MULTI-SPECIFIC ANTIBODIES AND METHODS OF MAKING AND USING THEREOF

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of U.S. Provisional Patent Application No. 62524557 filed June, 25, 2017, which application is expressly incorporated herein by reference in its entirety.

TECHNICAL FIELD

The present disclosure generally relates to the technical field of biologic therapeutics, and more particularly relates to making and using multi-specific antibodies.

BACKGROUND

Cancer cells develop various strategies to evade the immune system. One of the underlying mechanisms for the immune escape is the reduced recognition of cancer cells by the immune system. Defective presentation of cancer specific antigens or lack of thereof results in immune tolerance and cancer progression. In the presence of effective immune recognition tumors use other mechanisms to avoid elimination by the immune system. Immunocompetent tumors create suppressive microenvironment to downregulate the immune response. Multiple players are involved in shaping the suppressive tumor microenvironment, including tumor cells, regulatory T cells, Myeloid-Derived Suppressor cells, stromal cells, and other cell types. The suppression of immune response may be executed in a cell contact-dependent format as well as in and a contact-independent manner, via secretion of immunosuppressive cytokines or elimination of essential survival factors from the local environment. Cell contact-dependent suppression relies on molecules expressed on the cell surface, e.g. Programmed Death Ligand 1 (PD-L1), T-lymphocyte-associated protein 4 (CTLA-4) and others [Dunn, et al., 2004, Immunity, 21(2): 137-48; Adachi & Tamada, 2015, Cancer Sci., 106(8): 945-50].

As the mechanisms by which tumors evade recognition by the immune system continue to be better understood new treatment modalities that target these mechanisms have recently emerged. On March 25, 2011, the U. S. Food and Drug Administration (FDA) approved ipilimumab injection (Yervoy, Bristol-Myers Squibb) for the treatment of unresectable or metastatic melanoma. Yervoy binds to cytotoxic T-lymphocyte-associated protein 4 (CTLA-4) expressed on activated T cells and blocks the interaction of CTLA-4 with CD80/86 on antigen-presenting cells thereby blocking the negative or inhibitory signal delivered into the T cell through CTLA-4 resulting in re-activation of the antigen-specific T cell leading to, in many patients, eradication of the tumor. A few years later in 2014 the FDA approved Keytruda (Pembrolizumab, Merck) and Opdivo (Nivolumab, Bristol-Myers Squibb) for treatment of advanced melanoma. These monoclonal antibodies bind to PD-1 which is expressed on activated and/or exhausted T cells and block the interaction of PD-1 with PD-L1 expressed on tumors thereby eliminating the inhibitory signal through PD-1 into the T cell resulting in re-activation of the antigen-specific T cell leading to again, in many patients, eradication of the tumor. Since then additional clinical trials have been performed comparing the single monoclonal antibody Yervoy to the combination of the monoclonal antibodies Yervoy and Opdivo in the treatment of advanced melanoma which showed improvement in overall survival and progression-free survival in the patients treated with the

combination of antibodies. (Hodi et al., 2016, Lancet Oncol. 17(11):1558-1568, Hellman et al., 2018, Cancer Cell 33(5): 853-861). However, as many clinical trials have shown a great benefit of treating cancer patients with monoclonal antibodies that are specific for one or more immune checkpoint molecules data has emerged that only those patients with a high mutational burden that generates a novel T cell epitope(s) which is recognized by antigen-specific T cells show a clinical response (Snyder et al., 2014, NEJM 371:2189-2199). Those patients that have a low tumor mutational load mostly do not show an objective clinical response (Snyder et al., 2014, NEJM 371:2189-2199, Hellman et al., 2018, Cancer Cell 33(5): 853-861).

In recent years, other groups have developed an alternate approach that does not require the presence of neoepitope presentation by antigen-presenting cells to activate T cells. One example is the development of a bi-specific antibody where the binding domain of an antibody which is specific for a tumor associated antigen, e.g., CD19, is linked to and antibody binding domain specific for CD3 on T cells thus creating a bi-specific T cell engager or BiTe molecule. In 2014, the FDA approved a bi-specific antibody called Blinatumomab for the treatment of Precursor B-Cell Acute Lymphoblastic Leukemia. Blinatumomab links the scFv specific for CD19 expressed on leukemic cells with the scFv specific for CD3 expressed on T cells (Bejnjamin and Stein 2016, Ther Adv Hematol 7(3):142-146). However, despite an initial response rate of >50% in patients with relapsed or refractory ALL many patients are resistant to Blinatumomab therapy or relapse after successful treatment with Blinatumomab. Evidence is emerging that the resistant to Blinatumomab or who relapse after Blinatumomab treatment is attributable to the expression of immune checkpoint inhibitory molecules expressed on tumor cells such as PD-L1 that drives an inhibitory signal through PD-1 expressed on activated T cells (Feucht et al., 2016, Oncotarget 7(47):76902-76919). In a case study of a patient who was resistant to therapy with Blinatumomab a second round of Blinatumomab therapy was performed but with the addition of a monoclonal antibody, pembrolizumab (Keytruda, Merck), which specific for PD-1 and blocks the interaction of T cell-expressed PD-1 with tumor cell expressed PD-L1 resulted in a dramatic response and reduction of tumor cells in the bone marrow from 45% to less than 5% in this one patient (Feucht et al., 2016, Oncotarget 7(47):76902-76919). These results show that combining a bi-specific BiTe molecule with one or more monoclonal antibodies may significantly increase clinical activity compared to either agent alone.

