] T cells from a human donor were incubated with the target cell lines, alongside increasing concentrations of the Ab-A2 (N67Q)XmAb^{2+1} molecule for 48 hours at 37 °C. After 48 hours, target cell viability was measured using steady glo (B) or cell titer glo to measure cell viability. Ab-A2(N67Q) XmAb^{2+1} killed all the cell lines with varying EC90.

[0290] Ab-A2 (N67Q) XmAb^{2+1} is capable of killing cancer cell lines with STEAP1 densities ranging from ~200,000 STEAP1 receptors per cell (SNU5 cell line) down to ~10,000 STEAP1 receptors per cell (LOX-IMV cell line). The potency of Ab-A2 (N67Q) XmAb^{2+1} decreases when the STEAP1 receptor density drops below 10,000 per cell. In this regard, Ab-A2 (N67Q) XmAb^{2+1} preferentially mediates T cell dependent killing of cells with a surface density of STEAP1 of greater than 10,000 (e.g., the EC90 is at least 10-fold less for cells with a surface density of STEAP1 of greater than 10,000 compared to cells having a surface density of STEAP1 less than 10,000).

[0291] The differential killing of cancer cells was assessed with other antibodies in the Xmab^{2+1} format (Ab-B-G52A XmAb^{2+1} and mouse antibody Ab-Cm XmAb^{2+1}) compared to Ab-A2-N67G XmAb^{2+1}. Ab-A2-N67G XmAb^{2+1} demonstrated differential killing between high- and low-STEAP1-expressing cells, whereas Ab-B-G52A XmAb^{2+1} did not discriminate between high- and low-STEAP1-expressing cells, instead killing every STEAP1 expressing cell. See Table 11. Ab-A2-N67G XmAb^{2+1} spares normal cells which express STEAP1 at lower levels (i.e., lower than 10,000/cell), such as HSMBC (primary human smooth muscle bronchial cells).

Table 11. Ab-B1 XmAb^{2+1} and Ab-Cm XmAb^{2+1} kill high- and low-STEAP1-expressing cells.

Ab (XmAb^{2+1})	C4-2B-Luc ~ 150,000 R/C		C4-2B K-O ~ 0 R/C		LOX-IMVI ~10,000 R/C		IM95-Luc ~8,000 R/C	
	Ec50 (pM)	EC90 (pM)	Ec50 (pM)	EC90 (pM)	Ec50 (pM)	EC90 (pM)	Ec50 (pM)	EC90 (pM)
Ab-A2-N67G	5	19.4	>30,000	>30,000	47.1	445.2	344.7	1,643
Ab-B1-G52A	48.9	205	>30,000	>30,000	22	45.6	13.2	37.7

Ab-Cm	23.3	64.3	>30,000	>30,000	27.6	464.7	6.6	21.1

Ab (XmAb^{2+1})	**HCT116-Luc ~ 4,000 R/C**		**HSMBC ~ 4,000 R/C**		**OVCARB Below FACS Detection**		**NB-4-Luc o R/C – No mRNA**	
	Ec50 (pM)	**EC90 (pM)**	**Ec50 (pM)**	**EC90 (pM)**	**Ec50 (pM)**	**EC90 (pM)**	**Ec50 (pM)**	**EC90 (pM)**
Ab-A2-N67G	336	1,796	2,008	>6000	3,623	12,946	>30,000	>30,000
Ab-B1-G52A	43.6	207.4	27.5	108	80.5	609	>30,000	>30,000
Ab-Cm	11.6	75.8	48.5	109.2	18.7	207.9	>30,000	>30,000

Example 9

[0292] This Example demonstrates that T-cell dependent cellular cytotoxicity is enhanced using a combination of an anti-CD3/anti-STEAP1 heterodimeric antibody described herein with an anti-PD-1 antibody.

