(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
25 January 2018 (25.01.2018)

WIPO | PCT

(10) International Publication Number
WO 2018/014260 A1

(51) International Patent Classification:
C07K 16/46 (2006.01) *C07K 16/24* (2006.01)
C07K 16/18 (2006.01) *A61K 39/395* (2006.01)
C07K 16/28 (2006.01) *A61P 35/00* (2006.01)
C07K 16/30 (2006.01) *A61P 37/00* (2006.01)

(21) International Application Number:
PCT/CN2016/090703

(22) International Filing Date:
20 July 2016 (20.07.2016)

(25) Filing Language: English

(26) Publication Language: English

(71) Applicant: **NANJING LEGEND BIOTECH CO., LTD.** [CN/CN]; No.6 Building of Nanjing Life Science Town, No. 568 Longmian Avenue, Jiangning District, Nanjing, Jiangsu 211100 (CN).

(72) Inventors: **CHOU, Chuan-Chu**; 909 Prospect Street, Westfield, New Jersey 07090 (US). **ZHANG, Yafeng**; 599 Lize Road, Building 35, Room 302, Moling Street, Jiangning District, Nanjing, Jiangsu 211100 (CN). **WU, Shu**; 28 Chengxu Road, Huayu Court, Building 3, Room 501, Moling Street, Jiangning District, Nanjing, Jiangsu 211100 (CN). **LIU, Zhenyu**; 228 Tianyuan East Road, Lai Yin Dong Jun, Yingxia Yuan #15-304, Jiangning District, Nanjing, Jiangsu 211100 (CN). **LI, Zhongdao**; 393 Zhushan South Road, Jiangning District, Nanjing, Jiangsu 211100 (CN). **ZHANG, Fangliang**; No. 28, Yongxi Road, Jiangning District, Nanjing, Jiangsu 211100 (CN).

(74) Agent: **CHENG & PENG INTELLECTUAL PROPERTY LAW OFFICE**; 821 Yufei Plaza, 42 Dongzhimenwai Avenue, Dongcheng District, Beijing 100027 (CN).

(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JP, KE, KG, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Published:
— *with international search report (Art. 21(3))*
— *with sequence listing part of description (Rule 5.2(a))*

WO 2018/014260 A1

(54) Title: MULTISPECIFIC ANTIGEN BINDING PROTEINS AND METHODS OF USE THEREOF

(57) Abstract: Disclosed herein are multispecific, such as bispecific, antigen binding proteins comprising a first antigen binding domain comprising a heavy chain variable domain and a light chain variable domain, and a second antigen binding domain comprising a single-domain antibody. Pharmaceutical compositions comprising the multispecific antigen binding proteins, kits and methods of use thereof are further provided.

MULTISPECIFIC ANTIGEN BINDING PROTEINS AND METHODS OF USE THEREOF

SUBMISSION OF SEQUENCE LISTING ON ASCII TEXT FILE

[0001] The content of the following submission on ASCII text file is incorporated herein by reference in its entirety: a computer readable form (CRF) of the Sequence Listing (file name: 761422000240SEQLIST.txt, date recorded: July 13, 2016, size: 12 KB).

FIELD OF THE INVENTION

[0002] The present invention relates to multispecific antigen binding proteins comprising at least one single-domain antibody and methods of use thereof.

BACKGROUND OF THE INVENTION

[0003] Monoclonal antibodies (mAbs) have been widely used as therapeutic agents to treat a variety of human diseases, such as cancer and autoimmune diseases. Currently, there are more than 30 monoclonal antibodies including murine, fully humanized, and chimeric antibodies that have been approved by the FDA for therapeutic use. Rituximab and trastuzumab are among the top-selling protein therapeutics against cancer. Recently, monoclonal antibodies targeting immune checkpoint molecules, such as ipilimumab and nivolumab, have shown encouraging clinical results by inducing T cell immunity against tumors. As many patients do not respond well to monotherapy approaches, monoclonal antibodies are often combined with other immunomodulatory approaches, such as monoclonal antibodies against other targets, to enhance their efficacy. For example, clinical studies have demonstrated that combination of nivolumab and ipilimumab results in improved rates of objective response among melanoma patients.

[0004] Multispecific (such as bispecific) antibodies are designed to simultaneously modulate two or more therapeutic targets in order to provide enhanced therapeutic efficacy and broadened potential utility. It has been reported that bispecific antibodies can be more effective than simple combination of two monoclonal antibodies. A variety of multispecific antibody formats have been developed. For example, bispecific antibodies have been made by fusing antigen binding (Fab) fragments or single chain variable fragments (scFvs) to monoclonal antibodies (see, for example, Weidle *et al. Cancer Genomics & Proteomics* 2013; 10: 1-18). Multispecific

antibodies of different formats differ in size, are frequently produced by different technologies, and have different *in vivo* distribution, tissue penetration, and pharmacokinetic properties.

[0005] Single-domain antibodies (sdAbs) are antibody fragments each having a single monomeric antibody variable domain. Despite their much smaller sizes than common monoclonal antibodies having two heavy chains and two light chains, sdAbs can bind antigens with similar affinity and specificity as mAbs. Used as building blocks, the sdAbs can be fused to IgG Fc domains to create IgG-like antibodies, including bivalent and bispecific antibodies (see, for example, Hmila I. *et al. Mol. Immunol.* 2008; 45: 3847-3856).

[0006] The disclosures of all publications, patents, patent applications and published patent applications referred to herein are hereby incorporated herein by reference in their entirety.

BRIEF SUMMARY OF THE INVENTION

[0007] The present application provides a multispecific antigen binding protein comprising one or more single-domain antibodies (sdAbs) fused to a full-length four-chain antibody or an antigen binding fragment derived therefrom.

[0008] Accordingly, one aspect of the present application provides a multispecific antigen binding protein comprising: (a) a first antigen binding portion comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a first epitope, and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds a second epitope, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the first epitope and the second epitope are from the same antigen. In some embodiments, the first epitope and the second epitope are from different antigens. In some embodiments, the multispecific antigen binding protein is bispecific.

[0009] In some embodiments according to any one of the multispecific antigen binding proteins described above, the first antigen binding portion is a full-length antibody consisting of two heavy chains and two light chains. In some embodiments, the first antigen binding portion is an antibody fragment comprising a heavy chain comprising the V_H and a light chain comprising the V_L. In some embodiments, the C terminus of the second antigen binding portion is fused to the N-terminus of at least one heavy chain of the first antigen binding portion. In some embodiments, the C terminus of the second antigen binding portion is fused to the N-terminus of at least one light chain of the first antigen binding portion. In some embodiments, the N terminus

of the second antigen binding portion is fused to the C-terminus of at least one heavy chain of the first antigen binding portion. In some embodiments, the N terminus of the second antigen binding portion is fused to the C-terminus of at least one light chain of the first antigen binding portion.

[0010] In some embodiments according to any one of the multispecific antigen binding proteins described above, the first antigen binding portion comprises a human, humanized or chimeric antibody or antigen binding fragment thereof.

[0011] In some embodiments according to any one of the multispecific antigen binding proteins described above, the first antigen binding portion comprises an Fc region. In some embodiments, the Fc region is an IgG1 Fc. In some embodiments, the Fc region is an IgG4 Fc, such as an IgG4 Fc having an S228P mutation.

[0012] In some embodiments according to any one of the multispecific antigen binding proteins described above, the first antigen binding portion and the second antigen binding portion are fused to each other via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20 or 15) amino acids long. In some embodiments, the peptide linker comprises the amino acid sequence of SEQ ID NO: 1. In some embodiments, the first antigen binding portion and the second antigen binding portion are fused to each other chemically.

[0013] In some embodiments according to any one of the multispecific antigen binding proteins described above, the single-domain antibody is a camelid, humanized, or human single-domain antibody.

[0014] In some embodiments according to any one of the multispecific antigen binding proteins described above, the first epitope is from an immune checkpoint molecule. In some embodiments, the immune checkpoint molecule is selected from the group consisting of PD-1, PD-L1, PD-L2, CTLA-4, B7-H3, TIM-3, LAG-3, VISTA, ICOS, 4-1BB, OX40, GITR, and CD40. In some embodiments, the first antigen binding portion is an anti-PD-1 antibody or antigen binding fragment thereof. In some embodiments, the anti-PD-1 antibody is selected from the group consisting of pembrolizumab and nivolumab. In some embodiments, the first antigen binding portion is an anti-PD-L1 antibody or antigen binding fragment thereof. In some embodiments, the anti-PD-L1 antibody is duravalumab or atezolizumab. In some embodiments, the single-domain antibody specifically binds an immune checkpoint molecule, such as an

immune checkpoint molecule selected from the group consisting of PD-1, PD-L1, PD-L2, CTLA-4, B7-H3, TIM-3, LAG-3, VISTA, ICOS, 4-1BB, OX40, GITR, and CD40. In some embodiments, the second antigen binding portion comprises an anti-CTLA-4 single-domain antibody.

[0015] In some embodiments according to any one of the multispecific antigen binding proteins described above, the first epitope is from a tumor antigen. In some embodiments, the tumor antigen is selected from the group consisting of HER2, BRAF, EGFR, VEGFR2, CD20, RANKL, CD38, and CD52. In some embodiments, the first antigen binding portion is an anti-HER2 antibody or antigen binding fragment thereof. In some embodiments, the anti-HER2 antibody is trastuzumab. In some embodiments, the second antigen binding portion comprises an anti-CD3 single-domain antibody.

[0016] In some embodiments according to any one of the multispecific antigen binding proteins described above, the first epitope is from a pro-inflammatory molecule. In some embodiments, the pro-inflammatory molecule is selected from the group consisting of IL-1β, TNF-α, IL-5, IL-6, IL-6R, and eotaxin-1. In some embodiments, the first antigen binding portion is an anti-TNF-α antibody or antigen binding fragment thereof. In some embodiments, the anti-TNF-α antibody is adalimumab. In some embodiments, the second antigen binding portion comprises an anti-IL-1β single-domain antibody. In some embodiments, the first antigen binding portion is an anti-IL-5 antibody or antigen binding fragment thereof. In some embodiments, the anti-IL-5 antibody is mepolizumab. In some embodiments, the second antigen binding portion comprises an anti-eotaxin-1 single-domain antibody.

[0017] Another aspect of the present application provides a pharmaceutical composition comprising any one of the multispecific antigen binding proteins described above and a pharmaceutically acceptable carrier.

[0018] Further provided in one aspect of the present application is a method of treating a disease in an individual, comprising administering to the individual an effective amount of any one of the pharmaceutical compositions described above. In some embodiments, the disease is a cancer. In some embodiments, the cancer is selected from the group consisting of breast cancer, renal cancer, melanoma, lung cancer, glioblastoma, head and neck cancer, prostate cancer, ovarian carcinoma, bladder carcinoma, and lymphoma. In some embodiments, the disease is an inflammatory or autoimmune disease. In some embodiments, the inflammatory or autoimmune

disease is selected from the group consisting of arthritis (such as rheumatoid arthritis, juvenile idiopathic arthritis, psoriatic arthritis, ankylosing spondylitis, and arthritic ulcerative colitis), colitis, psoriasis, severe asthma, and moderate to severe Crohn's disease.

BRIEF DESCRIPTION OF THE DRAWINGS

[0019] FIG. 1 depicts a schematic structure of an exemplary bispecific antigen binding protein comprising a monospecific full-length antibody having two identical heavy chains and two identical light chains, and a single-domain antibody, wherein the N-terminus of the single-domain antibody is fused to the C-terminus of one heavy chain via an optional peptide linker. The full-length antibody has two antigen binding sites that specifically bind the first epitope. The single-domain antibody specifically binds the second epitope.

[0020] FIG. 2 depicts a schematic structure of an exemplary bispecific antigen binding protein comprising a monospecific full-length antibody having two identical heavy chains and two identical light chains, and two identical single-domain antibodies, wherein the two single-domain antibodies are fused to each other, and the N-terminus of one single-domain antibody is fused to the C-terminus of a heavy chain via an optional peptide linker. The full-length antibody has two antigen binding sites that specifically bind the first epitope. The two single-domain antibodies specifically bind the second epitope.

[0021] FIG. 3 depicts a schematic structure of an exemplary trispecific antigen binding protein comprising a monospecific full-length antibody having two identical heavy chains and two identical light chains, a first single-domain antibody, and a second single-domain antibody, wherein the first single-domain antibody and the second single-domain antibody are fused to each other via an optional peptide linker, and the N-terminus of the first single-domain antibody is fused to the C-terminus of a heavy chain via an optional peptide linker. The full-length antibody has two antigen binding sites that specifically bind the first epitope. The first single-domain antibody specifically binds the second epitope. The second single-domain antibody specifically binds the third epitope.

[0022] FIG. 4 depicts a schematic structure of an exemplary trispecific antigen binding protein comprising a monospecific full-length antibody having two identical heavy chains and two identical light chains, and two identical single-domain antibodies, wherein the N-terminus of each single-domain antibody is fused to the C terminus of one heavy chain via an optional peptide linker. The full-length antibody has two antigen binding sites that specifically bind a first

epitope. The two single-domain antibodies specifically bind the second epitope. In alternative formats, each single-domain antibody may be replaced with two copies of the single-domain antibody fused to each other.

[0023] FIG. 5 depicts a schematic structure of an exemplary bispecific antigen binding protein comprising a monospecific Fab having a heavy chain and a light chain, and two identical single-domain antibodies, wherein the N-terminus of a single-domain antibody is fused to the C-terminus of the heavy chain via an optional peptide linker, and the other single-domain antibody is fused to the C-terminus of the light chain of the Fab via an optional peptide linker. The Fab specifically binds the first epitope. The two single-domain antibodies specifically bind the second epitope. In alternative formats, each single-domain antibody may be omitted, or replaced with two identical or different single-domain antibodies fused to each other.

[0024] FIG. 6 depicts a schematic structure of an exemplary trispecific antigen binding protein comprising a bispecific full-length antibody having two heavy chains and two light chains, and two identical single-domain antibodies, wherein the N-terminus of each single-domain antibody is fused to one heavy chain via an optional peptide linker. The full-length antibody has a first antigen binding site that specifically binds the first epitope, and a second antigen binding site that specifically binds the third epitope. The two single-domain antibodies specifically bind to the second epitope. In alternative formats, each single-domain antibody may be omitted, or replaced with two identical or different single-domain antibodies fused to each other.

[0025] FIG. 7 depicts a schematic structure of an exemplary trispecific antigen binding protein comprising a monospecific full-length antibody having two identical heavy chains and two identical light chains, a first single-domain antibody, and a second single-domain antibody, wherein the N-terminus of each single-domain antibody is fused to one heavy chain via an optional peptide linker. The full-length antibody has two antigen binding sites that specifically bind the first epitope. The first single-domain antibody specifically binds the second epitope. The second single-domain antibody specifically binds the third epitope. In alternative formats, each single-domain antibody may be omitted, or replaced with two identical or different single-domain antibodies fused to each other. The monospecific full-length antibody may be replaced with a bispecific full-length antibody to further expand binding specificity.

[0026] FIG. 8 depicts a schematic structure of an exemplary tetraspecific antigen binding protein comprising a bispecific full-length antibody having two heavy chains and two light

chains, a first single-domain antibody, and a second single-domain antibody, wherein the N-terminus of each single-domain antibody is fused to one heavy chain via an optional peptide linker. The full-length antibody has a first antigen binding site that specifically binds the first epitope, and a second antigen binding site that specifically binds the third epitope. The first single-domain antibody specifically binds the second epitope. The second single-domain antibody specifically binds the fourth epitope. In alternative formats, each single-domain antibody may be omitted, or replaced with two identical or different single-domain antibodies fused to each other.

[0027] FIG. 9 depicts a schematic structure of an exemplary bispecific antigen binding protein comprising a monospecific full-length antibody having two identical heavy chains and two identical light chains, and two identical single-domain antibodies, wherein the C-terminus of each single-domain antibody is fused to the N-terminus of one heavy chain. The full-length antibody has two antigen binding sites that specifically bind a first epitope. The two single-domain antibodies specifically bind the second epitope. In alternative formats, each single-domain antibody may be omitted, or replaced with two identical or different single-domain antibodies fused to each other. The monospecific full-length antibody may be replaced with a bispecific full-length antibody to further expand binding specificity.

[0028] FIG. 10 depicts a schematic structure of an exemplary trispecific antigen binding protein comprising a monospecific full-length antibody having two identical heavy chains and two identical light chains, a first single-domain antibody, and a second single-domain antibody, wherein the C-terminus of each single-domain antibody is fused to the N-terminus of one heavy chain. The full-length antibody has two antigen binding sites that specifically bind the first epitope. The first single-domain antibody specifically binds the second epitope. The second single-domain antibody specifically binds the third epitope. In alternative formats, each single-domain antibody may be omitted, or replaced with two identical or different single-domain antibodies fused to each other. The monospecific full-length antibody may be replaced with a bispecific full-length antibody to further expand binding specificity.

[0029] FIG. 11 depicts a schematic structure of an exemplary bispecific antigen binding protein comprising a monospecific full-length antibody having two identical heavy chains and two identical light chains, and two identical single-domain antibodies, wherein the N-terminus of each single-domain antibody is fused to the C-terminus of one light chain via an optional peptide

linker. The full-length antibody has two antigen binding sites that specifically bind a first epitope. The two single-domain antibodies specifically bind the second epitope. In alternative formats, each single-domain antibody may be omitted, or replaced with two identical or different single-domain antibodies fused to each other. The monospecific full-length antibody may be replaced with a bispecific full-length antibody to further expand binding specificity.

[0030] FIG. 12 depicts a schematic structure of an exemplary trispecific antigen binding protein comprising a monospecific full-length antibody having two identical heavy chains and two identical light chains, a first single-domain antibody, and a second single-domain antibody, wherein the N-terminus of each single-domain antibody is fused to the C-terminus of one light chain via an optional peptide linker. The full-length antibody has two antigen binding sites that specifically bind a first epitope. The first single-domain antibody specifically binds the second epitope. The second single-domain antibody specifically binds the third epitope. In alternative formats, each single-domain antibody may be omitted, or replaced with two identical or different single-domain antibodies fused to each other. The monospecific full-length antibody may be replaced with a bispecific full-length antibody to further expand binding specificity.

[0031] FIG. 13 depicts a schematic structure of an exemplary bispecific antigen binding protein comprising a monospecific full-length antibody having two identical heavy chains and two identical light chains, and two identical single-domain antibodies, wherein the C-terminus of each single-domain antibody is fused to the N-terminus of one light chain via an optional peptide linker. The full-length antibody has two antigen binding sites that specifically bind a first epitope. The two single-domain antibodies specifically bind the second epitope. In alternative formats, each single-domain antibody may be omitted, or replaced with two identical or different single-domain antibodies fused to each other. The monospecific full-length antibody may be replaced with a bispecific full-length antibody to further expand binding specificity.

[0032] FIG. 14 depicts a schematic structure of an exemplary trispecific antigen binding protein comprising a monospecific full-length antibody having two identical heavy chains and two identical light chains, a first single-domain antibody, and a second single-domain antibody, wherein the C-terminus of each single-domain antibody is fused to the N-terminus of one light chain via an optional peptide linker. The full-length antibody has two antigen binding sites that specifically bind a first epitope. The first single-domain antibody specifically binds the second epitope. The second single-domain antibody specifically binds the third epitope. In alternative

formats, each single-domain antibody may be omitted, or replaced with two identical or different single-domain antibodies fused to each other. The monospecific full-length antibody may be replaced with a bispecific full-length antibody to further expand binding specificity.

[0033] FIG. 15 depicts a schematic structure of an exemplary trispecific antigen binding protein comprising a monospecific full-length antibody having two identical heavy chains and two identical light chains, two identical first single-domain antibodies, and two identical second single-domain antibodies, wherein the C-terminus of each first single-domain antibody is fused to the N-terminus of one heavy chain via an optional peptide linker, and the N-terminus of each second single-domain antibody is fused to the C-terminus of one heavy chain via an optional peptide linker. The full-length antibody has two antigen binding sites that specifically bind a first epitope. The first single-domain antibody specifically binds the second epitope. The second single-domain antibody specifically binds the third epitope. In alternative formats, each single-domain antibody may be omitted, or replaced with two identical or different single-domain antibodies fused to each other. The monospecific full-length antibody may be replaced with a bispecific full-length antibody to further expand binding specificity.

[0034] FIG. 16 depicts a schematic structure of an exemplary trispecific antigen binding protein comprising a monospecific full-length antibody having two identical heavy chains and two identical light chains, two identical first single-domain antibodies, and two identical second single-domain antibodies, wherein the C-terminus of each first single-domain antibody is fused to the N-terminus of one light chain via an optional peptide linker, and the N-terminus of each second single-domain antibody is fused to the C-terminus of one heavy chain via an optional peptide linker. The full-length antibody has two antigen binding sites that specifically bind a first epitope. The first single-domain antibody specifically binds the second epitope. The second single-domain antibody specifically binds the third epitope. In alternative formats, each single-domain antibody may be omitted, or replaced with two identical or different single-domain antibodies fused to each other. The monospecific full-length antibody may be replaced with a bispecific full-length antibody to further expand binding specificity.

DETAILED DESCRIPTION OF THE INVENTION

[0035] The present application provides a multispecific antigen binding protein comprising a single-domain antibody (sdAb) fused to a full-length antibody or antigen binding fragment that comprise a heavy chain variable domain (V_H) and a light chain variable domain (V_L). The sdAb

specifically binds a target (such as an epitope or antigen) that is distinct from the target(s) recognized by the full-length antibody or antigen binding fragment, thereby conferring a broadened targeting capability. As a building block in a multispecific antigen binding protein, sdAb has several advantages over other antigen binding fragments such as Fab and scFv used in currently known multispecific antibody formats, including, but not limited to, small size, high solubility and stability, weak immunogenicity in human, and ability to target a variety of epitopes. Thus, multispecific antigen binding proteins described herein can have similar molecular weight and pharmacokinetic properties compared to those of the full-length antibody or antigen binding fragment component. For example, a multispecific antigen binding protein can be designed by fusing one or more sdAbs to a monoclonal antibody with proven clinical efficacy and safety to provide increased clinical benefits and desirable pharmacokinetic properties without impeding the expressibility of the multispecific construct. The multispecific antigen binding protein format of the present application can be adopted to target a variety of disease-related epitope or antigen combinations, such as a combination of immune checkpoint molecules, a combination of cell surface antigens (such as tumor antigens), or a combination of pro-inflammatory molecules, thereby providing agents that are useful for treating a variety of diseases and conditions, such as cancer, inflammation, and autoimmune diseases.

[0036] Accordingly, one aspect of the present application provides a multispecific antigen binding protein comprising: (a) a first antigen binding portion comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a first epitope, and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds a second epitope, wherein the first antigen binding portion and the second antigen binding portion are fused to each other.

[0037] One aspect of the present application provides a multispecific antigen binding protein comprising: (a) a first antigen binding portion comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a first immune checkpoint molecule, and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds a second immune checkpoint molecule, wherein the first antigen binding portion and the second antigen binding portion are fused to each other.

[0038] One aspect of the present application provides a multispecific antigen binding protein comprising: (a) a first antigen binding portion comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a first pro-inflammatory molecule, and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds a second pro-inflammatory molecule, wherein the first antigen binding portion and the second antigen binding portion are fused to each other.

[0039] One aspect of the present application provides a multispecific antigen binding protein comprising: (a) a first antigen binding portion comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a first tumor antigen, and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds a cell surface antigen (such as tumor antigen, or a cell surface antigen on an immune effector cell), wherein the first antigen binding portion and the second antigen binding portion are fused to each other.

[0040] Also provided are pharmaceutical compositions, kits and articles manufacture comprising the multispecific antigen binding proteins, and methods of treating a disease using the multispecific antigen binding proteins described herein.

I. Definitions

[0041] The practice of the present invention will employ, unless indicated specifically to the contrary, conventional methods of virology, immunology, microbiology, molecular biology and recombinant DNA techniques within the skill of the art, many of which are described below for the purpose of illustration. Such techniques are explained fully in the literature. See, *e.g.*, Current Protocols in Molecular Biology or Current Protocols in Immunology, John Wiley & Sons, New York, N.Y.(2009); Ausubel *et al*, Short Protocols in Molecular Biology, 3rd ed., Wiley & Sons, 1995; Sambrook and Russell, Molecular Cloning: A Laboratory Manual (3rd Edition, 2001); Maniatis *et al.* Molecular Cloning: A Laboratory Manual (1982); DNA Cloning: A Practical Approach, vol. I & II (D. Glover, ed.); Oligonucleotide Synthesis (N. Gait, ed., 1984); Nucleic Acid Hybridization (B. Hames & S. Higgins, eds., 1985); Transcription and Translation (B. Hames & S. Higgins, eds., 1984); Animal Cell Culture (R. Freshney, ed., 1986); Perbal, A Practical Guide to Molecular Cloning (1984) and other like references.

[0042] As used herein, the term "treatment" refers to clinical intervention designed to alter the natural course of the individual or cell being treated during the course of clinical pathology. Desirable effects of treatment include decreasing the rate of disease progression, ameliorating or palliating the disease state, and remission or improved prognosis. For example, an individual is successfully "treated" by the multispecific antigen binding protein of the present application if one or more symptoms associated with the disease or condition being treated (such as cancer, inflammatory or autoimmune disease) are mitigated or eliminated.

[0043] As used herein, an "effective amount" refers to an amount of an agent or drug effective to treat a disease or condition in a subject. In the case of cancer, the effective amount of the multispecific antigen binding protein of the present application may reduce the number of cancer cells; reduce the tumor size; inhibit (*i.e.*, slow to some extent and preferably stop) cancer cell infiltration into peripheral organs; inhibit (*i.e.*, slow to some extent and preferably stop) tumor metastasis; inhibit, to some extent, tumor growth; and/or relieve to some extent one or more of the symptoms associated with the cancer. As is understood in the clinical context, an effective amount of a drug, compound, or pharmaceutical composition may or may not be achieved in conjunction with another drug, compound, or pharmaceutical composition. Thus, an "effective amount" may be considered in the context of administering one or more therapeutic agents, and a single agent may be considered to be given in an effective amount if, in conjunction with one or more other agents, a desirable result may be or is achieved.

[0044] As used herein, an "individual" or a "subject" refers to a mammal, including, but not limited to, human, bovine, horse, feline, canine, rodent, or primate. In some embodiments, the individual is a human.

[0045] The term "antibody" includes monoclonal antibodies (including full length 4-chain antibodies which have an immunoglobulin Fc region), antibody compositions with polyepitopic specificity, multispecific antibodies (*e.g.*, bispecific antibodies, diabodies, and single-chain molecules, as well as antibody fragments (*e.g.*, Fab, $F(ab')_2$, and Fv). The term "immunoglobulin" (Ig) is used interchangeably with "antibody" herein. Antibodies contemplated herein include heavy-chain only antibodies and single-domain antibodies.

[0046] The basic 4-chain antibody unit is a heterotetrameric glycoprotein composed of two identical light (L) chains and two identical heavy (H) chains. An IgM antibody consists of 5 of the basic heterotetramer units along with an additional polypeptide called a J chain, and contains

10 antigen binding sites, while IgA antibodies comprise from 2-5 of the basic 4-chain units which can polymerize to form polyvalent assemblages in combination with the J chain. In the case of IgGs, the 4-chain unit is generally about 150,000 daltons. Each L chain is linked to an H chain by one covalent disulfide bond, while the two H chains are linked to each other by one or more disulfide bonds depending on the H chain isotype. Each H and L chain also has regularly spaced intrachain disulfide bridges. Each H chain has at the N-terminus, a variable domain (V_H) followed by three constant domains (C_H) for each of the α and γ chains and four C_H domains for μ and ε isotypes. Each L chain has at the N-terminus, a variable domain (V_L) followed by a constant domain at its other end. The V_L is aligned with the V_H and the C_L is aligned with the first constant domain of the heavy chain (C_H1). Particular amino acid residues are believed to form an interface between the light chain and heavy chain variable domains. The pairing of a V_H and V_L together forms a single antigen-binding site. For the structure and properties of the different classes of antibodies, see *e.g.*, *Basic and Clinical Immunology,* 8th Edition, Daniel P. Sties, Abba I. Terr and Tristram G. Parsolw (eds), Appleton & Lange, Norwalk, Conn., 1994, page 71 and Chapter 6. The L chain from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains. Depending on the amino acid sequence of the constant domain of their heavy chains (C_H), immunoglobulins can be assigned to different classes or isotypes. There are five classes of immunoglobulins: IgA, IgD, IgE, IgG and IgM, having heavy chains designated α, δ, ε, γ and μ, respectively. The γ and α classes are further divided into subclasses on the basis of relatively minor differences in the C_H sequence and function, *e.g.*, humans express the following subclasses: IgG1, IgG2A, IgG2B, IgG3, IgG4, IgA1 and IgA2.

[0047] An "isolated" antibody is one that has been identified, separated and/or recovered from a component of its production environment (*E.g.*, natural or recombinant). Preferably, the isolated polypeptide is free of association with all other components from its production environment. Contaminant components of its production environment, such as that resulting from recombinant transfected cells, are materials that would typically interfere with research, diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the polypeptide will be purified: (1) to greater than 95% by weight of antibody as determined by, for example, the Lowry method, and in some embodiments, to greater than 99% by weight; (1) to a degree

sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody in situ within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, an isolated polypeptide or antibody will be prepared by at least one purification step.

[0048] The "variable region" or "variable domain" of an antibody refers to the amino-terminal domains of the heavy or light chain of the antibody. The variable domains of the heavy chain and light chain may be referred to as "V_H" and "V_L", respectively. These domains are generally the most variable parts of the antibody (relative to other antibodies of the same class) and contain the antigen binding sites. Heavy-chain only antibodies from the *Camelidae* species have a single heavy chain variable region, which is referred to as "V_HH". V_HH is thus a special type of V_H.

[0049] The term "variable" refers to the fact that certain segments of the variable domains differ extensively in sequence among antibodies. The V domain mediates antigen binding and defines the specificity of a particular antibody for its particular antigen. However, the variability is not evenly distributed across the entire span of the variable domains. Instead, it is concentrated in three segments called hypervariable regions (HVRs) both in the light-chain and the heavy chain variable domains. The more highly conserved portions of variable domains are called the framework regions (FR). The variable domains of native heavy and light chains each comprise four FR regions, largely adopting a beta-sheet configuration, connected by three HVRs, which form loops connecting, and in some cases forming part of, the beta-sheet structure. The HVRs in each chain are held together in close proximity by the FR regions and, with the HVRs from the other chain, contribute to the formation of the antigen binding site of antibodies (see Kabat *et al.*, *Sequences of Immunological Interest*, Fifth Edition, National Institute of Health, Bethesda, Md. (1991)). The constant domains are not involved directly in the binding of antibody to an antigen, but exhibit various effector functions, such as participation of the antibody in antibody-dependent cellular toxicity.

[0050] The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, *i.e.*, the individual antibodies comprising the population are identical except for possible naturally occurring mutations and/or post-translation modifications (*e.g.*, isomerizations, amidations) that may be present in minor amounts.

Monoclonal antibodies are highly specific, being directed against a single antigenic site. In contrast to polyclonal antibody preparations which typically include different antibodies directed against different determinants (epitopes), each monoclonal antibody is directed against a single determinant on the antigen. In addition to their specificity, the monoclonal antibodies are advantageous in that they are synthesized by the hybridoma culture, uncontaminated by other immunoglobulins. The modifier "monoclonal" indicates the character of the antibody as being obtained from a substantially homogeneous population of antibodies, and is not to be construed as requiring production of the antibody by any particular method. For example, the monoclonal antibodies to be used in accordance with the present application may be made by a variety of techniques, including, for example, the hybridoma method (*e.g.*, Kohler and Milstein., *Nature,* 256:495-97 (1975); Hongo *et al.*, *Hybridoma,* 14 (3): 253-260 (1995), Harlow *et al.*, *Antibodies: A Laboratory Manual*, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988); Hammerling *et al.*, in: *Monoclonal Antibodies and T-Cell Hybridomas* 563-681 (Elsevier, N.Y., 1981)), recombinant DNA methods (see, *e.g.*, U.S. Pat. No. 4,816,567), phage-display technologies (see, *e.g.*, Clackson *et al.*, *Nature,* 352: 624-628 (1991); Marks *et al.*, *J. Mol. Biol.* 222: 581-597 (1992); Sidhu *et al.*, *J. Mol. Biol.* 338(2): 299-310 (2004); Lee *et al.*, *J. Mol. Biol.* 340(5): 1073-1093 (2004); Fellouse, *Proc. Natl. Acad. Sci. USA* 101(34): 12467-12472 (2004); and Lee *et al.*, *J. Immunol. Methods* 284(1-2): 119-132 (2004), and technologies for producing human or human-like antibodies in animals that have parts or all of the human immunoglobulin loci or genes encoding human immunoglobulin sequences (see, *e.g.*, WO 1998/24893; WO 1996/34096; WO 1996/33735; WO 1991/10741; Jakobovits *et al.*, *Proc. Natl. Acad. Sci. USA* 90: 2551 (1993); Jakobovits *et al.*, *Nature* 362: 255-258 (1993); Bruggemann *et al.*, *Year in Immunol.* 7:33 (1993); U.S. Pat. Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; and 5,661,016; Marks *et al.*, *Bio/Technology* 10: 779-783 (1992); Lonberg *et al.*, *Nature* 368: 856-859 (1994); Morrison, *Nature* 368: 812-813 (1994); Fishwild *et al.*, *Nature Biotechnol.* 14: 845-851 (1996); Neuberger, *Nature Biotechnol.* 14: 826 (1996); and Lonberg and Huszar, *Intern. Rev. Immunol.* 13: 65-93 (1995).

[0051] The term "naked antibody" refers to an antibody that is not conjugated to a cytotoxic moiety or radiolabel.

[0052] The terms "full-length antibody," "intact antibody" or "whole antibody" are used interchangeably to refer to an antibody in its substantially intact form, as opposed to an antibody

fragment. Specifically full-length 4-chain antibodies include those with heavy and light chains including an Fc region. The constant domains may be native sequence constant domains (*e.g.*, human native sequence constant domains) or amino acid sequence variants thereof. In some cases, the intact antibody may have one or more effector functions.

[0053] An "antibody fragment" comprises a portion of an intact antibody, preferably the antigen binding and/or the variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', $F(ab')_2$ and Fv fragments; diabodies; linear antibodies (see U.S. Pat. No. 5,641,870, Example 2; Zapata *et al.*, *Protein Eng.* 8(10): 1057-1062 [1995]); single-chain antibody molecules and multispecific antibodies formed from antibody fragments. Papain digestion of antibodies produced two identical antigen-binding fragments, called "Fab" fragments, and a residual "Fc" fragment, a designation reflecting the ability to crystallize readily. The Fab fragment consists of an entire L chain along with the variable region domain of the H chain (V_H), and the first constant domain of one heavy chain (C_H1). Each Fab fragment is monovalent with respect to antigen binding, *i.e.*, it has a single antigen-binding site. Pepsin treatment of an antibody yields a single large $F(ab')_2$ fragment which roughly corresponds to two disulfide linked Fab fragments having different antigen-binding activity and is still capable of cross-linking antigen. Fab' fragments differ from Fab fragments by having a few additional residues at the carboxy terminus of the C_H1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. $F(ab')_2$ antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

[0054] The Fc fragment comprises the carboxy-terminal portions of both H chains held together by disulfides. The effector functions of antibodies are determined by sequences in the Fc region, the region which is also recognized by Fc receptors (FcR) found on certain types of cells.