SUMMARY

The present disclosure provides, among others, tetra-specific antibody monomers, antibodies containing tetra-specific monomers, antigen-binding fragments thereof, multi-specific antibodies, immuno-conjugates comprising the disclosed antibodies, methods of making disclosed monomers, antigen-binding fragments, and antibodies, and methods of using the disclosed molecules for treating cancer.

In one aspect, the present disclosure refers to a tetra-specific antibody monomer having a N-terminal and a C-terminal, comprising in tandem from the N-terminal to the C-terminal, a first scFv domain at the N-terminal, a Fab domain, a Fc domain, a second scFv domain, and a third scFv domain at the C-terminal, wherein the first scFv domain, the Fab domain, the second scFv domain, and the third scFv domain each has a binding specificity against a different antigen, wherein the first scFv domain, the Fab domain, the second scFv domain, and the third scFv domain each independently has a binding specificity against: (i) an antigen selected from CD3, PD-L1, 4-1BB, and ROR1; or (ii) an antigen selected from CD3,

PD-L1, 4-1 BB, and CD19; or (iii) an antigen selected from CD3, PD-L1, 4-1 BB, and EGFRvIII; and wherein the monomer comprises: (a) 3 complementarity determining regions (CDRs) of SEQ ID NO: 30, 3 CDRs of SEQ NO: 32, 3 CDRs of SEQ NO: 10, 3 CDRs of SEQ NO: 12, 3 CDRs of SEQ NO: 38, 3 CDRs of SEQ NO: 40, 3 CDRs of SEQ NO: 2, and 3 CDRs of SEQ NO: 4; or (b) 3 CDRs of SEQ ID NO: 26, 3 CDRs of SEQ NO:28, 3 CDRs of SEQ NO:10, 3 CDRs of SEQ NO:12, 3 CDRs of SEQ NO:38, 3 CDRs of SEQ NO:40, 3 CDRs of SEQ NO:2, and 3 CDRs of SEQ NO:4; or (c) 3 CDRs of SEQ ID NO:2, 3 CDRs of SEQ NO:4, 3 CDRs of SEQ NO:54, 3 CDRs of SEQ NO:56, 3 CDRs of SEQ NO:14, 3 CDRs of SEQ NO:16, 3 CDRs of SEQ NO:26, and 3 CDRs of SEQ NO:28; or (d) 3 CDRs of SEQ ID NO: 2, 3 CDRs of SEQ NO: 4, 3 CDRs of SEQ NO: 50, 3 CDRs of SEQ NO: 52, 3 CDRs of SEQ NO: 14, 3 CDRs of SEQ NO: 16, 3 CDRs of SEQ NO: 22, and 3 CDRs of SEQ NO: 24.

In yet another aspect, the present disclosure refers to a tetra-specific antibody monomer having a N-terminal and a C-terminal, comprising in tandem from the N-terminal to the C-terminal, a first scFv domain at the N-terminal, a Fab domain, a Fc domain, a second scFv domain, and a third scFv domain at the C-terminal, wherein the first scFv domain, the Fab domain, the second scFv domain, and the third scFv domain each has a binding specificity against a different antigen, wherein the first scFv domain, the Fab domain, the second scFv domain, and the third scFv domain each independently has a binding specificity against: (i) an antigen selected from CD3, PD-L1, 4-1BB, and ROR1; or (ii) an antigen selected from CD3, PD-L1, 4-1 BB, and CD19; or (iii) an antigen selected from CD3, PD-L1, 4-1 BB, and EGFRvIII; and wherein the monomer comprises: (a) an amino acid sequence having a percentage homology to SEQ ID NO: 30, an amino acid sequence having a percentage homology to SEQ ID NO: 32, an amino acid sequence having a percentage homology to SEQ ID NO: 10, an amino acid sequence having a percentage homology to SEQ ID NO: 12, an amino acid sequence having a percentage homology to SEQ ID NO: 38, an amino acid sequence having a percentage homology to SEQ ID NO: 40, an amino acid sequence having a percentage homology to SEQ ID NO: 2 and an amino acid sequence having a percentage homology to SEQ ID NO: 4, wherein the percentage homology is not less than 98%; or (b) an amino acid sequence having a percentage homology to SEQ ID NO: 26, an amino acid sequence having a percentage homology to SEQ ID NO: 28, an amino acid sequence having a percentage homology to SEQ ID NO: 10, an amino acid sequence having a percentage homology to SEQ ID NO: 12, an amino acid sequence having a percentage homology to SEQ ID NO: 38, an amino acid sequence having a percentage homology to SEQ ID NO: 40, an amino acid sequence having a percentage homology to SEQ ID NO: 2 and an amino acid sequence having a percentage homology to SEQ ID NO: 4, wherein the percentage homology is not less than 98%; or (c) an amino acid sequence having a percentage homology to SEQ ID NO: 2, an amino acid sequence having a percentage homology to SEQ ID NO: 4, an amino acid sequence having a percentage homology to SEQ ID NO: 54, an amino acid sequence having a percentage homology to SEQ ID NO: 56, an amino acid sequence having a percentage homology to SEQ ID NO: 14, an amino acid sequence having a percentage homology to SEQ ID NO: 16, an amino acid sequence having a percentage homology to SEQ ID NO: 26 and an amino acid sequence having a percentage homology to SEQ ID NO: 28, wherein the percentage homology is not less than 98%; or (d) an amino acid sequence having a percentage homology to SEQ ID NO: 2, an amino acid sequence having a percentage homology to SEQ ID NO: 4, an amino acid sequence having a percentage homology to SEQ ID NO: 50, an amino acid sequence having a percentage homology to SEQ ID NO: 52, an amino acid sequence having a percentage homology to SEQ ID NO: 14, an amino acid sequence having a percentage homology to SEQ ID NO: 16, an amino acid sequence having a percentage homology to SEQ ID NO: 22 and an amino acid

sequence having a percentage homology to SEQ ID NO: 24, wherein the percentage homology is not less than 98%.