[0293] *Generation of PD-L1 overexpression cell lines*: GP2-293 cells were cultured in DMEM media supplemented with 10% fetal bovine serum, 1% Pen/Strep, 1% HEPES, and 1% GlutaMAX. Cells were plated at 75% confluency in 10 cm dishes and incubated at 37°C, 5% CO_2 overnight. The next morning, cells were transfected. To tube A, 45 µL of Lipofectamine 3000 and 500 µL of OptiMEM media were added. To tube B, 15 µg of MSCV_GFP_PD-L1 plasmid, 1.8 µg of VSV-g plasmid, 30 µL P3000 reagent, and 500 µL of OptiMEM media were added. Tubes A and B were mixed and incubated at room temperature for 10 minutes. The mixture was added dropwise to dishes of GP2-293 cells which were incubated at 37°C, 5% CO_2 overnight. The next morning, the media was removed and replaced with 10 mL of fresh culture media. That afternoon, target cells were plated at 75% confluence in 6 well plates and incubated at 37°C, 5% CO_2 overnight. The following morning, viral supernatants were collected from GP2-293 cells and centrifuged (5 minutes, 1200 rpm). Supernatants were collected in a new tube, and polybrene was added at 1:1000. Media was removed from plates containing target cells and 2 mL of viral supernatant was added. For suspension cells, 1E6 cells were centrifuged at 1500 rpm for 5 minutes, resuspended in 500 µL RPMI supplemented with 10% fetal bovine serum and 1% pen/strep, and plated in 6 wells plates to which was added 2 mL of viral supernatant. Plates containing target cells and viral supernatants were centrifuged for 1.5 hours at 1200 x g at 32°C then incubated at 37°C, 5% CO_2. Culture media was added after 5 hours. Four days later, cells

were analyzed for GFP and PD-L1 expression by flow cytometry with a FACSymphony. PD-L1 was detected using a PE-conjugated antibody, clone 29E.2A3. Cells < 70% positive for PD-L1 expression were sorted on a BD Melody sorter to select for cells expressing high levels of PD-L1.

[0294] *T cell dependent cellular cytotoxicity (TDCC) assay*: Ab-A2 (N67Q) XmAb^{2+1} was diluted in cell culture media (RPMI, 10% heat inactivated fetal bovine serum, 1X GlutaMAX, 1X Pen/Strep), serially diluted (1:3, 22 total) and transferred to black, clear bottom 384-well plates using a Bravo liquid handling robot. Human pan T cells (n = 4), pre-activated with CD3/CD28 Dynabeads (1:1, 48 hours) were separated from beads using a magnet and diluted in cell culture media. (An aliquot of activated T cells from each donor was assessed for PD-1 expression by flow cytometry. Cells were stained as described above and data was collected on a FACSymphony flow cytometer and analyzed using FlowJo v10.1.) Activated T cells (2500 cells/20 µL; 4 rows/donor) followed by target cells overexpressing PD-L1 were plated in 384-well assay plates (2500 cells/20 µL; full plate) such that the final effector to target cell (E:T) ratio was 1:1. An anti-PD-1 antibody of the disclosure comprising CDR sequences of SEQ ID NOs: 189-194 (10 µg/mL final in 5 µL) was added to two rows of each T cell donor. Plates were covered with MicroClime lids and incubated at 37°C, 5% CO_2 for 24 hours. For assays with target cells expressing luciferase, 30 µL of Steady-Glo, Bright-Glo, or One-Glo reagent (Promega) was added. Plates with adherent target cells not expressing luciferase were washed with PBS to remove T cells using EL406 plate washer and 25 µL Cell Titer Glo reagent was added. Plates were incubated with reagent for 10 minutes in the dark at room temperature. Luminescence was detected using a BioTek Neo plate reader. Specific cytotoxicity was calculated relative to target cells incubated with T cells without Ab-A2 XmAb^{2+1}. Graphpad Prism software was used to plot dose curves and calculate EC50 values with four parameter variable slope curve fitting.

[0295] The results of the TDCC assay are illustrated in Figures 20A and 20B. The combination of Ab-A2 (N67Q) XmAb^{2+1} and anti-PD-1 antibody demonstrated enhanced cytotoxicity and reduced EC50 compared to Ab-A2 (N67Q) XmAb^{2+1} alone.

Example 10

[0296] This Example demonstrates the ability of a heterodimeric antibody of the disclosure (e.g., Ab-A2 (N67Q) XmAb^{2+1}) to reduce Ewing sarcoma tumor volumes *in vivo*.

[0297] Sub-lethally irradiated NOD/SCID female immuno-compromised mice were transplanted with $5x10^6$ cells STEAP1-expressing SK-N-MC tumor cells on day 1. On day 8, $2x10^7$ CD3+ human T cells were injected intra-peritoneally. Ab-A2 (N67Q) $XmAb^{2+1}$ or vehicle control was administered by intravenous (IV) bolus injection at 0.01, 0.1 or 1 mg/kg on days 12, 19 and 26. Tumor volume data over time are presented graphically (Figure 22).