[0055] "Fv" is the minimum antibody fragment which contains a complete antigen-recognition and -binding site. This fragment consists of a dimer of one heavy- and one light-chain variable region domain in tight, non-covalent association. From the folding of these two domains emanate six hypervariable loops (3 loops each from the H and L chain) that contribute the amino acid residues for antigen binding and confer antigen binding specificity to the antibody. However,

even a single variable domain (or half of an Fv comprising only three HVRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

[0056] "Single-chain Fv" also abbreviated as "sFv" or "scFv" are antibody fragments that comprise the V_H and V_L antibody domains connected into a single polypeptide chain. Preferably, the sFv polypeptide further comprises a polypeptide linker between the V_H and V_L domains which enables the sFv to form the desired structure for antigen binding. For a review of the sFv, see Pluckthun in *The Pharmacology of Monoclonal Antibodies*, vol. 113, Rosenburg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994).

[0057] "Functional fragments" of the antibodies described herein comprise a portion of an intact antibody, generally including the antigen binding or variable region of the intact antibody or the Fc region of an antibody which retains or has modified FcR binding capability. Examples of antibody fragments include linear antibody, single-chain antibody molecules and multispecific antibodies formed from antibody fragments.

[0058] The term "diabodies" refers to small antibody fragments prepared by constructing sFv fragments (see preceding paragraph) with short linkers (about 5-10) residues) between the V_H and V_L domains such that inter-chain but not intra-chain pairing of the V domains is achieved, thereby resulting in a bivalent fragment, *i.e.*, a fragment having two antigen-binding sites. Bispecific diabodies are heterodimers of two "crossover" sFv fragments in which the V_H and V_L domains of the two antibodies are present on different polypeptide chains. Diabodies are described in greater detail in, for example, EP 404,097; WO 93/11161; Hollinger *et al.*, *Proc. Natl. Acad. Sci. USA* 90: 6444-6448 (1993).

[0059] The monoclonal antibodies herein specifically include "chimeric" antibodies (immunoglobulins) in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is(are) identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, so long as they exhibit the desired biological activity (U.S. Pat. No. 4,816,567; Morrison *et al.*, *Proc. Natl. Acad. Sci. USA,* 81:6851-6855 (1984)). Chimeric antibodies of interest herein include PRIMATTZFD® antibodies wherein the antigen-binding region of the

antibody is derived from an antibody produced by, *e.g.*, immunizing macaque monkeys with an antigen of interest. As used herein, "humanized antibody" is used a subset of "chimeric antibodies."

[0060] "Humanized" forms of non-human (*e.g.*, murine) antibodies are chimeric antibodies that contain minimal sequence derived from non-human immunoglobulin. In one embodiment, a humanized antibody is a human immunoglobulin (recipient antibody) in which residues from an HVR (hereinafter defined) of the recipient are replaced by residues from an HVR of a non-human species (donor antibody) such as mouse, rat, rabbit or non-human primate having the desired specificity, affinity, and/or capacity. In some instances, framework ("FR") residues of the human immunoglobulin are replaced by corresponding non-human residues. Furthermore, humanized antibodies may comprise residues that are not found in the recipient antibody or in the donor antibody. These modifications may be made to further refine antibody performance, such as binding affinity. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the hypervariable loops correspond to those of a non-human immunoglobulin sequence, and all or substantially all of the FR regions are those of a human immunoglobulin sequence, although the FR regions may include one or more individual FR residue substitutions that improve antibody performance, such as binding affinity, isomerization, immunogenicity, etc. The number of these amino acid substitutions in the FR is typically no more than 6 in the H chain, and in the L chain, no more than 3. The humanized antibody optionally will also comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. For further details, see, *e.g.*, Jones *et al.*, *Nature* 321:522-525 (1986); Riechmann *et al.*, *Nature* 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.* 2:593-596 (1992). See also, for example, Vaswani and Hamilton, *Ann. Allergy, Asthma & Immunol.* 1:105-115 (1998); Harris, *Biochem. Soc. Transactions* 23:1035-1038 (1995); Hurle and Gross, *Curr. Op. Biotech.* 5:428-433 (1994); and U.S. Pat. Nos. 6,982,321 and 7,087,409.

[0061] A "human antibody" is an antibody that possesses an amino-acid sequence corresponding to that of an antibody produced by a human and/or has been made using any of the techniques for making human antibodies as disclosed herein. This definition of a human antibody specifically excludes a humanized antibody comprising non-human antigen-binding residues. Human antibodies can be produced using various techniques known in the art,

including phage-display libraries. Hoogenboom and Winter, *J. Mol. Biol.,* 227:381 (1991); Marks *et al.*, *J. Mol. Biol.,* 222:581 (1991). Also available for the preparation of human monoclonal antibodies are methods described in Cole *et al.*, *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, p. 77 (1985); Boerner *et al.*, *J. Immunol.,* 147(1):86-95 (1991). See also van Dijk and van de Winkel, *Curr. Opin. Pharmacol.,* 5: 368-74 (2001). Human antibodies can be prepared by administering the antigen to a transgenic animal that has been modified to produce such antibodies in response to antigenic challenge, but whose endogenous loci have been disabled, *e.g.*, immunized xenomice (see, *e.g.*, U.S. Pat. Nos. 6,075,181 and 6,150,584 regarding XENOMOUSE™ technology). See also, for example, Li *et al.*, *Proc. Natl. Acad. Sci. USA,* 103:3557-3562 (2006) regarding human antibodies generated via a human B-cell hybridoma technology.

[0062] The term "hypervariable region," "HVR," or "HV," when used herein refers to the regions of an antibody variable domain which are hypervariable in sequence and/or form structurally defined loops. Generally, 4-chain antibodies comprise six HVRs; three in the V_H (H1, H2, H3), and three in the V_L (L1, L2, L3). Single-domain antibodies comprise three HVRs, such as three in the V_HH (H1, H2, H3). In native 4-chain antibodies, H3 and L3 display the most diversity of the six HVRs, and H3 in particular is believed to play a unique role in conferring fine specificity to antibodies. See, *e.g.*, Xu *et al.*, *Immunity* 13:37-45 (2000); Johnson and Wu, in *Methods in Molecular Biology* 248:1-25 (Lo, ed., Human Press, Totowa, N.J., 2003). Indeed, naturally occurring camelid antibodies consisting of a heavy chain only are functional and stable in the absence of light chain. See, *e.g.*, Hamers-Casterman *et al.*, *Nature* 363:446-448 (1993); Sheriff *et al.*, *Nature Struct. Biol.* 3:733-736 (1996).

[0063] The term "Complementarity Determining Region" or "CDR" are used to refer to hypervariable regions as defined by the Kabat system. See Kabat *et al.*, *Sequences of Proteins of Immunological Interest,* 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md. (1991)

[0064] A number of HVR delineations are in use and are encompassed herein. The Kabat Complementarity Determining Regions (CDRs) are based on sequence variability and are the most commonly used (Kabat *et al.*, *Sequences of Proteins of Immunological Interest,* 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md. (1991)). Chothia refers instead to the location of the structural loops (Chothia and Lesk, *J. Mol. Biol.* 196:901-917

(1987)). The AbM HVRs represent a compromise between the Kabat HVRs and Chothia structural loops, and are used by Oxford Molecular's AbM antibody modeling software. The "contact" HVRs are based on an analysis of the available complex crystal structures. The residues from each of these HVRs are noted below in Table 1.

Table 1. HVR delineations.

Loop	Kabat	AbM	Chothia	Contact
L1	L24-L34	L24-L34	L26-L32	L30-L36
L2	L50-L56	L50-L56	L50-L52	L46-L55
L3	L89-L97	L89-L97	L91-L96	L89-L96
H1	H31-H35B	H26-H35B	H26-H32	H30-H35B
		(Kabat Numbering)		
H1	H31-H35	H26-H35	H26-H32	H30-H35
		(Chothia Numbering)		
H2	H50-H65	H50-H58	H53-H55	H47-H58
H3	H95-H102	H95-H102	H96-H101	H93-H101

[0065] HVRs may comprise "extended HVRs" as follows: 24-36 or 24-34 (L1), 46-56 or 50-56 (L2) and 89-97 or 89-96 (L3) in the V_L and 26-35 (H1), 50-65 or 49-65 (H2) and 93-102, 94-102, or 95-102 (H3) in the V_H. The variable domain residues are numbered according to Kabat *et al.*, supra, for each of these definitions.

[0066] The expression "variable-domain residue-numbering as in Kabat" or "amino-acid-position numbering as in Kabat," and variations thereof, refers to the numbering system used for heavy-chain variable domains or light-chain variable domains of the compilation of antibodies in Kabat *et al.*, supra. Using this numbering system, the actual linear amino acid sequence may contain fewer or additional amino acids corresponding to a shortening of, or insertion into, a FR or HVR of the variable domain. For example, a heavy-chain variable domain may include a single amino acid insert (residue 52a according to Kabat) after residue 52 of H2 and inserted residues (*e.g.* residues 82a, 82b, and 82c, etc. according to Kabat) after heavy-chain FR residue 82. The Kabat numbering of residues may be determined for a given antibody by alignment at regions of homology of the sequence of the antibody with a "standard" Kabat numbered sequence.

[0067] "Framework" or "FR" residues are those variable-domain residues other than the HVR residues as herein defined.

[0068] A "human consensus framework" or "acceptor human framework" is a framework that represents the most commonly occurring amino acid residues in a selection of human immunoglobulin V_L or V_H framework sequences. Generally, the selection of human immunoglobulin V_L or V_H sequences is from a subgroup of variable domain sequences. Generally, the subgroup of sequences is a subgroup as in Kabat *et al.*, *Sequences of Proteins of Immunological Interest,* 5th Ed. Public Health Service, National Institutes of Health, Bethesda, Md. (1991). Examples include for the V_L, the subgroup may be subgroup kappa I, kappa II, kappa III or kappa IV as in Kabat *et al.*, supra. Additionally, for the VH, the subgroup may be subgroup I, subgroup II, or subgroup III as in Kabat *et al.* Alternatively, a human consensus framework can be derived from the above in which particular residues, such as when a human framework residue is selected based on its homology to the donor framework by aligning the donor framework sequence with a collection of various human framework sequences. An acceptor human framework "derived from" a human immunoglobulin framework or a human consensus framework may comprise the same amino acid sequence thereof, or it may contain pre-existing amino acid sequence changes. In some embodiments, the number of pre-existing amino acid changes are 10 or less, 9 or less, 8 or less, 7 or less, 6 or less, 5 or less, 4 or less, 3 or less, or 2 or less.

[0069] An "amino-acid modification" at a specified position, *e.g.* of the Fc region, refers to the substitution or deletion of the specified residue, or the insertion of at least one amino acid residue adjacent the specified residue. Insertion "adjacent" to a specified residue means insertion within one to two residues thereof. The insertion may be N-terminal or C-terminal to the specified residue. The preferred amino acid modification herein is a substitution.

[0070] An "affinity-matured" antibody is one with one or more alterations in one or more HVRs thereof that result in an improvement in the affinity of the antibody for antigen, compared to a parent antibody that does not possess those alteration(s). In one embodiment, an affinity-matured antibody has nanomolar or even picomolar affinities for the target antigen. Affinity-matured antibodies are produced by procedures known in the art. For example, Marks *et al.*, *Bio/Technology* 10:779-783 (1992) describes affinity maturation by V_H- and V_L -domain shuffling. Random mutagenesis of HVR and/or framework residues is described by, for example: Barbas *et al. Proc Nat. Acad. Sci. USA* 91:3809-3813 (1994); Schier *et al. Gene* 169:147-155

(1995); Yelton *et al. J. Immunol.* 155:1994-2004 (1995); Jackson *et al., J. Immunol.* 154(7):3310-9 (1995); and Hawkins *et al, J. Mol. Biol.* 226:889-896 (1992).

[0071] As use herein, the term "specifically binds" or is "specific for" refers to measurable and reproducible interactions such as binding between a target and an antibody, which is determinative of the presence of the target in the presence of a heterogeneous population of molecules including biological molecules. For example, an antibody that specifically binds a target (which can be an epitope) is an antibody that binds this target with greater affinity, avidity, more readily, and/or with greater duration than it binds other targets. In one embodiment, the extent of binding of an antibody to an unrelated target is less than about 10% of the binding of the antibody to the target as measured, *e.g.*, by a radioimmunoassay (RIA). In certain embodiments, an antibody that specifically binds a target has a dissociation constant (Kd) of ≦1 μM, ≦100 nM, ≦10 nM, ≦1 nM, or ≦0.1 nM. In certain embodiments, an antibody specifically binds an epitope on a protein that is conserved among the protein from different species. In another embodiment, specific binding can include, but does not require exclusive binding.

[0072] The term "specificity" refers to selective recognition of an antigen binding protein or antibody for a particular epitope of an antigen. Natural antibodies, for example, are monospecific. The term "multispecific" as used herein denotes that an antigen binding protein or an antibody has two or more antigen-binding sites of which at least two bind a different antigen or a different epitope of the same antigen. "Bispecific" as used herein denotes that an antigen binding protein or an antibody has two different antigen-binding specificities. The term "monospecific" antibody as used herein denotes an antibody that has one or more binding sites each of which bind the same epitope of the same antigen.

[0073] The term "valent" as used herein denotes the presence of a specified number of binding sites in an antigen binding protein or antibody molecule. A natural antibody for example or a full length antibody has two binding sites and is bivalent. As such, the terms "trivalent", "tetravalent", "pentavalent" and "hexavalent" denote the presence of two binding site, three binding sites, four binding sites, five binding sites, and six binding sites, respectively, in an antigen binding protein or antibody molecule. The multispecific antigen binding proteins of the present application are at least "bivalent," for example, the multispecific antigen binding proteins can be "trivalent," or "tetravalent."

[0074] A "blocking" antibody or an "antagonist" antibody is one that inhibits or reduces a biological activity of the antigen it binds. In some embodiments, blocking antibodies or antagonist antibodies substantially or completely inhibit the biological activity of the antigen.

[0075] An "agonist" or activating antibody is one that enhances or initiates signaling by the antigen to which it binds. In some embodiments, agonist antibodies cause or activate signaling without the presence of the natural ligand.

[0076] "Antibody effector functions" refer to those biological activities attributable to the Fc region (a native sequence Fc region or amino acid sequence variant Fc region) of an antibody, and vary with the antibody isotype. Examples of antibody effector functions include: C1q binding and complement dependent cytotoxicity; Fc receptor binding; antibody—dependent cell-mediated cytotoxicity (ADCC); phagocytosis; down regulation of cell surface receptors (*e.g.*, B cell receptors); and B cell activation. "Reduced or minimized" antibody effector function means that which is reduced by at least 50% (alternatively 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%) from the wild type or unmodified antibody. The determination of antibody effector function is readily determinable and measurable by one of ordinary skill in the art. In a preferred embodiment, the antibody effector functions of complement binding, complement dependent cytotoxicity and antibody dependent cytotoxicity are affected. In some embodiments, effector function is eliminated through a mutation in the constant region that eliminated glycosylation, *e.g.*, "effector-less mutation." In one aspect, the effector-less mutation is an N297A or DANA mutation (D265A+N297A) in the C_H2 region. Shields *et al.*, *J. Biol. Chem.* 276 (9): 6591-6604 (2001). Alternatively, additional mutations resulting in reduced or eliminated effector function include: K322A and L234A/L235A (LALA). Alternatively, effector function can be reduced or eliminated through production techniques, such as expression in host cells that do not glycosylate (*e.g.*, *E. coli.*) or in which result in an altered glycosylation pattern that is ineffective or less effective at promoting effector function (*e.g.*, Shinkawa *et al.*, *J. Biol. Chem.* 278(5): 3466-3473 (2003).

[0077] "Antibody-dependent cell-mediated cytotoxicity" or ADCC refers to a form of cytotoxicity in which secreted Ig bound onto Fc receptors (FcRs) present on certain cytotoxic cells (*e.g.*, natural killer (NK) cells, neutrophils and macrophages) enable these cytotoxic effector cells to bind specifically to an antigen-bearing target cell and subsequently kill the target cell with cytotoxins. The antibodies "arm" the cytotoxic cells and are required for killing of the target

cell by this mechanism. The primary cells for mediating ADCC, NK cells, express FcγRIII only, whereas monocytes express FcγRI, FcγRII and FcγRIII. Fc expression on hematopoietic cells is summarized in Table 3 on page 464 of Ravetch and Kinet, *Annu. Rev. Immunol.* 9: 457-92 (1991). To assess ADCC activity of a molecule of interest, an *in vitro* ADCC assay, such as that described in U.S. Pat. No. 5,500,362 or 5,821,337 may be performed. Useful effector cells for such assays include peripheral blood mononuclear cells (PBMC) and natural killer (NK) cells. Alternatively, or additionally, ADCC activity of the molecule of interest may be assessed *in vivo*, *e.g.*, in an animal model such as that disclosed in Clynes *et al.*, *PNAS USA* 95:652-656 (1998).

[0078] Unless indicated otherwise herein, the numbering of the residues in an immunoglobulin heavy chain is that of the EU index as in Kabat *et al.*, supra. The "EU index as in Kabat" refers to the residue numbering of the human IgG1 EU antibody.

[0079] The term "Fc region" herein is used to define a C-terminal region of an immunoglobulin heavy chain, including native-sequence Fc regions and variant Fc regions. Although the boundaries of the Fc region of an immunoglobulin heavy chain might vary, the human IgG heavy-chain Fc region is usually defined to stretch from an amino acid residue at position Cys226, or from Pro230, to the carboxyl-terminus thereof. The C-terminal lysine (residue 447 according to the EU numbering system) of the Fc region may be removed, for example, during production or purification of the antibody, or by recombinantly engineering the nucleic acid encoding a heavy chain of the antibody. Accordingly, a composition of intact antibodies may comprise antibody populations with all K447 residues removed, antibody populations with no K447 residues removed, and antibody populations having a mixture of antibodies with and without the K447 residue. Suitable native-sequence Fc regions for use in the antibodies described herein include human IgG1, IgG2 (IgG2A, IgG2B), IgG3 and IgG4.

[0080] "Fc receptor" or "FcR" describes a receptor that binds the Fc region of an antibody. The preferred FcR is a native sequence human FcR. Moreover, a preferred FcR is one which binds an IgG antibody (a gamma receptor) and includes receptors of the FcγRI, FcγRII, and FcγRIII subclasses, including allelic variants and alternatively spliced forms of these receptors, FcγRII receptors include FcγRIIA (an "activating receptor") and FcγRIIB (an "inhibiting receptor"), which have similar amino acid sequences that differ primarily in the cytoplasmic domains thereof. Activating receptor FcγRIIA contains an immunoreceptor tyrosine-based activation motif (ITAM) in its cytoplasmic domain. Inhibiting receptor FcγRIIB contains an

immunoreceptor tyrosine-based inhibition motif (ITIM) in its cytoplasmic domain. (see M. Daëron, *Annu. Rev. Immunol.* 15:203-234 (1997). FcRs are reviewed in Ravetch and Kinet, *Annu. Rev. Immunol.* 9: 457-92 (1991); Capel *et al.*, *Immunomethods* 4: 25-34 (1994); and de Haas *et al.*, *J. Lab. Clin. Med.* 126: 330-41 (1995). Other FcRs, including those to be identified in the future, are encompassed by the term "FcR" herein.

[0081] The term "Fc receptor" or "FcR" also includes the neonatal receptor, FcRn, which is responsible for the transfer of maternal IgGs to the fetus. Guyer *et al.*, *J. Immunol.* 117: 587 (1976) and Kim *et al.*, *J. Immunol.* 24: 249 (1994). Methods of measuring binding to FcRn are known (see, *e.g.*, Ghetie and Ward, *Immunol. Today* 18: (12): 592-8 (1997); Ghetie *et al.*, *Nature Biotechnology* 15 (7): 637-40 (1997); Hinton *et al.*, *J. Biol. Chem.* 279 (8): 6213-6 (2004); WO 2004/92219 (Hinton *et al.*). Binding to FcRn *in vivo* and serum half-life of human FcRn high-affinity binding polypeptides can be assayed, *e.g.*, in transgenic mice or transfected human cell lines expressing human FcRn, or in primates to which the polypeptides having a variant Fc region are administered. WO 2004/42072 (Presta) describes antibody variants which improved or diminished binding to FcRs. See also, *e.g.*, Shields *et al.*, *J. Biol. Chem.* 9(2): 6591-6604 (2001).

[0082] "Effector cells" are leukocytes which express one or more FcRs and perform effector functions. In one aspect, the effector cells express at least FcγRIII and perform ADCC effector function. Examples of human leukocytes which mediate ADCC include peripheral blood mononuclear cells (PBMC), natural killer (NK) cells, monocytes, cytotoxic T cells and neutrophils. The effector cells may be isolated from a native source, *e.g.*, blood. Effector cells generally are lymphocytes associated with the effector phase, and function to produce cytokines (helper T cells), killing cells in infected with pathogens (cytotoxic T cells) or secreting antibodies (differentiated B cells).

[0083] "Complement dependent cytotoxicity" or "CDC" refers to the lysis of a target cell in the presence of complement. Activation of the classical complement pathway is initiated by the binding of the first component of the complement system (C1q) to antibodies (of the appropriate subclass) which are bound to their cognate antigen. To assess complement activation, a CDC assay, *e.g.*, as described in Gazzano-Santoro *et al.*, *J. Immunol. Methods* 202: 163 (1996), may be performed. Antibody variants with altered Fc region amino acid sequences and increased or decreased C1q binding capability are described in U.S. Pat. No. 6,194,551B1 and WO99/51642.

The contents of those patent publications are specifically incorporated herein by reference. See, also, Idusogie *et al. J. Immunol.* 164: 4178-4184 (2000).

[0084] The term "heavy chain-only antibody" or "HCAb" refers to a functional antibody, which comprises heavy chains, but lacks the light chains usually found in antibodies. Camelid animals (such as camels, llamas, or alpacas) are known to produce HCAbs.

[0085] The term "single-domain antibody" or "sdAb" refers to a single antigen-binding polypeptide having three complementary determining regions (CDRs). The sdAb alone is capable of binding to the antigen without pairing with a corresponding CDR-containing polypeptide. In some cases, single-domain antibodies are engineered from camelid HCAbs, and their heavy chain variable domains are referred herein as "V_HHs". Camelid sdAb is one of the smallest known antigen-binding antibody fragments (see, *e.g.,* Hamers-Casterman *et al.*, Nature 363:446-8 (1993); Greenberg *et al.*, Nature 374:168-73 (1995); Hassanzadeh-Ghassabeh *et al.*, Nanomedicine (Lond), 8:1013-26 (2013)).

[0086] "Binding affinity" generally refers to the strength of the sum total of non-covalent interactions between a single binding site of a molecule (*e.g.*, an antibody) and its binding partner (*e.g.*, an antigen). Unless indicated otherwise, as used herein, "binding affinity" refers to intrinsic binding affinity that reflects a 1:1 interaction between members of a binding pair (*e.g.*, antibody and antigen). The affinity of a molecule X for its partner Y can generally be represented by the dissociation constant (Kd). Affinity can be measured by common methods known in the art, including those described herein. Low-affinity antibodies generally bind antigen slowly and tend to dissociate readily, whereas high-affinity antibodies generally bind antigen faster and tend to remain bound longer. A variety of methods of measuring binding affinity are known in the art, any of which can be used for purposes of the present application. Specific illustrative and exemplary embodiments for measuring binding affinity are described in the following.

[0087] The "Kd" or "Kd value" as used herein is in one embodiment measured by a radiolabeled antigen binding assay (RIA) performed with the Fab version of the antibody and antigen molecule as described by the following assay that measures solution binding affinity of Fabs for antigen by equilibrating Fab with a minimal concentration of (^{125}I)-labeled antigen in the presence of a titration series of unlabeled antigen, then capturing bound antigen with an anti-Fab antibody-coated plate (Chen, *et al.*, (1999) *J. Mol. Biol* 293:865-881). To establish conditions for the assay, microtiter plates (Dynex) are coated overnight with 5 μg/ml of a

capturing anti-Fab antibody (Cappel Labs) in 50 mM sodium carbonate (pH 9.6), and subsequently blocked with 2% (w/v) bovine serum albumin in PBS for two to five hours at room temperature (approximately 23° C.). In a non-adsorbent plate (Nunc #269620), 100 pM or 26 pM [^{125}I]-antigen are mixed with serial dilutions of a Fab of interest (consistent with assessment of an anti-VEGF antibody, Fab-12, in Presta *et al.*, (1997) *Cancer Res.* 57:4593-4599). The Fab of interest is then incubated overnight; however, the incubation may continue for a longer period (*e.g.*, 65 hours) to insure that equilibrium is reached. Thereafter, the mixtures are transferred to the capture plate for incubation at room temperature for one hour. The solution is then removed and the plate washed eight times with 0.1% Tween-20 in PBS. When the plates have dried, 150 µl/well of scintillant (MicroScint-20; Packard) is added, and the plates are counted on a Topcount gamma counter (Packard) for ten minutes. Concentrations of each Fab that give less than or equal to 20% of maximal binding are chosen for use in competitive binding assays.

[0088] According to another embodiment, the Kd is measured by using surface-plasmon resonance assays using a BIACORE®-2000 or a BIACORE®-3000 instrument (BIAcore, Inc., Piscataway, N.J.) at 25° C. with immobilized antigen CM5 chips at ~10 response units (RU). Briefly, carboxymethylated dextran biosensor chips (CM5, BIAcore Inc.) are activated with N-ethyl-N′-(3-dimethylaminopropyl)-carbodiimide hydrochloride (EDC) and N-hydroxysuccinimide (NHS) according to the supplier's instructions. Antigen is diluted with 10 mM sodium acetate, pH 4.8, to 5 µg/ml (~0.2 µM) before injection at a flow rate of 5 µL/minute to achieve approximately 10 response units (RU) of coupled protein. Following the injection of antigen, 1 M ethanolamine is injected to block unreacted groups. For kinetics measurements, two-fold serial dilutions of Fab (0.78 nM to 500 nM) are injected in PBS with 0.05% TWEEN 20™ surfactant (PBST) at 25° C. at a flow rate of approximately 25 µL/min. Association rates (k_{on}) and dissociation rates (k_{off}) are calculated using a simple one-to-one Langmuir binding model (BIAcore® Evaluation Software version 3.2) by simultaneously fitting the association and dissociation sensorgrams. The equilibrium dissociation constant (Kd) is calculated as the ratio k_{off}/k_{on}. See, *e.g.*, Chen *et al.*, *J. Mol. Biol.* 293:865-881 (1999). If the on-rate exceeds $10^6 M^{-1} s^{-1}$ by the surface-plasmon resonance assay above, then the on-rate can be determined by using a fluorescent quenching technique that measures the increase or decrease in fluorescence-emission intensity (excitation=295 nm; emission=340 nm, 16 nm band-pass) at 25° C. of a 20 nM anti-antigen antibody (Fab form) in PBS, pH 7.2, in the presence of increasing concentrations of

antigen as measured in a spectrometer, such as a stop-flow-equipped spectrophotometer (Aviv Instruments) or a 8000-series SLM-AMINCO™ spectrophotometer (ThermoSpectronic) with a stirred cuvette.

[0089] An "on-rate," "rate of association," "association rate," or "k_{on}" as used herein can also be determined as described above using a BIACORE®-2000 or a BIACORE®-3000 system (BIAcore, Inc., Piscataway, N.J.) at 25° C. with immobilized antigen CM5 chips at about 10 response units (RU). Briefly, carboxymethylated dextran biosensor ships (CM5, BIAcore Inc.) are activated with N-ethyl-N′-(3-dimethylamino propyl)-carbodiimide hydrochloride (ECD) and N-hydroxysuccinimide (NHS) according to the supplier's instructions. Antigen is diluted with 10 mM sodium acetate, ph 4.8, into 5 mg/ml 0.2 mM) before injection at a flow rate of 5 ml/min. to achieve approximately 10 response units (RU) of coupled protein. Following the injection of antigen, 1M ethanolamine is added to block unreacted groups. For kinetics measurements, two-fold serial dilutions of Fab (0.78 nM to 500 nM) are injected in PBS with 0.05% Tween 20 (PBST) at 25° C. at a flow rate of approximately 25 μl/min. Association rates (k_{on}) and dissociation rates (k_{off}) are calculated using a simple one-to-one Langmuir binding model (BIAcore Evaluation Software version 3.2) by simultaneous fitting the association and dissociation sensorgram. The equilibrium dissociation constant (Kd) was calculated as the ratio k_{off}/k_{on}. See, *e.g.*, Chen, Y., *et al.*, (1999) *J. Mol. Biol* 293:865-881. However, if the on-rate exceeds $10^6\ M^{-1}\ S^{-1}$ by the surface plasmon resonance assay above, then the on-rate is preferably determined by using a fluorescent quenching technique that measures the increase or decrease in fluorescence emission intensity (excitation=295 nm; emission=340 nm, 16 nm band-pass) at 25° C. of a 20 nM anti-antigen antibody (Fab form) in PBS, pH 7.2, in the presence of increasing concentrations of antigen as measured in a spectrometer, such as a stop-flow equipped spectrophometer (Aviv Instruments) or a 8000-series SLM-Aminco spectrophotometer (ThermoSpectronic) with a stirred cuvette.

[0090] "Percent (%) amino acid sequence identity" and "homology" with respect to a peptide, polypeptide or antibody sequence are defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the specific peptide or polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid

sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or MEGALIGN™ (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared.

[0091] An "isolated" nucleic acid molecule encoding the multispecific antigen binding protein or single-domain antibody herein is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the environment in which it was produced. Preferably, the isolated nucleic acid is free of association with all components associated with the production environment. The isolated nucleic acid molecules encoding the polypeptides and antibodies herein is in a form other than in the form or setting in which it is found in nature. Isolated nucleic acid molecules therefore are distinguished from nucleic acid encoding the polypeptides and antibodies herein existing naturally in cells.

[0092] The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

[0093] Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

[0094] "Carriers" as used herein include pharmaceutically acceptable carriers, excipients, or stabilizers that are nontoxic to the cell or mammal being exposed thereto at the dosages and concentrations employed. Often the physiologically acceptable carrier is an aqueous pH buffered

solution. Examples of physiologically acceptable carriers 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) polypeptide; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, 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 counterions such as sodium; metal complexes (*e.g.* Zn-protein complexes); and/or nonionic surfactants such as TWEEN™, polyethylene glycol (PEG), and PLURONICS™ or polyethylene glycol (PEG).

[0095] The "diluent" of interest herein is one which is pharmaceutically acceptable (safe and non-toxic for administration to a human) and is useful for the preparation of a liquid formulation, such as a formulation reconstituted after lyophilization. Exemplary diluents include sterile water, bacteriostatic water for injection (BWFI), a pH buffered solution (*e.g.* phosphate-buffered saline), sterile saline solution, Ringer's solution or dextrose solution. In an alternative embodiment, diluents can include aqueous solutions of salts and/or buffers.

[0096] A "preservative" is a compound which can be added to the formulations herein to reduce bacterial activity. The addition of a preservative may, for example, facilitate the production of a multi-use (multiple-dose) formulation. Examples of potential preservatives include octadecyldimethylbenzyl ammonium chloride, hexamethonium chloride, benzalkonium chloride (a mixture of alkylbenzyldimethylammonium chlorides in which the alkyl groups are long-chain compounds), and benzethonium chloride. Other types of preservatives include aromatic alcohols such as phenol, butyl and benzyl alcohol, alkyl parabens such as methyl or propyl paraben, catechol, resorcinol, cyclohexanol, 3-pentanol, and m-cresol. The most preferred preservative herein is benzyl alcohol.

[0097] The term "pharmaceutical formulation" refers to a preparation that is in such form as to permit the biological activity of the active ingredient to be effective, and that contains no additional components that are unacceptably toxic to a subject to which the formulation would be

administered. Such formulations are sterile. A "sterile" formulation is aseptic or free from all living microorganisms and their spores.

[0098] A "stable" formulation is one in which the protein therein essentially retains its physical and chemical stability and integrity upon storage. Various analytical techniques for measuring protein stability are available in the art and are reviewed in *Peptide and Protein Drug Delivery,* 247-301, Vincent Lee Ed., Marcel Dekker, Inc., New York, N.Y., Pubs. (1991) and Jones, A. *Adv. Drug Delivery Rev.* 10: 29-90 (1993). Stability can be measured at a selected temperature for a selected time period. For rapid screening, the formulation may be kept at 40° C. for 2 weeks to 1 month, at which time stability is measured. Where the formulation is to be stored at 2-8° C., generally the formulation should be stable at 30° C. or 40° C. for at least 1 month and/or stable at 2-8° C. for at least 2 years. Where the formulation is to be stored at 30° C., generally the formulation should be stable for at least 2 years at 30° C. and/or stable at 40° C. for at least 6 months. For example, the extent of aggregation during storage can be used as an indicator of protein stability. Thus, a "stable" formulation may be one wherein less than about 10% and preferably less than about 5% of the protein are present as an aggregate in the formulation. In other embodiments, any increase in aggregate formation during storage of the formulation can be determined.

[0099] A "reconstituted" formulation is one which has been prepared by dissolving a lyophilized protein or antibody formulation in a diluent such that the protein is dispersed throughout. The reconstituted formulation is suitable for administration (*e.g.* subcutaneous administration) to a patient to be treated with the protein of interest and, in certain embodiments, may be one which is suitable for parenteral or intravenous administration.

[0100] An "isotonic" formulation is one which has essentially the same osmotic pressure as human blood. Isotonic formulations will generally have an osmotic pressure from about 250 to 350 mOsm. The term "hypotonic" describes a formulation with an osmotic pressure below that of human blood. Correspondingly, the term "hypertonic" is used to describe a formulation with an osmotic pressure above that of human blood. Isotonicity can be measured using a vapor pressure or ice-freezing type osmometer, for example. The formulations of the present application can be hypertonic as a result of the addition of salt and/or buffer.

[0101] "Immune checkpoint molecules" refers to molecules in the immune system that either turn up a signal or turn down a signal. "Stimulatory immune checkpoint molecules" or "co-

stimulatory molecules" are immune checkpoint molecules that turn up a signal in the immune system. "Inhibitory immune checkpoint molecules" are immune checkpoint molecules that turn down a signal in the immune system.

[0102] It is understood that embodiments described herein include "consisting" and/or "consisting essentially of" embodiments.

[0103] Reference to "about" a value or parameter herein includes (and describes) variations that are directed to that value or parameter *per se*. For example, description referring to "about X" includes description of "X".

[0104] As used herein, reference to "not" a value or parameter generally means and describes "other than" a value or parameter. For example, the method is not used to treat cancer of type X means the method is used to treat cancer of types other than X.

[0105] The term "about X-Y" used herein has the same meaning as "about X to about Y."

[0106] As used herein and in the appended claims, the singular forms "a," "or," and "the" include plural referents unless the context clearly dictates otherwise.

II. Multispecific antigen binding proteins

[0107] One aspect of the present application provides a multispecific antigen binding protein comprising: (a) a first antigen binding portion comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a first epitope, and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds a second epitope, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the first epitope is from a first immune checkpoint molecule, and the second epitope is from a second immune checkpoint molecule. In some embodiments, the first epitope is from a first tumor antigen, and the second epitope is from a second tumor antigen. In some embodiments, the first epitope is from a tumor antigen, and the second epitope is from a cell surface molecule, such as CD3. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the first epitope is from a first pro-inflammatory molecule, and the second epitope is from a second pro-inflammatory molecule. In some embodiments, the first antigen binding portion comprises a heavy chain comprising the V_H and a light chain comprising the V_L. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of the heavy chain, the N-terminus of the

light chain, the C-terminus of the heavy chain, or the C-terminus of the light chain. In some embodiments, the first antigen binding portion comprises a full-length 4-chain antibody. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG1 Fc or IgG4 Fc.

[0108] The multispecific antigen binding proteins of the present application have at least two antigen binding portions that can specifically bind at least two different epitopes. Some of the at least two antigen binding portions may be identical, so long as the multispecific antigen binding protein has binding sites for two different epitopes. The multispecific antigen binding proteins can be symmetric or asymmetric. For example, the multispecific antigen binding protein may comprise one or two copies of the first antigen binding portion, and one to eight copies of the second antigen binding portion. In some embodiments, the multispecific antigen binding protein comprises two different antigen binding portions that each comprise a V_H domain and a V_L domain that together form a different antigen binding site. For example, the first antigen binding portion can be a bispecific antibody. In some embodiments, the first antigen binding portion is a monospecific full-length antibody or antigen binding fragment thereof, such as a Fab.