In yet another aspect, the present disclosure refers to a tetra-specific antibody comprising a tetra-specific antibody monomer having a N-terminal and a C-terminal, comprising in tandem from the N-terminal to the C-terminal, a first scFv domain at the N-terminal, a Fab domain, a Fc domain, a second scFv domain, and a third scFv domain at the C-terminal, wherein the first scFv domain, the Fab domain, the second scFv domain, and the third scFv domain each has a binding specificity against a different antigen, wherein the first scFv domain, the Fab domain, the second scFv domain, and the third scFv domain each independently has a binding specificity against an antigen selected from CD3, PD-L1, 4-1BB, and ROR1; and wherein the tetra-specific antibody comprises an amino acid sequence having a percentage homology to SEQ ID NO. 66, and an amino acid sequence having a percentage homology to SEQ ID NO. 68, wherein the percentage homology is not less than 98%.

In yet another aspect, the present disclosure refers to a tetra-specific antibody, comprising a tetra-specific antibody monomer as disclosed herein. In still another aspect, the present disclosure refers to an isolated nucleic acid sequence, encoding a tetra-

specific antibody monomer as disclosed herein. In still another aspect, the present disclosure refers to an expression vector, comprising the isolated nucleic acid sequence of the present disclosure. In still a further aspect, the present disclosure refers to a host cell comprising the isolated nucleic acid sequence of the present disclosure. In yet another aspect, the present disclosure refers to a method for producing a tetra-specific antibody as disclosed herein or a tetra-specific antibody monomer as disclosed herein, wherein the method comprises culturing a host cell capable of expressing the antibody or the monomer such that the tetra-specific antibody or monomer is expressed, and purifying said tetra-specific antibody or monomer, wherein the host cell capable of expressing the antibody or monomer is a host cell as disclosed herein. In yet another aspect, the present disclosure refers to a pharmaceutical composition, comprising a pharmaceutically acceptable carrier and a tetra-specific antibody as disclosed herein. In yet another aspect, the present disclosure refers to the use of the tetra-specific antibody according to the present disclosure in the manufacture of a medicament for treating cancer.

In one example, the application provides tetra-specific antibody monomers. In one example, the tetra-specific antibody monomer has a N-terminal and a C-terminal and include in tandem from the N-terminal to the C-terminal, a first scFv domain at the N-terminal, a Fab domain, a Fc domain, a second scFv domain, and a third scFv at the C-terminal. The first scFv domain, the Fab domain, the second scFv domain, and the third scFv domain each has a binding specificity against a different antigen.

In one example, the antigen includes a tumor antigen, an immune signalling antigen, or a combination thereof. In one example, the first scFv domain, the Fab domain, the second scFv domain, and the third scFv domain each has a binding specificity against a tumor antigen or an immune signalling antigen. In one example, the first scFv domain has a binding specificity against a tumor antigen. In one example, the first scFv domain has a binding specificity against an immune signalling antigen. In one example, the Fab domain has a binding specificity against a tumor antigen. In one example, the Fab domain has a binding specificity against an immune signalling antigen. In one example, the second scFv domain has a binding specificity against a tumor antigen. In one example, the second scFv domain has a binding specificity against an immune signalling antigen. In one example, the third scFv domain has a binding specificity against a tumor antigen. In one example, the third scFv domain has a binding specificity against a tumor antigen.

In one example, the tetra-specific monomer includes the scFv domain, the Fab domain, the second scFv domain, and the third scFv domain each independently has a binding specificity against an antigen selected from ROR1, PD-L1, CD3, CD28, 4-1BB, CEA, HER2, EGFR VIII, EGFR, LMP1, LMP2A, Mesothelin, PSMA, EpCAM, glypimay-3, gpA33, GD2, TROP2, NKG2D, BCMA, CD19, CD20, CD33, CD123, CD22, CD30, PD-L1, PD1, OX40, 4-1BB, GITR, TIGIT, TIM-3, LAG-3, CTLA4, CD40, VISTA, ICOS, BTLA, LIGHT, HVEM, CSF1R, CD73, and CD39. In one example, the scFv domain, the Fab domain, the second scFv domain, and the third scFv domain each independently has a binding specificity against tumor specific antigens including, but not limited to, ROR1, CEA, HER2, EGFR, EGFR VIII, LMP1, LMP2A, Mesothelin, PSMA, EpCAM, glypimay-3, gpA33, GD2, TROP2, BCMA, CD3, CD19, CD20, CD33, CD123, CD22, CD30, or immune checkpoint modulators including, without limitation, PD-L1, PD1, OX40, 4-1BB, GITR, TIGIT, TIM-3, LAG-3, CTLA4, CD40, VISTA, ICOS, BTLA, Light, HVEM, CD73, CD39, etc. In one example, one set of scFv domain may specifically bind to an immune checkpoint modulators or a tumor antigen. In one example, the scFv specific to CD3 may be on either C or N terminal of heave or light chains.

In one example, the first scFv domain, the Fab domain, the second scFv domain, and the third scFv domain each independently has a binding specificity against an antigen selected from CD3, EGRF VIII, PD-L1, and 4-1BB. In one example, the first scFv domain has a binding specificity against CD3. In one example, the Fab domain has a binding specificity against EGRF VIII. In one example, the second scFv domain has a binding specificity against PD-L1. In one example, the third scFv domain has a binding specificity against 4-1BB. In one example, the first scFv domain has a binding specificity against CD3, the Fab domain has a binding specificity against EGRF VIII, the second scFv domain has a binding specificity against PD-L1, and the third scFv domain has a binding specificity against 4-1BB.