[0298] Ab-A2 (N67Q) $XmAb^{2+1}$ induced an initial tumor regression with relative tumor volumes (RTV) being < 1 in all dose groups between days 15 and 22, while the RTV of vehicle-treated animals increased continuously until study end. Tumors from animals receiving the lowest dose of Ab-A2 (N67Q) $XmAb^{2+1}$ (0.01 mg/kg) started to regrow after day 22, while the mean RTV for mice treated with higher Ab-A2 (N67Q) $XmAb^{2+1}$ doses (0.1 and 1 mg/kg) were < 1 until days 28 and 25, respectively (Table 12).

Table 12. Relative Tumor Volumes as Compared to Day 11

Dose Group	Parameter	Day 11	Day 13	Day 15	Day 18	Day 20	Day 22	Day 25	Day 28
2. Vehicle	Mean	1.00	1.19	1.36	1.88	2.40	2.93	3.89	5.29
	SEM	0.00	0.05	0.05	0.13	0.20	0.30	0.39	0.45
1. Vehicle w/o T cells	Mean	1.00	1.07	1.46	1.88	2.87	3.48	4.17	5.02
	SEM	0.00	0.02	0.14	0.17	0.44	0.32	0.39	0.52
3. Ab-A2 $XmAb^{2+1}$ (1.0 mg/kg)	Mean	1.00	1.09	0.91	0.51	0.47	0.37	0.41	0.61
	SEM	0.00	0.05	0.07	0.13	0.17	0.19	0.27	0.46
4. Ab-A2 $XmAb^{2+1}$ (0.1 mg/kg)	Mean	1.00	1.03	0.79	0.49	0.42	0.27	0.51	1.13
	SEM	0.00	0.07	0.06	0.05	0.06	0.07	0.22	0.39
5. Ab-A2 $XmAb^{2+1}$ (0.01 mg/kg)	Mean	1.00	1.18	0.86	0.75	0.63	0.93	2.46	4.24
	SEM	0.00	0.09	0.08	0.08	0.08	0.15	0.35	0.54

[0299] Between day 15 and day 22, p-values < 0.001 were achieved at all Ab-A2 (N67Q) $XmAb^{2+1}$ dose levels, and after day 22, p-values < 0.001 were achieved at the 0.1 and 1 mg/kg Ab-A2 (N67Q) $XmAb^{2+1}$ doses, when compared to vehicle-treated control group 2 (Figure 23). On day 28, tumors of vehicle-treated mice (group 2) had on average 5.29-times larger volumes relative to their starting volumes before treatment initiation, while the group mean RTV in the Ab-A2 (N67Q) $XmAb^{2+1}$-treated groups were 0.61 (group 3), 1.13 (group 4) and 4.24 (group 5) (Table 1). At the end of the in-life phase on day 28, 9/10 animals in the highest Ab-A2 (N67Q) $XmAb^{2+1}$ dose group (group 3) were considered tumor-free with tumor growth inhibition (TGI) of 97% (Table 13).

Table 13. Tumor Growth Inhibition (Tumor Volumes)

Dose Group	Parameter	Day 11	Day 13	Day 15	Day 18	Day 20	Day 22	Day 25	Day 28
2. Vehicle	Median	196.61	225.01	253.27	348.93	468.93	590.08	837.07	955.14
	T/C (%)	100	100	100	100	100	100	100	100
1. Vehicle w/o T cells	Median	203.63	229.86	286.81	323.09	563.09	598.48	673.42	885.10
	T/C (%)	104	102	113	93	120	101	80	93
	TGI (%)	-4	-2	-13	7	-20	-1	20	7
3. Ab-A2 XmAb^{2+1} (1.0 mg/kg)	Median	197.87	206.94	166.09	78.41	59.90	33.53	27.07	29.77
	T/C (%)	101	92	66	22	13	6	3	3
	TGI (%)	-1	8	34	78	87	94	97	97
4. Ab-A2 XmAb^{2+1} (0.1 mg/kg)	Median	197.59	198.67	144.59	88.07	76.73	41.56	55.86	106.87
	T/C (%)	100	88	57	25	16	7	7	11
	TGI (%)	0	12	43	75	84	93	93	89
5. Ab-A2 XmAb^{2+1} (0.01 mg/kg)	Median	200.97	217.31	150.74	121.75	115.60	202.07	431.89	867.08
	T/C (%)	102	97	60	35	25	34	52	91
	TGI (%)	-2	3	40	65	75	66	48	9

[0300] Thus, in clinically relevant xenograft model, Ab-A2 (N67Q) XmAb^{2+1} exhibited compelling anti-tumor activity.