[0109] In some embodiments, the multispecific antigen binding protein comprises any one of 1, 2, 3, 4, 5, 6, 7, 8, or more different antigen binding portions that each comprises a single-domain antibody. In some embodiments, two identical single-domain antibodies are fused to each other, which is further fused to the first antigen binding portion. In some embodiments, two different single-domain antibodies are fused to each other, which is further fused to the first antigen binding portion.

[0110] The multispecific antigen binding proteins may have any suitable number of valencies for each epitope, and any suitable number of specificity. In some embodiments, the multispecific antigen binding protein is bivalent, trivalent, tetravalent, pentavalent, hexavalent, or of higher valencies for the first epitope. In some embodiments, the multispecific antigen binding protein is bivalent, trivalent, tetravalent, pentavalent, hexavalent, or of higher valencies for the second epitope. In some embodiments, the multispecific antigen binding protein is bispecific. In some

embodiments, the multispecific antigen binding protein is trispecific. In some embodiments, the multispecific antigen binding protein is tetraspecific. In some embodiments, the multispecific antigen binding protein has more than four specificities. Exemplary multispecific antigen binding proteins are depicted in FIGs. 1-16.

[0111] In some embodiments, there is provided a bispecific antigen binding protein comprising: (a) a single copy of a first antigen binding portion comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a first epitope, and (b) one or more copies (such as 2) of a second antigen binding portion comprising a single-domain antibody that specifically binds a second epitope, wherein each copy of the second antigen binding portion is fused to the first antigen binding portion. An example is shown in FIG. 5. In some embodiments, one or more of the single-domain antibodies is each further fused to another identical or different single-domain antibody.

[0112] In some embodiments, there is provided a multispecific antigen binding protein comprising: (a) a plurality (such as 2, 3, 4, 5, 6, or more) of a first antigen binding portion comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a first epitope, and (b) a plurality (such as 2, 3, 4, 5, 6, 7, 8, or more) of identical or different single-domain antibodies that each specifically binds an epitope that is different from the first epitope, wherein the single-domain antibodies are fused to each other, and/or to the first antigen binding portion.

[0113] In some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) two copies of a first antigen binding portion each comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a first epitope, and (b) a single copy of a second antigen binding portion comprising a single-domain antibody that specifically binds a second epitope, wherein the second antigen binding portion is fused to one of the two copies of the first antigen binding portion. An example is shown in FIG. 1.

[0114] In some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) two copies of a first antigen binding portion each comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a first epitope, and (b) a plurality

(such as 2, 3, or 4) of identical or different single-domain antibodies that each specifically binds an epitope that is different from the first epitope, wherein the single-domain antibodies are fused to each other, and/or to the first antigen binding portion. Examples are shown in FIGs. 2 and 3.

[0115] In some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) two copies of a first antigen binding portion each comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a first epitope, and (b) two copies of a second antigen binding portion each comprising a single-domain antibody that specifically binds a second epitope, wherein one copy of the second antigen binding portion is fused to each copy of the first antigen binding portion. Examples are shown in FIGs. 4, 9, 11, and 13. In some embodiments, one or more of the single-domain antibodies is each further fused to another identical or different single-domain antibody.

[0116] In some embodiments, there is provided a multispecific (such as trispecific) antigen binding protein comprising: (a) a first copy and a second copy of a first antigen binding portion each comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a first epitope, (b) a second antigen binding portion comprising a single-domain antibody that specifically binds a second epitope, and (c) a third antigen binding portion comprising a second single-domain antibody that specifically binds a third epitope, wherein the second antigen binding portion is fused to the first copy of the first antigen binding portion, and wherein the third antigen binding portion is fused to the second copy of the first antigen binding portion. Examples are shown in FIGs. 7, 10, 12, and 14. In some embodiments, one or more of the single-domain antibodies is each further fused to another identical or different single-domain antibody.

[0117] In some embodiments, there is provided a multispecific (such as trispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a first heavy chain variable domain (V_H) and a first light chain variable domain (V_L), wherein the first V_H and first V_L together form a first antigen-binding site that specifically binds a first epitope; (b) one to four copies of a second antigen binding portion comprising a single-domain antibody that specifically binds a second epitope; and (c) a third antigen binding portion comprising a third heavy chain variable domain (V_H) and a third light chain variable domain (V_L), wherein the third V_H and third

V_L together form a third antigen-binding site that specifically binds a third epitope; and wherein the second antigen binding portion is fused to the first antigen binding portion and/or the third antigen binding portion. An example is shown in FIG. 6. In some embodiments, one or more of the single-domain antibodies is each further fused to another identical or different single-domain antibody.

[0118] In some embodiments, there is provided a multispecific (such as tetraspecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a first heavy chain variable domain (V_H) and a first light chain variable domain (V_L), wherein the first V_H and first V_L together form a first antigen-binding site that specifically binds a first epitope; (b) a second antigen binding portion comprising a single-domain antibody that specifically binds a second epitope; (c) a third antigen binding portion comprising a third heavy chain variable domain (V_H) and a third light chain variable domain (V_L), wherein the third V_H and third V_L together form a third antigen-binding site that specifically binds a third epitope; and (d) a fourth antigen binding portion comprising a second single-domain antibody that specifically binds a fourth epitope; wherein the first antigen binding portion and the second antigen binding portion are fused to each other, and wherein the third antigen binding portion and the fourth antigen binding portion are fused to each other. An example is shown in FIG. 8. In some embodiments, one or more of the single-domain antibodies is each further fused to another identical or different single-domain antibody.

Epitopes and antigens

[0119] Any of the multispecific antigen binding proteins described herein can specifically bind at least two different epitopes. The at least two different epitopes recognized can be located on the same antigen, or on different antigens. In some embodiments, the antigens are cell surface molecules. In some embodiments, the antigens are extracellular molecules.

[0120] Thus, in some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a first antigen, and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds a second antigen, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or

human single-domain antibody. In some embodiments, the first antigen binding portion comprises a heavy chain comprising the V_H and a light chain comprising the V_L. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of the heavy chain, the N-terminus of the light chain, the C-terminus of the heavy chain, or the C-terminus of the light chain. In some embodiments, the first antigen binding portion comprises a full-length 4-chain antibody. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG1 Fc or IgG4 Fc.

[0121] In some embodiments, the first epitope and/or the second epitope is an immune checkpoint molecule. In some embodiments, the immune checkpoint molecule is a stimulatory immune checkpoint molecule. Exemplary stimulatory immune checkpoint molecules include, but are not limited to, CD28, OX40, ICOS, GITR, 4-1BB, CD27, CD40, CD3, HVEM, and TCR (*e.g.*, MHC class I or class II molecules). In some embodiments, the immune checkpoint molecule is an inhibitory immune checkpoint molecule. Exemplary inhibitory immune checkpoint molecules include, but are not limited to, CTLA-4, TIM-3, A2a Receptor, LAG-3, BTLA, KIR, PD-1, IDO, CD47, and ligands thereof such as B7.1, B7.2, PD-L1, PD-L2, HVEM, B7-H4, NKTR-218, and SIRP-alpha receptor.

[0122] Thus, in some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a first immune checkpoint molecule, and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds a second immune checkpoint molecule, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the first immune checkpoint molecule and/or the second immune checkpoint molecule is selected from the group consisting of PD-1, PD-L1, PD-L2, CTLA-4, B7-H3, TIM-3, LAG-3, VISTA, ICOS, 4-1BB, OX40, GITR, and CD40. In some embodiments, the first antigen binding portion

comprises a heavy chain comprising the V_H and a light chain comprising the V_L. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of the heavy chain, the N-terminus of the light chain, the C-terminus of the heavy chain, or the C-terminus of the light chain. In some embodiments, the first antigen binding portion comprises a full-length 4-chain antibody. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG4 Fc.

[0123] In some embodiments, the first epitope and/or the second epitope is a cell surface antigen. In some embodiments, the cell surface antigen is an antigen on immune effector cells, such as T cells (*e.g.*, helper T cells, cytotoxic T cells, memory T cells, *etc.*), B cells, macrophages, and Natural Killer (NK) cells. In some embodiments, the cell surface antigen is a T cell surface antigen, such as CD3.

[0124] In some embodiments, the cell surface antigen is a tumor antigen. Tumor antigens are proteins that are produced by tumor cells that can elicit an immune response, particularly T-cell mediated immune responses. The selection of the targeted antigen described herein will depend on the particular type of cancer to be treated. Exemplary tumor antigens include, for example, a glioma-associated antigen, carcinoembryonic antigen (CEA), β-human chorionic gonadotropin, alphafetoprotein (AFP), lectin-reactive AFP, thyroglobulin, RAGE-1, MN-CAIX, human telomerase reverse transcriptase, RU1, RU2 (AS), intestinal carboxyl esterase, mut hsp70-2, M-CSF, prostase, prostate-specific antigen (PSA), PAP, NY-ESO-1, LAGE-la, p53, prostein, PSMA, HER2/neu, survivin and telomerase, prostate-carcinoma tumor antigen-1 (PCTA-1), MAGE, ELF2M, neutrophil elastase, ephrinB2, CD22, insulin growth factor (IGF)-I, IGF-II, IGF-I receptor and mesothelin.

[0125] In some embodiments, the tumor antigen comprises one or more antigenic cancer epitopes associated with a malignant tumor. Malignant tumors express a number of proteins that can serve as target antigens for an immune attack. These molecules include but are not limited to tissue-specific antigens such as MART-1, tyrosinase and gp100 in melanoma and prostatic acid phosphatase (PAP) and prostate-specific antigen (PSA) in prostate cancer. Other target

molecules belong to the group of transformation-related molecules such as the oncogene HER2/Neu/ErbB-2. Yet another group of target antigens are onco-fetal antigens such as carcinoembryonic antigen (CEA). In B-cell lymphoma the tumor-specific idiotype immunoglobulin constitutes a truly tumor-specific immunoglobulin antigen that is unique to the individual tumor. B-cell differentiation antigens such as CD 19, CD20 and CD37 are other candidates for target antigens in B-cell lymphoma.

[0126] In some embodiments, the tumor antigen is a tumor-specific antigen (TSA) or a tumor-associated antigen (TAA). A TSA is unique to tumor cells and does not occur on other cells in the body. A TAA associated antigen is not unique to a tumor cell, and instead is also expressed on a normal cell under conditions that fail to induce a state of immunologic tolerance to the antigen. The expression of the antigen on the tumor may occur under conditions that enable the immune system to respond to the antigen. TAAs may be antigens that are expressed on normal cells during fetal development, when the immune system is immature, and unable to respond or they may be antigens that are normally present at extremely low levels on normal cells, but which are expressed at much higher levels on tumor cells.

[0127] Non-limiting examples of TSA or TAA antigens include the following: Differentiation antigens such as MART-1/MelanA (MART-I), gp 100 (Pmel 17), tyrosinase, TRP-1, TRP-2 and tumor-specific multilineage antigens such as MAGE-1, MAGE-3, BAGE, GAGE-1, GAGE-2, pl5; overexpressed embryonic antigens such as CEA; overexpressed oncogenes and mutated tumor-suppressor genes such as p53, Ras, HER2/neu; unique tumor antigens resulting from chromosomal translocations; such as BCR-ABL, E2A-PRL, H4-RET, IGH-IGK, MYL-RAR; and viral antigens, such as the Epstein Barr virus antigens EBVA and the human papillomavirus (HPV) antigens E6 and E7. Other large, protein-based antigens include TSP-180, MAGE-4, MAGE-5, MAGE-6, RAGE, NY-ESO, pl85erbB2, pl80erbB-3, c-met, nm-23HI, PSA, TAG-72, CA 19-9, CA 72-4, CAM 17.1, NuMa, K-ras, beta-Catenin, CDK4, Mum-1, p 15, p 16, 43-9F, 5T4, 791Tgp72, alpha-fetoprotein, beta-HCG, BCA225, BTAA, CA 125, CA 15-3\CA 27.29\BCAA, CA 195, CA 242, CA-50, CAM43, CD68\P1, CO-029, FGF-5, G250, Ga733\EpCAM, HTgp-175, M344, MA-50, MG7-Ag, MOV18, NB/70K, NY-CO- 1, RCAS 1, SDCCAG16, TA-90\Mac-2 binding protein\cyclophilin C-associated protein, TAAL6, TAG72, TLP, and TPS.

[0128] Thus, in some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a first tumor antigen, and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds a second tumor antigen, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the first tumor antigen and/or the second tumor antigen is selected from the group consisting of HER2, BRAF, EGFR, VEGFR2, CD20, RANKL, CD38, and CD52. In some embodiments, the first antigen binding portion comprises a heavy chain comprising the V_H and a light chain comprising the V_L. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of the heavy chain, the N-terminus of the light chain, the C-terminus of the heavy chain, or the C-terminus of the light chain. In some embodiments, the first antigen binding portion comprises a full-length 4-chain antibody. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG1 Fc.

[0129] In some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a tumor antigen, and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds a cell surface antigen on an immune effector cell (such as T cell), wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the tumor antigen is selected from the group consisting of HER2, BRAF, EGFR, VEGFR2, CD20, RANKL, CD38, and CD52. In some embodiments, the first antigen binding portion comprises a heavy chain comprising the V_H and a light chain comprising the V_L. In some embodiments, the

second antigen binding portion is fused to the first antigen binding portion at the N-terminus of the heavy chain, the N-terminus of the light chain, the C-terminus of the heavy chain, or the C-terminus of the light chain. In some embodiments, the first antigen binding portion comprises a full-length 4-chain antibody. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG1 Fc or IgG4 Fc.

[0130] In some embodiments, the first epitope and/or the second epitope is a pro-inflammatory molecule. "Pro-inflammatory molecule" refers to any molecule produced or expressed by an immune cell (such as monocytes, macrophages, lymphocytes and leukocytes) that up-regulates inflammatory reactions. In some embodiments, the pro-inflammatory molecule is a pro-inflammatory cytokine, such as lymphokine, monokine, chemokine, or interleukin. Exemplary pro-inflammatory molecules include, but are not limited to, IL-1β, TNF-α, IL-6, IL-6R, IL-5, IL-17, IL-23, IL- 22, IL-21, IL-12, and eotaxin-1 (*i.e.*, CCL11).

[0131] Thus, in some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a first pro-inflammatory molecule, and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds a second pro-inflammatory molecule, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the first pro-inflammatory molecule and/or the second pro-inflammatory molecule is selected from the group consisting of IL-1β, TNF-α, IL-5, IL-6, IL-6R, and eotaxin-1. In some embodiments, the first antigen binding portion comprises a heavy chain comprising the V_H and a light chain comprising the V_L. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of the heavy chain, the N-terminus of the light chain, the C-terminus of the heavy chain, or the C-terminus of the light chain. In some embodiments, the first antigen binding portion comprises a full-length 4-chain antibody. In some embodiments,

the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG1 Fc.

Fusion polypeptides

[0132] The first antigen binding portion and the second antigen binding portion of the multispecific antigen binding protein are fused (*i.e.*, covalently linked) to each other. Thus, the multispecific antigen binding proteins of the present application comprise one or more fusion polypeptides. Each fusion polypeptide may comprise the second antigen binding portion and a polypeptide from the first antigen binding portion.

[0133] The first antigen binding portion and the second antigen binding portion may be linked directly by a single chemical bond (such as peptide bond) or via a peptide linker. The second antigen binding portion may be fused at either the N-terminus or the C-terminus of any one (including each) polypeptide of the first antigen binding portion, or may be fused at an internal position of any one (including each) polypeptide of the first antigen binding portion. The fusion polypeptides may be obtained either recombinantly or chemically. In some embodiments, the C-terminus of the second antigen binding portion is fused to the N-terminus of any (including each) polypeptide of the first antigen binding portion via a chemical bond (such as peptide bond) or a peptide linker. In some embodiments, the N-terminus of the second antigen binding portion is fused to the C-terminus of any (including each) polypeptide of the first antigen binding portion via a chemical bond (such as peptide bond) or a peptide linker. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a chemical bond that is not a peptide bond involving the main chain chemical groups of amino acids.

[0134] In some embodiments, the first antigen binding portion comprises a single-chain antibody fragment comprising the V_H and V_L. In some embodiments, the first antigen binding portion comprises an scFv. In some embodiments, the multispecific antigen binding protein comprises a fusion polypeptide comprising in the N-terminus to C-terminus direction: the second antigen binding portion comprising the sdAb, an optional peptide linker, the V_H domain and the V_L domain. In some embodiments, the multispecific antigen binding protein comprises a fusion

polypeptide comprising in the N-terminus to C-terminus direction: the second antigen binding portion comprising the sdAb, an optional peptide linker, the V_L domain and the V_H domain. In some embodiments, the multispecific antigen binding protein comprises a fusion polypeptide comprising in the N-terminus to C-terminus direction: the V_H domain, the V_L domain, an optional peptide linker, and the second antigen binding portion comprising the sdAb. In some embodiments, the multispecific antigen binding protein comprises a fusion polypeptide comprising in the N-terminus to C-terminus direction: the V_L domain, the V_H domain, an optional peptide linker, and the second antigen binding portion comprising the sdAb.

[0135] In some embodiments, the first antigen binding portion comprises a heavy chain comprising the V_H domain, and a light chain comprising the V_L domain. In some embodiments, the heavy chain further comprises one or more heavy chain constant domains, such as C_H1, C_H2, C_H4, and C_H3, and/or an antibody hinge region (HR). In some embodiments, the light chain further comprises a light chain constant domain (C_L), such as the lambda C_L domain or kappa C_L domain. In some embodiments, the N-terminus of the second antigen binding portion is fused to the C-terminus of the heavy chain. In some embodiments, the C-terminus of the second antigen binding portion is fused to the N-terminus of the heavy chain. In some embodiments, the N-terminus of the second antigen binding portion is fused to the C-terminus of the light chain. In some embodiments, the C-terminus of the second antigen binding portion is fused to the N-terminus of the light chain. In some embodiments, the multispecific antigen binding protein comprises a first polypeptide comprising from the N-terminus to the C-terminus: the heavy chain, an optional peptide linker, and the second antigen binding portion comprising the sdAb; and a second polypeptide comprising the light chain. In some embodiments, the multispecific antigen binding protein comprises a first polypeptide comprising from the N-terminus to the C-terminus: the second antigen binding portion comprising the sdAb, an optional peptide linker, and the heavy chain; and a second polypeptide comprising the light chain. In some embodiments, the multispecific antigen binding protein comprises a first polypeptide comprising from the N-terminus to the C-terminus: the light chain, an optional peptide linker, and the second antigen binding portion comprising the sdAb; and a second polypeptide comprising the heavy chain. In some embodiments, the multispecific antigen binding protein comprises a first polypeptide comprising from the N-terminus to the C-terminus: the second antigen binding portion

comprising the sdAb, an optional peptide linker, and the light chain; and a second polypeptide comprising the heavy chain.

[0136] In some embodiments, the first antigen binding portion comprises a full-length antibody consisting of two heavy chains and two light chains. In some embodiments, the full-length antibody is a full-length monoclonal antibody consisting of two identical heavy chains and two identical light chains. In some embodiments, the multispecific antigen binding protein comprises two identical first polypeptides each comprising from the N-terminus to the C-terminus: the heavy chain, an optional peptide linker, and the second antigen binding portion comprising the sdAb; and two second polypeptides each comprising the light chain (see, for example, FIG. 4). In some embodiments, the multispecific antigen binding protein comprises two identify first polypeptides each comprising from the N-terminus to the C-terminus: the second antigen binding portion comprising the sdAb, an optional peptide linker, and the heavy chain; and two identical second polypeptides each comprising the light chain (see, for example, FIG. 9). In some embodiments, the multispecific antigen binding protein comprises two identical first polypeptides each comprising from the N-terminus to the C-terminus: the light chain, an optional peptide linker, and the second antigen binding portion comprising the sdAb; and two identical second polypeptides each comprising the heavy chain (see, for example, FIG. 11). In some embodiments, the multispecific antigen binding protein comprises two identical first polypeptides each comprising from the N-terminus to the C-terminus: the second antigen binding portion comprising the sdAb, an optional peptide linker, and the light chain; and two identical second polypeptides comprising the heavy chain (see, for example, FIG. 13).

[0137] In some embodiments, the multispecific antigen binding protein comprises: (a) a full-length antibody consisting of two heavy chains and two light chains, wherein the full-length antibody specifically recognizes a first epitope; (b) a first single-domain antibody that specifically recognizes a second epitope; and (c) a second single-domain antibody that specifically recognizes a third epitope, wherein the C-terminus of the first single domain antibody is fused to the N-terminus of each heavy chain, and wherein the N-terminus of the second single-domain antibody is fused to the C-terminus of each heavy chain. In some embodiments, the multispecific antigen binding protein comprises two identical first polypeptides each comprising from the N-terminus to the C-terminus: the first single-domain antibody, an optional peptide linker, the heavy chain, an optional peptide linker, and the second

single-domain antibody; and two identical second polypeptides each comprising the light chain. See, for example, FIG. 15.

[0138] In some embodiments, the multispecific antigen binding protein comprises: (a) a full-length antibody consisting of two heavy chains and two light chains, wherein the full-length antibody specifically recognizes a first epitope; (b) a first single-domain antibody that specifically recognizes a second epitope; and (c) a second single-domain antibody that specifically recognizes a third epitope, wherein the C-terminus of the first single domain antibody is fused to the N-terminus of each light chain, and wherein the N-terminus of the second single-domain antibody is fused to the C-terminus of each heavy chain. In some embodiments, the multispecific antigen binding protein comprises two identical first polypeptides each comprising from the N-terminus to the C-terminus: the heavy chain, an optional peptide linker, and the second single-domain antibody; and two identical second polypeptides each comprising the first single-domain antibody, an optional peptide linker, and the light chain. See, for example, FIG. 16.

[0139] Thus, in some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a heavy chain comprising a heavy chain variable domain (V_H) and a light chain comprising a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a first epitope, and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds a second epitope, wherein the N-terminus of the second antigen binding portion is fused to the C-terminus of the heavy chain of the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the first epitope is from a first immune checkpoint molecule, and the second epitope is from a second immune checkpoint molecule. In some embodiments, the first epitope is from a first tumor antigen, and the second epitope is from a second tumor antigen. In some embodiments, the first epitope is from a tumor antigen, and the second epitope is from a cell surface molecule, such as CD3. In some embodiments, the first epitope is from a first pro-inflammatory molecule, and the second epitope is from a second pro-inflammatory molecule. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino

acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG1 Fc or IgG4 Fc.

[0140] In some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a heavy chain comprising a heavy chain variable domain (V_H) and a light chain comprising a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a first epitope, and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds a second epitope, wherein the C-terminus of the second antigen binding portion is fused to the N-terminus of the heavy chain of the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the first epitope is from a first immune checkpoint molecule, and the second epitope is from a second immune checkpoint molecule. In some embodiments, the first epitope is from a first tumor antigen, and the second epitope is from a second tumor antigen. In some embodiments, the first epitope is from a tumor antigen, and the second epitope is from a cell surface molecule, such as CD3. In some embodiments, the first epitope is from a first pro-inflammatory molecule, and the second epitope is from a second pro-inflammatory molecule. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG1 Fc or IgG4 Fc.

[0141] In some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a heavy chain comprising a heavy chain variable domain (V_H) and a light chain comprising a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a first epitope, and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds a second epitope, wherein the N-terminus of the second antigen binding portion is fused to the C-terminus of the light chain of the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the first epitope is from a first immune checkpoint molecule, and the second epitope is from a second immune checkpoint molecule. In some embodiments, the first epitope is from a first tumor

antigen, and the second epitope is from a second tumor antigen. In some embodiments, the first epitope is from a tumor antigen, and the second epitope is from a cell surface molecule, such as CD3. In some embodiments, the first epitope is from a first pro-inflammatory molecule, and the second epitope is from a second pro-inflammatory molecule. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG1 Fc or IgG4 Fc.

[0142] In some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a heavy chain comprising a heavy chain variable domain (V_H) and a light chain comprising a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a first epitope, and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds a second epitope, wherein the C-terminus of the second antigen binding portion is fused to the N-terminus of the light chain of the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the first epitope is from a first immune checkpoint molecule, and the second epitope is from a second immune checkpoint molecule. In some embodiments, the first epitope is from a first tumor antigen, and the second epitope is from a second tumor antigen. In some embodiments, the first epitope is from a tumor antigen, and the second epitope is from a cell surface molecule, such as CD3. In some embodiments, the first epitope is from a first pro-inflammatory molecule, and the second epitope is from a second pro-inflammatory molecule. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG1 Fc or IgG4 Fc.

[0143] In some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a full-length antibody comprising two heavy chains and two light chains, wherein the full-length antibody specifically binds a first epitope, and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds a second epitope, wherein the N-terminus of the second antigen binding portion is fused to the C-terminus of one or each of the two heavy chains of the first

antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the first epitope is from a first immune checkpoint molecule, and the second epitope is from a second immune checkpoint molecule. In some embodiments, the first epitope is from a first tumor antigen, and the second epitope is from a second tumor antigen. In some embodiments, the first epitope is from a tumor antigen, and the second epitope is from a cell surface molecule, such as CD3. In some embodiments, the first epitope is from a first pro-inflammatory molecule, and the second epitope is from a second pro-inflammatory molecule. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG1 Fc or IgG4 Fc.

[0144] In some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a full-length antibody comprising two heavy chains and two light chains, wherein the full-length antibody specifically binds a first epitope, and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds a second epitope, wherein the C-terminus of the second antigen binding portion is fused to the N-terminus of one or each of the two heavy chains of the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the first epitope is from a first immune checkpoint molecule, and the second epitope is from a second immune checkpoint molecule. In some embodiments, the first epitope is from a first tumor antigen, and the second epitope is from a second tumor antigen. In some embodiments, the first epitope is from a tumor antigen, and the second epitope is from a cell surface molecule, such as CD3. In some embodiments, the first epitope is from a first pro-inflammatory molecule, and the second epitope is from a second pro-inflammatory molecule. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG1 Fc or IgG4 Fc.

[0145] In some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a full-length antibody comprising two heavy chains and two light chains, wherein the full-length antibody specifically

binds a first epitope, and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds a second epitope, wherein the N-terminus of the second antigen binding portion is fused to the C-terminus of one or each of the two light chains of the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the first epitope is from a first immune checkpoint molecule, and the second epitope is from a second immune checkpoint molecule. In some embodiments, the first epitope is from a first tumor antigen, and the second epitope is from a second tumor antigen. In some embodiments, the first epitope is from a tumor antigen, and the second epitope is from a cell surface molecule, such as CD3. In some embodiments, the first epitope is from a first pro-inflammatory molecule, and the second epitope is from a second pro-inflammatory molecule. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG1 Fc or IgG4 Fc.

[0146] In some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a full-length antibody comprising two heavy chains and two light chains, wherein the full-length antibody specifically binds a first epitope, and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds a second epitope, wherein the C-terminus of the second antigen binding portion is fused to the N-terminus of one or each of the two light chains of the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the first epitope is from a first immune checkpoint molecule, and the second epitope is from a second immune checkpoint molecule. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the first epitope is from a first tumor antigen, and the second epitope is from a second tumor antigen. In some embodiments, the first epitope is from a tumor antigen, and the second epitope is from a cell surface molecule, such as CD3. In some embodiments, the first epitope is from a first pro-inflammatory molecule, and the second epitope is from a second pro-inflammatory molecule. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG1 Fc or IgG4 Fc.

[0147] The multispecific antigen binding proteins described herein may comprise one or more peptide linkers situated between the first antigen binding portion and the second antigen binding portion. In some embodiments, the peptide linker between the heavy chain polypeptide of the first antigen binding portion and the second antigen binding portion is the same as the peptide linker between the light chain polypeptide of the first antigen binding portion and the second antigen binding portion. In some embodiments, the peptide linker between the heavy chain polypeptide of the first antigen binding portion and the second antigen binding portion is different from the peptide linker between the light chain polypeptide of the first antigen binding portion and the second antigen binding portion. In some embodiments, the first antigen binding portion and the second antigen binding portion are directly fused to each other without a peptide linker disposed therebetween.

[0148] The various antigen binding portions of the multispecific antigen binding proteins may be fused to each other via a peptide linker. The peptide linkers connecting different antigen binding portions may be the same or different. Each peptide linker can be optimized individually. The peptide linker can be of any suitable length. In some embodiments, the peptide linker is at least about any of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 50 or more amino acids long. In some embodiments, the peptide linker is no more than about any of 50, 40, 35, 30, 25, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5 or fewer amino acids long. In some embodiments, the length of the peptide linker is any of about 1 amino acid to about 10 amino acids, about 1 amino acids to about 20 amino acids, about 1 amino acid to about 30 amino acids, about 5 amino acids to about 15 amino acids, about 10 amino acids to about 25 amino acids, about 5 amino acids to about 30 amino acids, about 10 amino acids to about 30 amino acids long, about 30 amino acids to about 50 amino acids, or about 1 amino acid to about 50 amino acids.

[0149] The peptide linker may have a naturally occurring sequence, or a non-naturally occurring sequence. For example, a sequence derived from the hinge region of heavy chain only antibodies may be used as the linker. *See,* for example, WO1996/34103. In some embodiments, the peptide linker is a flexible linker. Exemplary flexible linkers include glycine polymers $(G)_n$, glycine-serine polymers (including, for example, $(GS)_n$, $(GSGGS)_n$ and $(GGGS)_n$, where n is an integer of at least one), glycine-alanine polymers, alanine-serine polymers, and other flexible

linkers known in the art. In some embodiments, the peptide linker comprises the amino acid sequence GGGGSGGGS (SEQ ID NO:1).

[0150] In some embodiments, the first antigen binding portion and the second antigen binding portion are fused to each other chemically. For example, the second antigen binding portion and one or more polypeptides of the first antigen binding portion may be conjugated using one or more reactive sites via a linking group. Reactive sites in polypeptides that are useful for chemical conjugation are well known in the art, including, but not limited to primary amino groups present on amino acid residue such as the epsilon amino group of lysine, and the alpha amino group of N-terminal amino acids, thiol groups in cysteine residues, the carboxylic group of the C-terminal amino acids, and carbohydrate groups in glycosylated antibodies. In some embodiments, the reactive site is introduced into the second antigen binding portion or the first antigen binding portion by site-directed mutagenesis, incorporation of selenocysteines or unnatural amino acids, incorporation of bifunctional linkers (such as bis-alkylating reagents), and/or glycoengineering. In some embodiments, one or more primary amino groups of a polypeptide can be converted to a thiol-containing group (*e.g.*, from a cysteine or homocysteine residue), an electrophilic unsaturated group such as a maleimide group, or halogenated group such as a bromoacetyl group, for conjugation to thiol reactive polypeptides. Any linking groups and conjugation methods known in the art can be used to chemically fuse the second antigen binding portion to the first antigen binding portion. In some embodiments, the conjugation can be achieved, for example, by using succinimide esters (such as succinimidyl 4-[N-maleimidomethyl]cyclohexane-1-carboxylate (SMCC), or N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS)), glutaraldehyde, carbodiimide (such as 1-ethyl-3-(3-dimethylaminopropyl) carbodiimide (EDCI)), benzidine (BDB), periodate, or isothiocyanate (such as N-acetyl homocysteine thiolactone (NAHT)).

Antigen binding portion comprising single-domain antibody

[0151] The multispecific antigen binding proteins of the present application comprise at least one antigen binding portion comprising a single-domain antibody. Exemplary sdAbs include, but are not limited to, heavy chain variable domains from heavy-chain only antibodies (*e.g.*, V_HH or V_{NAR}), binding molecules naturally devoid of light chains, single domains (such as V_H or V_L) derived from conventional 4-chain antibodies, humanized heavy-chain only antibodies, human single-domain antibodies produced by transgenic mice or rats expressing human heavy chain

segments, and engineered domains and single domain scaffolds other than those derived from antibodies. Any sdAbs known in the art or developed by the inventors may be used to construct the multispecific antigen binding proteins of the present application. The sdAbs may be derived from any species including, but not limited to mouse, rat, human, camel, llama, lamprey, fish, shark, goat, rabbit, and bovine. Single-domain antibodies contemplated herein also include naturally occurring single-domain antibody molecules from species other than *Camelidae* and sharks.

[0152] In some embodiments, the sdAb is derived from a naturally occurring single-domain antigen binding molecule known as heavy chain antibody devoid of light chains (also referred herein as "heavy chain only antibodies"). Such single domain molecules are disclosed in WO 94/04678 and Hamers-Casterman, C. *et al.* (1993) *Nature* 363:446-448, for example. For clarity reasons, the variable domain derived from a heavy chain molecule naturally devoid of light chain is known herein as a V_HH to distinguish it from the conventional VH of four chain immunoglobulins. Such a V_HH molecule can be derived from antibodies raised in *Camelidae* species, for example, camel, llama, vicuna, dromedary, alpaca and guanaco. Other species besides Camelidae may produce heavy chain molecules naturally devoid of light chain, and such V_HHs are within the scope of the present application.

[0153] V_HH molecules from Camelids are about 10 times smaller than IgG molecules. They are single polypeptides and can be very stable, resisting extreme pH and temperature conditions. Moreover, they can be resistant to the action of proteases which is not the case for conventional antibodies. Furthermore, *in vitro* expression of V_HH s produces high yield, properly folded functional V_HHs. In addition, antibodies generated in Camelids can recognize epitopes other than those recognized by antibodies generated *in vitro* through the use of antibody libraries or via immunization of mammals other than Camelids (see, for example, WO9749805). As such, multispecific antigen binding proteins comprising one or more V_HH domains may interact more efficiently with targets than conventional antibodies. Since V_HHs are known to bind into 'unusual' epitopes such as cavities or grooves, the affinity of multispecific antigen binding proteins comprising such V_HHs may be more suitable for therapeutic treatment than conventional multispecific polypeptides.

[0154] In some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a heavy chain variable

domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a first epitope, and (b) a second antigen binding portion comprising a V_HH domain that specifically binds a second epitope, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the first epitope is from a first immune checkpoint molecule, and the second epitope is from a second immune checkpoint molecule. In some embodiments, the first epitope is from a first tumor antigen, and the second epitope is from a second tumor antigen. In some embodiments, the first epitope is from a tumor antigen, and the second epitope is from a cell surface molecule, such as CD3. In some embodiments, the first epitope is from a first pro-inflammatory molecule, and the second epitope is from a second pro-inflammatory molecule. In some embodiments, the first antigen binding portion comprises a heavy chain comprising the V_H and a light chain comprising the V_L. In some embodiments, the V_HH domain is humanized. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of the heavy chain, the N-terminus of the light chain, the C-terminus of the heavy chain, or the C-terminus of the light chain. In some embodiments, the first antigen binding portion comprises a full-length 4-chain antibody. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG1 Fc or IgG4 Fc.

[0155] In some embodiments, the sdAb is derived from a variable region of the immunoglobulin found in cartilaginous fish. For example, the sdAb can be derived from the immunoglobulin isotype known as Novel Antigen Receptor (NAR) found in the serum of shark. Methods of producing single domain molecules derived from a variable region of NAR ("IgNARs") are described in WO 03/014161 and Streltsov (2005) *Protein Sci.* 14:2901-2909.

[0156] In some embodiments, the sdAb is recombinant, CDR-grafted, humanized, camelized, de-immunized and/or *in vitro* generated (*e.g.*, selected by phage display). In some embodiments, the sdAb is a human single-domain antibody produced by transgenic mice or rats expressing human heavy chain segments. See, *e.g.*, US20090307787A1, U.S. Pat. No. 8,754,287,

US20150289489A1, US20100122358A1, and WO2004049794. In some embodiments, the sdAb is affinity matured.