Fc domain may be humanized. In one example, the Fc domain is a human IgG1 Fc.

The scFv domain may include a linker linking the scFv domain to the heavy chain or light chain of the antibody. In one example, the linker may include more than 10 amino acids. In one example, the linker may include more than 15 amino acids long. In one example, the linker may include less than 20 amino acids.

In one example, the linker may comprises a gly-gly-gly-gly-ser (G4S)n linker, and n may be an integral between 1 to 20. For example, n may be 2, 4, or 6. In one example, the first scFv domain, the second scFv domain, or the third scFv domain may comprise a gly-gly-gly-gly-ser (G4S)n linker, wherein n is 2 or 4.

In one example, the application provides a tetra-specific antibody monomers having an amino acid sequence having a percentage homology to SEQ ID NO. 02, 04, 06, 08, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, and 60. The percentage homology is not less than 70%, 80%, 90%, 95%, 98% or 99%.

The application further provides antigen-binding fragments. In one example, the application provides scFv domains. In one example, the scFv domain has an amino acid sequence having a percentage homology to SEQ ID NO. 02, 04, 06, 08, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, and 60, wherein the percentage homology is not less than 70%, 80%, 90%,

95%, 98% or 99%. In one example, the application provides Fab domains. In one example, the Fab domain includes an amino acid sequence having a percentage homology to SEQ ID NO. 02, 04, 06, 08, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 and 60, wherein the percentage homology is not less than 70%, 80%, 90%, 95%, 98% or 99%. The antigen-binding fragments disclosed herein may be used to construct the tetra-specific antibody monomers or multi-specific antibodies.

In one example, the application provides multi-specific antibodies. In one example, the multi-specific antibody includes tetra-specific antibody monomers. In one example, the multi-specific antibody includes two tetra-specific antibody monomers disclosed herein. As each tetra-specific antibody monomer has four antigen-binding domains, the multi-specific antibody disclosed may include 8 antigen-binding domains. In one example, the antigen binding domains in such multi-specific antibody each independently has a binding specificity against a different antigen therefor providing an octa-specific antibody. In one example, the multi-specific antibody is a penta-specific antibody. In one example, the multi-specific antibody is a penta-specific antibody. In one example, the multi-specific antibody is a penta-specific antibody a hexa-specific antibody. In one example, the multi-specific antibody is a penta-specific antibody a hepta-specific antibody.

In one example, the multi-specific antibody includes a dimer of a tetra-specific antibody monomer therefor providing a tetra-specific antibody. In one example, the application provides an isolated, purified, or non-natural existing multi-specific antibodies. In one example, the application provides a tetra-specific antibody having an amino acid sequence having a percentage homology to SEQ ID 66 and 68. The percentage homology is not less than 70%, 80%, 90%, 95%, 98% or 99%.

The application further provides isolated nucleic acid sequence encoding the tetra-specific antibody monomers, the multi-specific antibodies, or the antigen-binding fragments thereof. In one example, the nucleic acid encodes an amino acid sequence having a percentage homology to the tetra-specific antibody monomer having a SEQ ID NO. 01, 03, 05, 07, 09, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, and 59. The percentage homology is not less than 70%, 80%, 90%, 95%, 98% or 99%.

The application further provides expression vectors and host cells comprising the nucleic acid sequences disclosed herein. In one example, the host cell includes the expression vector. The host cell may be a prokaryotic cell or a eukaryotic cell.

The application further provides immuno-conjugates. In one example, the immuno-conjugate includes a cytotoxic agent or an imaging agent linked to the multi-specific antibody disclosed herein through a linker.

The linker may be cleavable or non-cleavable. The linker may include a covalent bond such as an ester bond, an ether bond, an amid bond, a disulphide bond, an imide bond, a sulfone bond, a phosphate bond, a phosphorus ester bond, a peptide bond, or a combination thereof. In one example, the linker comprises a hydrophobic poly(ethylene glycol) linker.

The cytotoxic agent may include a chemotherapeutic agent, a growth inhibitory agent, a cytotoxic agent from class of calicheamicin, an antimitotic agent, a toxin, a radioactive isotope, a therapeutic agent, or a combination thereof. In one example, the cytotoxic agent comprises a calicheamicin, ozogamicin, monomethyl auristatin E, emtansine, a derivative or a combination thereof.

The imaging agent may be any compound useful for imaging purpose. In one example, the imaging agent may be radionuclide, a florescent agent, a quantum dots, or a combination thereof.

The application further provides pharmaceutical composition. In one example, the pharmaceutical composition comprises a pharmaceutically acceptable carrier and the tetra-specific antibody monomer disclosed herein. In one example, the pharmaceutical composition comprises a pharmaceutically acceptable carrier and the multi-specific antibody disclosed herein. In one example, the pharmaceutical composition comprises a pharmaceutically acceptable carrier and the antigen-binding fragment disclosed herein. In one example, the pharmaceutical composition comprises a pharmaceutically acceptable carrier and the immuno-conjugate disclosed herein.