WHAT IS CLAIMED IS:

1. An antigen-binding protein that binds STEAP1 of SEQ ID NO: 2 and comprises:

(a) heavy chain CDRs comprising amino acid sequences that differ by no more than 3, 2, or 1 amino acid from i) vhCDR1 SEQ ID NO: 14, vhCDR2 SEQ ID NO: 15 or vhCDR2 SEQ ID NO: 21, and vhCDR3 SEQ ID NO: 16, or ii) vhCDR1 SEQ ID NO: 33, vhCDR2 SEQ ID NO: 34, and vhCDR3 SEQ ID NO: 35; or

(b) light chain CDRs comprising amino acid sequences that differ by no more than 3, 2, or 1 amino acid from i) vlCDR1 SEQ ID NO: 11, vlCDR2 SEQ ID NO: 12, and vlCDR3 SEQ ID NO: 13; or ii) vlCDR1 SEQ ID NO: 30, vlCDR2 SEQ ID NO: 31, and vlCDR3 SEQ ID NO: 32; or

(c) a light chain variable domain comprising an amino acid sequence at least 90% identical to SEQ ID NO: 183 or SEQ ID NO: 186; or

(d) a heavy chain variable domain comprising an amino acid sequence at least 90% identical to SEQ ID NO: 182, SEQ ID NO: 184, or SEQ ID NO: 185.

2. The antigen-binding protein of claim 1, comprising CDR sequences

a) vhCDR1 comprising SEQ ID NO: 14, vhCDR2 comprising SEQ ID NO: 15 or SEQ ID NO: 21, and vhCDR3 comprising SEQ ID NO:16; or

b) vhCDR1 comprising SEQ ID NO:33, vhCDR2 comprising SEQ ID NO: 34, and vhCDR3 comprising SEQ ID NO: 35.

3. The antigen-binding protein of claim 1 or claim 2, comprising CDR sequences selected from

a) vlCDR1 comprising SEQ ID NO: 11, vlCDR2 comprising SEQ ID NO: 12, and vlCDR3 comprising SEQ ID NO: 13; or

b) vlCDR1 comprising SEQ ID NO: 30, vlCDR2 comprising SEQ ID NO: 31, and vlCDR3 comprising SEQ ID NO: 32.

4. The antigen-binding protein of any one of claims 1-3, comprising

vhCDR1 comprising SEQ ID NO: 14,

vhCDR2 comprising SEQ ID NO: 15 or SEQ ID NO: 21,

vhCDR3 comprising SEQ ID NO: 16,

vlCDR1 comprising SEQ ID NO: 11,
vlCDR2 comprising SEQ ID NO: 12, and
vlCDR3 comprising SEQ ID NO: 13.

5. The antigen-binding protein of any one of claims 1-3, comprising vhCDR1 comprising SEQ ID NO: 33, vhCDR2 comprising SEQ ID NO: 34, vhCDR3 comprising SEQ ID NO: 35, vlCDR1 comprising SEQ ID NO: 30, vlCDR2 comprising SEQ ID NO: 31, and vlCDR3 comprising SEQ ID NO: 32.

6. The antigen-binding protein of any one of claims 1-3, comprising a variable heavy domain comprising SEQ ID NO: 182, SEQ ID NO: 184, or SEQ ID NO: 185.

7. The antigen-binding protein of any one of claims 1-3, comprising a variable light domain comprising SEQ ID NO: 183 or SEQ ID NO: 186.

8. The antigen-binding protein of any one of claims 1-3, comprising a variable heavy domain comprising SEQ ID NO: 182 or SEQ ID NO: 184 and a variable light domain comprising SEQ ID NO: 183.

9. The antigen-binding protein of any one of claims 1-3, comprising a variable heavy domain comprising SEQ ID NO: 185 and a variable light domain comprising SEQ ID NO: 186.

10. An antigen-binding protein that cross-blocks the binding of a reference antigen-binding protein of any one of claims 1-9 to STEAP1 or which is cross-blocked from binding to STEAP1 by a reference antigen-binding protein any one of claims 1-9.