[0157] Single-domain antibodies comprising a V_HH domain can be humanized to have human-like sequences. In some embodiments, the FR regions of the V_HH domain used herein comprise at least about any one of 50%, 60%, 70%, 80%, 90%, 95% or more of amino acid sequence homology to human VH framework regions. One exemplary class of humanized V_HH domains is characterized in that the V_HHs carry an amino acid from the group consisting of glycine, alanine, valine, leucine, isoleucine, proline, phenylalanine, tyrosine, tryptophan, methionine, serine, threonine, asparagine, or glutamine at position 45, such as, for example, L45 and a tryptophan at position 103, according to the Kabat numbering. As such, polypeptides belonging to this class show a high amino acid sequence homology to human VH framework regions and said polypeptides might be administered to a human directly without expectation of an unwanted immune response therefrom, and without the burden of further humanization.

[0158] Another exemplary class of humanized Camelidae single-domain antibodies has been described in WO 03/035694 and contains hydrophobic FR2 residues typically found in conventional antibodies of human origin or from other species, but compensating this loss in hydrophilicity by the charged arginine residue on position 103 that substitutes the conserved tryptophan residue present in V_H from double-chain antibodies. As such, peptides belonging to these two classes show a high amino acid sequence homology to human V_H framework regions and said peptides might be administered to a human directly without expectation of an unwanted immune response therefrom, and without the burden of further humanization.

[0159] In some embodiments, the multispecific antigen binding protein comprises an antigen binding portion comprising an sdAb having a suitable affinity to its epitope. For example, the affinity of the sdAb may affect the overall affinity and avidity of the multispecific antigen binding protein to the target cell or tissue, which may further affect the efficacy of the multispecific antigen binding protein. In some embodiments, the sdAb binds its epitope with high affinity. A high-affinity sdAb binds its epitope with a dissociation constant (Kd) in the low nanomolar (10^{-9} M) range, such as no more than about any of 5 nM, 4 nM, 3 nM, 2 nM, 1 nM, 0.5 nM, 0.2 nM, 0.1 nM, 0.05 nM, 0.02 nM, 0.01 nM, 5 pM, 2 pM, 1 pM or less. In some embodiments, the sdAb binds its epitope with low affinity. A low-affinity sdAb binds its epitope with a Kd in the low micromolar (10^{-6} M) range or higher, such as more than about any of 1 μM,

2 μM, 3 μM, 4 μM, 5 μM, 6 μM, 7 μM, 8 μM, 9 μM, 10 μM or more. In some embodiments, the sdAb binds its epitope with medium affinity. A medium-affinity sdAb binds its epitope with a Kd lower than that of a low-affinity sdAb but higher than that of a high-affinity sdAb. In some embodiments, a medium-affinity sdAb binds its epitope with a Kd of any one of about 1 nM to about 10 nM, about 10 nM to about 100 nM, about 100 nM to about 500 nM, about 500 nM to about 1 μM, about 1 nM to about 100 nM, about 10 nM to about 500 nM, or about 1 nM to about 1 μM.

[0160] In some embodiments, the sdAb specifically binds an immune checkpoint molecule. In some embodiments, the sdAb specifically binds a stimulatory immune checkpoint molecule. In some embodiments, the sdAb specifically binds an inhibitory immune checkpoint molecule. In some embodiments, the sdAb specifically binds an immune checkpoint molecule selected from the group consisting of PD-1, PD-L1, PD-L2, CTLA-4, B7-H3, TIM-3, LAG-3, VISTA, ICOS, 4-1BB, OX40, GITR, and CD40. In some embodiments, the sdAb is an agonist for the immune checkpoint molecule. In some embodiments, the sdAb is an antagonist against the immune checkpoint molecule.

[0161] Thus, in some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a first epitope, and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds a second epitope of an immune checkpoint molecule, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the immune checkpoint molecule is selected from the group consisting of PD-1, PD-L1, PD-L2, CTLA-4, B7-H3, TIM-3, LAG-3, VISTA, ICOS, 4-1BB, OX40, GITR, and CD40. In some embodiments, the first epitope is from a second immune checkpoint molecule. In some embodiments, the first epitope is from a pro-inflammatory molecule, such as a pro-inflammatory cytokine. In some embodiments, the pro-inflammatory molecule is selected from the group consisting of IL-1β, TNF-α, IL-5, IL-6, IL-6R and eotaxin-1. In some embodiments, the first antigen binding portion comprises a heavy chain comprising the V_H and a light chain comprising the V_L. In some embodiments, the second antigen binding portion is fused to the first antigen

binding portion at the N-terminus of the heavy chain, the N-terminus of the light chain, the C-terminus of the heavy chain, or the C-terminus of the light chain. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG4 Fc.

[0162] In some embodiments, the sdAb specifically binds CTLA-4. In some embodiments, the sdAb binds CTLA-4 with high affinity. In some embodiments, the sdAb binds CTLA-4 with medium affinity. In some embodiments, the sdAb binds CTLA-4 with low affinity.

[0163] In some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds an epitope of an immune checkpoint molecule, and (b) a second antigen binding portion comprising a single-domain antibody (*e.g.*, a V_HH) that specifically binds CTLA-4, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the immune checkpoint molecule is an epitope of CTLA-4 that is different from the epitope specifically recognized by the single-domain antibody. In some embodiments, the immune checkpoint molecule is selected from the group consisting of PD-1, PD-L1, PD-L2, B7-H3, TIM-3, LAG-3, VISTA, ICOS, 4-1BB, OX40, GITR, and CD40. In some embodiments, the first antigen binding portion comprises a full-length anti-PD-1 monoclonal antibody (such as pembrolizumab or nivolumab) or antigen binding fragment thereof. In some embodiments, the first antigen binding portion comprises a full-length anti-PD-L1 monoclonal antibody (such as duravalumab or atezolizumab) or antigen binding fragment thereof. In some embodiments, the sdAb binds CTLA-4 with high affinity. In some embodiments, the sdAb binds CTLA-4 with medium affinity. In some embodiments, the sdAb binds CTLA-4 with low affinity. In some embodiments, the first antigen binding portion comprises a heavy chain comprising the V_H and a light chain comprising the V_L. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of the heavy chain, the N-terminus of the light chain, the C-

terminus of the heavy chain, or the C-terminus of the light chain. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG4 Fc.

[0164] In some embodiments, the sdAb specifically binds TIM-3. In some embodiments, the sdAb binds TIM-3 with high affinity. In some embodiments, the sdAb binds TIM-3 with medium affinity. In some embodiments, the sdAb binds TIM-3 with low affinity.

[0165] Thus, in some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds an epitope of an immune checkpoint molecule, and (b) a second antigen binding portion comprising a single-domain antibody (*e.g.*, a V_HH) that specifically binds TIM-3, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the immune checkpoint molecule is selected from the group consisting of CTLA-4, PD-1, PD-L1, PD-L2, B7-H3, LAG-3, VISTA, ICOS, 4-1BB, OX40, GITR, and CD40. In some embodiments, the first antigen binding portion comprises a full-length anti-PD-1 monoclonal antibody (such as pembrolizumab or nivolumab) or antigen binding fragment thereof. In some embodiments, the first antigen binding portion comprises a full-length anti-PD-L1 monoclonal antibody (such as duravalumab or atezolizumab) or antigen binding fragment thereof. In some embodiments, the first antigen binding portion comprises a heavy chain comprising the V_H and a light chain comprising the V_L. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of the heavy chain, the N-terminus of the light chain, the C-terminus of the heavy chain, or the C-terminus of the light chain. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In

some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG4 Fc.

[0166] In some embodiments, the sdAb specifically binds LAG-3. In some embodiments, the sdAb binds LAG-3 with high affinity. In some embodiments, the sdAb binds LAG-3 with medium affinity. In some embodiments, the sdAb binds LAG-3 with low affinity.

[0167] Thus, in some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds an epitope of an immune checkpoint molecule, and (b) a second antigen binding portion comprising a single-domain antibody (*e.g.*, a V_HH) that specifically binds LAG-3, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the immune checkpoint molecule is selected from the group consisting of CTLA-4, PD-1, PD-L1, PD-L2, B7-H3, TIM-3, VISTA, ICOS, 4-1BB, OX40, GITR, and CD40. In some embodiments, the first antigen binding portion comprises a full-length anti-PD-1 monoclonal antibody (such as pembrolizumab or nivolumab) or antigen binding fragment thereof. In some embodiments, the first antigen binding portion comprises a full-length anti-PD-L1 monoclonal antibody (such as duravalumab or atezolizumab) or antigen binding fragment thereof. In some embodiments, the first antigen binding portion comprises a heavy chain comprising the V_H and a light chain comprising the V_L. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of the heavy chain, the N-terminus of the light chain, the C-terminus of the heavy chain, or the C-terminus of the light chain. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG4 Fc.

[0168] In some embodiments, the sdAb specifically binds VISTA. In some embodiments, the sdAb binds VISTA with high affinity. In some embodiments, the sdAb binds VISTA with medium affinity. In some embodiments, the sdAb binds VISTA with low affinity.

[0169] Thus, in some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds an epitope of an immune checkpoint molecule, and (b) a second antigen binding portion comprising a single-domain antibody (*e.g.*, a V_HH) that specifically binds VISTA, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the immune checkpoint molecule is selected from the group consisting of CTLA-4, PD-1, PD-L1, PD-L2, B7-H3, TIM-3, LAG-3, ICOS, 4-1BB, OX40, GITR, and CD40. In some embodiments, the first antigen binding portion comprises a full-length anti-PD-1 monoclonal antibody (such as pembrolizumab or nivolumab) or antigen binding fragment thereof. In some embodiments, the first antigen binding portion comprises a full-length anti-PD-L1 monoclonal antibody (such as duravalumab or atezolizumab) or antigen binding fragment thereof. In some embodiments, the first antigen binding portion comprises a heavy chain comprising the V_H and a light chain comprising the V_L. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of the heavy chain, the N-terminus of the light chain, the C-terminus of the heavy chain, or the C-terminus of the light chain. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG4 Fc.

[0170] In some embodiments, the sdAb specifically binds a cell surface antigen. In some embodiments, the cell surface antigen is a tumor antigen. In some embodiments, the sdAb specifically binds a cell surface antigen on an immune effector cell, such as T cell, or Natural Killer cell.

[0171] In some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a first tumor antigen, and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds a second tumor antigen, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the first tumor antigen and/or the second tumor antigen is selected from the group consisting of HER2, BRAF, EGFR, VEGFR2, CD20, RANKL, CD38, and CD52. In some embodiments, the first antigen binding portion comprises a full-length anti-HER-2 monoclonal antibody (such as trastuzumab) or antigen binding fragment thereof. In some embodiments, the first antigen binding portion comprises a heavy chain comprising the V_H and a light chain comprising the V_L. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of the heavy chain, the N-terminus of the light chain, the C-terminus of the heavy chain, or the C-terminus of the light chain. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG1 Fc.

[0172] In some embodiments, the sdAb specifically binds CD3. In some embodiments, the sdAb binds CD3 with high affinity. In some embodiments, the sdAb binds CD3 with medium affinity. In some embodiments, the sdAb binds CD3 with low affinity.

[0173] Thus, in some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds an epitope of a tumor antigen, and (b) a second antigen binding portion comprising a single-domain antibody (*e.g.*, a V_HH) that specifically binds CD3, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid,

humanized, or human single-domain antibody. In some embodiments, the tumor antigen is selected from the group consisting of HER2, BRAF, EGFR, VEGFR2, CD20, RANKL, CD38, and CD52. In some embodiments, the first antigen binding portion comprises a full-length anti-HER-2 monoclonal antibody (such as trastuzumab) or antigen binding fragment thereof. In some embodiments, the first antigen binding portion comprises a heavy chain comprising the V_H and a light chain comprising the V_L. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of the heavy chain, the N-terminus of the light chain, the C-terminus of the heavy chain, or the C-terminus of the light chain. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG4 Fc.

[0174] In some embodiments, the sdAb specifically binds an extracellular protein, such as a secreted protein.

[0175] In some embodiments, the sdAb specifically binds a pro-inflammatory molecule.

[0176] In some embodiments, the sdAb specifically binds IL-1β. In some embodiments, the sdAb binds IL-1β with high affinity. In some embodiments, the sdAb binds IL-1β with medium affinity. In some embodiments, the sdAb binds IL-1β with low affinity.

[0177] Thus, in some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds an epitope of a pro-inflammatory molecule, and (b) a second antigen binding portion comprising a single-domain antibody (*e.g.*, a V_HH) that specifically binds IL-1β, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the pro-inflammatory molecule is selected from the group consisting of TNF-α, IL-5, IL-6, IL-6R and eotaxin-1. In some embodiments, the first antigen binding portion comprises a full-length anti-TNF-α monoclonal antibody (such as adalimumab) or antigen binding fragment thereof. In some

embodiments, the first antigen binding portion comprises a heavy chain comprising the V_H and a light chain comprising the V_L. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of the heavy chain, the N-terminus of the light chain, the C-terminus of the heavy chain, or the C-terminus of the light chain. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG1 Fc.

[0178] In some embodiments, the sdAb specifically binds eotaxin-1, *i.e.*, CCL11.

[0179] Thus, in some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds an epitope of a pro-inflammatory molecule, and (b) a second antigen binding portion comprising a single-domain antibody (*e.g.*, a V_HH) that specifically binds eotaxin-1, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the pro-inflammatory molecule is selected from the group consisting of IL-1β, TNF-α, IL-5, IL-6 and IL-6R. In some embodiments, the first antigen binding portion comprises a full-length anti-IL-5 monoclonal antibody (such as mepolizumab) or antigen binding fragment thereof. In some embodiments, the first antigen binding portion comprises a heavy chain comprising the V_H and a light chain comprising the V_L. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of the heavy chain, the N-terminus of the light chain, the C-terminus of the heavy chain, or the C-terminus of the light chain. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long.

In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG1 Fc.

Antigen binding portion comprising V_H and V_L

[0180] The multispecific antigen binding proteins of the present application comprise at least one antigen binding portion comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L). Such antigen binding portion can be a full-length conventional antibody consisting of two heavy chains and two light chains, or an antigen binding fragment derived therefrom.

[0181] In some embodiments, the first antigen binding portion is an antigen binding fragment comprising a heavy chain comprising the V_H domain and a light chain comprising the V_L domain. Exemplary antigen binding fragments contemplated herein include, but are not limited to, Fab, Fab', $F(ab')_2$, and Fv fragments; diabodies; linear antibodies; single-chain antibody molecules (such as scFv); and multispecific antibodies formed from antibody fragments.

[0182] In some embodiments, the first antigen binding portion comprises an Fc region, such as a human Fc region. In some embodiments, the Fc region is derived from an IgG molecule, such as any one of the IgG1, IgG2, IgG3, or IgG4 subclass. In some embodiments, the Fc region is capable of mediating an antibody effector function, such as ADCC (antibody- dependent cell-mediated cytotoxicity) and/or CDC (complement-dependent cytotoxicity). For example, antibodies of subclass IgGl, IgG2, and IgG3 with wildtype Fc sequences usually show complement activation including CIq and C3 binding, whereas IgG4 does not activate the complement system and does not bind CIq and/or C3. In some embodiments, the Fc region comprises a modification that reduces binding affinity of the Fc region to an Fc receptor. In some embodiments, the Fc region is an IgG1 Fc. In some embodiments, the IgG1 Fc comprises one or mutations in positions 233-236, such as L234A and/or L235A. In some embodiments, the Fc region is an IgG4 Fc. In some embodiments, the IgG4 Fc comprises a mutation in positions 327, 330 and/or 331. See, for example, Armour KL *et al.*, *Eur J. Immunol.* 1999; 29: 2613; and Shields RL *et al.*, J. Biol. Chem. 2001; 276: 6591. In some embodiments, the Fc region comprises a P329G mutation.

[0183] In some embodiments, the Fc region comprises a modification that promotes heterodimerization of two non-identical heavy chains. Such modified Fc regions may be of particular interest for multispecific antigen binding proteins described herein having an

asymmetric design. In some embodiments, said modification is a knob-into-hole modification, comprising a knob modification in one of the heavy chains or heavy chain fusion polypeptides and a hole modification in the other one of the two heavy chains or heavy chain fusion polypeptides. In one embodiment, the Fc region comprises a modification within the interface between the two heavy chains in the CH3 domain, wherein i) in the CH3 domain of one heavy chain, an amino acid residue is replaced with an amino acid residue having a larger side chain volume, thereby generating a protuberance ("knob") within the interface in the CH3 domain of one heavy chain which is positionable in a cavity ("hole") within the interface in the CH3 domain of the other heavy chain, and ii) in the CH3 domain of the other heavy chain, an amino acid residue is replaced with an amino acid residue having a smaller side chain volume, thereby generating a cavity ("hole") within the interface in the second CH3 domain within which a protuberance ("knob") within the interface in the first CH3 domain is positionable. Examples of knob-into-hole modifications have been described, for example, in US 2011/0287009, US2007/0178552, WO 96/027011, WO 98/050431, and Zhu *et al.*, 1997, *Protein Science* 6:781-788. Other modifications to the Fc region that promote heterodimerization are also contemplated herein. For example, electrostatic steering effects can be engineered into the Fc region to provide Fc-heterodimeric molecules (see, *e.g.*, US4676980, and Brennan *et al.*, *Science*, 229: 81 (1985)).

[0184] In some embodiments, the Fc region comprises a modification that inhibits Fab arm exchange. For example, the S228P mutation in IgG4 Fc prevents Fab arm exchange.

[0185] In some embodiments, the first antigen binding portion comprises a kappa light chain constant region. In some embodiments, the first antigen binding portion comprises a lambda light chain constant region. In some embodiments, the first antigen binding portion comprises a light chain constant region comprising the amino acid sequence of SEQ ID NO: 6.

[0186] In some embodiments, the first antigen binding portion comprises a heavy chain constant region comprising the amino acid sequence of SEQ ID NO: 7.

[0187] In some embodiments, the first antigen binding portion is a full-length antibody consisting of two heavy chains and two light chains. In some embodiments, the first antigen binding portion comprises a monoclonal antibody consisting of two heavy chains and two light chains (also referred herein as “4-chain antibody”). In some embodiments, the first antigen binding portion comprises a multispecific (such as bispecific) full-length antibody consisting of two heavy chains and two light chains. In some embodiments, the first antigen binding portion

comprises a full-length antibody of human IgGl subclass, or of human IgGl subclass with the mutations L234A and L235A. In some embodiments, the first antigen binding portion comprises a full-length antibody of human IgG2 subclass. In some embodiments, the first antigen binding portion comprises a full-length antibody of human IgG3 subclass. In some embodiments, the first antigen binding portion comprises a full-length antibody of human IgG4 subclass or, of human IgG4 subclass with the additional mutation S228P.

[0188] Any full-length 4-chain antibody known in the art or antigen binding fragments derived therefrom can be used as the first antigen binding portion in the multispecific antigen binding protein of the present application. Antibodies or antibody fragments with proven clinical efficacy, safety, and pharmacokinetics profile are of particular interest. In some embodiments, the antibody or antibody fragment known in the art is further engineered, such as humanized or mutagenized to select for a variant with a suitable affinity, prior to fusion with the second antigen binding portion to provide the multispecific antigen binding protein. In some embodiments, the first antigen binding portion comprises the V_H and V_L domains of a monoclonal antibody or antibody fragment known in the art, and modified heavy chain constant region and/or light chain constant region. In some embodiments, the first antigen binding portion comprises the monoclonal antibody known in the art and a modified Fc region, such as an IgG4 Fc with an S228P mutation. In some embodiments, the first antigen binding portion comprises a human, humanized, or chimeric full-length antibody or antibody fragments.

[0189] In some embodiments, the first antigen binding portion is derived from an approved (such as by FDA and/or EMA) or investigational monoclonal antibody or antibody fragment (such as Fab). In some embodiments, the first antigen binding portion is an approved (such as by FDA and/or EMA) or investigational monoclonal antibody or antibody fragment (such as Fab).

[0190] In some embodiments, the first antigen binding portion specifically binds an immune checkpoint molecule. In some embodiments, the first antigen binding portion comprises a full-length antibody (such as antagonist antibody) or antigen binding fragment derived therefrom that specifically binds an inhibitory immune checkpoint protein. In some embodiments, the first antigen binding portion comprises a full-length antibody (such as agonist antibody) or antigen binding fragment derived therefrom that specifically binds a stimulatory checkpoint molecule. In some embodiments, the immune checkpoint molecule is selected from the group consisting of

PD-1, PD-L1, PD-L2, CTLA-4, B7-H3, TIM-3, LAG-3, VISTA, ICOS, 4-1BB, OX40, GITR, and CD40. In some embodiments, the first antigen binding portion is an anti-PD-1 antibody or antigen binding fragment thereof. In some embodiments, the anti-PD-1 antibody is selected from the group consisting of pembrolizumab and nivolumab. In some embodiments, the first antigen binding portion is an anti-PD-L1 antibody or antigen binding fragment thereof. In some embodiments, the anti-PD-L1 antibody is duravalumab or atezolizumab. In some embodiments, the first antigen binding portion is an anti-CTLA-4 antibody or antigen binding fragment thereof. In some embodiments, the anti-CTLA-4 antibody is ipilimumab.

[0191] In some embodiments, the first antigen binding portion comprises pembrolizumab or antigen binding fragment thereof. In some embodiments, the first antigen binding portion comprises a V_H domain comprising the amino acid sequence of SEQ ID NO: 2 and a V_L domain comprising the amino acid sequence of SEQ ID NO: 3. In some embodiments, the first antigen binding portion comprises an IgG4 Fc. In some embodiments, the first antigen binding portion comprises a heavy chain comprising the amino acid sequence of SEQ ID NO: 4. In some embodiments, the first antigen binding portion comprises a light chain comprising the amino acid sequence of SEQ ID NO: 5. In some embodiments, the first antigen binding portion comprises an IgG4 Fc.

[0192] Pembrolizumab (KETRUDA®) is a humanized antibody used in cancer immunotherapy. It targets the programmed cell death 1 (PD-1) receptor. The drug was initially used in treating metastatic melanoma. On September 4, 2014 the US Food and Drug Administration (FDA) approved KETRUDA® under the FDA Fast Track Development Program. It is approved for use in advanced melanoma. On October 2, 2015, the US FDA approved KETRUDA® for the treatment of metastatic non-small cell lung cancer in patients whose tumors express PD-L1 and who have failed treatments with other chemotherapeutic agents.

[0193] Ipilimumab (YERVOY®) is a fully human anti-CTLA-4 immunoglobulin G1 (IgG1) monoclonal antibody (mAb) that blocks the down-regulation of T-cell activation. Ipilimumab is a CTLA-4 immune checkpoint inhibitor that blocks T-cell inhibitory signals induced by the CTLA-4 pathway, and increases the number of tumor reactive T effector cells. Ipilimumab was used in combination with nivolumab (OPDIVO®) to investigate the effects of concurrent inhibition of the PD-1 and CTLA-4 receptors in nonhuman primates. Nivolumab has demonstrated clinical efficacy either as monotherapy or in combination with ipilimumab in

treating several tumor types, including renal cell carcinoma, melanoma, NSCLC, and some lymphomas. BMS recently announced the treatment results of immune combination therapy nivolumab and ipilimumab for treating melanoma. Compared with ipilimumab monotherapy, the combined therapy achieved a very high objective response rate (61% vs 11%) and complete remission rate of 22%, while disease progression or death risk decreased by 60%. This kind of therapy demonstrated the great potential of different combinations of immune therapeutic agents in clinical treatment of cancer.

[0194] In some embodiments, the first antigen binding portion specifically binds a tumor antigen. In some embodiments, the tumor antigen is selected from the group consisting of HER2, BRAF, EGFR, VEGFR2, CD20, RANKL, CD38, and CD52. In some embodiments, the first antigen binding portion is an anti-HER2 antibody or antigen binding fragment thereof. In some embodiments, the anti-HER2 antibody is trastuzumab.

[0195] Trastuzumab (HERCEPTIN®), one of the five top selling therapeutic antibodies, is a humanized anti-HER2 receptor monoclonal antibody that has significantly increased the survival rate in patients with HER2-positive breast cancer. The HER receptors are proteins that are embedded in the cell membrane and communicate molecular signals from outside the cell (molecules called EGFs) to inside the cell, and turn genes on and off. The HER protein, Human Epidermal Growth Factor Receptor, binds Human Epidermal Growth Factor, and stimulates cell proliferation. In some cancers, notably certain types of breast cancer, HER2 is over-expressed, and causes cancer cells to reproduce uncontrollably. However, among breast cancer patients, only 15-20% of them exhibit amplification and overexpression of the human epidermal growth factor receptor 2 (HER2), most HER2- patients do not respond to trastuzumab. In addition, some of the HER2+ patients have developed resistance to trastuzumab after initial treatment. As the epidermal growth factor RTK family consists of four members: EGFR, HER2, HER3 and HER4, some bispecific antibodies have been developed to target two of these antigens, which have shown advantages over conventional monospecific antibodies.

[0196] In some embodiments, the first antigen binding portion specifically binds a pro-inflammatory molecule. In some embodiments, the pro-inflammatory molecule is selected from the group consisting of IL-1β, TNF-α, IL-5, IL-6, IL-6R and eotaxin-1. In some embodiments, the first antigen binding portion is an anti-TNF-α antibody or antigen binding fragment thereof. In some embodiments, the anti-TNF-α antibody is adalimumab.

Exemplary multispecific antigen binding proteins

[0197] In some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a full-length antibody (such as pembrolizumab or nivolumab) consisting of two heavy chains and two light chains, wherein the full-length antibody specifically binds PD-1; and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds CTLA-4, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the single-domain antibody binds CTLA-4 with a high affinity. In some embodiments, the single-domain antibody binds CTLA-4 with a medium affinity. In some embodiments, the single-domain antibody binds CTLA-4 with a low affinity. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of one or each of the two heavy chains, the N-terminus of one or each of the two light chains, the C-terminus of one or each of the two heavy chains, or the C-terminus of one or each of the two light chains. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the peptide linker comprises the amino acid sequence of SEQ ID NO: 1. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG4 Fc.

[0198] In some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a full-length antibody (such as pembrolizumab or nivolumab) consisting of two heavy chains and two light chains, wherein the full-length antibody specifically binds PD-1; and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds TIM-3, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of one or each of the two heavy chains, the N-terminus of one or each of the two light chains, the C-terminus of one or each of the two heavy chains, or the C-

terminus of one or each of the two light chains. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the peptide linker comprises the amino acid sequence of SEQ ID NO: 1. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG4 Fc.

[0199] In some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a full-length antibody (such as pembrolizumab or nivolumab) consisting of two heavy chains and two light chains, wherein the full-length antibody specifically binds PD-1; and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds LAG-3, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of one or each of the two heavy chains, the N-terminus of one or each of the two light chains, the C-terminus of one or each of the two heavy chains, or the C-terminus of one or each of the two light chains. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the peptide linker comprises the amino acid sequence of SEQ ID NO: 1. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG4 Fc.

[0200] In some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a full-length antibody (such as pembrolizumab or nivolumab) consisting of two heavy chains and two light chains, wherein the full-length antibody specifically binds PD-1; and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds VISTA, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain

antibody. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of one or each of the two heavy chains, the N-terminus of one or each of the two light chains, the C-terminus of one or each of the two heavy chains, or the C-terminus of one or each of the two light chains. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the peptide linker comprises the amino acid sequence of SEQ ID NO: 1. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG4 Fc.

[0201] In some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a heavy chain comprising a V_H domain comprising the amino acid sequence of SEQ ID NO: 2 and a light chain comprising a V_L domain comprising the amino acid sequence of SEQ ID NO: 3; and (b) a second antigen binding portion comprising an anti-CTLA-4 single-domain antibody, and wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the first antigen binding portion is full-length pembrolizumab. In some embodiments, the N-terminus of the second antigen binding portion is fused to the C-terminus of the heavy chain of the first antigen binding portion via an optional peptide linker. In some embodiments, the C-terminus of the second antigen binding portion is fused to the N-terminus of the heavy chain of the first antigen binding portion via an optional peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the peptide linker comprises the amino acid sequence of SEQ ID NO: 1. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG4 Fc.

[0202] In some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a full-length antibody (such as duravalumab or atezolizumab) consisting of two heavy chains and two light chains, wherein the full-length antibody specifically binds PD-L1; and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds CTLA-4, wherein the first

antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the single-domain antibody binds CTLA-4 with a high affinity. In some embodiments, the single-domain antibody binds CTLA-4 with a medium affinity. In some embodiments, the single-domain antibody binds CTLA-4 with a low affinity. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of one or each of the two heavy chains, the N-terminus of one or each of the two light chains, the C-terminus of one or each of the two heavy chains, or the C-terminus of one or each of the two light chains. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the peptide linker comprises the amino acid sequence of SEQ ID NO: 1. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG4 Fc.

[0203] In some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a full-length antibody (such as duravalumab or atezolizumab) consisting of two heavy chains and two light chains, wherein the full-length antibody specifically binds PD-L1; and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds TIM-3, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of one or each of the two heavy chains, the N-terminus of one or each of the two light chains, the C-terminus of one or each of the two heavy chains, or the C-terminus of one or each of the two light chains. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the

peptide linker comprises the amino acid sequence of SEQ ID NO: 1. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG4 Fc.

[0204] In some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a full-length antibody (such as duravalumab or atezolizumab) consisting of two heavy chains and two light chains, wherein the full-length antibody specifically binds PD-L1; and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds LAG-3, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of one or each of the two heavy chains, the N-terminus of one or each of the two light chains, the C-terminus of one or each of the two heavy chains, or the C-terminus of one or each of the two light chains. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the peptide linker comprises the amino acid sequence of SEQ ID NO: 1. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG4 Fc.

[0205] In some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a full-length antibody (such as duravalumab or atezolizumab) consisting of two heavy chains and two light chains, wherein the full-length antibody specifically binds PD-L1; and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds VISTA, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of one or each of the two heavy chains, the N-terminus of one or each of the two light chains, the C-terminus of one or each of the two heavy chains, or the C-terminus of one or each of the two light chains. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments,

the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the peptide linker comprises the amino acid sequence of SEQ ID NO: 1. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG4 Fc.

[0206] In some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a full-length antibody (such as trastuzumab) consisting of two heavy chains and two light chains, wherein the full-length antibody specifically binds HER2 receptor; and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds CD3, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of one or each of the two heavy chains, the N-terminus of one or each of the two light chains, the C-terminus of one or each of the two heavy chains, or the C-terminus of one or each of the two light chains. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the peptide linker comprises the amino acid sequence of SEQ ID NO: 1. In some embodiments, the first antigen binding fragment comprises an Fc region, such as IgG4 Fc.

[0207] In some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a full-length antibody (such as adalimumab) consisting of two heavy chains and two light chains, wherein the full-length antibody specifically binds TNF-α; and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds IL-1β, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of one or each of the two heavy chains, the N-terminus of one or each of the two

light chains, the C-terminus of one or each of the two heavy chains, or the C-terminus of one or each of the two light chains. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the peptide linker comprises the amino acid sequence of SEQ ID NO: 1. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG1 Fc.

[0208] In some embodiments, there is provided a multispecific (such as bispecific) antigen binding protein comprising: (a) a first antigen binding portion comprising a full-length antibody (such as mepolizumab) consisting of two heavy chains and two light chains, wherein the full-length antibody specifically binds IL-5; and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds eotaxin-1, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of one or each of the two heavy chains, the N-terminus of one or each of the two light chains, the C-terminus of one or each of the two heavy chains, or the C-terminus of one or each of the two light chains. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the peptide linker comprises the amino acid sequence of SEQ ID NO: 1. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG1 Fc.

III. Pharmaceutical compositions

[0209] Further provided by the present application are pharmaceutical compositions comprising any one of the multispecific antigen binding proteins as described herein, and a pharmaceutically acceptable carrier. Pharmaceutical compositions can be prepared by mixing a multispecific 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.

[0210] Acceptable carriers, excipients, or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers, antioxidants including ascorbic acid, methionine, Vitamin E, sodium metabisulfite; preservatives, isotonicifiers, stabilizers, metal complexes (*e.g.* Zn-protein complexes); chelating agents such as EDTA and/or non-ionic surfactants.

[0211] Buffers are used to control the pH in a range which optimizes the therapeutic effectiveness, especially if stability is pH dependent. Buffers are preferably present at concentrations ranging from about 50 mM to about 250 mM. Suitable buffering agents for use in the present application include both organic and inorganic acids and salts thereof. For example, citrate, phosphate, succinate, tartrate, fumarate, gluconate, oxalate, lactate, acetate. Additionally, buffers may comprise histidine and trimethylamine salts such as Tris.

[0212] Preservatives are added to retard microbial growth, and are typically present in a range from 0.2%-1.0% (w/v). Suitable preservatives for use in the present application include octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium halides (*e.g.*, chloride, bromide, iodide), benzethonium chloride; thimerosal, phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol, 3-pentanol, and m-cresol.

[0213] Tonicity agents, sometimes known as "stabilizers" are present to adjust or maintain the tonicity of liquid in a composition. When used with large, charged biomolecules such as proteins and antibodies, they are often termed "stabilizers" because they can interact with the charged groups of the amino acid side chains, thereby lessening the potential for inter and intra-molecular interactions. Tonicity agents can be present in any amount between 0.1% to 25% by weight, preferably 1 to 5%, taking into account the relative amounts of the other ingredients. Preferred tonicity agents include polyhydric sugar alcohols, preferably trihydric or higher sugar alcohols, such as glycerin, erythritol, arabitol, xylitol, sorbitol and mannitol.

[0214] Additional excipients include agents which can serve as one or more of the following: (1) bulking agents, (2) solubility enhancers, (3) stabilizers and (4) and agents preventing denaturation or adherence to the container wall. Such excipients include: polyhydric sugar alcohols (enumerated above); amino acids such as alanine, glycine, glutamine, asparagine,

histidine, arginine, lysine, ornithine, leucine, 2-phenylalanine, glutamic acid, threonine, etc.; organic sugars or sugar alcohols such as sucrose, lactose, lactitol, trehalose, stachyose, mannose, sorbose, xylose, ribose, ribitol, myoinisitose, myoinisitol, galactose, galactitol, glycerol, cyclitols (*e.g.*, inositol), polyethylene glycol; sulfur containing reducing agents, such as urea, glutathione, thioctic acid, sodium thioglycolate, thioglycerol, α-monothioglycerol and sodium thio sulfate; low molecular weight proteins such as human serum albumin, bovine serum albumin, gelatin or other immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; monosaccharides (*e.g.*, xylose, mannose, fructose, glucose; disaccharides (*e.g.*, lactose, maltose, sucrose); trisaccharides such as raffinose; and polysaccharides such as dextrin or dextran.

[0215] Non-ionic surfactants or detergents (also known as "wetting agents") are present to help solubilize the therapeutic agent as well as to protect the therapeutic protein against agitation-induced aggregation, which also permits the formulation to be exposed to shear surface stress without causing denaturation of the active therapeutic protein or antibody. Non-ionic surfactants are present in a range of about 0.05 mg/ml to about 1.0 mg/ml, preferably about 0.07 mg/ml to about 0.2 mg/ml.

[0216] Suitable non-ionic surfactants include polysorbates (20, 40, 60, 65, 80, etc.), polyoxamers (184, 188, etc.), PLURONIC® polyols, TRITON®, polyoxyethylene sorbitan monoethers (TWEEN®-20, TWEEN®-80, etc.), lauromacrogol 400, polyoxyl 40 stearate, polyoxyethylene hydrogenated castor oil 10, 50 and 60, glycerol monostearate, sucrose fatty acid ester, methyl celluose and carboxymethyl cellulose. Anionic detergents that can be used include sodium lauryl sulfate, dioctyle sodium sulfosuccinate and dioctyl sodium sulfonate. Cationic detergents include benzalkonium chloride or benzethonium chloride.