In one example, the pharmaceutical composition further includes a therapeutic agent. Example therapeutic agents include without limitation a radioisotope, radionuclide, a toxin, a chemotherapeutic agent or a combination thereof. In one example, the therapeutic agent comprises an antibody, an enzyme, or a combination thereof. In one example, the therapeutic agent comprises an anti-estrogen agent, a receptor tyrosine kinase inhibitor, a kinase inhibitor, a cell cycle inhibitor, a DNA, RNA or protein synthesis inhibitor, a RAS inhibitor, or a combination thereof. In one example, the therapeutic agent comprises a check point inhibitor. In one example, the therapeutic agent comprises an inhibitor of PD1, PDL1, CTLA4, 4-1BB, OX40, GITR, ICOS, LIGHT, TIM3, LAG3, TIGIT, CD40, CD27, HVEM, BTLA, VISTA, B7H4, CSF1R, NKG2D, CD73, a derivative or a combination thereof.

In a further example, the application provides methods for making the tetra-specific antibody monomers, the multi-specific antibodies, the antigen-binding fragments thereof, and immuno-conjugates thereof. In one example, the method includes the steps of culturing the host cell containing the nucleic acid sequences disclosed herein such that the DNA sequence encoding the antibody is expressed and purifying the antibody. In one example, the antibody is a tetra-specific antibody.

In a further example, the application provides methods of using the tetra-specific antibody monomers, the multi-specific antibodies, the antigen-binding fragments thereof, and immuno-conjugates thereof for cancer treatment. In one example, the method includes the step of administering tetra-specific antibody monomers, the multi-specific antibodies, the antigen-binding fragments thereof, and immuno-conjugates thereof, or pharmaceutical composition thereof to a subject in need of such treatment. In one example, the method includes the step of administering to the subject an effective amount of the tetra-specific antibody.

In one example, the method includes directly injecting into the tumour site an effective amount of multi-specific monomers, multi-specific antibodies, the immuno-conjugates, the antigen-binding fragment thereof.

Varieties of cancer may be prevented or treated. In one example, the cancer may have cells expressing ROR1, CEA, HER2, EGFR, EGFR VIII, LMP1, LMP2A, Mesothelin, PSMA, EpCAM, glypimay-3, gpA33, GD2, TROP2, NKG2D, BCMA, CD19, CD20, CD33, CD123, CD22, or CD30. Example cancers include without limitation breast cancer, colorectal cancer, anal cancer, pancreatic cancer, gallbladder cancer, bile duct cancer, head and neck cancer, nasopharyngeal cancer, skin cancer, melanoma, ovarian cancer, prostate cancer, urethral cancer, lung cancer, non-small lung cell cancer, small cell lung cancer, brain tumor, glioma, neuroblastoma, oesophageal cancer, gastric cancer, liver cancer, kidney cancer, bladder cancer, cervical cancer, endometrial cancer, thyroid cancer, eye cancer, sarcoma, bone cancer, leukemia, myeloma or lymphoma.

In one example, the method may further include co-administering an effective amount of a therapeutic agent. In one example, the therapeutic agent may include an antibody, a chemotherapy agent, an enzyme, or a combination thereof. In one example, the therapeutic agent may include an anti-estrogen agent, a receptor tyrosine kinase inhibitor, a kinase inhibitor, a cell cycle inhibitor, a DNA, RNA or protein synthesis inhibitor, a RAS inhibitor, or a combination thereof. In one example, the therapeutic agent may include a check point inhibitor. In one example, the therapeutic agent may include an inhibitor of PD1, PD-L1, CTLA4, 4-1BB, OX40, GITR, ICOS, LIGHT, TIM3, LAG3, TIGIT, CD40, CD27, HVEM, BTLA, VISTA, B7H4, CSF1R, NKG2D, CD73, a derivative or a combination thereof.

In one example, the therapeutic agent may comprises capecitabine, cisplatin, Cyclophosphamide, methotrexate, 5-fluorouracil, Doxorubicin, cyclophosphamide, Mustine, vincristine, procarbazine, prednisolone, bleomycin, vinblastine, dacarbazine, etoposide, Epirubicin, pemetrexed, folinic acid, gemicitabine, oxaliplatin, irinotecan, topotecan, camptothecin, docetaxel, paclitaxel, , fulvestrant, tamoxifen, letrozole, exemestane, anastrozole, aminoglutethimide, testolactone, vorozole, formestane, fadrozole, erlotinib, lafatinib, dasatinib, gefitinib, osimertinib, vandertanib, afatinib, imatinib, pazopinib, lapatinib, sunitinib, nilotinib, sorafenib, nab-palitaxel, Everolimus, temsirolimus, Dabrafenib,

vemurafenib, trametinib, vintafolide, apatinib, crizotinib, periforsine, olaparib, Bortezomib, tofacitinib, trastuzumab,a derivative or a combination thereof.

The subject may be a human. In one embodiment, the subject may be suffering from cancer. The application further provides solutions comprising an effective concentration of the multi-specific antibodies, monomers, or immuno-conjugates disclosed herein. In one embodiment, the solution is blood plasma in a subject.

The objectives and advantages of the disclosure may become apparent from the following detailed description of example embodiments thereof in connection with the accompanying drawings. Still other embodiments may become readily apparent to those skilled in the art from the following detailed description, wherein are described embodiments by way of illustrating the best mode contemplated. As may be realized, other and different embodiments are possible and the embodiments' several details are capable of modifications in various obvious respects, all without departing from their spirit and the scope. Accordingly, the drawings and detailed description are to be regarded as illustrative in nature and not as restrictive.