11. The antigen-binding protein of claim 10, wherein the cross-blocking is detected by surface plasmon resonance or ELISA.

12. The antigen-binding protein of claim 10, which does not bind extracellular loop 2 of STEAP1.

13. The antigen-binding protein of claim 10, which preferentially mediates T cell dependent killing of cells with a surface density of STEAP1 of greater than 10,000.

14. An antigen-binding protein which binds a region of STEAP1 within amino acids 92-118 and amino acids 279-290.

15. The antigen-binding protein of any one of claims 1-14, wherein the antigen-binding protein is an antibody.

16. The antigen-binding protein of claim 15, which is a monoclonal antibody, a chimeric antibody, or a humanized antibody.

17. The antigen-binding protein of any one of claims 1-14, wherein the antigen-binding protein is an antigen-binding antibody fragment.

18. The antigen-binding protein of any one of claims 1-14, comprising a single chain antibody, a diabody, a triabody, a tetrabody, or a domain antibody.

19. A pharmaceutical composition comprising the antigen-binding protein of any one of claims 1-18 and a physiologically acceptable carrier.

20. The pharmaceutical composition of claim 19, further comprising an anti-PD-1 antigen-binding protein comprising a vhCDR1 comprising the amino acid sequence set forth in SEQ ID NO: 189, a vhCDR2 comprising the amino acid sequence set forth in SEQ ID NO: 190, a vhCDR3 comprising the amino acid sequence set forth in SEQ ID NO: 191, a vlCDR1 comprising the amino acid sequence set forth in SEQ ID NO: 192, a vhCDR2 comprising the amino acid sequence set forth in SEQ ID NO: 193, and a vl CDR3 comprising the amino acid sequence set forth in SEQ ID NO: 194.

21. A method of treating cancer, the method comprising administering to a subject in need thereof the antigen-binding protein of any one of claims 1-18.

22. The method of claim 21, further comprising administering to the subject an anti-PD-1 antigen-binding protein.

23. Use of the antigen-binding protein of any one of claims 1-18 in the preparation of a medicament for treating cancer in a subject in need thereof.

24. The use of claim 23, wherein the medicament is for administering an effective amount of the anti-STEAP1 antigen-binding protein in association with an effective amount of an anti-PD-1 antigen-binding protein.

25. The antigen-binding protein of any one of claims 1-18 for use in treating cancer in a subject in need thereof.

26. The antigen-binding protein for use of claim 25, wherein the antigen-binding protein is administered with an anti-PD1 antigen-binding protein.

27. The method, use, or antigen-binding protein for use of claim 22, 24, or 26, wherein the anti-PD1 antigen-binding protein comprises a vhCDR1 comprising the amino acid sequence set forth in SEQ ID NO: 189 a vhCDR2 comprising the amino acid sequence set forth in SEQ ID NO: 190, a vhCDR3 comprising the amino acid sequence set forth in SEQ ID NO: 191, a vlCDR1 comprising the amino acid sequence set forth in SEQ ID NO: 192, a vhCDR2 comprising the amino acid sequence set forth in SEQ ID NO: 193, and a vl CDR3 comprising the amino acid sequence set forth in SEQ ID NO: 194.

28. The method, use, or antigen-binding protein for use of claim 27, wherein the anti-PD1 antigen-binding protein comprises a heavy chain variable domain comprising an amino acid sequence at least 90% identical to the amino acid sequence of SEQ ID NO: 195 and a light chain variable domain comprising an amino acid sequence at least 90% identical to the amino acid sequence of SEQ ID NO: 196.

29. The method, use, or antigen-binding protein for use of claim 28, wherein the anti-PD1 antigen-binding protein comprises a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 195and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 196.

30. The method, use, or antigen-binding protein for use of any one of claims 27-29, wherein the anti-PD-1 antigen-binding protein is an antigen-binding antibody fragment.

31. The method, use, or antigen-binding protein for use of any one of claims 27-29, wherein the anti-PD-1 antigen-binding protein is an antibody.

32. The method, use, or antigen-binding protein for use of any one of claims 27-29, wherein the anti-PD-1 antigen-binding protein is a monoclonal antibody, a chimeric antibody, or a humanized antibody.

33. The method, use, or antigen-binding protein for use of any one of claims 27-31, wherein the anti-PD1 antigen-binding protein comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 197 and a light chain comprising the amino acid sequence of SEQ ID NO: 198.