[0217] In order for the pharmaceutical compositions to be used for *in vivo* administration, they must be sterile. The pharmaceutical composition may be rendered sterile by filtration through sterile filtration membranes. The pharmaceutical compositions herein generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

[0218] The route of administration is in accordance with known and accepted methods, such as by single or multiple bolus or infusion over a long period of time in a suitable manner, *e.g.*, injection or infusion by subcutaneous, intravenous, intraperitoneal, intramuscular, intraarterial,

intralesional or intraarticular routes, topical administration, inhalation or by sustained release or extended-release means.

[0219] Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semi-permeable matrices of solid hydrophobic polymers containing the antagonist, which matrices are in the form of shaped articles, *e.g.* films, 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. 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.

[0220] The pharmaceutical compositions herein 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. Alternatively, or in addition, the composition may comprise a cytotoxic agent, chemotherapeutic agent, cytokine, immunosuppressive agent, or growth inhibitory agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

[0221] The active ingredients may also be entrapped in microcapsules prepared, for example, by coascervation 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* 18th edition.

[0222] An exemplary pharmaceutical formulation of the multispecific antigen binding protein is a liquid formulation comprising sodium citrate, sodium chloride, mannitol, diethylenetriaminepentacetic acid (pentetic acid), and polysorbate 80 (Tween 80), at pH 6.0.

IV. Methods of use

[0223] The multispecific antigen binding proteins described herein, and the compositions (such as pharmaceutical compositions) thereof are useful for a variety of applications, such as in diagnosis, molecular assays, and therapy.

[0224] In some embodiments, there is a method of treating a disease or a condition in an individual in need thereof, comprising administering an effective amount of a pharmaceutical composition comprising a multispecific (such as bispecific) antigen binding protein and a pharmaceutically acceptable carrier, wherein the multispecific antigen binding protein comprises (a) a first antigen binding portion comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a first epitope, and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds a second epitope, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the first antigen binding portion comprises a heavy chain comprising the V_H and a light chain comprising the V_L. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of the heavy chain, the N-terminus of the light chain, the C-terminus of the heavy chain, or the C-terminus of the light chain. In some embodiments, the first antigen binding portion comprises a full-length 4-chain antibody. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG1 Fc or IgG4 Fc.

Methods of treating a cancer

[0225] In some embodiments, there is provided a method of treating a cancer in an individual in need thereof, comprising administering an effective amount of a pharmaceutical composition comprising a multispecific (such as bispecific) antigen binding protein and a pharmaceutically acceptable carrier, wherein the multispecific antigen binding protein comprises: (a) a first antigen binding portion comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a first epitope, and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds a second epitope, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments,

the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the cancer is selected from the group consisting of breast cancer, renal cancer, melanoma, lung cancer, glioblastoma, head and neck cancer, prostate cancer, ovarian carcinoma, bladder carcinoma, and lymphoma. In some embodiments, the first antigen binding portion comprises a heavy chain comprising the V_H and a light chain comprising the V_L. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of the heavy chain, the N-terminus of the light chain, the C-terminus of the heavy chain, or the C-terminus of the light chain. In some embodiments, the first antigen binding portion comprises a full-length 4-chain antibody. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG1 Fc or IgG4 Fc.

[0226] In some embodiments, there is provided a method of treating a cancer in an individual in need thereof, comprising administering an effective amount of a pharmaceutical composition comprising a multispecific (such as bispecific) antigen binding protein and a pharmaceutically acceptable carrier, wherein the multispecific antigen binding protein comprises: (a) a first antigen binding portion comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a first immune checkpoint molecule, and (b) a second antigen binding portion comprising a single-domain antibody (*e.g.*, a V_HH) that specifically binds a second immune checkpoint molecule, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the first immune checkpoint molecule and/or the second immune checkpoint molecule is selected from the group consisting of PD-1, PD-L1, PD-L2, CTLA-4, B7-H3, TIM-3, LAG-3, VISTA, ICOS, 4-1BB, OX40, GITR, and CD40. In some embodiments, the cancer is selected from the group consisting of breast cancer, renal cancer, melanoma, lung cancer, glioblastoma, head and neck cancer, prostate cancer, ovarian carcinoma, bladder carcinoma, and lymphoma. In some embodiments, the first antigen binding portion comprises a heavy chain comprising the V_H and a light chain

comprising the V_L. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of the heavy chain, the N-terminus of the light chain, the C-terminus of the heavy chain, or the C-terminus of the light chain. In some embodiments, the first antigen binding portion comprises a full-length 4-chain antibody. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG4 Fc.

[0227] In some embodiments, there is provided a method of treating a cancer in an individual in need thereof, comprising administering an effective amount of a pharmaceutical composition comprising a multispecific (such as bispecific) antigen binding protein and a pharmaceutically acceptable carrier, wherein the multispecific antigen binding protein comprises: (a) a first antigen binding portion comprising a full-length antibody (such as pembrolizumab or nivolumab) consisting of two heavy chains and two light chains, wherein the full-length antibody specifically binds PD-1; and (b) a second antigen binding portion comprising a single-domain antibody (*e.g.*, a V_HH) that specifically binds CTLA-4, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the single-domain antibody binds CTLA-4 with a high affinity. In some embodiments, the single-domain antibody binds CTLA-4 with a medium affinity. In some embodiments, the single-domain antibody binds CTLA-4 with a low affinity. In some embodiments, the cancer is selected from the group consisting of breast cancer, renal cancer, melanoma, lung cancer, glioblastoma, head and neck cancer, prostate cancer, ovarian carcinoma, bladder carcinoma, and lymphoma. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of one or each of the two heavy chains, the N-terminus of one or each of the two light chains, the C-terminus of one or each of the two heavy chains, or the C-terminus of one or each of the two light chains. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker.

In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG4 Fc.

[0228] In some embodiments, there is provided a method of treating a cancer in an individual in need thereof, comprising administering an effective amount of a pharmaceutical composition comprising a multispecific (such as bispecific) antigen binding protein and a pharmaceutically acceptable carrier, wherein the multispecific antigen binding protein comprises: (a) a first antigen binding portion comprising a full-length antibody (such as pembrolizumab or nivolumab) consisting of two heavy chains and two light chains, wherein the full-length antibody specifically binds PD-1; and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds TIM-3, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the cancer is selected from the group consisting of breast cancer, renal cancer, melanoma, lung cancer, glioblastoma, head and neck cancer, prostate cancer, ovarian carcinoma, bladder carcinoma, and lymphoma. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of one or each of the two heavy chains, the N-terminus of one or each of the two light chains, the C-terminus of one or each of the two heavy chains, or the C-terminus of one or each of the two light chains. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG4 Fc.

[0229] In some embodiments, there is provided a method of treating a cancer in an individual in need thereof, comprising administering an effective amount of a pharmaceutical composition comprising a multispecific (such as bispecific) antigen binding protein and a pharmaceutically acceptable carrier, wherein the multispecific antigen binding protein comprises: (a) a first antigen binding portion comprising a full-length antibody (such as pembrolizumab or nivolumab) consisting of two heavy chains and two light chains, wherein the full-length antibody specifically binds PD-1; and (b) a second antigen binding portion comprising a single-domain antibody that

specifically binds LAG-3, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the cancer is selected from the group consisting of breast cancer, renal cancer, melanoma, lung cancer, glioblastoma, head and neck cancer, prostate cancer, ovarian carcinoma, bladder carcinoma, and lymphoma. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of one or each of the two heavy chains, the N-terminus of one or each of the two light chains, the C-terminus of one or each of the two heavy chains, or the C-terminus of one or each of the two light chains. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG4 Fc.

[0230] In some embodiments, there is provided a method of treating a cancer in an individual in need thereof, comprising administering an effective amount of a pharmaceutical composition comprising a multispecific (such as bispecific) antigen binding protein and a pharmaceutically acceptable carrier, wherein the multispecific antigen binding protein comprises: (a) a first antigen binding portion comprising a full-length antibody (such as pembrolizumab or nivolumab) consisting of two heavy chains and two light chains, wherein the full-length antibody specifically binds PD-1; and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds VISTA, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the cancer is selected from the group consisting of breast cancer, renal cancer, melanoma, lung cancer, glioblastoma, head and neck cancer, prostate cancer, ovarian carcinoma, bladder carcinoma, and lymphoma. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of one or each of the two heavy chains, the N-terminus of one or each of the two light chains, the C-terminus of one or each of the two heavy chains, or the C-terminus of one or each of the two light chains. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments,

the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG4 Fc.

[0231] In some embodiments, there is provided a method of treating a cancer in an individual in need thereof, comprising administering an effective amount of a pharmaceutical composition comprising a multispecific (such as bispecific) antigen binding protein and a pharmaceutically acceptable carrier, wherein the multispecific antigen binding protein comprises: (a) a first antigen binding portion comprising pembrolizumab consisting of two heavy chains and two light chains; and (b) a second antigen binding portion comprising an anti-CTLA-4 single-domain antibody, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the cancer is selected from the group consisting of breast cancer, renal cancer, melanoma, lung cancer, glioblastoma, head and neck cancer, prostate cancer, ovarian carcinoma, bladder carcinoma, and lymphoma. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of one or each of the two heavy chains, the N-terminus of one or each of the two light chains, the C-terminus of one or each of the two heavy chains, or the C-terminus of one or each of the two light chains. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the peptide linker comprises the amino acid sequence of SEQ ID NO: 1. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG4 Fc.

[0232] In some embodiments, there is provided a method of treating a cancer in an individual in need thereof, comprising administering an effective amount of a pharmaceutical composition comprising a multispecific (such as bispecific) antigen binding protein and a pharmaceutically acceptable carrier, wherein the multispecific antigen binding protein comprises: (a) a first antigen binding portion comprising a full-length antibody (such as durvalumab or atezolizumab) consisting of two heavy chains and two light chains, wherein the full-length antibody specifically

binds PD-L1; and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds CTLA-4, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the single-domain antibody binds CTLA-4 with a high affinity. In some embodiments, the single-domain antibody binds CTLA-4 with a medium affinity. In some embodiments, the single-domain antibody binds CTLA-4 with a low affinity. In some embodiments, the cancer is selected from the group consisting of breast cancer, renal cancer, melanoma, lung cancer, glioblastoma, head and neck cancer, prostate cancer, ovarian carcinoma, bladder carcinoma, and lymphoma. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of one or each of the two heavy chains, the N-terminus of one or each of the two light chains, the C-terminus of one or each of the two heavy chains, or the C-terminus of one or each of the two light chains. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG4 Fc.

[0233] In some embodiments, there is provided a method of treating a cancer in an individual in need thereof, comprising administering an effective amount of a pharmaceutical composition comprising a multispecific (such as bispecific) antigen binding protein and a pharmaceutically acceptable carrier, wherein the multispecific antigen binding protein comprises: (a) a first antigen binding portion comprising a full-length antibody (such as durvalumab or atezolizumab) consisting of two heavy chains and two light chains, wherein the full-length antibody specifically binds PD-L1; and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds TIM-3, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the cancer is selected from the group consisting of breast cancer, renal cancer, melanoma, lung cancer, glioblastoma, head and neck cancer, prostate cancer, ovarian carcinoma, bladder carcinoma, and lymphoma. In some embodiments, the second antigen binding portion is fused to the first antigen

binding portion at the N-terminus of one or each of the two heavy chains, the N-terminus of one or each of the two light chains, the C-terminus of one or each of the two heavy chains, or the C-terminus of one or each of the two light chains. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG4 Fc.

[0234] In some embodiments, there is provided a method of treating a cancer in an individual in need thereof, comprising administering an effective amount of a pharmaceutical composition comprising a multispecific (such as bispecific) antigen binding protein and a pharmaceutically acceptable carrier, wherein the multispecific antigen binding protein comprises: (a) a first antigen binding portion comprising a full-length antibody (such as durvalumab or atezolizumab) consisting of two heavy chains and two light chains, wherein the full-length antibody specifically binds PD-L1; and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds LAG-3, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the cancer is selected from the group consisting of breast cancer, renal cancer, melanoma, lung cancer, glioblastoma, head and neck cancer, prostate cancer, ovarian carcinoma, bladder carcinoma, and lymphoma. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of one or each of the two heavy chains, the N-terminus of one or each of the two light chains, the C-terminus of one or each of the two heavy chains, or the C-terminus of one or each of the two light chains. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG4 Fc.

[0235] In some embodiments, there is provided a method of treating a cancer in an individual in need thereof, comprising administering an effective amount of a pharmaceutical composition

comprising a multispecific (such as bispecific) antigen binding protein and a pharmaceutically acceptable carrier, wherein the multispecific antigen binding protein comprises: (a) a first antigen binding portion comprising a full-length antibody (such as durvalumab or atezolizumab) consisting of two heavy chains and two light chains, wherein the full-length antibody specifically binds PD-L1; and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds VISTA, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the cancer is selected from the group consisting of breast cancer, renal cancer, melanoma, lung cancer, glioblastoma, head and neck cancer, prostate cancer, ovarian carcinoma, bladder carcinoma, and lymphoma. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of one or each of the two heavy chains, the N-terminus of one or each of the two light chains, the C-terminus of one or each of the two heavy chains, or the C-terminus of one or each of the two light chains. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG4 Fc.

[0236] In some embodiments, there is provided a method of treating a cancer in an individual in need thereof, comprising administering an effective amount of a pharmaceutical composition comprising a multispecific (such as bispecific) antigen binding protein and a pharmaceutically acceptable carrier, wherein the multispecific antigen binding protein comprises: (a) a first antigen binding portion comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a first tumor antigen, and (b) a second antigen binding portion comprising a single-domain antibody (*e.g.*, a V_HH) that specifically binds a second tumor antigen, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the first tumor antigen and/or the second tumor antigen is selected from the group consisting of HER2, BRAF, EGFR, VEGFR2, CD20, RANKL, CD38,

and CD52. In some embodiments, the first antigen binding portion comprises a full-length anti-HER-2 monoclonal antibody (such as trastuzumab) or antigen binding fragment thereof. In some embodiments, the cancer is selected from the group consisting of breast cancer, renal cancer, melanoma, lung cancer, glioblastoma, head and neck cancer, prostate cancer, ovarian carcinoma, bladder carcinoma, and lymphoma. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of one or each of the two heavy chains, the N-terminus of one or each of the two light chains, the C-terminus of one or each of the two heavy chains, or the C-terminus of one or each of the two light chains. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG1 Fc.

[0237] In some embodiments, there is provided a method of treating a cancer in an individual in need thereof, comprising administering an effective amount of a pharmaceutical composition comprising a multispecific (such as bispecific) antigen binding protein and a pharmaceutically acceptable carrier, wherein the multispecific antigen binding protein comprises: (a) a first antigen binding portion comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a tumor antigen, and (b) a second antigen binding portion comprising a single-domain antibody (*e.g.*, a V_HH) that specifically binds a cell surface antigen on an immune effector cell (such as T cell), wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the tumor antigen is selected from the group consisting of HER2, BRAF, EGFR, VEGFR2, CD20, RANKL, CD38, and CD52. In some embodiments, the first antigen binding portion comprises a full-length anti-HER-2 monoclonal antibody (such as trastuzumab) or antigen binding fragment thereof. In some embodiments, the cancer is selected from the group consisting of breast cancer, renal cancer, melanoma, lung cancer, glioblastoma, head and neck cancer, prostate cancer, ovarian carcinoma, bladder carcinoma, and lymphoma. In some embodiments, the second antigen binding portion is

fused to the first antigen binding portion at the N-terminus of one or each of the two heavy chains, the N-terminus of one or each of the two light chains, the C-terminus of one or each of the two heavy chains, or the C-terminus of one or each of the two light chains. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG1 Fc.

[0238] In some embodiments, there is provided a method of treating a cancer (such as breast cancer) in an individual in need thereof, comprising administering an effective amount of a pharmaceutical composition comprising a multispecific (such as bispecific) antigen binding protein and a pharmaceutically acceptable carrier, wherein the multispecific antigen binding protein comprises: (a) a first antigen binding portion comprising a full-length antibody (such as trastuzumab) consisting of two heavy chains and two light chains, wherein the full-length antibody specifically binds HER2 receptor; and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds CD3, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of one or each of the two heavy chains, the N-terminus of one or each of the two light chains, the C-terminus of one or each of the two heavy chains, or the C-terminus of one or each of the two light chains. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG4 Fc.

[0239] The methods described herein are suitable for treating various cancers, including both solid cancer and liquid cancer. The methods are applicable to cancers of all stages, including early stage, advanced stage and metastatic cancer. The methods described herein may be used as

a first therapy, second therapy, third therapy, or combination therapy with other types of cancer therapies known in the art, such as chemotherapy, surgery, radiation, gene therapy, immunotherapy, bone marrow transplantation, stem cell transplantation, targeted therapy, cryotherapy, ultrasound therapy, photodynamic therapy, radio-frequency ablation or the like, in an adjuvant setting or a neoadjuvant setting.

Methods of treating inflammatory or autoimmune disease

[0240] In some embodiments, there is provided a method of treating an inflammatory or autoimmune disease in an individual in need thereof, comprising administering an effective amount of a pharmaceutical composition comprising a multispecific (such as bispecific) antigen binding protein and a pharmaceutically acceptable carrier, wherein the multispecific antigen binding protein comprises: (a) a first antigen binding portion comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a first epitope, and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds a second epitope, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the inflammatory or autoimmune disease is selected from the group consisting of arthritis (such as rheumatoid arthritis, juvenile idiopathic arthritis, psoriatic arthritis, ankylosing spondylitis, and arthritic ulcerative colitis), colitis, psoriasis, severe asthma, and moderate to severe Cronh's disease. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of one or each of the two heavy chains, the N-terminus of one or each of the two light chains, the C-terminus of one or each of the two heavy chains, or the C-terminus of one or each of the two light chains. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG1 Fc.

[0241] In some embodiments, there is provided a method of treating an inflammatory or autoimmune disease in an individual in need thereof, comprising administering an effective

amount of a pharmaceutical composition comprising a multispecific (such as bispecific) antigen binding protein and a pharmaceutically acceptable carrier, wherein the multispecific antigen binding protein comprises: (a) a first antigen binding portion comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a first pro-inflammatory molecule, and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds a second pro-inflammatory molecule, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the inflammatory or autoimmune disease is selected from the group consisting of arthritis (such as rheumatoid arthritis, juvenile idiopathic arthritis, psoriatic arthritis, ankylosing spondylitis, and arthritic ulcerative colitis), colitis, psoriasis, severe asthma, and moderate to severe Cronh's disease. In some embodiments, the first pro-inflammatory molecule and/or the second pro-inflammatory molecule is selected from the group consisting of IL-1β, TNF-α, IL-5, IL-6, IL-6R, and eotaxin-1. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of one or each of the two heavy chains, the N-terminus of one or each of the two light chains, the C-terminus of one or each of the two heavy chains, or the C-terminus of one or each of the two light chains. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG1 Fc.

[0242] In some embodiments, there is provided a method of treating an inflammatory or autoimmune disease in an individual in need thereof, comprising administering an effective amount of a pharmaceutical composition comprising a multispecific (such as bispecific) antigen binding protein and a pharmaceutically acceptable carrier, wherein the multispecific antigen binding protein comprises: (a) a first antigen binding portion comprising a full-length antibody (such as adalimumab) consisting of two heavy chains and two light chains, wherein the full-length antibody specifically binds TNF-α; and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds IL-1β, wherein the first antigen binding portion

and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the inflammatory or autoimmune disease is selected from the group consisting of arthritis (such as rheumatoid arthritis, juvenile idiopathic arthritis, psoriatic arthritis, ankylosing spondylitis, and arthritic ulcerative colitis), colitis, psoriasis, severe asthma, and moderate to severe Cronh's disease. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of one or each of the two heavy chains, the N-terminus of one or each of the two light chains, the C-terminus of one or each of the two heavy chains, or the C-terminus of one or each of the two light chains. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG1 Fc.

[0243] In some embodiments, there is provided a method of treating an inflammatory or autoimmune disease in an individual in need thereof, comprising administering an effective amount of a pharmaceutical composition comprising a multispecific (such as bispecific) antigen binding protein and a pharmaceutically acceptable carrier, wherein the multispecific antigen binding protein comprises: (a) a first antigen binding portion comprising a full-length antibody (such as mepolizumab) consisting of two heavy chains and two light chains, wherein the full-length antibody specifically binds IL-5; and (b) a second antigen binding portion comprising a single-domain antibody that specifically binds eotaxin-1, wherein the first antigen binding portion and the second antigen binding portion are fused to each other. In some embodiments, the single-domain antibody is a camelid, humanized, or human single-domain antibody. In some embodiments, the inflammatory or autoimmune disease is selected from the group consisting of arthritis (such as rheumatoid arthritis, juvenile idiopathic arthritis, psoriatic arthritis, ankylosing spondylitis, and arthritic ulcerative colitis), colitis, psoriasis, severe asthma, and moderate to severe Cronh's disease. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion at the N-terminus of one or each of the two heavy chains, the N-terminus of one or each of the two light chains, the C-terminus of one or each of the two heavy chains, or the C-terminus of one or each of the two light chains. In some embodiments, the

second antigen binding portion is fused to the first antigen binding portion chemically. In some embodiments, the second antigen binding portion is fused to the first antigen binding portion via a peptide bond or a peptide linker. In some embodiments, the peptide linker is no more than about 30 (such as no more than about any one of 25, 20, or 15) amino acids long. In some embodiments, the first antigen binding fragment comprises an Fc region, such as an IgG1 Fc.

Dosage and routes of administration

[0244] Dosages and desired drug concentrations of pharmaceutical compositions of the present application may vary depending on the particular use envisioned. The determination of the appropriate dosage or route of administration is well within the skill of an ordinary artisan. Animal experiments provide reliable guidance for the determination of effective doses for human therapy. Interspecies scaling of effective doses can be performed following the principles laid down by Mordenti, J. and Chappell, W. "The Use of Interspecies Scaling in Toxicokinetics," In *Toxicokinetics and New Drug Development*, Yacobi *et al.*, Eds, Pergamon Press, New York 1989, pp. 42-46.

[0245] When *in vivo* administration of the multispecific antigen binding proteins described herein are used, normal dosage amounts may vary from about 10 ng/kg up to about 100 mg/kg of mammal body weight or more per day, preferably about 1 mg/kg/day to 10 mg/kg/day, depending upon the route of administration. It is within the scope of the present application that different formulations will be effective for different treatments and different disorders, and that administration intended to treat a specific organ or tissue may necessitate delivery in a manner different from that to another organ or tissue. Moreover, dosages may be administered by one or more separate administrations, or by continuous infusion. For repeated administrations over several days or longer, depending on the condition, the treatment is sustained until a desired suppression of disease symptoms occurs. However, other dosage regimens may be useful. The progress of this therapy is easily monitored by conventional techniques and assays.

[0246] In some embodiments, the pharmaceutical composition is administered for a single time. In some embodiments, the pharmaceutical composition is administered for multiple times (such as any of 2, 3, 4, 5, 6, or more times). In some embodiments, the pharmaceutical composition is administered once per week, once 2 weeks, once 3 weeks, once 4 weeks, once per month, once per 2 months, once per 3 months, once per 4 months, once per 5 months, once per 6 months, once per 7 months, once per 8 months, once per 9 months, or once per year. In some

embodiments, the interval between administrations is about any one of 1 week to 2 weeks, 2 weeks to 1 month, 2 weeks to 2 months, 1 month to 2 months, 1 month to 3 months, 3 months to 6 months, or 6 months to a year. The optimal dosage and treatment regime for a particular patient can readily be determined by one skilled in the art of medicine by monitoring the patient for signs of disease and adjusting the treatment accordingly.

[0247] The pharmaceutical compositions of the present application, including but not limited to reconstituted and liquid formulations, are administered to an individual in need of treatment with the multispecific antigen binding proteins, preferably a human, in accord with known methods, such as intravenous administration as a bolus or by continuous infusion over a period of time, by intramuscular, intraperitoneal, intracerobrospinal, subcutaneous, intra-articular, intrasynovial, intrathecal, oral, topical, or inhalation routes.

[0248] In some embodiments, the pharmaceutical compositions are administered to the individual by subcutaneous (*i.e.* beneath the skin) administration. For such purposes, the pharmaceutical compositions may be injected using a syringe. However, other devices for administration of the pharmaceutical compositions are available such as injection devices; injector pens; auto-injector devices, needleless devices; and subcutaneous patch delivery systems.

[0249] In some embodiments, the pharmaceutical compositions are administered to the individual intravenously. In some embodiments, the pharmaceutical composition is administered to an individual by infusion, such as intravenous infusion. Infusion techniques for immunotherapy are known in the art (see, *e.g.*, Rosenberg *et al.*, New Eng. J. of Med. 319: 1676 (1988)).

V. Methods of preparation

[0250] The present application also provides isolated nucleic acids encoding the multispecific antigen binding proteins, vectors and host cells comprising such isolated nucleic acids, and recombinant methods for the production of the multispecific antigen binding proteins.

[0251] For recombinant production of the multispecific antigen binding protein, the nucleic acids encoding the full-length antibody or antigen binding fragment of the first antigen binding portion, and the single-domain antibody are isolated and inserted into a replicable vector for further cloning (amplification of the DNA) or for expression. In some embodiments, the nucleic acid encoding the full-length antibody or antigen binding fragment of the first antigen binding portion is recombinantly fused to the nucleic acid encoding the single-domain antibody of the

second antigen binding portion and optionally via a nucleic acid encoding a peptide linker, all in frame for translation with respect to each other to provide a nucleic acid encoding the multispecific antigen binding protein. DNA encoding the multispecific antigen binding protein, components thereof, or the single-domain antibody is readily isolated and sequenced using conventional procedures (*e.g.*, by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of the antibody). Many vectors are available. The choice of vector depends in part on the host cell to be used. Generally, preferred host cells are of either prokaryotic or eukaryotic (generally mammalian) origin. Alternatively, the first antigen binding fragment and the second antigen binding fragment are each prepared recombinantly using prokaryotic or eukaryotic host cells comprising nucleic acids that encode the first antigen binding fragment and the second antigen binding fragment respectively. The expressed first antigen binding fragment and the second antigen binding fragment are then conjugated chemically, and purified in order to provide the multispecific antigen binding protein.

1. Protein production in Prokaryotic Cells

a) Vector Construction

[0252] Polynucleotide sequences encoding polypeptide components of the multispecific antigen binding protein of the present application can be obtained using standard recombinant techniques. Desired polynucleotide sequences may be isolated and sequenced from antibody producing cells such as hybridoma cells. Alternatively, polynucleotides can be synthesized using nucleotide synthesizer or PCR techniques. Once obtained, sequences encoding the polypeptides are inserted into a recombinant vector capable of replicating and expressing heterologous polynucleotides in prokaryotic hosts. Many vectors that are available and known in the art can be used for the purpose of the present application. Selection of an appropriate vector will depend mainly on the size of the nucleic acids to be inserted into the vector and the particular host cell to be transformed with the vector. Each vector contains various components, depending on its function (amplification or expression of heterologous polynucleotide, or both) and its compatibility with the particular host cell in which it resides. The vector components generally include, but are not limited to: an origin of replication, a selection marker gene, a promoter, a ribosome binding site (RBS), a signal sequence, the heterologous nucleic acid insert and a transcription termination sequence.

[0253] In general, plasmid vectors containing replicon and control sequences which are derived from species compatible with the host cell are used in connection with these hosts. The vector ordinarily carries a replication site, as well as marking sequences which are capable of providing phenotypic selection in transformed cells. For example, *E. coli* is typically transformed using pBR322, a plasmid derived from an *E. coli* species. pBR322 contains genes encoding ampicillin (Amp) and tetracycline (Tet) resistance and thus provides easy means for identifying transformed cells. pBR322, its derivatives, or other microbial plasmids or bacteriophage may also contain, or be modified to contain, promoters which can be used by the microbial organism for expression of endogenous proteins. Examples of pBR322 derivatives used for expression of particular antibodies are described in detail in Carter *et al.*, U.S. Pat. No. 5,648,237.

[0254] In addition, phage vectors containing replicon and control sequences that are compatible with the host microorganism can be used as transforming vectors in connection with these hosts. For example, bacteriophage such as GEM™-11 may be utilized in making a recombinant vector which can be used to transform susceptible host cells such as *E. coli* LE392.

[0255] The expression vector described herein may comprise two or more promoter-cistron pairs, encoding each of the polypeptide components. A promoter is an untranslated regulatory sequence located upstream (5′) to a cistron that modulates its expression. Prokaryotic promoters typically fall into two classes, inducible and constitutive. Inducible promoter is a promoter that initiates increased levels of transcription of the cistron under its control in response to changes in the culture condition, *e.g.* the presence or absence of a nutrient or a change in temperature.

[0256] A large number of promoters recognized by a variety of potential host cells are well known. The selected promoter can be operably linked to cistron DNA encoding the light or heavy chain by removing the promoter from the source DNA via restriction enzyme digestion and inserting the isolated promoter sequence into the vector. Both the native promoter sequence and many heterologous promoters may be used to direct amplification and/or expression of the target genes. In some embodiments, heterologous promoters are utilized, as they generally permit greater transcription and higher yields of expressed target gene as compared to the native target polypeptide promoter.

[0257] Promoters suitable for use with prokaryotic hosts include the PhoA promoter, the -galactamase and lactose promoter systems, a tryptophan (trp) promoter system and hybrid promoters such as the tac or the trc promoter. However, other promoters that are functional in

bacteria (such as other known bacterial or phage promoters) are suitable as well. Their nucleotide sequences have been published, thereby enabling a skilled worker operably to ligate them to cistrons encoding the target light and heavy chains (Siebenlist *et al.* (1980) *Cell* 20: 269) using linkers or adaptors to supply any required restriction sites.

[0258] In one aspect, each cistron within the recombinant vector comprises a secretion signal sequence component that directs translocation of the expressed polypeptides across a membrane. In general, the signal sequence may be a component of the vector, or it may be a part of the target polypeptide DNA that is inserted into the vector. The signal sequence selected for the purpose of this application should be one that is recognized and processed (*i.e.* cleaved by a signal peptidase) by the host cell. For prokaryotic host cells that do not recognize and process the signal sequences native to the heterologous polypeptides, the signal sequence is substituted by a prokaryotic signal sequence selected, for example, from the group consisting of the alkaline phosphatase, penicillinase, Ipp, or heat-stable enterotoxin II (STII) leaders, LamB, PhoE, PelB, OmpA and MBP. In some embodiments, the signal sequences used in both cistrons of the expression system are STII signal sequences or variants thereof.

[0259] In some embodiments, the production of the multispecific antigen binding proteins can occur in the cytoplasm of the host cell, and therefore does not require the presence of secretion signal sequences within each cistron. In some embodiments, polypeptide components, such as the polypeptide encoding the V_H domain of the first antigen binding portion optionally fused to the second antigen binding portion, and the polypeptide encoding the V_L domain of the first antigen binding portion optionally fused to the second antigen binding portion, are expressed, folded and assembled to form functional multispecific antigen binding proteins within the cytoplasm. Certain host strains (*e.g.*, the *E. coli* trxB$^-$ strains) provide cytoplasm conditions that are favorable for disulfide bond formation, thereby permitting proper folding and assembly of expressed protein subunits. Proba and Pluckthun *Gene,* 159:203 (1995).

[0260] The present application provides an expression system in which the quantitative ratio of expressed polypeptide components can be modulated in order to maximize the yield of secreted and properly assembled the multispecific antigen binding proteins of the present application. Such modulation is accomplished at least in part by simultaneously modulating translational strengths for the polypeptide components. One technique for modulating translational strength is disclosed in Simmons *et al.*, U.S. Pat. No. 5,840,523. It utilizes variants of the translational

initiation region (TIR) within a cistron. For a given TIR, a series of amino acid or nucleic acid sequence variants can be created with a range of translational strengths, thereby providing a convenient means by which to adjust this factor for the desired expression level of the specific chain. TIR variants can be generated by conventional mutagenesis techniques that result in codon changes which can alter the amino acid sequence, although silent changes in the nucleotide sequence are preferred. Alterations in the TIR can include, for example, alterations in the number or spacing of Shine-Dalgarno sequences, along with alterations in the signal sequence. One method for generating mutant signal sequences is the generation of a "codon bank" at the beginning of a coding sequence that does not change the amino acid sequence of the signal sequence (*i.e.*, the changes are silent). This can be accomplished by changing the third nucleotide position of each codon; additionally, some amino acids, such as leucine, serine, and arginine, have multiple first and second positions that can add complexity in making the bank. This method of mutagenesis is described in detail in Yansura *et al.* (1992) *METHODS: A Companion to Methods in Enzymol.* 4:151-158.

[0261] Preferably, a set of vectors is generated with a range of TIR strengths for each cistron therein. This limited set provides a comparison of expression levels of each chain as well as the yield of the desired multispecific antigen binding protein products under various TIR strength combinations. TIR strengths can be determined by quantifying the expression level of a reporter gene as described in detail in Simmons *et al.* U.S. Pat. No. 5,840,523. Based on the translational strength comparison, the desired individual TIRs are selected to be combined in the expression vector constructs of the present application.

b) Prokaryotic Host Cells.

[0262] Prokaryotic host cells suitable for expressing the multispecific antigen binding proteins of the present application include Archaebacteria and Eubacteria, such as Gram-negative or Gram-positive organisms. Examples of useful bacteria include *Escherichia* (*e.g.*, *E. coli*), *Bacilli* (*e.g.*, *B. subtilis*), Enterobacteria, *Pseudomonas* species (*e.g.*, *P. aeruginosa*), *Salmonella typhimurium, Serratia marcescans, Klebsiella, Proteus, Shigella, Rhizobia, Vitreoscilla*, or *Paracoccus*. In one embodiment, gram-negative cells are used. In one embodiment, *E. coli* cells are used as hosts. Examples of *E. coli* strains include strain W3110 (Bachmann, *Cellular and Molecular Biology*, vol. 2 (Washington, D.C.: American Society for Microbiology, 1987), pp. 1190-1219; ATCC Deposit No. 27,325) and derivatives thereof, including strain 33D3 having

genotype W3110 AfhuA (AtonA) ptr3 lac Iq lacL8 AompT A(nmpc-fepE) degP41 kan^R (U.S. Pat. No. 5,639,635). Other strains and derivatives thereof, such as *E. coli* 294 (ATCC 31,446), *E. coli* B, *E. coli* 1776 (ATCC 31,537) and *E. coli* RV308(ATCC 31,608) are also suitable. These examples are illustrative rather than limiting. Methods for constructing derivatives of any of the above-mentioned bacteria having defined genotypes are known in the art and described in, for example, Bass *et al.*, *Proteins,* 8:309-314 (1990). It is generally necessary to select the appropriate bacteria taking into consideration replicability of the replicon in the cells of a bacterium. For example, *E. coli, Serratia*, or *Salmonella* species can be suitably used as the host when well known plasmids such as pBR322, pBR325, pACYC177, or pKN410 are used to supply the replicon.

[0263] Typically the host cell should secrete minimal amounts of proteolytic enzymes, and additional protease inhibitors may desirably be incorporated in the cell culture.

c) Protein Production

[0264] Host cells are transformed with the above-described expression vectors and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. Transformation means introducing DNA into the prokaryotic host so that the DNA is replicable, either as an extrachromosomal element or by chromosomal integrant. Depending on the host cell used, transformation is done using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride is generally used for bacterial cells that contain substantial cell-wall barriers. Another method for transformation employs polyethylene glycol/DMSO. Yet another technique used is electroporation.

[0265] Prokaryotic cells used to produce the multispecific antigen binding proteins of the present application are grown in media known in the art and suitable for culture of the selected host cells. Examples of suitable media include luria broth (LB) plus necessary nutrient supplements. In some embodiments, the media also contains a selection agent, chosen based on the construction of the expression vector, to selectively permit growth of prokaryotic cells containing the expression vector. For example, ampicillin is added to media for growth of cells expressing ampicillin resistant gene.