BRIEF DESCRIPTION OF FIGURES

The foregoing and other features of this disclosure may become more fully apparent from the following description and appended claims, taken in conjunction with the accompanying drawings. Understanding that these drawings depict only several embodiments arranged in accordance with the disclosure and are, therefore, not to be considered limiting of its scope, the disclosure may be described with additional specificity and detail through use of the accompanying drawings, in which:

FIGURE 1 is a diagram of a tetra-specific antibody with Domains 1-4 as antigen binding domains. CD3 x EGFRvIII x PD-L1 x 4-1BB tetra-specific antibody is shown as an example in accordance to one embodiment.

FIGURE 2 depicts experiment results showing Redirected PBMC (peripheral blood mononuclear cells) cytotoxicity against astrocytoma cell line U87 that was transfected with EGFRvIII. Tumor lysis activity of tetra-specific antibodies used is listed in TABLE 1.

FIGURE 3 depicts experiment results showing Redirected PBMC (peripheral blood mononuclear cells) cytotoxicity against acute lymphoblastic leukemia cell line Kasumi-2.

FIGURE 4 depicts experiment results showing Redirected PBMC (peripheral blood mononuclear cells) cytotoxicity against astrocytoma cell line U87 that was transfected with EGFRvIII. Functional activities of different 4-1BB domains and functional impact of PD-L1 and 4-1BB domains are shown.

FIGURE 5 is a depiction of experiment results showing FACS analysis of tetra-specific antibodies binding to human ROR1 transfected CHO cells according to some embodiments.

FIGURE 6 is a depiction of experiment results showing FACS analysis of tetra-specific antibodies binding to human 4-1BB transfected CHO cells according to some embodiments.

FIGURE 7 is a depiction of experiment results showing FACS analysis of tetra-specific antibodies binding to human PD-L1 transfected CHO cells according to some embodiments.

FIGURE 8 is a depiction of experiment results showing redirected T cell cytotoxicity (RTCC) assay, meditated by tetra-specific antibodies with the binding domain 323H7 which is specific for the Ig domain of ROR1, with peripheral blood mononuclear cells as effectors and the B-ALL cell line Kasumi2 as targets according to some embodiments.

FIGURE 8 is a depiction of experiment results showing redirected T cell cytotoxicity (RTCC) assay, meditated by tetra-specific antibodies with the binding domain 323H7 which is specific for the Ig domain of ROR1, with peripheral blood mononuclear cells as effectors and the B-ALL cell line Kasumi2 as targets according to some embodiments.

FIGURE 9 is a depiction of experiment results showing redirected T cell cytotoxicity (RTCC) assay, meditated by tetra-specific antibodies with the binding domain 323H7 which is specific for the Ig domain of ROR1, with CD8+, CD45RO+ memory T cells as effectors and the B-ALL cell line Kasumi2 as targets according to some embodiments.

FIGURE 10 is a depiction of experiment results showing redirected T cell cytotoxicity (RTCC) assay, meditated by tetra-specific antibodies with the binding domain 323H7 which is specific for the Ig domain of ROR1, with CD8+, CD45RA+ naive T cells as effectors and the B-ALL cell line Kasumi2 as targets according to some embodiments.

FIGURE 11 is a depiction of experiment results showing redirected T cell cytotoxicity (RTCC) assay, meditated by tetra-specific antibodies with the binding domain 338H4 which is specific for the Frizzled domain of ROR1, with peripheral blood mononuclear cells as effectors and the B-ALL cell line Kasumi2 as targets according to some embodiments.

FIGURE 12 is a depiction of experiment results showing redirected T cell cytotoxicity (RTCC) assay, meditated by tetra-specific antibodies with the binding domain 338H4 which is specific for the Frizzled domain of ROR1, with CD8+, CD45RO+ memory T cells as effectors and the B-ALL cell line Kasumi2 as targets according to some embodiments.

FIGURE 13 is a depiction of experiment results showing redirected T cell cytotoxicity (RTCC) assay, meditated by tetra-specific antibodies with the binding domain 338H4 which is specific for the Frizzled domain of ROR1, with CD8+, CD45RA+ naive T cells as effectors and the B-ALL cell line Kasumi2 as targets according to some embodiments.

DETAILED DESCRIPTION

In the following detailed description, reference is made to the accompanying drawings, which form a part hereof. In the drawings, similar symbols typically identify similar components, unless context dictates otherwise. The illustrative embodiments described in the detailed description, drawings, and claims are not meant to be limiting. Other embodiments may be utilized, and other changes may be made, without departing from the spirit or scope of the subject matter presented herein. It may be

readily understood that the aspects of the present disclosure, as generally described herein, and illustrated in the FIGUREs, may be arranged, substituted, combined, separated, and designed in a wide variety of different configurations, all of which are explicitly contemplated herein.

The disclosure provides, among others, isolated antibodies, methods of making such antibodies, tetra-specific or multi-specific molecules, antibody-drug conjugates and/or immuno-conjugates composed from such antibodies or antigen binding fragments, pharmaceutical compositions containing the antibodies, tetra-specific or multi-specific molecules, antibody-drug conjugates and/or immuno-conjugates, method of making thereof, and method of using the disclosed molecules or composition for treatment of cancer.