34. The method, use, or antigen-binding protein for use of any one of claims 21-33, wherein the cancer is prostate cancer.

35. The method, use, or antigen-binding protein for use of any one of claims 21-33, wherein the cancer is Ewing sarcoma.

36. A polynucleotide comprising a nucleic acid sequence encoding the light chain variable domain and/or heavy chain variable domain of the antigen-binding protein of any one of claims 1-14.

37. An expression vector comprising the polynucleotide of claim 36.

38. A composition comprising a polynucleotide comprising a nucleic acid sequence encoding the light chain variable domain of the antigen-binding protein of any one of claims 1-14 and a polynucleotide comprising a nucleic acid sequence encoding the heavy chain variable domain of the antigen-binding protein of any one of claims 1-14.

39. A method of making an antigen-binding protein, the method comprising contacting a host cell with the polynucleotide of claim 36 or the composition of claim 38 under conditions that allow expression of the light chain variable domain and the heavy chain variable domain.

40. A bispecific antigen-binding protein comprising the antigen-binding protein of any one of claims 1-14.

41. The bispecific antigen-binding protein of claim 40, which binds STEAP1 and CD3.

42. The bispecific antigen-binding protein of claim 41, comprising a CD3 binding domain comprising CDR sequences of SEQ ID NOs: 170-172 and 174-176.

43. A heterodimeric antibody comprising:

a) a first monomer comprising a first heavy chain comprising:

1) a first variable heavy domain;

2) a first constant heavy chain comprising a first CH1 domain and a first Fc domain;

3) a scFv that binds human CD3 and comprises a scFv variable light domain, an scFv linker and a scFv variable heavy domain; wherein said scFv is covalently attached between the C-terminus of said CH1 domain and the N-terminus of said first Fc domain using domain linker(s);

b) a second monomer comprising a second heavy chain comprising a second variable heavy domain and a second constant heavy chain comprising a second Fc domain; and

c) a common light chain comprising a variable light domain and a constant light domain;

wherein said first variable heavy domain and said variable light domain bind human STEAP1, said second variable heavy domain and said variable light domain bind human STEAP1, and wherein

(i) the first variable heavy domain and the second variable heavy domain comprise heavy chain CDRs comprising amino acid sequences that differ by no more than 3, 2, or 1 amino acid from (a) vhCDR1 SEQ ID NO: 14, (b) vhCDR2 SEQ ID NO: 15 or SEQ ID NO: 21, and (3) vhCDR3 SEQ ID NO: 16, and the variable light domain comprises light chain CDRs comprising amino acid sequences that differ by no more than 3, 2, or 1 amino acid from vlCDR1 SEQ ID NO: 11, vlCDR2 SEQ ID NO: 12, and vlCDR3 SEQ ID NO: 13; or

(ii) the first variable heavy domain and the second variable heavy domain comprise heavy chain CDRs comprising amino acid sequences that differ by no more than 3, 2, or 1 amino acid from vhCDR1 SEQ ID NO: 33, vhCDR2 SEQ ID NO: 34, and vhCDR3

SEQ ID NO: 35, and the variable light domain comprises light chain CDRs comprising amino acid sequences that differ by no more than 3, 2, or 1 amino acid from vlCDR1 SEQ ID NO: 30, vlCDR2 SEQ ID NO: 31, and vlCDR3 SEQ ID NO: 32; or

(iii) the first variable heavy domain and the second variable heavy domain comprise an amino acid sequence at least 90% identical to SEQ ID NO: 182 or 184 and the variable light domain comprises an amino acid sequence at least 90% identical to SEQ ID NO: 183; or

(iv) the first variable heavy domain and the second variable heavy domain comprise an amino acid sequence at least 90% identical to SEQ ID NO: 185 and the variable light domain comprises an amino acid sequence at least 90% identical to SEQ ID NO: 186.

44. The heterodimeric antibody of claim 43, wherein the first monomer comprises amino acid substitutions E233P, L235V, G236A, S267K, R292C, N297G, V302C, E357Q, and S364K; the second monomer comprises the amino acid substitutions N208D, E233P, L235V, G236A, S267K, R292C, Q295E, N297G, V302C, L368D, K370S, N384D, Q418E, and N421D; and both monomers comprise a deletion at position 234.