[0266] Any necessary supplements besides carbon, nitrogen, and inorganic phosphate sources may also be included at appropriate concentrations introduced alone or as a mixture with another

supplement or medium such as a complex nitrogen source. Optionally the culture medium may contain one or more reducing agents selected from the group consisting of glutathione, cysteine, cystamine, thioglycollate, dithioerythritol and dithiothreitol.

[0267] The prokaryotic host cells are cultured at suitable temperatures. For *E. coli* growth, for example, the preferred temperature ranges from about 20° C. to about 39° C., more preferably from about 25° C. to about 37° C., even more preferably at about 30° C. The pH of the medium may be any pH ranging from about 5 to about 9, depending mainly on the host organism. For *E. coli*, the pH is preferably from about 6.8 to about 7.4, and more preferably about 7.0.

[0268] If an inducible promoter is used in the expression vector, protein expression is induced under conditions suitable for the activation of the promoter. In some embodiments, PhoA promoters are used for controlling transcription of the polypeptides. Accordingly, the transformed host cells are cultured in a phosphate-limiting medium for induction. Preferably, the phosphate-limiting medium is the C.R.A.P medium (see, *e.g.*, Simmons *et al.*, *J. Immunol. Methods* (2002), 263:133-147). A variety of other inducers may be used, according to the vector construct employed, as is known in the art.

[0269] The expressed multispecific antigen binding proteins of the present application are secreted into and recovered from the periplasm of the host cells. Protein recovery typically involves disrupting the microorganism, generally by such means as osmotic shock, sonication or lysis. Once cells are disrupted, cell debris or whole cells may be removed by centrifugation or filtration. The proteins may be further purified, for example, by affinity resin chromatography. Alternatively, proteins can be transported into the culture media and isolated therein. Cells may be removed from the culture and the culture supernatant being filtered and concentrated for further purification of the proteins produced. The expressed polypeptides can be further isolated and identified using commonly known methods such as polyacrylamide gel electrophoresis (PAGE) and Western blot assay.

[0270] Alternatively, protein production is conducted in large quantity by a fermentation process. Various large-scale fed-batch fermentation procedures are available for production of recombinant proteins. Large-scale fermentations have at least 1000 liters of capacity, preferably about 1,000 to 100,000 liters of capacity. These fermentors use agitator impellers to distribute oxygen and nutrients, especially glucose (the preferred carbon/energy source). Small scale

fermentation refers generally to fermentation in a fermentor that is no more than approximately 100 liters in volumetric capacity, and can range from about 1 liter to about 100 liters.

[0271] During the fermentation process, induction of protein expression is typically initiated after the cells have been grown under suitable conditions to a desired density, *e.g.*, an OD_{550} of about 180-220, at which stage the cells are in the early stationary phase. A variety of inducers may be used, according to the vector construct employed, as is known in the art and described above. Cells may be grown for shorter periods prior to induction. Cells are usually induced for about 12-50 hours, although longer or shorter induction time may be used.

[0272] To improve the production yield and quality of the multispecific antigen binding proteins of the present application, various fermentation conditions can be modified. For example, to improve the proper assembly and folding of the secreted polypeptides, additional vectors overexpressing chaperone proteins, such as Dsb proteins (DsbA, DsbB, DsbC, DsbD and or DsbG) or FkpA (a peptidylprolyl cis,trans-isomerase with chaperone activity) can be used to co-transform the host prokaryotic cells. The chaperone proteins have been demonstrated to facilitate the proper folding and solubility of heterologous proteins produced in bacterial host cells. Chen *et al.* (1999) *J Bio Chem* 274:19601-19605; Georgiou *et al.*, U.S. Pat. No. 6,083,715; Georgiou *et al.*, U.S. Pat. No. 6,027,888; Bothmann and Pluckthun (2000) J. Biol. Chem. 275:17100-17105; Ramm and Pluckthun (2000) J. Biol. Chem. 275:17106-17113; Arie *et al.* (2001) *Mol. Microbiol.* 39:199-210.

[0273] To minimize proteolysis of expressed heterologous proteins (especially those that are proteolytically sensitive), certain host strains deficient for proteolytic enzymes can be used for the present application. For example, host cell strains may be modified to effect genetic mutation(s) in the genes encoding known bacterial proteases such as Protease III, OmpT, DegP, Tsp, Protease I, Protease Mi, Protease V, Protease VI and combinations thereof. Some *E. coli* protease-deficient strains are available and described in, for example, Joly *et al.* (1998), supra; Georgiou *et al.*, U.S. Pat. No. 5,264,365; Georgiou *et al.*, U.S. Pat. No. 5,508,192; Hara *et al.*, *Microbial Drug Resistance,* 2:63-72 (1996).

[0274] *E. coli* strains deficient for proteolytic enzymes and transformed with plasmids overexpressing one or more chaperone proteins may be used as host cells in the expression system encoding the multispecific antigen binding proteins of the present application.

d) Protein Purification

[0275] The multispecific antigen binding proteins produced herein are further purified to obtain preparations that are substantially homogeneous for further assays and uses. Standard protein purification methods known in the art can be employed. The following procedures are exemplary of suitable purification procedures: fractionation on immunoaffinity or ion-exchange columns, ethanol precipitation, reverse phase HPLC, chromatography on silica or on a cation-exchange resin such as DEAE, chromatofocusing, SDS-PAGE, ammonium sulfate precipitation, and gel filtration using, for example, Sephadex G-75.

[0276] In some embodiments, Protein A immobilized on a solid phase is used for immunoaffinity purification of the multispecific antigen binding proteins comprising an Fc region described herein. Protein A is a 411(D cell wall protein from *Staphylococcus aureas* which binds with a high affinity to the Fc region of antibodies. Lindmark *et al* (1983) *J. Immunol. Meth.* 62:1-13. The solid phase to which Protein A is immobilized is preferably a column comprising a glass or silica surface, more preferably a controlled pore glass column or a silicic acid column. In some applications, the column has been coated with a reagent, such as glycerol, in an attempt to prevent nonspecific adherence of contaminants. The solid phase is then washed to remove contaminants non-specifically bound to the solid phase. Finally the multispecific antigen binding proteins of interest is recovered from the solid phase by elution.

2. Protein Production in Eukaryotic Cells

[0277] For Eukaryotic expression, the vector components generally include, but are not limited to, one or more of the following, a signal sequence, an origin of replication, one or more marker genes, and enhancer element, a promoter, and a transcription termination sequence.

a) Signal Sequence Component

[0278] A vector for use in a eukaryotic host may also an insert that encodes a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. The heterologous signal sequence selected preferably is one that is recognized and processed (*i.e.*, cleaved by a signal peptidase) by the host cell. In mammalian cell expression, mammalian signal sequences as well as viral secretory leaders, for example, the herpes simplex gD signal, are available.

[0279] The DNA for such precursor region is ligated in reading frame to DNA encoding the multispecific antigen binding proteins of the present application.

b) Origin of Replication

[0280] Generally, the origin of replication component is not needed for mammalian expression vectors (the SV40 origin may typically be used only because it contains the early promoter).

c) Selection Gene Component

[0281] Expression and cloning vectors may contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, *e.g.*, ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, *e.g.*, the gene encoding D-alanine racemase for Bacilli.

[0282] One example of a selection scheme utilizes a drug to arrest growth of a host cell. Those cells that are successfully transformed with a heterologous gene produce a protein conferring drug resistance and thus survive the selection regimen. Examples of such dominant selection use the drugs neomycin, mycophenolic acid and hygromycin.

[0283] Another example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up nucleic acid encoding the multispecific antigen binding proteins of the present application, such as DHFR, thymidine kinase, metallothionein-I and -II, preferably primate metallothionein genes, adenosine deaminase, ornithine decarboxylase, etc.

[0284] For example, cells transformed with the DHFR selection gene are first identified by culturing all of the transformants in a culture medium that contains methotrexate (Mtx), a competitive antagonist of DHFR. An appropriate host cell when wild-type DHFR is employed is the Chinese hamster ovary (CHO) cell line deficient in DHFR activity (*e.g.*, ATCC CRL-9096).

[0285] Alternatively, host cells (particularly wild-type hosts that contain endogenous DHFR) transformed or co-transformed with the polypeptide encoding-DNA sequences, wild-type DHFR protein, and another selectable marker such as aminoglycoside 3′-phosphotransferase (APH) can be selected by cell growth in medium containing a selection agent for the selectable marker such as an aminoglycosidic antibiotic, *e.g.*, kanamycin, neomycin, or G418. See U.S. Pat. No. 4,965,199.

d) Promoter Component

[0286] Expression and cloning vectors usually contain a promoter that is recognized by the host organism and is operably linked to the nucleic acid encoding the desired polypeptide sequences. Virtually all eukaryotic genes have an AT-rich region located approximately 25 to 30 based upstream from the site where transcription is initiated. Another sequence found 70 to 80 bases upstream from the start of the transcription of many genes is a CNCAAT region where N may be any nucleotide. A the 3′ end of most eukaryotic is an AATAAA sequence that may be the signal for addition of the poly A tail to the 3′ end of the coding sequence. All of these sequences may be inserted into eukaryotic expression vectors.

[0287] Other promoters suitable for use with prokaryotic hosts include the phoA promoter, -lactamase and lactose promoter systems, alkaline phosphatase promoter, a tryptophan (trp) promoter system, and hybrid promoters such as the tac promoter. However, other known bacterial promoters are suitable. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding the multispecific antigen binding proteins.

[0288] Polypeptide transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus, adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and most preferably Simian Virus 40 (SV40), from heterologous mammalian promoters, *e.g.*, the actin promoter or an immunoglobulin promoter, from heat-shock promoters, provided such promoters are compatible with the host cell systems.

[0289] The early and late promoters of the SV40 virus are conveniently obtained as an SV40 restriction fragment that also contains the SV40 viral origin of replication. The immediate early promoter of the human cytomegalovirus is conveniently obtained as a HindIII E restriction fragment. A system for expressing DNA in mammalian hosts using the bovine papilloma virus as a vector is disclosed in U.S. Pat. No. 4,419,446. A modification of this system is described in U.S. Pat. No. 4,601,978. See also Reyes *et al.*, *Nature* 297:598-601 (1982) on expression of human-interferon cDNA in mouse cells under the control of a thymidine kinase promoter from herpes simplex virus. Alternatively, the Rous Sarcoma Virus long terminal repeat can be used as the promoter.

e) Enhancer Element Component

[0290] Transcription of a DNA encoding the multispecific antigen binding proteins of the present application by higher eukaryotes is often increased by inserting an enhancer sequence into the vector. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, α-fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. See also Yaniv, *Nature* 297:17-18 (1982) on enhancing elements for activation of eukaryotic promoters. The enhancer may be spliced into the vector at a position 5′ or 3′ to the polypeptide encoding sequence, but is preferably located at a site 5′ from the promoter.

f) Transcription Termination Component

[0291] Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5′ and, occasionally 3′, untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the polypeptide-encoding mRNA. One useful transcription termination component is the bovine growth hormone polyadenylation region. See WO94/11026 and the expression vector disclosed therein.

g) Selection and Transformation of Host Cells

[0292] Suitable host cells for cloning or expressing the DNA in the vectors herein include higher eukaryote cells described herein, including vertebrate host cells. Propagation of vertebrate cells in culture (tissue culture) has become a routine procedure. Examples of useful mammalian host cell lines are monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham *et al.*, *J. Gen Virol.* 36:59 (1977)); baby hamster kidney cells (BHK, ATCC CCL 10); Chinese hamster ovary cells/−DHFR (CHO, Urlaub *et al.*, *Proc. Natl. Acad. Sci. USA* 77:4216 (1980)); mouse sertoli cells (TM4, Mather, *Biol. Reprod.* 23:243-251 (1980)); monkey kidney cells (CV1 ATCC CCL 70); African green monkey kidney cells (VERO-76, ATCC CRL-1587);

human cervical carcinoma cells (HELA, ATCC CCL 2); canine kidney cells (MDCK, ATCC CCL 34); buffalo rat liver cells (BRL 3A, ATCC CRL 1442); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); mouse mammary tumor (MMT 060562, ATCC CCL51); TR1 cells (Mather *et al.*, *Annals N.Y. Acad. Sci.* 383:44-68 (1982)); MRC 5 cells; FS4 cells; and a human hepatoma line (Hep G2).

[0293] Host cells are transformed with the above-described expression or cloning vectors for multispecific antigen binding proteins production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences.

h) Culturing the Host Cells

[0294] The host cells used to produce the multispecific antigen binding proteins of the present application may be cultured in a variety of media. Commercially available media such as Ham's F10 (Sigma), Minimal Essential Medium ((MEM), (Sigma), RPMI-1640 (Sigma), and Dulbecco's Modified Eagle's Medium ((DMEM), Sigma) are suitable for culturing the host cells. In addition, any of the media described in Ham *et al.*, *Meth. Enz.* 58:44 (1979), Barnes *et al.*, *Anal. Biochem.* 102:255 (1980), U.S. Pat. No. 4,767,704; 4,657,866; 4,927,762; 4,560,655; or 5,122,469; WO 90/03430; WO 87/00195; or U.S. Pat. Re. 30,985 may be used as culture media for the host cells. Any of these media may be supplemented as necessary with hormones and/or other growth factors (such as insulin, transferrin, or epidermal growth factor), salts (such as sodium chloride, calcium, magnesium, and phosphate), buffers (such as HEPES), nucleotides (such as adenosine and thymidine), antibiotics (such as GENTAMYCIN™ drug), trace elements (defined as inorganic compounds usually present at final concentrations in the micromolar range), and glucose or an equivalent energy source. Any other necessary supplements may also be included at appropriate concentrations that would be known to those skilled in the art. The culture conditions, such as temperature, pH, and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

i) Protein Purification

[0295] When using recombinant techniques, the multispecific antigen binding proteins can be produced intracellularly, in the periplasmic space, or directly secreted into the medium. If the multispecific antigen binding protein or the single-domain antibody is produced intracellularly,

as a first step, the particulate debris, either host cells or lysed fragments, are removed, for example, by centrifugation or ultrafiltration. Carter *et al.*, *Bio/Technology* 10:163-167 (1992) describe a procedure for isolating antibodies which are secreted to the periplasmic space of *E. coli*. Briefly, cell paste is thawed in the presence of sodium acetate (pH 3.5), EDTA, and phenylmethylsulfonylfluoride (PMSF) over about 30 min. Cell debris can be removed by centrifugation. Where the multispecific antigen binding protein or the single-domain antibody is secreted into the medium, supernatants from such expression systems are generally first concentrated using a commercially available protein concentration filter, for example, an Amicon or Millipore Pellicon ultrafiltration unit. A protease inhibitor such as PMSF may be included in any of the foregoing steps to inhibit proteolysis and antibiotics may be included to prevent the growth of adventitious contaminants.

[0296] The protein composition prepared from the cells can be purified using, for example, hydroxylapatite chromatography, gel electrophoresis, dialysis, and affinity chromatography, with affinity chromatography being the preferred purification technique. The suitability of protein A as an affinity ligand depends on the species and isotype of any immunoglobulin Fc domain that is present in the multispecific antigen binding protein. Protein A can be used to purify the multispecific antigen binding proteins that are based on human immunoglobulins containing 1, 2, or 4 heavy chains (Lindmark *et al.*, *J. Immunol. Meth.* 62:1-13 (1983)). Protein G is recommended for all mouse isotypes and for human 3 (Guss *et al.*, *EMBO J.* 5:15671575 (1986)). The matrix to which the affinity ligand is attached is most often agarose, but other matrices are available. Mechanically stable matrices such as controlled pore glass or poly(styrene-divinyl)benzene allow for faster flow rates and shorter processing times than can be achieved with agarose. Where the multispecific antigen binding protein comprises a C_H3 domain, the Bakerbond ABXTMresin (J. T. Baker, Phillipsburg, N.J.) is useful for purification. Other techniques for protein purification such as fractionation on an ion-exchange column, ethanol precipitation, Reverse Phase HPLC, chromatography on silica, chromatography on heparin SEPHAROSE™ chromatography on an anion or cation exchange resin (such as a polyaspartic acid column), chromatofocusing, SDS-PAGE, and ammonium sulfate precipitation are also available depending on the multispecific antigen binding protein or the single-domain antibody to be recovered.

[0297] Following any preliminary purification step(s), the mixture comprising the multispecific antigen binding protein or the single-domain antibody of interest and contaminants may be subjected to low pH hydrophobic interaction chromatography using an elution buffer at a pH between about 2.5-4.5, preferably performed at low salt concentrations (*e.g.*, from about 0-0.25M salt).

3. Antibody production

[0298] Components of the multispecific antigen binding proteins, such as conventional 4-chain antibodies, antigen-binding fragments, and single-domain antibodies, can be produced using any known methods in the art, including methods described below.

[0299] The single-domain antibodies (such as V_HHs) may be obtained using methods known in the art such as by immunizing a *Camelidae* species (such as camel or llama) and obtaining hybridomas therefrom, or by cloning a library of single-domain antibodies using molecular biology techniques known in the art and subsequent selection by ELISA with individual clones of unselected libraries or by using phage display.

1) Monoclonal Antibodies

[0300] Monoclonal antibodies are obtained from a population of substantially homogeneous antibodies, *i.e.*, the individual antibodies comprising the population are identical except for possible naturally occurring mutations and/or post-translational modifications (*e.g.*, isomerizations, amidations) that may be present in minor amounts. Thus, the modifier "monoclonal" indicates the character of the antibody as not being a mixture of discrete antibodies.

[0301] For example, the monoclonal antibodies may be made using the hybridoma method first described by Kohler *et al.*, *Nature*, 256:495 (1975), or may be made by recombinant DNA methods (U.S. Pat. No. 4,816,567).

[0302] In the hybridoma method, a mouse or other appropriate host animal, such as a hamster, is immunized as hereinabove described to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind the protein used for immunization. Alternatively, lymphocytes may be immunized *in vitro*. Lymphocytes then are fused with myeloma cells using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, *Monoclonal Antibodies: Principles and Practice*, pp. 59-103 (Academic Press, 1986).

[0303] The immunizing agent will typically include the antigenic protein or a fusion variant thereof. Generally either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell. Goding, *Monoclonal Antibodies: Principles and Practice*, Academic Press (1986), pp. 59-103.

[0304] Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells thus prepared are seeded and grown in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, parental myeloma cells. For example, if the parental myeloma cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine (HAT medium), which are substances that prevent the growth of HGPRT-deficient cells.

[0305] Preferred immortalized myeloma cells are those that fuse efficiently, support stable high-level production of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. Among these, preferred are murine myeloma lines, such as those derived from MOPC-21 and MPC-11 mouse tumors available from the Salk Institute Cell Distribution Center, San Diego, Calif. USA, and SP-2 cells (and derivatives thereof, *e.g.*, X63-Ag8-653) available from the American Type Culture Collection, Manassas, Va. USA. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, *J. Immunol.*, 133:3001 (1984); Brodeur *et al.*, *Monoclonal Antibody Production Techniques and Applications*, pp. 51-63 (Marcel Dekker, Inc., New York, 1987)).

[0306] Culture medium in which hybridoma cells are growing is assayed for production of monoclonal antibodies directed against the antigen. Preferably, the binding specificity of monoclonal antibodies produced by hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunosorbent assay (ELISA).

[0307] The culture medium in which the hybridoma cells are cultured can be assayed for the presence of monoclonal antibodies directed against the desired antigen. Preferably, the binding

affinity and specificity of the monoclonal antibody can be determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked assay (ELISA). Such techniques and assays are known in the in art. For example, binding affinity may be determined by the Scatchard analysis of Munson *et al.*, *Anal. Biochem.*, 107:220 (1980).

[0308] After hybridoma cells are identified that produce antibodies of the desired specificity, affinity, and/or activity, the clones may be subcloned by limiting dilution procedures and grown by standard methods (Goding, supra). Suitable culture media for this purpose include, for example, D-MEM or RPMI-1640 medium. In addition, the hybridoma cells may be grown *in vivo* as tumors in a mammal.

[0309] The monoclonal antibodies secreted by the subclones are suitably separated from the culture medium, ascites fluid, or serum by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

[0310] Monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Pat. No. 4,816,567, and as described above. DNA encoding the monoclonal antibodies is readily isolated and sequenced using conventional procedures (*e.g.*, by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as *E. coli* cells, simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, in order to synthesize monoclonal antibodies in such recombinant host cells. Review articles on recombinant expression in bacteria of DNA encoding the antibody include Skerra *et al.*, *Curr. Opinion in Immunol.*, 5:256-262 (1993) and Pliickthun, *Immunol. Revs.* 130:151-188 (1992).

[0311] In a further embodiment, antibodies can be isolated from antibody phage libraries generated using the techniques described in McCafferty *et al.*, *Nature*, 348:552-554 (1990). Clackson *et al.*, *Nature*, 352:624-628 (1991) and Marks *et al.*, *J. Mol. Biol.*, 222:581-597 (1991) describe the isolation of murine and human antibodies, respectively, using phage libraries. Subsequent publications describe the production of high affinity (nM range) human antibodies by chain shuffling (Marks *et al.*, *Bio/Technology*, 10:779-783 (1992)), as well as combinatorial infection and *in vivo* recombination as a strategy for constructing very large phage libraries

(Waterhouse *et al.*, *Nucl. Acids Res.*, 21:2265-2266 (1993)). Thus, these techniques are viable alternatives to traditional monoclonal antibody hybridoma techniques for isolation of monoclonal antibodies.

[0312] The DNA also may be modified, for example, by substituting the coding sequence for human heavy- and light-chain constant domains in place of the homologous murine sequences (U.S. Pat. No. 4,816,567; Morrison, *et al.*, *Proc. Natl Acad. Sci. USA*, 81:6851 (1984)), or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Typically such non-immunoglobulin polypeptides are substituted for the constant domains of an antibody, or they are substituted for the variable domains of one antigen-combining site of an antibody to create a chimeric bivalent antibody comprising one antigen-combining site having specificity for an antigen and another antigen-combining site having specificity for a different antigen.

[0313] The monoclonal antibodies described herein may by monovalent, the preparation of which is well known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and a modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent heavy chain crosslinking. Alternatively, the relevant cysteine residues may be substituted with another amino acid residue or are deleted so as to prevent crosslinking. *In vitro* methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly Fab fragments, can be accomplished using routine techniques known in the art.

[0314] Chimeric or hybrid antibodies also may be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide-exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate.

2) Humanized Antibodies

[0315] The antibodies may further comprise humanized or human antibodies. Humanized forms of non-human (*e.g.*, murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', $F(ab')_2$ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues

from a complementarity determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domain, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. Jones *et al.*, *Nature* 321: 522-525 (1986); Riechmann *et al.*, *Nature* 332: 323-329 (1988) and Presta, *Curr. Opin. Struct. Biol.* 2: 593-596 (1992).

[0316] Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers, Jones *et al.*, *Nature* 321:522-525 (1986); Riechmann *et al.*, *Nature* 332:323-327 (1988); Verhoeyen *et al.*, *Science* 239:1534-1536 (1988), or through substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Pat. No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

[0317] The choice of human variable domains, both light and heavy, to be used in making the humanized antibodies is very important to reduce antigenicity. According to the so-called "best-fit" method, the sequence of the variable domain of a rodent antibody is screened against the entire library of known human variable-domain sequences. The human sequence which is closest to that of the rodent is then accepted as the human framework (FR) for the humanized antibody. Sims *et al.*, *J. Immunol.*, 151:2296 (1993); Chothia *et al.*, *J. Mol. Biol.*, 196:901 (1987). Another method uses a particular framework derived from the consensus sequence of all human

antibodies of a particular subgroup of light or heavy chains. The same framework may be used for several different humanized antibodies. Carter *et al.*, *Proc. Natl. Acad. Sci. USA*, 89:4285 (1992); Presta *et al.*, *J. Immunol.*, 151:2623 (1993).

[0318] It is further important that antibodies be humanized with retention of high affinity for the antigen and other favorable biological properties. To achieve this goal, according to a preferred method, humanized antibodies are prepared by a process of analysis of the parental sequences and various conceptual humanized products using three-dimensional models of the parental and humanized sequences. Three-dimensional immunoglobulin models are commonly available and are familiar to those skilled in the art. Computer programs are available which illustrate and display probable three-dimensional conformational structures of selected candidate immunoglobulin sequences. Inspection of these displays permits analysis of the likely role of the residues in the functioning of the candidate immunoglobulin sequence, *i.e.*, the analysis of residues that influence the ability of the candidate immunoglobulin to bind its antigen. In this way, FR residues can be selected and combined from the recipient and import sequences so that the desired antibody characteristic, such as increased affinity for the target antigen(s), is achieved. In general, the CDR residues are directly and most substantially involved in influencing antigen binding.

[0319] Various forms of the humanized antibody are contemplated. For example, the humanized antibody may be an antibody fragment, such as an Fab, which is optionally conjugated with one or more cytotoxic agent(s) in order to generate an immunoconjugate. Alternatively, the humanized antibody may be an intact antibody, such as an intact IgG1 antibody.

[0320] In some embodiments, the single-domain antibodies are modified, such as humanized, without diminishing the native affinity of the domain for antigen and while reducing its immunogenicity with respect to a heterologous species. For example, the amino acid residues of the antibody variable domain (V_HH) of an llama antibody can be determined, and one or more of the Camelidae amino acids, for example, in the framework regions, are replaced by their human counterpart as found in the human consensus sequence, without that polypeptide losing its typical character, *i.e.* the humanization does not significantly affect the antigen binding capacity of the resulting polypeptide. Humanization of Camelidae single-domain antibodies requires the introduction and mutagenesis of a limited amount of amino acids in a single polypeptide chain.

This is in contrast to humanization of scFv, Fab', (Fab')2 and IgG, which requires the introduction of amino acid changes in two chains, the light and the heavy chain and the preservation of the assembly of both chains.

3) Human Antibodies

[0321] As an alternative to humanization, human antibodies can be generated. For example, it is now possible to produce transgenic animals (*e.g.*, mice) that are capable, upon immunization, of producing a full repertoire of human antibodies in the absence of endogenous immunoglobulin production. For example, it has been described that the homozygous deletion of the antibody heavy-chain joining region (J_H) gene in chimeric and germ-line mutant mice results in complete inhibition of endogenous antibody production. Transfer of the human germ-line immunoglobulin gene array in such germ-line mutant mice will result in the production of human antibodies upon antigen challenge. See, *e.g.*, Jakobovits *et al.*, *Proc. Natl. Acad. Sci. USA*, 90:2551 (1993); Jakobovits *et al.*, *Nature*, 362:255-258 (1993); Bruggermann *et al.*, *Year in Immuno.*, 7:33 (1993); U.S. Pat. No. 5,591,669 and WO 97/17852. Transgenic mice or rats capable of producing fully human single-domain antibodies are known in the art. See, *e.g.*, US20090307787A1, U.S. Pat. No. 8,754,287, US20150289489A1, US20100122358A1, and WO2004049794.

[0322] Alternatively, phage display technology can be used to produce human antibodies and antibody fragments *in vitro*, from immunoglobulin variable (V) domain gene repertoires from unimmunized donors. McCafferty *et al.*, *Nature* 348:552-553 (1990); Hoogenboom and Winter, *J. Mol. Biol.* 227: 381 (1991). According to this technique, antibody V domain genes are cloned in-frame into either a major or minor coat protein gene of a filamentous bacteriophage, such as M13 or fd, and displayed as functional antibody fragments on the surface of the phage particle. Because the filamentous particle contains a single-stranded DNA copy of the phage genome, selections based on the functional properties of the antibody also result in selection of the gene encoding the antibody exhibiting those properties. Thus, the phage mimics some of the properties of the B-cell. Phage display can be performed in a variety of formats, reviewed in, *e.g.*, Johnson, Kevin S, and Chiswell, David *J., Curr. Opin Struct. Biol.* 3:564-571 (1993). Several sources of V-gene segments can be used for phage display. Clackson *et al.*, Nature 352:624-628 (1991) isolated a diverse array of anti-oxazolone antibodies from a small random combinatorial library of V genes derived from the spleens of immunized mice. A repertoire of V genes from unimmunized human donors can be constructed and antibodies to a diverse array of antigens

(including self-antigens) can be isolated essentially following the techniques described by Marks *et al.*, J. Mol. Biol. 222:581-597 (1991), or Griffith *et al.*, EMBO J. 12:725-734 (1993). See also, U.S. Pat. Nos. 5,565,332 and 5,573,905.

[0323] The techniques of Cole *et al.*, and Boerner *et al.*, are also available for the preparation of human monoclonal antibodies (Cole *et al.*, Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, p. 77 (1985) and Boerner *et al.*, *J. Immunol.* 147(1): 86-95 (1991). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, *e.g.*, mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly and antibody repertoire. This approach is described, for example, in U.S. Pat. Nos. 5,545,807; 5,545,806, 5,569,825, 5,625,126, 5,633,425, 5,661,016 and in the following scientific publications: Marks *et al.*, *Bio/Technology* 10: 779-783 (1992); Lonberg *et al.*, *Nature* 368: 856-859 (1994); Morrison, *Nature* 368: 812-13 (1994), Fishwild *et al.*, *Nature Biotechnology* 14: 845-51 (1996), Neuberger, *Nature Biotechnology* 14: 826 (1996) and Lonberg and Huszar, *Intern. Rev. Immunol.* 13: 65-93 (1995).

[0324] Finally, human antibodies may also be generated *in vitro* by activated B cells (see U.S. Pat. Nos. 5,567,610 and 5,229,275).

4) Antibody Fragments

[0325] In certain circumstances there are advantages to using antibody fragments, such as antigen binding fragments, rather than whole antibodies. Smaller fragment sizes allow for rapid clearance, and may lead to improved access to solid tumors.

[0326] Various techniques have been developed for the production of antibody fragments. Traditionally, these fragments were derived via proteolytic digestion of intact antibodies (see, *e.g.*, Morimoto *et al.*, *J Biochem Biophys. Method.* 24:107-117 (1992); and Brennan *et al.*, *Science* 229:81 (1985)). However, these fragments can now be produced directly by recombinant host cells. Fab, Fv and scFv antibody fragments can all be expressed in and secreted from *E. coli*, thus allowing the facile production of large amounts of these fragments. Antibody fragments can be isolated from the antibody phage libraries discussed above. Alternatively, Fab'-SH fragments can be directly recovered from *E. coli* and chemically coupled to form $F(ab')_2$ fragments (Carter *et al.*, *Bio/Technology* 10:163-167 (1992)). According to another approach, $F(ab')_2$ fragments can

be isolated directly from recombinant host cell culture. Fab and $F(ab')_2$ with increase *in vivo* half-life is described in U.S. Pat. No. 5,869,046. In other embodiments, the antibody of choice is a single chain Fv fragment (scFv). See WO 93/16185; U.S. Pat. No. 5,571,894 and U.S. Pat. No. 5,587,458. The antibody fragment may also be a "linear antibody", *e.g.*, as described in U.S. Pat. No. 5,641,870. Such linear antibody fragments may be monospecific or bispecific.

5) Bispecific and Multispecific Antibodies

[0327] Bispecific antibodies (BsAbs) are antibodies that have binding specificities for at least two different epitopes, including those on the same or another protein. Alternatively, one arm can bind the target antigen, and another arm can be combined with an arm that binds a triggering molecule on a leukocyte such as a T-cell receptor molecule (*e.g.*, CD3), or Fc receptors for IgG (FcγR) such as FcγR1 (CD64), FcγRII (CD32) and FcγRIII (CD16), so as to focus and localize cellular defense mechanisms to the target antigen-expressing cell. Such antibodies can be derived from full length antibodies or antibody fragments (*e.g.* $F(ab')_2$ bispecific antibodies).

[0328] Bispecific antibodies may also be used to localize cytotoxic agents to cells which express the target antigen. Such antibodies possess one arm that binds the desired antigen and another arm that binds the cytotoxic agent (*e.g.*, saporin, anti-interferon-α, vinca alkoloid, ricin A chain, methotrexate or radioactive isotope hapten). Examples of known bispecific antibodies include anti-ErbB2/anti-FcgRIII (WO 96/16673), anti-ErbB2/anti-FcgRI (U.S. Pat. No. 5,837,234), anti-ErbB2/anti-CD3 (U.S. Pat. No. 5,821,337).

[0329] Methods for making bispecific antibodies are known in the art. Traditional production of full length bispecific antibodies is based on the coexpression of two immunoglobulin heavy-chain/light chain pairs, where the two chains have different specificities. Millstein *et al.*, *Nature*, 305:537-539 (1983). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of 10 different antibody molecules, of which only one has the correct bispecific structure. Purification of the correct molecule, which is usually done by affinity chromatography steps, is rather cumbersome, and the product yields are low. Similar procedures are disclosed in WO 93/08829 and in Traunecker *et al.*, *EMBO J.*, 10:3655-3659 (1991).

[0330] According to a different approach, antibody variable domains with the desired binding specificities (antibody-antigen combining sites) are fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy chain constant domain,

comprising at least part of the hinge, C_H2, and C_H3 regions. It is preferred to have the first heavy-chain constant region (C_H1) containing the site necessary for light chain binding, present in at least one of the fusions. DNAs encoding the immunoglobulin heavy chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. This provides for great flexibility in adjusting the mutual proportions of the three polypeptide fragments in embodiments when unequal ratios of the three polypeptide chains used in the construction provide the optimum yields. It is, however, possible to insert the coding sequences for two or all three polypeptide chains in one expression vector when the expression of at least two polypeptide chains in equal ratios results in high yields or when the ratios are of no particular significance.

[0331] In a preferred embodiment of this approach, the bispecific antibodies are composed of a hybrid immunoglobulin heavy chain with a first binding specificity in one arm, and a hybrid immunoglobulin heavy chain-light chain pair (providing a second binding specificity) in the other arm. It was found that this asymmetric structure facilitates the separation of the desired bispecific compound from unwanted immunoglobulin chain combinations, as the presence of an immunoglobulin light chain in only one half of the bispecific molecules provides for an easy way of separation. This approach is disclosed in WO 94/04690. For further details of generating bispecific antibodies, see, for example, Suresh *et al.*, *Methods in Enzymology* 121: 210 (1986).

[0332] According to another approach described in WO 96/27011 or U.S. Pat. No. 5,731,168, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the C_H3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (*e.g.*, tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chains(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (*e.g.*, alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

[0333] Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical linkage. Brennan *et al.*, *Science* 229: 81 (1985) describe a procedure wherein intact antibodies

are proteolytically cleaved to generate $F(ab')_2$ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

[0334] Fab' fragments may be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby *et al.*, *J. Exp. Med.* 175: 217-225 (1992) describes the production of fully humanized bispecific antibody $F(ab')_2$ molecules. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling *in vitro* to form the bispecific antibody. The bispecific antibody thus formed was able to bind cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

[0335] Various techniques for making and isolating bivalent antibody fragments directly from recombinant cell culture have also been described. For example, bivalent heterodimers have been produced using leucine zippers. Kostelny *et al.*, *J. Immunol.*, 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. The "diabody" technology described by Hollinger *et al.*, *Proc. Natl. Acad. Sci. USA*, 90: 6444-6448 (1993) has provided an alternative mechanism for making bispecific/bivalent antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific/bivalent antibody fragments by the use of single-chain Fv (scFv) dimers has also been reported. See Gruber *et al.*, *J. Immunol.*, 152:5368 (1994).

[0336] Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt *et al.*, *J. Immunol.* 147: 60 (1991).

[0337] Exemplary bispecific antibodies may bind two different epitopes on a given molecule. Alternatively, an anti-protein arm may be combined with an arm which binds a triggering

molecule on a leukocyte such as a T-cell receptor molecule (*e.g.*, CD2, CD3, CD28 or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular protein. Bispecific antibodies may also be used to localize cytotoxic agents to cells which express a particular protein. Such antibodies possess a protein-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA or TETA. Another bispecific antibody of interest binds the protein of interest and further binds tissue factor (TF).