The term "antibody" is used in the broadest sense and specifically covers single monoclonal antibodies (including agonist and antagonist antibodies), antibody compositions with polyepitopic specificity, as well as antibody fragments (e.g., Fab, $F(ab')_2$, and Fv), so long as they exhibit the desired biological activity. In some embodiments, the antibody may be monoclonal, polyclonal, chimeric, single chain, tetra-specific or bi-effective, simianized, human and humanized antibodies as well as active fragments thereof. Examples of active fragments of molecules that bind to known antigens include Fab, $F(ab')_2$, scFv and Fv fragments, including the products of an Fab immunoglobulin expression library and epitope-binding fragments of any of the antibodies and fragments mentioned above. In some embodiments, antibody may include immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, i.e. molecules that contain a binding site that immunospecifically bind an antigen. The immunoglobulin may be of any type (IgG, IgM, IgD, IgE, IgA and IgY) or class (IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2) or subclasses of immunoglobulin molecule. In one embodiment, the antibody may be whole antibodies and any antigen-binding fragment derived from the whole antibodies. A typical antibody refers to hetero-tetrameric protein comprising typically of two heavy (H) chains and two light (L) chains. Each heavy chain is comprised of a heavy chain variable domain (abbreviated as VH) and a heavy chain constant domain. Each light chain is comprised of a light chain variable domain (abbreviated as VL) and a light chain constant domain. The VH and VL regions may be further subdivided into domains of hypervariable complementarity determining regions (CDR), and more conserved regions called framework regions (FR). Each variable domain (either VH or VL) is typically composed of three CDRs and four FRs, arranged in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4 from amino-terminus to carboxy-terminus. Within the variable regions of the light and heavy chains there are binding regions that interacts with the antigen.

The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally occurring mutations that may be present in minor amounts. Monoclonal antibodies are highly specific, being directed against a single antigenic site. Furthermore, in contrast to conventional (polyclonal) antibody preparations which typically include different antibodies directed against different determinants (epitopes), each monoclonal antibody is directed against a single determinant on the antigen. In addition to their specificity, the monoclonal antibodies may be 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 disclosure may be made by the hybridoma method first described by Kohler & Milstein, *Nature,* 256:495 (1975), or may be made by recombinant DNA methods (see, e.g., U.S. Pat. No. 4,816,567).

The monoclonal antibodies may 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 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; and Morrison et al., *Proc. Natl. Acad. Sci. USA,* 81:6851-6855 [1984]).

Monoclonal antibodies may be produced using various methods including mouse hybridoma or phage display (see Siegel. Transfus. Clin. Biol. 9:15-22 (2002) for a review) or from molecular cloning of antibodies directly from primary B cells (see Tiller. New Biotechnol. 28:453-7 (2011)). In the present disclosure antibodies were created by the immunization of rabbits with both human PD-L1 protein and cells transiently expressing human PD-L1 on the cell surface. Rabbits are known to create antibodies of high affinity, diversity and specificity (Weber et al. Exp. Mol. Med. 49:e305). B cells from immunized animals were cultured in vitro and screened for the production of anti-PD-L1 antibodies. The antibody variable genes were isolated using recombinant DNA techniques and the resulting antibodies were expressed recombinantly and further screened for desired features such as ability to inhibit the binding of PD-L1 to PD-1, the ability to bind to non-human primate PD-L1 and the ability to enhance human T-cell activation. This general method of antibody discovery is similar to that described in Seeber et al. PLOS One. 9:e86184 (2014).

The term "antigen- or epitope-binding portion or fragment" refers to fragments of an antibody that are capable of binding to an antigen (PD-L1 in this case). These fragments may be capable of the antigen-binding function and additional functions of the intact antibody. Examples of binding fragments include, but are not limited to a single-chain Fv fragment (scFv) consisting of the VL and VH domains of a single arm of an antibody connected in a single polypeptide chain by a synthetic linker or a Fab fragment which is a monovalent fragment consisting of the VL, constant light (CL), VH and constant heavy 1 (CH1) domains. Antibody fragments may be even smaller sub-fragments and may consist of domains as small as a single CDR domain, in particular the CDR3 regions from either the VL and/or VH domains (for example see Beiboer et al., J. Mol. Biol. 296:833-49 (2000)). Antibody fragments are produced using conventional methods known to those skilled in the art. The antibody fragments are may be screened for utility using the same techniques employed with intact antibodies.

The "antigen-or epitope-binding fragments" may be derived from an antibody of the present disclosure by a number of art-known techniques. For example, purified monoclonal antibodies may be cleaved with an enzyme, such as pepsin, and subjected to HPLC gel filtration. The appropriate fraction containing Fab fragments may then be collected and concentrated by membrane filtration and the like. For further

description of general techniques for the isolation of active fragments of antibodies, see for example, Khaw, B. A. et al. J. Nucl. Med. 23:1011-1019 (1982); Rousseaux et al. Methods Enzymology, 121:663-69, Academic Press, 1986.

Papain digestion of antibodies produces two identical antigen binding fragments, called "Fab" fragments, each with a single antigen binding site, and a residual "Fc" fragment, whose name reflects its ability to crystallize readily. Pepsin treatment yields an $F(ab')_2$ fragment that has two antigen combining sites and is still capable of cross-linking antigen.

The Fab fragment may contain the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab' fragments differ from Fab fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 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.

"Fv" is the minimum antibody fragment which contains a complete antigen recognition and binding site. This region consists of a dimer of one heavy and one light chain variable domain in tight, non-covalent association. It is in this configuration that the three CDRs of each variable domain interact to define an antigen binding site on the surface of the VH-VL dimer. Collectively, the six CDRs confer antigen binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

The "light chains" of antibodies (immunoglobulins) from any vertebrate species may be assigned to one of two clearly distinct types, called kappa and lambda (λ), based on the amino acid sequences of their constant domains.

Depending on the amino acid sequence of the constant domain of their heavy chains, immunoglobulins may be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG and IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG-1, IgG-2, IgG-3, and IgG-4; IgA-1 and IgA-2. The heavy chain constant domains that correspond to the different classes of immunoglobulins are called α, delta, epsilon, γ, and μ, respectively. The subunit structures and three-dimensional configurations of different classes of immunoglobulins are well known.