45. The heterodimeric antibody of claim 43 or claim 44, wherein said scFv comprises

(i) a variable heavy domain comprising heavy chain CDRs comprising amino acid sequences that differ by no more than 3, 2, or 1 amino acid from vhCDR1 SEQ ID NO: 170, vhCDR2 SEQ ID NO: 171, and vhCDR3 SEQ ID NO: 172, and a variable light domain comprising light chain CDRs comprising amino acid sequences that differ by no more than 3, 2, or 1 amino acid from vlCDR1 SEQ ID NO: 174, vlCDR2 SEQ ID NO:175, and vlCDR3 SEQ ID NO: 176; or

(ii) a variable heavy domain comprising an amino acid sequence at least 90% identical to SEQ ID NO:169 and a variable light domain comprising an amino acid sequence at least 90% identical to SEQ ID NO: 173.

46. The heterodimeric antibody of claim 43 or claim 44, wherein said scFv comprises CDRs comprising vhCDR1 comprising SEQ ID NO: 170, vhCDR2 comprising SEQ ID NO: 171, vhCDR3 comprising SEQ ID NO: 172, vlCDR1 comprising SEQ ID NO:174, vlCDR2 comprising SEQ ID NO: 175, and vlCDR3 comprising SEQ ID NO: 176.

47. The heterodimeric antibody of any one of claims 43-45, wherein said scFv comprises a variable heavy region and a variable light region of SEQ ID NO:169 and SEQ ID NO:173.

48. The heterodimeric antibody of any one of claims 43-47, wherein said scFv has a charged scFv linker.

49. The heterodimeric antibody of claim 48, wherein the charged scFv linker has a positive charge from 3 to 8 and is selected from the group consisting of SEQ ID NOs: 143 to 153.

50. The heterodimeric antibody of claim 48, wherein the scFv linker comprises SEQ ID NO: 152.

51. The heterodimeric antibody of any one of claims 43-47, wherein said scFv comprises the sequence of SEQ ID NO: 44.

52. The heterodimeric antibody of any one of claims 43-51, wherein the first variable heavy domain and the second variable heavy domain comprise CDR sequences vhCDR1 comprising SEQ ID NO: 14, vhCDR2 comprising SEQ ID NO: 15 or SEQ ID NO: 21, vhCDR3 comprising SEQ ID NO: 16, and wherein the variable light domain comprises CDR sequences vlCDR1 comprising SEQ ID NO: 11, vlCDR2 comprising SEQ ID NO: 12, and vlCDR3 comprising SEQ ID NO: 13.

53. The heterodimeric antibody of any one of claims 43-51, wherein the first variable heavy domain and the second variable heavy domain comprise CDR sequences vhCDR1 comprising SEQ ID NO: 33, vhCDR2 comprising SEQ ID NO: 34, vhCDR3 comprising SEQ ID NO: 35, and wherein the variable light domain comprises CDR sequences vlCDR1 comprising SEQ ID NO: 30, vlCDR2 comprising SEQ ID NO: 31, and vlCDR3 comprising SEQ ID NO: 32.

54. The heterodimeric antibody of any of claims 43-51, wherein the first variable heavy domain and the second variable heavy domain comprise SEQ ID NO: 182 or SEQ ID NO: 184 and the variable light domain comprises SEQ ID NO: 183.

55. The heterodimeric antibody of any of claims 43-51, wherein the first variable heavy domain and the second variable heavy domain comprise SEQ ID NO: 185 and the variable light domain comprises SEQ ID NO: 186.

56. The heterodimeric antibody of claim 52 or claim 53 comprising the amino acid substitution N67Q and/or a substitution at one or more of positions 292, 297, or 302.

57. The heterodimeric antibody of claim 43, wherein

a) the first monomer comprises the sequence of SEQ ID NO: 19 or SEQ ID NO: 20, the second monomer comprises the sequence of SEQ ID NO:18 or 199, and the common light chain comprises the sequence of SEQ ID NO:17; or

b) the first monomer comprises the sequence of SEQ ID NO: 38, the second monomer comprises the sequence of SEQ ID NO: 37, and the common light chain comprises the sequence of SEQ ID NO:36.

58. The heterodimeric antibody of claim 43, wherein

a) the first monomer comprises the sequence of SEQ ID NO: 202, the second monomer comprises the sequence of SEQ ID NO: 201, and the common light chain comprises the sequence of SEQ ID NO:200;

b) the first monomer comprises the sequence of SEQ ID NO: 207, the second monomer comprises the sequence of SEQ ID NO: 203, and the common light chain comprises the sequence of SEQ ID NO:200; or

c) the first monomer comprises the sequence of SEQ ID NO: 206, the second monomer comprises the sequence of SEQ ID NO: 205, and the common light chain comprises the sequence of SEQ ID NO:204.