6) Multivalent Antibodies

[0338] A multivalent antibody may be internalized (and/or catabolized) faster than a bivalent antibody by a cell expressing an antigen to which the antibodies bind. The antibodies used as the first antigen binding portion in the multispecific antigen binding proteins of the present application can be multivalent antibodies (which are other than of the IgM class) with three or more antigen binding sites (*e.g.* tetravalent antibodies), which can be readily produced by recombinant expression of nucleic acid encoding the polypeptide chains of the antibody. The multivalent antibody can comprise a dimerization domain and three or more antigen binding sites. The preferred dimerization domain comprises (or consists of) an Fc region or a hinge region. In this scenario, the antibody will comprise an Fc region and three or more antigen binding sites amino-terminal to the Fc region. The preferred multivalent antibody herein comprises (or consists of) three to about eight, but preferably four, antigen binding sites. The multivalent antibody comprises at least one polypeptide chain (and preferably two polypeptide chains), wherein the polypeptide chain(s) comprise two or more variable domains. For instance, the polypeptide chain(s) may comprise VD1-$(X1)_n$-VD2-$(X_2)_n$-Fc, wherein VD1 is a first variable domain, VD2 is a second variable domain, Fc is one polypeptide chain of an Fc region, X1 and X2 represent an amino acid or polypeptide, and n is 0 or 1. For instance, the polypeptide chain(s) may comprise: V_H- C_H1-flexible linker-V_H-C_H1-Fc region chain; or V_H-C_H1-V_H-C_H1-Fc region chain. The multivalent antibody herein preferably further comprises at least two (and preferably four) light chain variable domain polypeptides. The multivalent antibody herein may, for instance, comprise from about two to about eight light chain variable domain polypeptides. The light chain variable domain polypeptides contemplated here comprise a light chain variable domain and, optionally, further comprise a C_L domain.

7) Heteroconjugate Antibodies

[0339] Heteroconjugate antibodies can also be used as the first antigen binding portion of the multispecific antigen binding proteins of the present application. Heteroconjugate antibodies are composed of two covalently joined antibodies. For example, one of the antibodies in the heteroconjugate can be coupled to avidin, the other to biotin. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells, U.S. Pat. No. 4,676,980, and for treatment of HIV infection. WO 91/00360, WO 92/200373 and EP 0308936. It is contemplated that the antibodies may be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Pat. No. 4,676,980. Heteroconjugate antibodies may be made using any convenient cross-linking methods. Suitable cross-linking agents are well known in the art, and are disclosed in U.S. Pat. No. 4,676,980, along with a number of cross-linking techniques.

8) Effector Function Engineering

[0340] It may be desirable to modify the multispecific antigen binding proteins of the present application with respect to Fc effector function, *e.g.*, so as to modify (*e.g.*, enhance or eliminate) antigen-dependent cell-mediated cytotoxicity (ADCC) and/or complement dependent cytotoxicity (CDC) of the antibody. In a preferred embodiment, Fc effector function of the multispecific antigen binding protein is reduced or eliminated. This may be achieved by introducing one or more amino acid substitutions in an Fc region of the antibody. Alternatively or additionally, cysteine residue(s) may be introduced in the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric multispecific antigen binding protein thus generated may have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron *et al.*, *J. Exp Med.* 176:1191-1195 (1992) and Shopes, B. *J. Immunol.* 148:2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity may also be prepared using heterobifunctional cross-linkers as described in Wolff *et al.*, *Cancer Research* 53:2560-2565 (1993). Alternatively, an antibody can be engineered which has dual Fc regions and may thereby

have enhanced complement lysis and ADCC capabilities. See Stevenson *et al.*, *Anti-Cancer Drug Design* 3:219-230 (1989).

[0341] To increase the serum half-life of the antibody, one may incorporate a salvage receptor binding epitope into the multispecific antigen binding protein as described in U.S. Pat. No. 5,739,277, for example. As used herein, the term "salvage receptor binding epitope" refers to an epitope of the Fc region of an IgG molecule (*e.g.*, IgG_1, IgG_2, IgG_3, or IgG_4) that is responsible for increasing the *in vivo* serum half-life of the IgG molecule.

9) Other Amino Acid Sequence Modifications

[0342] Amino acid sequence modification(s) of the antibodies, such as single chain antibodies or antibody components of the multispecific antigen binding proteins, described herein are contemplated. For example, it may be desirable to improve the binding affinity and/or other biological properties of the antibody. Amino acid sequence variants of the antibody are prepared by introducing appropriate nucleotide changes into the antibody nucleic acid, or by peptide synthesis. Such modifications include, for example, deletions from, and/or insertions into and/or substitutions of, residues within the amino acid sequences of the antibody. Any combination of deletion, insertion, and substitution is made to arrive at the final construct, provided that the final construct possesses the desired characteristics. The amino acid changes also may alter post-translational processes of the antibody, such as changing the number or position of glycosylation sites.

[0343] A useful method for identification of certain residues or regions of the antibody that are preferred locations for mutagenesis is called "alanine scanning mutagenesis" as described by Cunningham and Wells in *Science*, 244:1081-1085 (1989). Here, a residue or group of target residues are identified (*e.g.*, charged residues such as arg, asp, his, lys, and glu) and replaced by a neutral or negatively charged amino acid (most preferably alanine or polyalanine) to affect the interaction of the amino acids antigen. Those amino acid locations demonstrating functional sensitivity to the substitutions then are refined by introducing further or other variants at, or for, the sites of substitution. Thus, while the site for introducing an amino acid sequence variation is predetermined, the nature of the mutation per se need not be predetermined. For example, to analyze the performance of a mutation at a given site, ala scanning or random mutagenesis is conducted at the target codon or region and the expressed antibody variants are screened for the desired activity.

[0344] Amino acid sequence insertions include amino- and/or carboxyl-terminal fusions ranging in length from one residue to polypeptides containing a hundred or more residues, as well as intrasequence insertions of single or multiple amino acid residues. Examples of terminal insertions include an antibody with an N-terminal methionyl residue or the antibody fused to a cytotoxic polypeptide. Other insertional variants of the antibody molecule include the fusion to the N- or C-terminus of the antibody to an enzyme (*e.g.* for ADEPT) or a polypeptide which increases the serum half-life of the antibody.

[0345] Another type of variant is an amino acid substitution variant. These variants have at least one amino acid residue in the antibody molecule replaced by a different residue. The sites of greatest interest for substitutional mutagenesis include the hypervariable regions, but FR alterations are also contemplated. Conservative substitutions are shown in the Table 2 below under the heading of "preferred substitutions". If such substitutions result in a change in biological activity, then more substantial changes, denominated "exemplary substitutions" in Table 2, or as further described below in reference to amino acid classes, may be introduced and the products screened.

TABLE 2. Amino Acid Substitutions

Original Residue	Exemplary Substitutions	Preferred Substitutions
Ala (A)	val; leu; ile	val
Arg (R)	lys; gln; asn	lys
Asn (N)	gln; his; asp, lys; arg	gln
Asp (D)	glu; asn	glu
Cys (C)	ser; ala	ser
Gln (Q)	asn; glu	asn
Glu (E)	asp; gln	asp
Gly (G)	ala	ala
His (H)	asn; gln; lys; arg	arg
Ile (I)	leu; val; met; ala; phe; norleucine	leu
Leu (L)	norleucine; ile; val; met; ala; phe	ile
Lys (K)	arg; gln; asn	arg

TABLE 2. Amino Acid Substitutions

Met (M)	leu; phe; ile	leu
Phe (F)	leu; val; ile; ala; tyr	tyr
Pro (P)	Ala	ala
Ser (S)	Thr	thr
Thr (T)	Ser	ser
Trp (W)	tyr; phe	tyr
Tyr (Y)	trp; phe; thr; ser	phe
Val (V)	ile; leu; met; phe; ala; norleucine	leu

[0346] Substantial modifications in the biological properties of the antibody are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties:

(1) hydrophobic: norleucine, met, ala, val, leu, ile;

(2) neutral hydrophilic: cys, ser, thr;

(3) acidic: asp, glu;

(4) basic: asn, gln, his, lys, arg;

(5) residues that influence chain orientation: gly, pro; and

(6) aromatic: trp, tyr, phe.

[0347] Non-conservative substitutions will entail exchanging a member of one of these classes for another class.

[0348] Any cysteine residue not involved in maintaining the proper conformation of the antibody also may be substituted, generally with serine, to improve the oxidative stability of the molecule and prevent aberrant crosslinking. Conversely, cysteine bond(s) may be added to the antibody to improve its stability (particularly where the antibody is an antibody fragment such as an Fv fragment).

[0349] A particularly preferred type of substitutional variant involves substituting one or more hypervariable region residues of a parent antibody (*e.g.* a humanized or human antibody). Generally, the resulting variant(s) selected for further development will have improved

biological properties relative to the parent antibody from which they are generated. A convenient way for generating such substitutional variants involves affinity maturation using phage display. Briefly, several hypervariable region sites (*e.g.* 6-7 sites) are mutated to generate all possible amino substitutions at each site. The antibody variants thus generated are displayed in a monovalent fashion from filamentous phage particles as fusions to the gene III product of M13 packaged within each particle. The phage-displayed variants are then screened for their biological activity (*e.g.* binding affinity) as herein disclosed. In order to identify candidate hypervariable region sites for modification, alanine scanning mutagenesis can be performed to identify hypervariable region residues contributing significantly to antigen binding. Alternatively, or additionally, it may be beneficial to analyze a crystal structure of the antigen-antibody complex to identify contact points between the antibody and its target (*e.g.*, PD-L1, B7.1). Such contact residues and neighboring residues are candidates for substitution according to the techniques elaborated herein. Once such variants are generated, the panel of variants is subjected to screening as described herein and antibodies with superior properties in one or more relevant assays may be selected for further development.

[0350] Another type of amino acid variant of the antibody alters the original glycosylation pattern of the antibody. By altering is meant deleting one or more carbohydrate moieties found in the antibody, and/or adding one or more glycosylation sites that are not present in the antibody.

[0351] Glycosylation of antibodies 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 tripeptide 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 tripeptide sequences in a polypeptide creates a potential glycosylation site. O-linked glycosylation refers to the attachment of one of the sugars N-aceylgalactosamine, galactose, or xylose to a hydroxyamino acid, most commonly serine or threonine, although 5-hydroxyproline or 5-hydroxylysine may also be used.

[0352] 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 tripeptide 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 sequence of the original antibody (for O-linked glycosylation sites).

[0353] Nucleic acid molecules encoding amino acid sequence variants to the multispecific antigen binding proteins of the present application are prepared by a variety of methods known in the art. These methods include, but are not limited to, isolation from a natural source (in the case of naturally occurring amino acid sequence variants) or preparation by oligonucleotide-mediated (or site-directed) mutagenesis, PCR mutagenesis, and cassette mutagenesis of an earlier prepared variant or a non-variant versions.

10) Other Modifications

[0354] The multispecific antigen binding proteins of the present application can be further modified to contain additional nonproteinaceous moieties that are known in the art and readily available. Preferably, the moieties suitable for derivatization of the antibody are water-soluble polymers. Non-limiting examples of water-soluble polymers include, but are not limited to, polyethylene glycol (PEG), copolymers of ethylene glycol/propylene glycol, carboxymethylcellulose, dextran, polyvinyl alcohol, polyvinyl pyrrolidone, poly-1,3-dioxolane, poly-1,3,6-trioxane, ethylene/maleic anhydride copolymer, polyaminoacids (either homopolymers or random copolymers), and dextran or poly(n-vinyl pyrrolidone)polyethylene glycol, polypropylene glycol homopolymers, polypropylene oxide/ethylene oxide co-polymers, polyoxyethylated polyols (*e.g.*, glycerol), polyvinyl alcohol, and mixtures thereof. Polyethylene glycol propionaldehyde may have advantages in manufacturing due to its stability in water. The polymer may be of any molecular weight, and may be branched or unbranched. The number of polymers attached to the antibody may vary, and if more than one polymer is attached, they can be the same or different molecules. In general, the number and/or type of polymers used for derivatization can be determined based on considerations including, but not limited to, the particular properties or functions of the antibody to be improved, whether the antibody derivative will be used in a therapy under defined conditions, etc. Such techniques and other suitable formulations are disclosed in *Remington: The Science and Practice of Pharmacy,* 20th Ed., Alfonso Gennaro, Ed., Philadelphia College of Pharmacy and Science (2000).

VI. Kits and articles of manufacture

[0355] Further provided are kits, unit dosages, and articles of manufacture comprising any of the multispecific antigen binding proteins described herein. In some embodiments, a kit is provided comprising any one of the pharmaceutical compositions described herein and preferably provides instructions for its use.

[0356] The kits of the present application are in suitable packaging. Suitable packaging includes, but is not limited to, vials, bottles, jars, flexible packaging (*e.g.*, sealed Mylar or plastic bags), and the like. Kits may optionally provide additional components such as buffers and interpretative information. The present application thus also provides articles of manufacture, which include vials (such as sealed vials), bottles, jars, flexible packaging, and the like.

[0357] The article of manufacture can comprise a container and a label or package insert on or associated with the container. Suitable containers include, for example, bottles, vials, syringes, *etc.* The containers may be formed from a variety of materials such as glass or plastic. Generally, the container holds a composition which is effective for treating a disease or disorder described herein, and may have a sterile access port (for example the container may be an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection needle). The label or package insert indicates that the composition is used for treating the particular condition in an individual. The label or package insert will further comprise instructions for administering the composition to the individual. The label may indicate directions for reconstitution and/or use. The container holding the pharmaceutical composition may be a multi-use vial, which allows for repeat administrations (*e.g.* from 2-6 administrations) of the reconstituted formulation. Package insert refers to instructions customarily included in commercial packages of therapeutic products that contain information about the indications, usage, dosage, administration, contraindications and/or warnings concerning the use of such therapeutic products. Additionally, the article of manufacture may further comprise a second container comprising a pharmaceutically-acceptable buffer, such as bacteriostatic water for injection (BWFI), phosphate-buffered saline, Ringer's solution and dextrose solution. It may further include other materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, needles, and syringes.

[0358] The kits or article of manufacture may include multiple unit doses of the pharmaceutical composition and instructions for use, packaged in quantities sufficient for storage and use in pharmacies, for example, hospital pharmacies and compounding pharmacies.

EXAMPLES

[0359] The examples below are intended to be purely exemplary of the invention and should therefore not be considered to limit the invention in any way. The following examples and detailed description are offered by way of illustration and not by way of limitation.

Example 1: Construction and Expression of PD-1/CTLA-4 bispecific antigen binding protein

[0360] This example describes the construction and expression of exemplary PD-1/CTLA-4 bispecific antigen binding proteins. Two constructs were designed and expressed, each comprising two polypeptide chains as follows:

[0361] Construct 1: The first polypeptide comprises from the N-terminus to the C terminus: the V_HH domain of an anti-CTLA-4 sdAb, a peptide linker, the heavy chain variable domain V_H of pembrolizumab, and heavy chain constant domains of IgG4. The second polypeptide comprises from the N-terminus to the C-terminus: the light chain variable domain V_L of pembrolizumab, antibody kappa light chain C_L domain.

[0362] Construct 2: The first polypeptide comprises from the N-terminus to the C terminus: the heavy chain variable domain V_H of pembrolizumab, heavy chain constant domains of IgG4, a peptide linker, and the V_HH domain of an anti-CTLA-4 sdAb. The second polypeptide comprises from the N-terminus to the C-terminus: the light chain variable domain V_L of pembrolizumab, antibody kappa light chain C_L domain.

[0363] The bispecific antigen binding protein consists of two copies of the first polypeptide and two copies of the second polypeptide. An S228P mutation can be introduced to the IgG4 Fc region to inhibit Fab arm exchange. Furthermore, the Fc region of the bispecific antigen binding protein may be swapped with IgG Fc of a different isotype, for example, the IgG1 isotype. The Fc region of IgG4 isotype has low binding affinity to FcγRs, and thus is preferable over IgG1 isotype in some embodiments for avoiding ADCC-mediated depletion of PD-1 or CTLA-4 positive cells.

[0364] Stable cell lines expressing each of the two PD-1/CTLA-4 bispecific antigen binding protein constructs were generated. CHO-K1 SP cells were used to express the bispecific antigen

binding proteins, which were purified by chromatography through a column containing Protein A agarose resin followed by a size exclusion column.

[0365] The purified bispecific antigen binding proteins were formulated in a solution containing sodium citrate, sodium chloride, mannitol, diethylenetriaminepentacetic acid (pentetic acid), and polysorbate 80 (Tween 80), pH 6.0.

Example 2: *In vitro* functional assays of PD-1/CTLA-4 bispecific antigen binding proteins.

[0366] The PD-1/CTLA-4 bispecific antigen binding proteins prepared in Example 1 are tested in the *in vitro* assays described below to assess the functional blockade of PD-1 and CTLA-4 by the bispecific antigen binding proteins.

Target binding assays

[0367] The ability of the bispecific antigen binding proteins to bind PD-1 and CTLA-4 is determined using Surface Plasmon Resonance method (*e.g.*, BIACORE®), an enzyme-linked immunosorbent assay, a Fluorescence-Assisted Cell Sorting method (FACS), or a combination thereof. The analyses can be performed on activated T cells.

[0368] Binding of each of the bispecific antigen binding proteins to PD-1 and CTLA-4 expressed on activated T cells, such as Dendritic Cell-induced T cells, is determined using a fluorescence-activated cell sorting (FACS)-based assay. Cells bound to the bispecific antigen binding proteins are labeled by a fluorescein isothiocyanate (FITC)-conjugated anti-human kappa antibody (Jackson ImmunoResearch).

[0369] Binding kinetics of each bispecific antigen binding protein to PD-1 are determined using His-tagged human PD-1 protein captured on a CM5 sensor chip. Each bispecific antigen binding protein is flowed over the antigen-coated chip, and avidity is determined, using surface plasmon resonance. Alternatively, each bispecific antigen binding protein is captured on a CM5 chip pre-coated with an anti- C_H1 antibody, over which His-tagged human PD-1 protein is applied.

[0370] Binding kinetics of each bispecific antigen binding protein to CTLA-4 are determined using His-tagged human CTLA-4 coated on a CM5 (Biacore) sensor chip. Each bispecific antigen binding protein is flowed over the antigen-coated chip, and avidity was determined, using surface plasmon resonance. Alternatively, each bispecific antigen binding protein is

captured on a CM5 chip pre-coated with an anti- C_H1 antibody, over which His-tagged human CTLA-4 protein is applied.

Inhibition of ligand binding by FACS analysis

[0371] Inhibition of ligand binding by the bispecific antigen binding proteins can be assessed by a FACS assay.

[0372] To assess inhibition of PD-L1 by the bispecific antigen binding proteins, CHO cells expressing human PD-1 were dissociated from adherent culture flasks and mixed with varying concentrations of each bispecific antigen binding protein and a constant concentration of hPD-L1-Fc fusion protein having a biotin label. The mixture was equilibrated for 30 minutes at room temperature, and washed three times with FACS buffer (PBS containing 1% BSA). PE/Cy5 Streptavidin secondary antibody was then added to the mixtures and incubated for 15 minutes at room temperature. Subsequently, the cells were washed with FACS buffer and analyzed by flow cytometry. Data was analyzed with Prism (GraphPad Software, San Diego, CA) using non-linear regression, and IC50 values were calculated. The competition assays demonstrated the ability of the bispecific antigen binding proteins to efficiently inhibit PD-1/PD-L1 interactions at low concentrations (1-10 μg/ml).

[0373] To assess inhibition of B7-1 (a CTLA-4 ligand) by the bispecific antigen binding proteins, CHO cells expressing human B7-1 cells were dissociated from adherent culture flasks and mixed with varying concentrations of each bispecific antigen binding protein and a constant concentration of hCTLA-4-Fc fusion protein having a biotin-label. The mixture was equilibrated for 30 minutes at room temperature, and washed three times with FACS buffer (PBS containing 1% BSA). PE/Cy5 Streptavidin secondary antibody was then added to the mixtures and incubated for 15 minutes at room temperature. Subsequently, the cells were washed again with FACS buffer and analyzed by flow cytometry. Data were analyzed with Prism (GraphPad Software, San Diego, CA) using non-linear regression, and IC50 values were calculated. The competition assays demonstrated the ability of the bispecific antigen binding proteins to efficiently inhibit CTLA4-B7-1 interactions at low concentrations (1-10 μg/ml).

***In vitro* functional assays**

[0374] Blockade of the PD-1 and CTLA-4 pathways by the bispecific antigen binding proteins can be studied using a variety of bioassays that monitor T cell proliferation, IFN-γ release, IL-2

secretion or expression of reporter gene that is driven by signaling in the PD-1 or CTLA-4 pathway.

[0375] PD-1 pathway inhibition by the bispecific antigen binding proteins is studied by determining the IL-2 secretion level in mixed lymphocyte reactions (MLR) containing target cells expressing PD-L1 (such as dendritic cells), activated T cells, and each of the bispecific antigen binding proteins. Human $CD4^+$ T cells and allogeneic monocytes are purified from PBMC using isolation kits (Miltenyl Biotec). Monocytes are induced into dendritic cells. Each well contains10^5 $CD4^+$ T cells and 10^4 allogeneic dendritic cells with a final working volume of 200 μl. Each of the bispecific antigen binding proteins is added into each well at different concentrations. A no antibody well is used as the background control. Human IgG4 is used as the negative control and KEYTRUDA® is used as the positive anti-PD-1 antibody control. After incubating for 72 hours at 37°C in a 5% CO2 incubator, 100 μl medium is taken from each testing well for IL-2 measurement (Cisbio). Concentration-dependent secretion of IL-2 in the MLRs is used to extract an EC50 value for the bispecific antigen binding proteins against PD-1, which is compared with the EC50 value of control PD-1 antibody KEYTRUDA®.

[0376] CTLA-4 pathway inhibition by the bispecific antigen binding proteins is studied by determining IL-2 secretion level in mixed lymphocyte reactions containing target cells expressing CD80, activated T cells, and each of the bispecific antigen binding proteins. Human $CD4^+$ T cells are purified from PBMC using isolation kits (Miltenyl Biotec). Each well contains 10^5 $CD4^+$ T cells and 10^4 CHO-K1/human CD80 (CHO-K1 stably expressing human CD80) with a final working volume of 200 μl. Each of the bispecific antigen binding proteins is added into each well at different concentrations. A no antibody well is used as the background control. Human IgG4 is used as the negative control and YERVOY® is used as the positive anti-CTLA4 antibody control. CTLA4-Fc (GenScript, Z03373-50) is added into the system to initiate the reaction. After incubating for 24 hours at 37°C in a 5% CO2 incubator, 100 μl medium is taken from each testing well for IL-2 measurement (Cisbio). Concentration-dependent secretion of IL-2 in the CTLA-4 blockade bioassays is used to extract an EC50 value for the bispecific antigen binding proteins against CTLA-4, which is compared with the EC50 value of control CTLA-4 antibody YERVOY®.

Example 3: *In vivo* assay for bispecific antibody with PD-1 and CTLA-4.

[0377] This example describes *in vivo* experiments testing the functional blockade of PD-1 and CTLA-4 by the PD-1/CTLA-4 bispecific antigen binding proteins prepared in Example 1.

[0378] Anti-tumor efficacy is evaluated in tumor models developed with human CTLA-4 and PD-1 Knock-in mice. Humanization of both CTLA-4 and PD-1 in mice enables direct *in vivo* evaluation of the efficacy of PD-1/CTLA-4 bispecific antigen binding proteins in a mouse tumor xenograft model.

[0379] The mouse xenograft models are prepared by implanting tumor cells into NSG mice. Tumor cell lines, such as MC38 (a murine colon adenocarcinoma cell line) and CT26 (a murine colon carcinoma cell line), are used to prepare mouse models for colon cancer. B16, a murine melanoma cell line, is used to prepare a mouse model for melanoma. Renca, a murine renal cortical adenocarcinoma cell line, is used to prepare a mouse model for renal cancer.

[0380] The modelized mice are administered vehicle control, anti-PD-1 antibody, anti-CTLA-4 antibody, combination of anti-PD-1 antibody and anti-CTLA-4 antibody, or the bispecific antigen binding proteins intravenously. Efficacy of the bispecific antigen binding proteins can be evaluated for inhibition of tumor establishment, and/or inhibition of growth of established tumors. Tumor size may be monitored by *in vivo* bioluminescence imaging before and after the treatment.

[0381] Anti-tumor efficacy of the bispecific antigen binding proteins are compared with the efficacies of anti-PD-1 antibody, anti-CTLA-4 antibody, or combination of anti-PD-1 antibody and anti-CTLA-4 antibody in the same mouse tumor model. Syngeneic tumor models exhibit differential responses to either anti-PD-1 antibody or anti-CTLA-4 antibody alone. While the combination of anti-PD-1 antibody and anti-CTLA-4 antibody may demonstrate higher tumor inhibition efficacy over either monotherapy in the mouse tumor model, the efficacy of the PD-1/CTLA-4 bispecific antigen binding proteins may be higher than the anti-PD-1 antibody/anti-CTLA-4 antibody combination therapy over a certain range of doses.

[0382] All citations throughout the disclosure are hereby expressly incorporated by reference.

CLAIMS

What is claimed is:

1. A multispecific antigen binding protein comprising:
   (a) a first antigen binding portion comprising a heavy chain variable domain (V_H) and a light chain variable domain (V_L), wherein the V_H and V_L together form an antigen-binding site that specifically binds a first epitope, and
   (b) a second antigen binding portion comprising a single-domain antibody that specifically binds a second epitope,
   wherein the first antigen binding portion and the second antigen binding portion are fused to each other.
2. The multispecific antigen binding protein of claim 1, wherein the first epitope and the second epitope are from the same antigen.
3. The multispecific antigen binding protein of claim 1, wherein the first epitope and the second epitope are from different antigens.
4. The multispecific antigen binding protein of any one of claims 1-3, wherein the multispecific antigen binding protein is bispecific.
5. The multispecific antigen binding protein of any one of claims 1-4, wherein the first antigen binding portion is a full-length antibody consisting of two heavy chains and two light chains.
6. The multispecific antigen binding protein of any one of claims 1-4, wherein the first antigen binding portion is an antibody fragment comprising a heavy chain comprising the V_H and a light chain comprising the V_L.
7. The multispecific antigen binding protein of claim 5 or claim 6, wherein the C terminus of the second antigen binding portion is fused to the N-terminus of at least one heavy chain of the first antigen binding portion.
8. The multispecific antigen binding protein of claim 5 or claim 6, wherein the C terminus of the second antigen binding portion is fused to the N-terminus of at least one light chain of the first antigen binding portion.
9. The multispecific antigen binding protein of claim 5 or claim 6, wherein the N terminus of the second antigen binding portion is fused to the C-terminus of at least one heavy chain of the first antigen binding portion.

10. The multispecific antigen binding protein of claim 5 or claim 6, wherein the N terminus of the second antigen binding portion is fused to the C-terminus of at least one light chain of the first antigen binding portion.
11. The multispecific antigen binding protein of any one of claims 1-10, wherein the first antigen binding portion comprises a human, humanized or chimeric antibody or antigen binding fragment thereof.
12. The multispecific antigen binding protein of any one of claims 1-11, wherein the first antigen binding portion comprises an Fc region.
13. The multispecific antigen binding protein of claim 12, wherein the Fc region is an IgG1 Fc.
14. The multispecific antigen binding protein of claim 12, wherein the Fc region is an IgG4 Fc having an S228P mutation.
15. The multispecific antigen binding protein of any one of claims 1-14, wherein the first antigen binding portion and the second antigen binding portion are fused to each other via a peptide bond or a peptide linker.
16. The multispecific antigen binding protein of claim 15, wherein the peptide linker is no more than about 30 amino acids long.
17. The multispecific antigen binding protein of claim 16, wherein the peptide linker comprises the amino acid sequence of SEQ ID NO: 1.
18. The multispecific antigen binding protein of any one of claims 1-14, wherein the first antigen binding portion and the second antigen binding portion are fused to each other chemically.
19. The multispecific antigen binding protein of any one of claims 1-18, wherein the single-domain antibody is a camelid, humanized, or human single-domain antibody.
20. The multispecific antigen binding protein of any one of claims 1-19, wherein the first epitope is from an immune checkpoint molecule.
21. The multispecific antigen binding protein of claim 20, wherein the immune checkpoint molecule is selected from the group consisting of PD-1, PD-L1, PD-L2, CTLA-4, B7-H3, TIM-3, LAG-3, VISTA, ICOS, 4-1BB, OX40, GITR, and CD40.
22. The multispecific antigen binding protein of claim 21, wherein the first antigen binding portion is an anti-PD-1 antibody or antigen binding fragment thereof.

23. The multispecific antigen binding protein of claim 22, wherein the anti-PD-1 antibody is selected from the group consisting of pembrolizumab and nivolumab.
24. The multispecific antigen binding protein of claim 21, wherein the first antigen binding portion is an anti-PD-L1 antibody or antigen binding fragment thereof.
25. The multispecific antigen binding protein of claim 24, wherein the anti-PD-L1 antibody is duravalumab or atezolizumab.
26. The multispecific antigen binding protein of any one of claims 20-25, wherein the single-domain antibody specifically binds an immune checkpoint molecule.
27. The multispecific antigen binding protein of claim 26, wherein the immune checkpoint molecule is selected from the group consisting of PD-1, PD-L1, PD-L2, CTLA-4, B7-H3, TIM-3, LAG-3, VISTA, ICOS, 4-1BB, OX40, GITR, and CD40.
28. The multispecific antigen binding protein of claim 27, wherein the second antigen binding portion comprises an anti-CTLA-4 single-domain antibody.
29. The multispecific antigen binding protein of any one of claims 1-19, wherein the first epitope is from a tumor antigen.
30. The multispecific antigen binding protein of claim 29, wherein the tumor antigen is selected from the group consisting of HER2, BRAF, EGFR, VEGFR2, CD20, RANKL, CD38, and CD52.
31. The multispecific antigen binding protein of claim 30, wherein the first antigen binding portion is an anti-HER2 antibody or antigen binding fragment thereof.
32. The multispecific antigen binding protein of claim 31, wherein the anti-HER2 antibody is trastuzumab.
33. The multispecific antigen binding protein of any one of claims 29-32, wherein the second antigen binding portion comprises an anti-CD3 single-domain antibody.
34. The multispecific antigen binding protein of any one of claims 1-19, wherein the first epitope is from a pro-inflammatory molecule.
35. The multispecific antigen binding protein of claim 34, wherein the pro-inflammatory molecule is selected from the group consisting of IL-1β, TNF-α, IL-5, IL-6, IL-6R, and eotaxin-1.
36. The multispecific antigen binding protein of claim 35, wherein the first antigen binding portion is an anti-TNF-α antibody or antigen binding fragment thereof.

37. The multispecific antigen binding protein of claim 36, wherein the anti-TNF-α antibody is adalimumab.
38. The multispecific antigen binding protein of claim 37, wherein the second antigen binding portion comprises an anti-IL-1β single-domain antibody.
39. The multispecific antigen binding protein of claim 35, wherein the first antigen binding portion is an anti-IL-5 antibody or antigen binding fragment thereof.
40. The multispecific antigen binding protein of claim 39, wherein the anti-IL-5 antibody is mepolizumab.
41. The multispecific antigen binding protein of claim 40, wherein the second antigen binding portion comprises an anti-eotaxin-1 single-domain antibody.
42. A pharmaceutical composition comprising the multispecific antigen binding protein of any one of claims 1-41 and a pharmaceutically acceptable carrier.
43. A method of treating a disease in an individual, comprising administering to the individual an effective amount of the pharmaceutical composition of claim 42.
44. The method of claim 43, wherein the disease is a cancer.
45. The method of claim 44, wherein the cancer is selected from the group consisting of breast cancer, renal cancer, melanoma, lung cancer, glioblastoma, head and neck cancer, prostate cancer, ovarian carcinoma, bladder carcinoma, and lymphoma.
46. The method of claim 43, wherein the disease is an inflammatory or autoimmune disease.
47. The method of claim 46, wherein the inflammatory or autoimmune disease is selected from the group consisting of arthritis, colitis, psoriasis, severe asthma, and moderate to severe Crohn's disease.

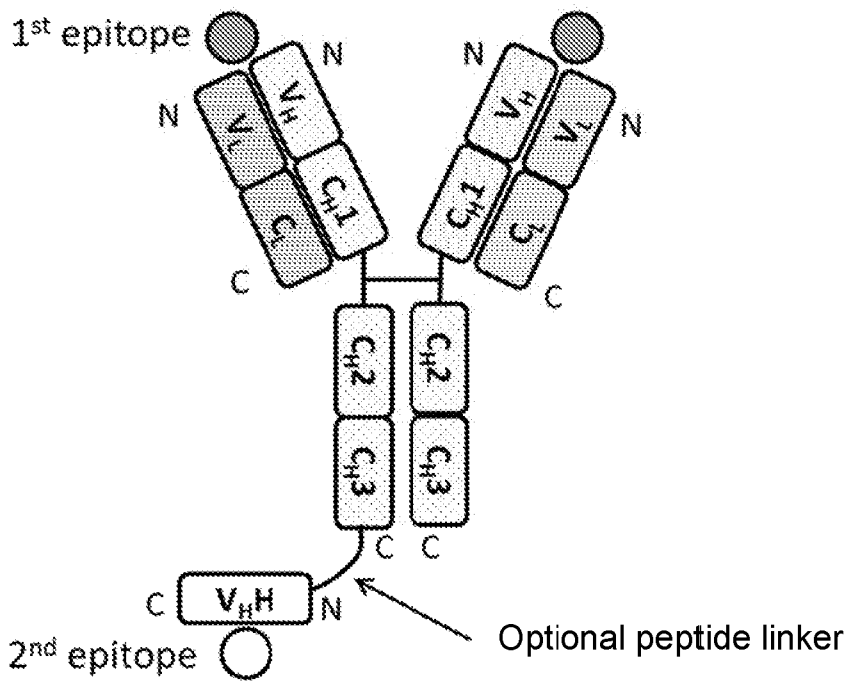
1st epitope
N
N
VH
VL
CH1
CL
C
N
N
VH
VL
CH1
CL
N
C
CH2
CH2
CH3
CH3
C
C
C
VHH
N
2nd epitope
Optional peptide linker

FIG. 1

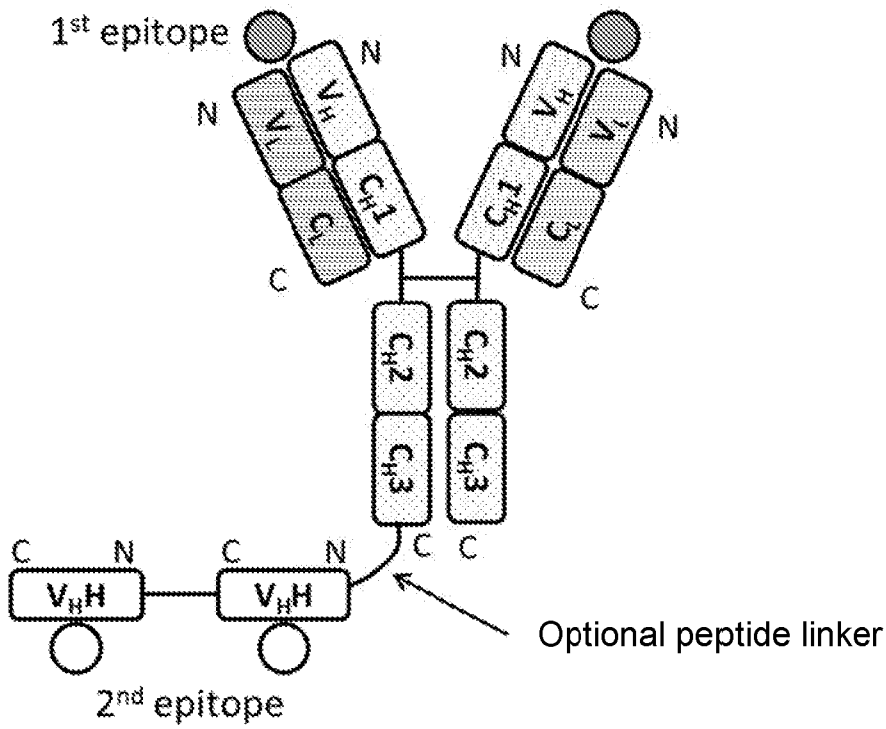
1st epitope
N
N
VH
VL
CH1
CL
C
N
N
VH
VL
CH1
CL
N
C
CH2
CH2
CH3
CH3
C
C
C
N
C
N
VHH
VHH
2nd epitope
Optional peptide linker

FIG. 2

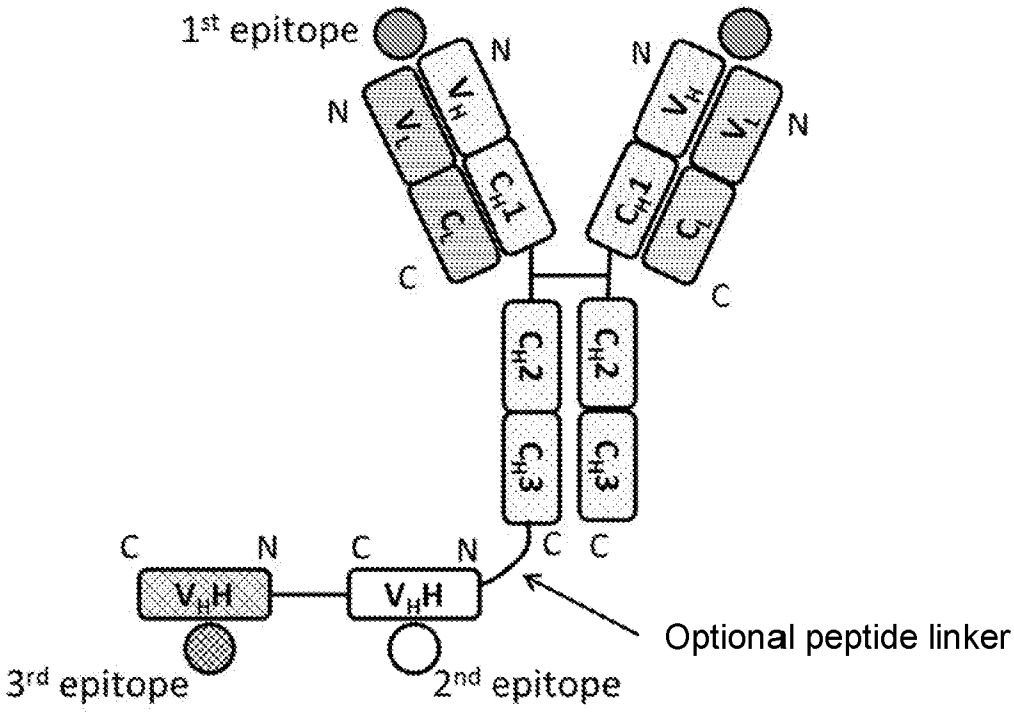
1st epitope
N
N
N
N
C
C
C
C
C
C
N
C
N
C
N
Optional peptide linker
3rd epitope
2nd epitope

FIG. 3

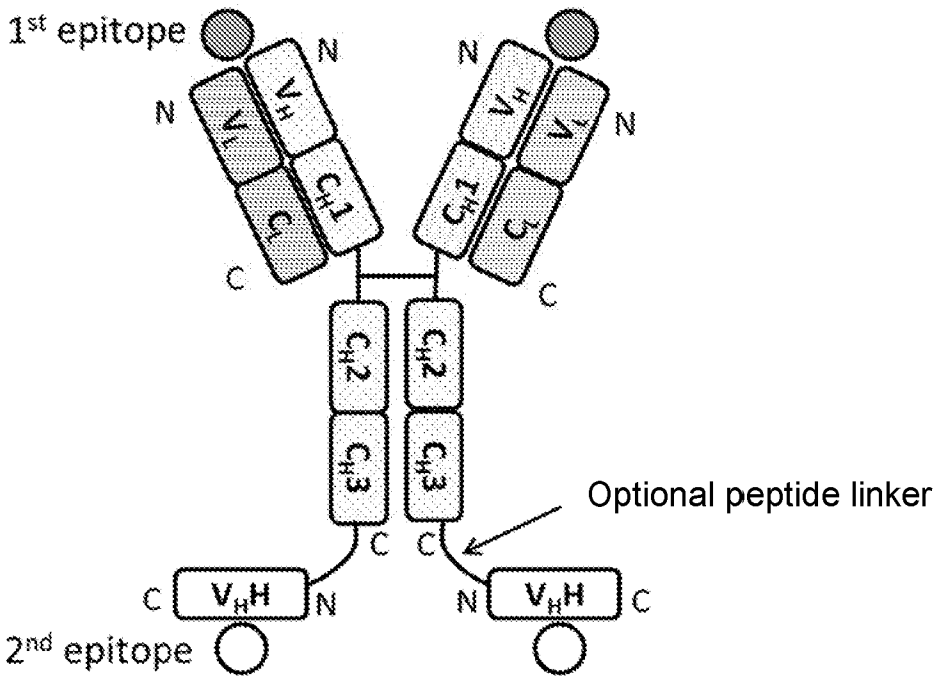
1st epitope
N
N
N
N
C
C
C
C
C
C
N
N
C
Optional peptide linker
2nd epitope

FIG. 4

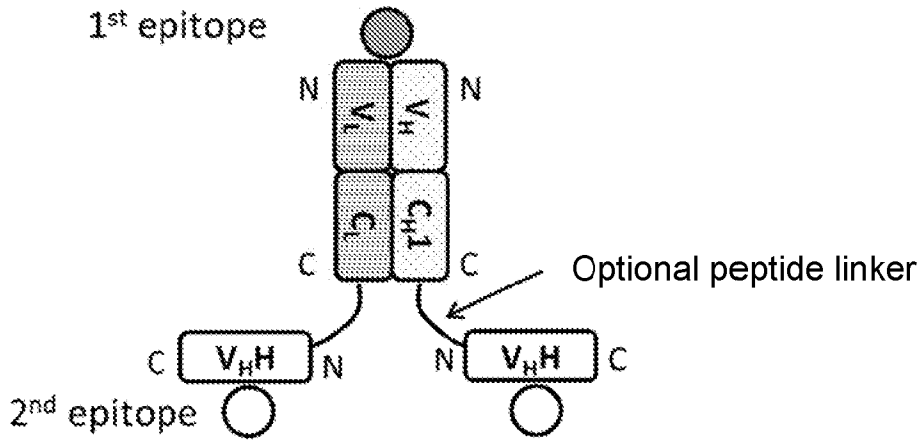
1st epitope
N
N
C
C
Optional peptide linker
C
N
N
C
2nd epitope

FIG. 5

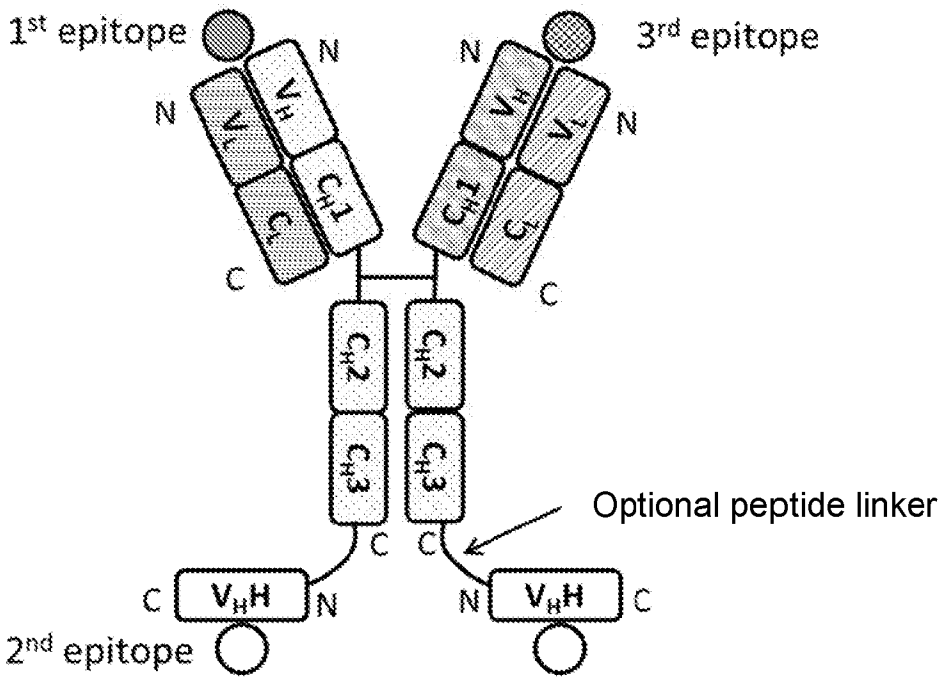
1st epitope
N
N
3rd epitope
N
N
C
C
Optional peptide linker
C
N
N
C
2nd epitope

FIG. 6

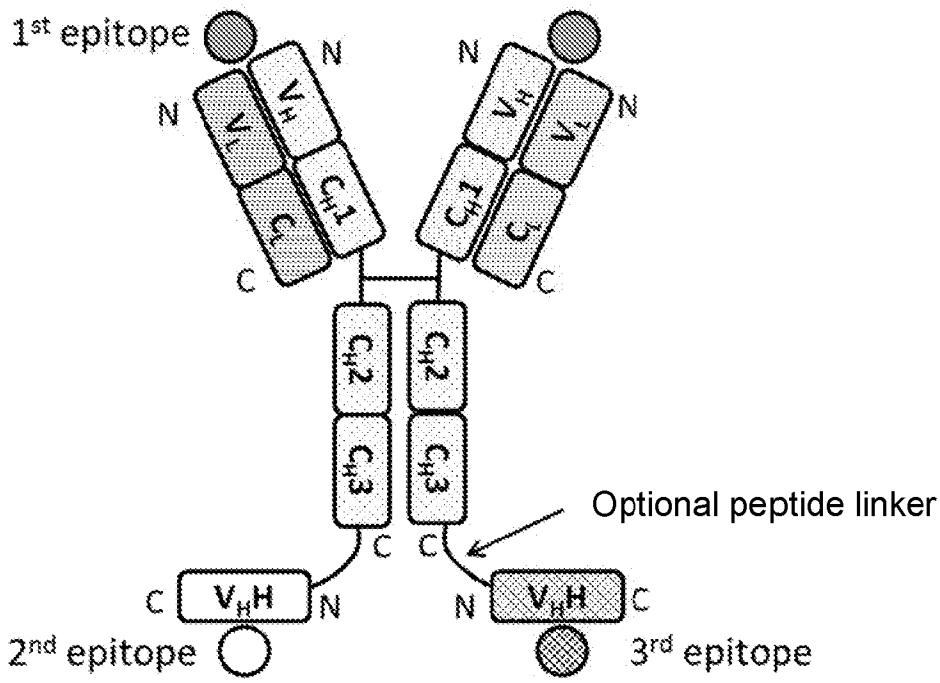
1st epitope
N
N
VH
VL
CH1
CL
C
C
N
N
VH
VL
CH1
CL
C
C
CH2
CH3
CH2
CH3
C
C
Optional peptide linker
C
VHH
N
N
VHH
C
2nd epitope
3rd epitope

FIG. 7

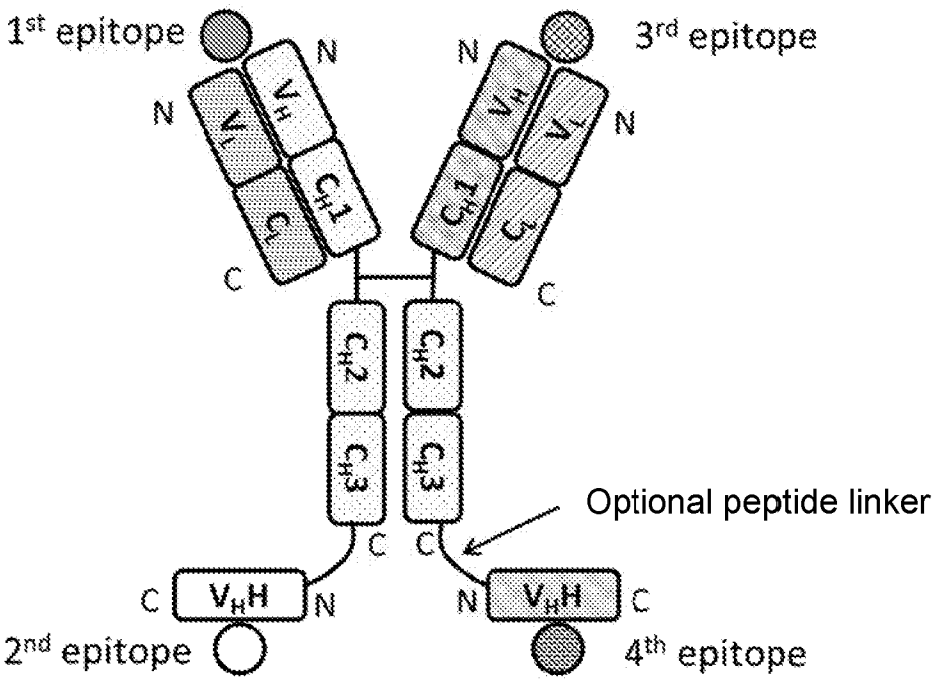
1st epitope
N
N
VH
VL
CH1
CL
C
C
3rd epitope
N
N
VH
VL
CH1
CL
C
C
CH2
CH3
CH2
CH3
C
C
Optional peptide linker
C
VHH
N
N
VHH
C
2nd epitope
4th epitope

FIG. 8

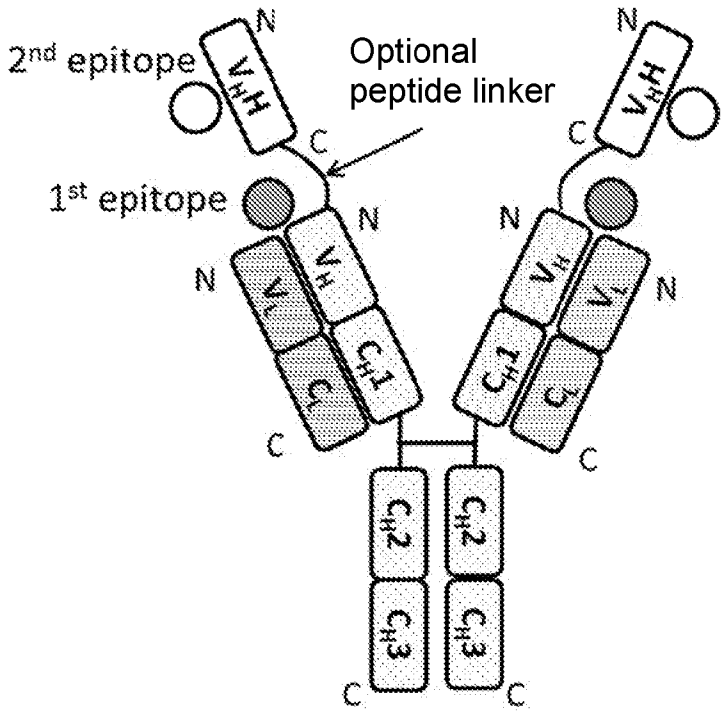
2nd epitope
Optional
peptide linker
1st epitope
N
C

FIG. 9

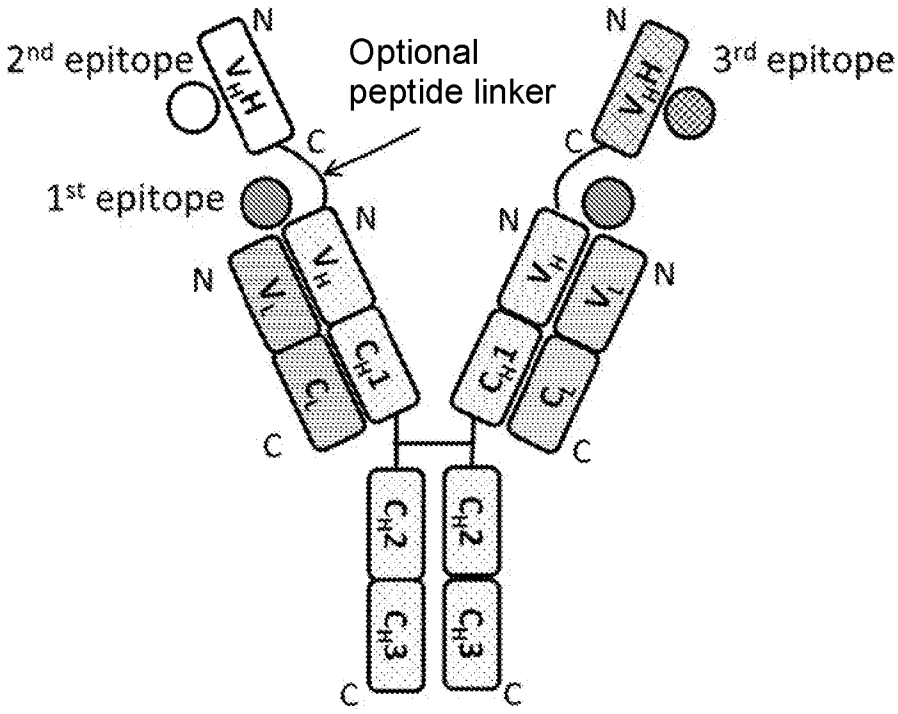
2nd epitope
Optional
peptide linker
3rd epitope
1st epitope
N
C

FIG. 10

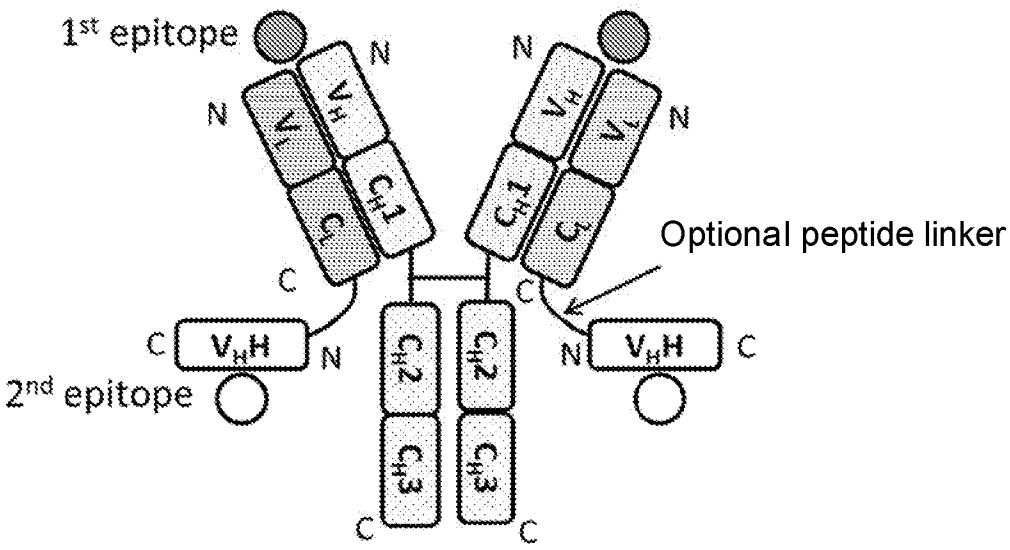
1st epitope
Optional peptide linker
2nd epitope

FIG. 11

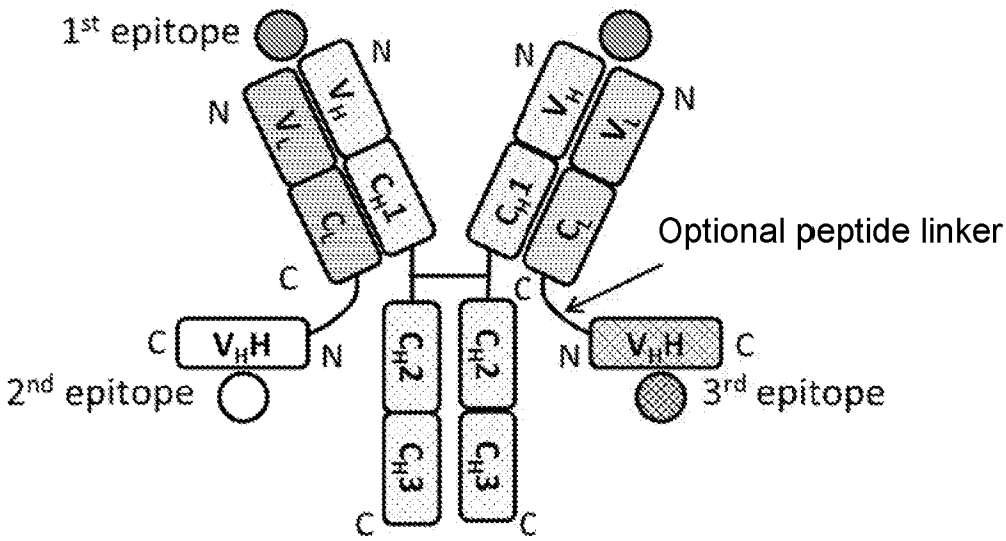
1st epitope
Optional peptide linker
2nd epitope
3rd epitope

FIG. 12

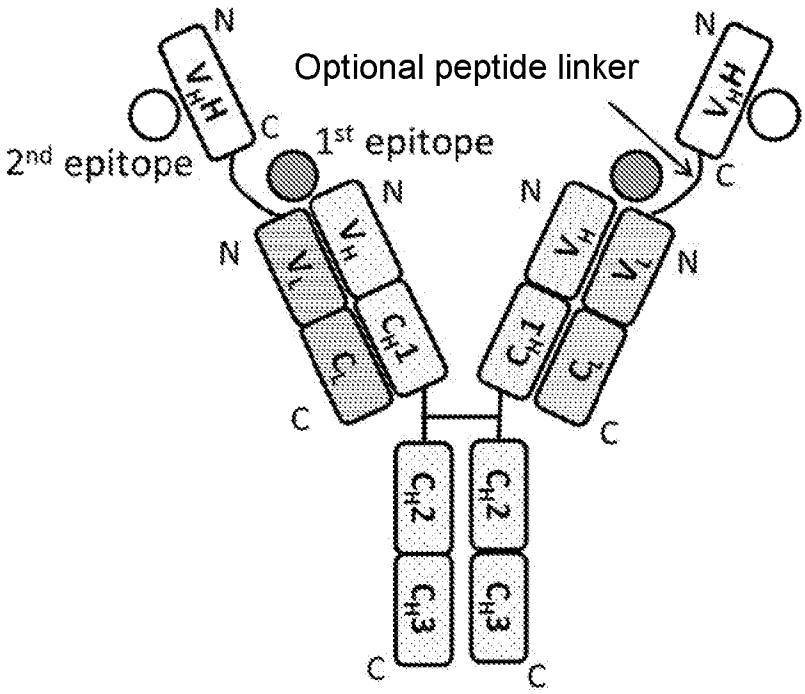
Optional peptide linker
2nd epitope
1st epitope
N
C

FIG. 13

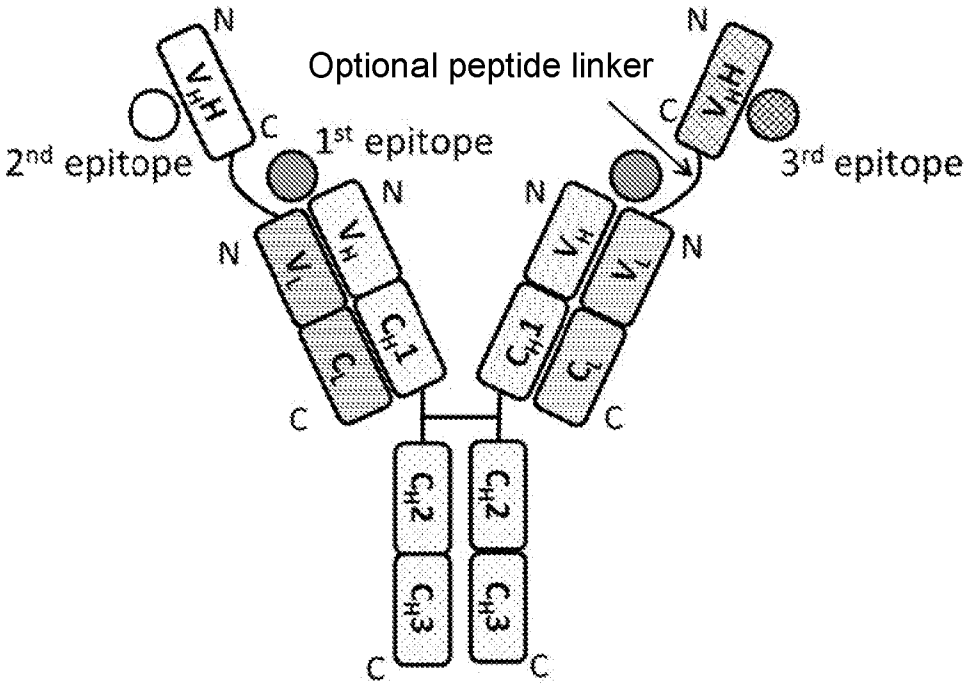
Optional peptide linker
2nd epitope
1st epitope
3rd epitope
N
C

FIG. 14

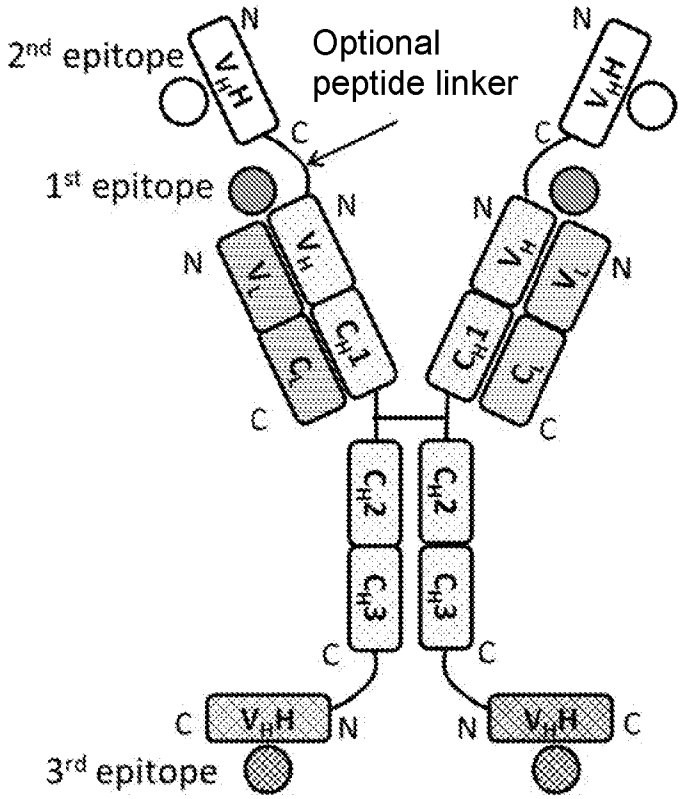
2nd epitope
Optional peptide linker
1st epitope
3rd epitope

FIG. 15

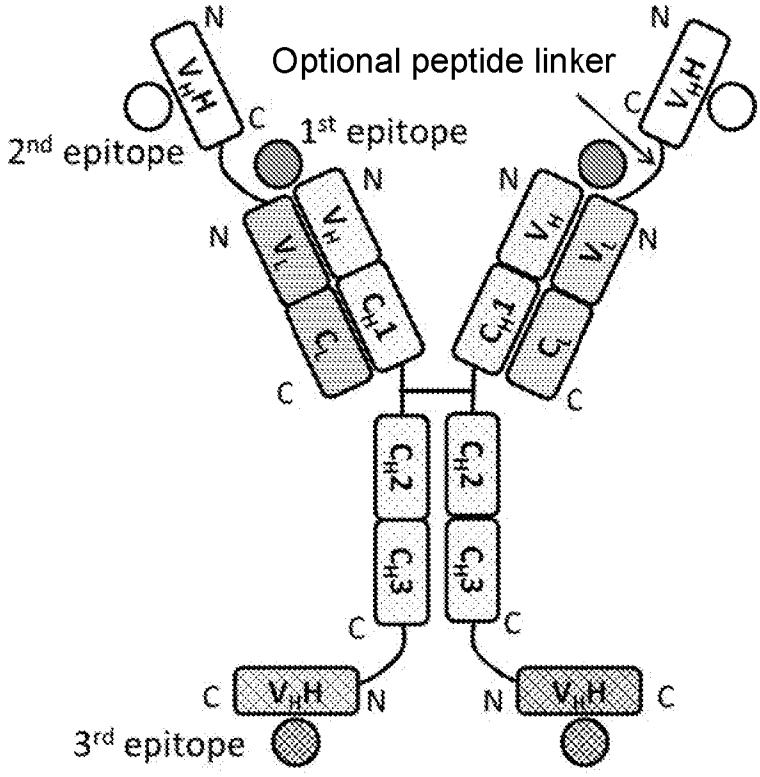
Optional peptide linker
2nd epitope
1st epitope
3rd epitope

FIG. 16

INTERNATIONAL SEARCH REPORT

International application No.
PCT/CN2016/090703

A. CLASSIFICATION OF SUBJECT MATTER

C07K 16/46(2006.01)i; C07K 16/18(2006.01)i; C07K 16/28(2006.01)i; C07K 16/30(2006.01)i; C07K 16/24(2006.01)i; A61K 39/395(2006.01)i; A61P 35/00(2006.01)i; A61P 37/00(2006.01)i

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

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

C07K; A61K; A61P

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

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

CNABS , VEN , CNTXT , USTXT , EPTXT , SIPOABS , DWPI , CNKI , GOOGLE, PubMed,ISI Web of Knowledge, NCBI GenBank, DDBJ, multispecific, bispecific, antibody, single domain antibody, dAb, nanobody, sdAb, Fc, linker, SEQ ID NO:1, PD-1, PD-L1, PD-L2, CTLA-4, B7-H3, TIM-3, LAG-3, VISTA, ICOS, 4-1BB, OX40, GITR, CD40,HER2, BRAF, EGFR, VEGFR2, CD20, RANKL, CD38, CD52, IL-1β, TNF-α, IL-5, IL-6, IL-6R, eotaxin-1, pembrolizumab, nivolumab, duravalumab, atezolizumab, trastuzumab, adalimumab, mepolizumab, cancer, inflammatory, autoimmune, Nanjingjinsirui Science & Technology Biology Corp, CHOU Chuanchu, ZHANG Yafeng, WU Shu, LIU Zhenyu, LI Zhongdao, ZHANG Fangliang

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2011036460 A1 (UCB PHARMA S.A.) 31 March 2011 (2011-03-31) description, page3, lines 1-5, 20-40, page 4, lines 9-26, page 7, lines 33-34, page 9, lines 21-25, page 11, line 2, page 13, lines 29-30, page 14, lines 18-21, page 30, lines 32-39, page 31, lines 7-14	1-4, 6-11, 15-21, 26-27, 29-30, 33-40, 42-47
X	US 2014127210 A1 (SAMSUNG ELECTRONICS CO., LTD.) 08 May 2014 (2014-05-08) description, para. 0025, 0030, 0031, 0033, 0066-0068	1-6, 12-15, 29-33, 42-47
X	CN 1388136 A (INST. GENETICS CAS. ET AL.) 01 January 2003 (2003-01-01) claims 1-9	1, 3-6, 11, 12, 15, 16, 19, 29, 33, 42-45

☑ Further documents are listed in the continuation of Box C. ☑ See patent family annex.

* Special categories of cited documents:

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

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

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

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

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

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

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

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

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
29 March 2017	**12 April 2017**
Name and mailing address of the ISA/CN **STATE INTELLECTUAL PROPERTY OFFICE OF THE P.R.CHINA** **6, Xitucheng Rd., Jimen Bridge, Haidian District, Beijing 100088** **China** Facsimile No. **(86-10)62019451**	Authorized officer **GUO,Tingting** Telephone No. **(86-10)62413903**

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 2011036460 A1 (UCB PHARMA S.A.) 31 March 2011 (2011-03-31) description, page3, lines 1-5, 20-40, page 4, lines 9-26, page 7, lines 33-34, page 9, lines 21-25, page 11, line 2, page 13, lines 29-30, page 14, lines 18-21, page 30, lines 32-39, page 31, lines 7-14	21-25, 27-28, 35, 41-47
Y	WO 2006138670 A2 (VIRXSYS CORPORATION) 28 December 2006 (2006-12-28) claims 1, 2, 6, 7, 9	21-25, 27-28, 42-47
Y	FULKERSON P.C. et al. "Targeting eosinophils in allergy, inflammation and beyond." *NATURE REVIEWS: DRUG DISCOVERY.*, Vol. 12, 21 January 2013 (2013-01-21), pages 117-129	35, 41-47
Y	CN 105754990 A (SHENZHEN GENTARGET MEDICAL TECH.CO.LTD.) 13 July 2016 (2016-07-13) claims 4-5	21-23, 27-28, 42-47

INTERNATIONAL SEARCH REPORT

International application No.
PCT/CN2016/090703

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing filed or furnished:

   a. (means)

   ☐ on paper

   ☑ in electronic form

   b. (time)

   ☑ in the international application as filed

   ☐ together with the international application in electronic form

   ☐ subsequently to this Authority for the purposes of search

2. ☐ In addition, in the case that more than one version or copy of a sequence listing has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that in the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments:

INTERNATIONAL SEARCH REPORT

International application No.
PCT/CN2016/090703

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

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

1. ☑ Claims Nos.: **43-47**
because they relate to subject matter not required to be searched by this Authority, namely:

[1] Claims 43-47 are directed to a method of treating a disease in an individual. The subject matter of claims 43-47 relates to the treatment of human body by therapy, therefore does not warrant an international search according to the criteria set out in PCT Rule 39.1(iv). An international search is still carried out on the basis of the use of the pharmaceutical composition of claim 42 for the manufacturing of a medicament for the treatment of cancer, inflammatory or autoimmune disease.

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

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

INTERNATIONAL SEARCH REPORT
Information on patent family members

International application No.
PCT/CN2016/090703

Patent document cited in search report	Publication date (day/month/year)	Patent family member(s)	Publication date (day/month/year)
WO 2011036460 A1	31 March 2011	JP 5931730 B2	08 June 2016
		EP 2480577 A1	01 August 2012
		CN 105315374 A	10 February 2016
		JP 2016106126 A	16 June 2016
		EA 201200526 A1	30 November 2012
		CN 102549018 B	25 November 2015
		CN 102549018 A	04 July 2012
		BR 112012006492 A2	22 November 2016
		US 2012316324 A1	13 December 2012
		IN 2535DEN2012 A	28 August 2015
		GB 201005063 D0	12 May 2010
		JP 2013505923 A	21 February 2013
		CA 2773286 A1	31 March 2011
US 2014127210 A1	08 May 2014	JP 2014090721 A	19 May 2014
		EP 2727940 A1	07 May 2014
		CN 103788212 A	14 May 2014
		KR 20140055536 A	09 May 2014
CN 1388136 A	01 January 2003	US 2005255115 A1	17 November 2005
		EP 1394253 A1	03 March 2004
		ES 2337237 T3	22 April 2010
		WO 03004648 A1	16 January 2003
		US 2008138339 A1	12 June 2008
		EP 1394253 B1	13 January 2010
		AT 454903 T	15 January 2010
		US 7262276 B2	28 August 2007
		EP 1394253 A4	15 March 2006
		DE 60235079 D1	04 March 2010
		RU 2003133973 A	10 May 2005
		CN 1195779 C	06 April 2005
WO 2006138670 A2	28 December 2006	CA 2612355 A1	28 December 2006
		WO 2006138670 A3	03 May 2007
CN 105754990 A	13 July 2016	None	