59. A nucleic acid composition comprising:

a) a first nucleic acid encoding the first monomer of any one of claims 43-58;

b) a second nucleic acid encoding the second monomer of any one of claims 43-58 and

c) a third nucleic acid encoding the common light chain of any one of claims 43-58.

60. A nucleic acid composition comprising:

a) a first expression vector comprising a first nucleic acid encoding the first monomer of any one of claims 43-58;

b) a second expression vector comprising a second nucleic acid encoding the second monomer of any one of claims 43-58; and

c) a third expression vector comprising a third nucleic acid encoding the common light chain of any one of claims 43-58.

61. A host cell comprising the nucleic acid composition of claim 59 or claim 60.

62. A pharmaceutical composition comprising the heterodimeric antibody of any one of claims 43-58.

63. A method of treating a subject in need thereof, the method comprising administering to the subject the heterodimeric antibody of any one of claims 43-58.

64. A method of treating cancer in a subject in need thereof, the method comprising administering to the subject the heterodimeric antibody of any one of claims 43-58.

65. The method of claim 63 or claim 64, further comprising administering to the subject an anti-PD-1 antigen-binding protein.

66. Use of the heterodimeric antibody of any one of claims 43-58 in the preparation of a medicament for treating cancer in a subject in need thereof.

67. The use of claim 66, wherein the medicament is for administering an effective amount of the heterodimeric antibody in association with an effective amount of an anti-PD-1 antigen-binding protein.

68. The heterodimeric antibody of any one of claims 43-58 for use in treating cancer in a subject in need thereof.

69. The heterodimeric antibody for use of claim 68, wherein the heterodimeric antibody is administered with an anti-PD1 antigen-binding protein.

70. The method, use, or antigen-binding protein for use of any one of claims 65, 67, or 69, wherein the anti-PD1 antigen-binding protein comprises a vhCDR1 comprising the amino acid sequence set forth in SEQ ID NO: 189, a vhCDR2 comprising the amino acid sequence set forth in SEQ ID NO: 190, a vhCDR3 comprising the amino acid sequence set forth in SEQ ID NO: 191, a vlCDR1 comprising the amino acid sequence set forth in SEQ ID NO: 192, a vhCDR2 comprising the amino acid sequence set forth in SEQ ID NO: 193, and a vl CDR3 comprising the amino acid sequence set forth in SEQ ID NO: 194.

71. The method, use, or antigen-binding protein for use of claim 70, wherein the anti-PD1 antigen-binding protein comprises a heavy chain variable domain comprising an amino acid sequence at least 90% identical to the amino acid sequence of SEQ ID NO: 195 and a light chain variable domain comprising an amino acid sequence at least 90% identical to the amino acid sequence of SEQ ID NO: 196.

72. The method, use, or antigen-binding protein for use of claim 71, wherein the anti-PD1 antigen-binding protein comprises a heavy chain variable domain comprising the amino acid sequence of SEQ ID NO: 195 and a light chain variable domain comprising the amino acid sequence of SEQ ID NO: 196.

73. The method, use, or heterodimeric antibody for use of any one of claims 70-72, wherein the anti-PD-1 antigen-binding protein is an antigen-binding antibody fragment.

74. The method, use, or heterodimeric antibody for use of any one of claims 70-72, wherein the anti-PD-1 antigen-binding protein is an antibody.

75. The method, use, or heterodimeric antibody for use of any one of claims 70-72, wherein the anti-PD-1 antigen-binding protein is a monoclonal antibody, a chimeric antibody, or a humanized antibody.

76. The method, use, or heterodimeric antibody for use of any one of claims 70-75, wherein the anti-PD1 antigen-binding protein comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 197 and a light chain comprising the amino acid sequence of SEQ ID NO: 198.

77. The method, use, or heterodimeric antibody for use of any one of claims 70-75, wherein the anti-PD1 antigen-binding protein comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 208 and a light chain comprising the amino acid sequence of SEQ ID NO: 209.

78. The method, use, or heterodimeric antibody for use of any one of claims 64-77, wherein the cancer is prostate cancer.

79. The method, use, or heterodimeric antibody for use of any one of claims 64-77, wherein the cancer is Ewing sarcoma.