A "humanized antibody" refers to a type of engineered antibody having its CDRs derived from a non-human donor immunoglobulin, the remaining immunoglobulin-derived parts of the molecule being derived from one (or more) human immunoglobulin(s). In some embodiments, framework support residues may be altered to preserve binding affinity. Methods to obtain "humanized antibodies" are well known to those skilled in the art. (see, e.g., Queen et al., Proc. Natl Acad Sci USA, 86:10029-10032 (1989), Hodgson et al., Bio/Technology, 9:421 (1991)).

The terms “polypeptide”, “peptide”, and “protein”, as used herein, are interchangeable and are defined to mean a biomolecule composed of amino acids linked by a peptide bond.

The terms “a”, “an” and “the” as used herein are defined to mean “one or more” and include the plural unless the context is inappropriate.

By “isolated” is meant a biological molecule free from at least some of the components with which it naturally occurs. "Isolated," when used to describe the various polypeptides disclosed herein, means a polypeptide that has been identified and separated and/or recovered from a cell or cell culture from which it was expressed. Ordinarily, an isolated polypeptide may be prepared by at least one purification step. An "isolated antibody," refers to an antibody which is substantially free of other antibodies having different antigenic specificities.

"Recombinant" means the antibodies are generated using recombinant nucleic acid techniques in exogeneous host cells.

The term “antigen” refers to an entity or fragment thereof which may induce an immune response in an organism, particularly an animal, more particularly a mammal including a human. The term includes immunogens and regions thereof responsible for antigenicity or antigenic determinants.

Also as used herein, the term “immunogenic” refers to substances which elicit or enhance the production of antibodies, T-cells or other reactive immune cells directed against an immunogenic agent and contribute to an immune response in humans or animals. An immune response occurs when an individual produces sufficient antibodies, T-cells and other reactive immune cells against administered immunogenic compositions of the present disclosure to moderate or alleviate the disorder to be treated.

"Specific binding" or "specifically binds to" or is "specific for" a particular antigen or an epitope means binding that is measurably different from a non-specific interaction. Specific binding may be measured, for example, by determining binding of a molecule compared to binding of a control molecule, which generally is a molecule of similar structure that does not have binding activity. For example, specific binding may be determined by competition with a control molecule that is similar to the target.

Specific binding for a particular antigen or an epitope may be exhibited, for example, by an antibody having a KD for an antigen or epitope of at least about 10^{-4} M, at least about 10^{-5} M, at least about 10^{-6} M, at least about 10^{-7} M, at least about 10^{-8} M, at least about 10^{-9} M, alternatively at least about 10^{-10} M, at least about 10^{-11} M, at least about 10^{-12} M, or greater, where KD refers to a dissociation rate of a particular antibody-antigen interaction. Typically, an antibody that specifically binds an antigen may have a KD that is 20-, 50-, 100-, 500-, 1000-, 5,000-, 10,000- or more times greater for a control molecule relative to the antigen or epitope.

Also, specific binding for a particular antigen or an epitope may be exhibited, for example, by an antibody having a KA or Ka for an antigen or epitope of at least 20-, 50-, 100-, 500-, 1000-, 5,000-,

10,000- or more times greater for the epitope relative to a control, where KA or Ka refers to an association rate of a particular antibody-antigen interaction.

"Homology" between two sequences is determined by sequence identity. If two sequences which are to be compared with each other differ in length, sequence identity preferably relates to the percentage of the nucleotide residues of the shorter sequence which are identical with the nucleotide residues of the longer sequence. Sequence identity may be determined conventionally with the use of computer programs. The deviations appearing in the comparison between a given sequence and the above-described sequences of the disclosure may be caused for instance by addition, deletion, substitution, insertion or recombination.

In one aspect, the application provides tetra-specific antibody monomers, antigen-binding fragments, and multi-specific antibodies. In one embodiment, the application provides tetra-specific antibodies.

In one embodiment, the disclosure provides tetra-specific antibodies with a binding specificity against four different antigen targets. In one embodiment, the antigen targets are tumor specific antigens, T cell receptor CD3 component, or immune checkpoint molecules. The tetra-specific antibodies may directly engage body's endogenous T cells to kill tumor cells independent of tumor antigen presentation by MHC to the antigen specific T cell receptors. In some embodiments, the immune checkpoint modulating component of the tetra-specific antibodies may overcome the immunosuppressive tumor microenvironment to fully activate the exhausted T cells within the tumor microenvironment.

The tetra-specific antibodies have unique properties of directly engaging T cells at the same time modulating immune checkpoint or inhibiting Treg or other inhibitory immune cells or targeting tumor with component against tumor antigens. It may show benefit to the patients where BiTE or CAR-T treatment isn't appropriate. In one embodiment, the tetra-specific antibodies could demonstrate clinical benefit in solid tumor where BiTE-like technology or CAR-T treatment yet to show clinical benefit due to the limitations imposed by the inhibitory tumor microenvironment.

In one embodiment, the application provides an engineered antibody with 4 different binding domains or a "tetra-specific antibody". One binding domain is specific for CD3 on T cells, a second binding domain is specific for a tumor associated antigen including but not limited to ROR1, CEA, HER2, EGFR, EGFRvIII, LMP1, LMP2A, Mesothelin, PSMA, EpCAM, glypimay-3, gpA33, GD2, TROP2, BCMA, CD19, CD20, CD33, CD123, CD22, CD30, and a third and fourth binding domains are specific for two distinct immune checkpoint modulators such as PD-L1, PD-1, OX40, 4-1BB, GITR, TIGIT, TIM-3, LAG-3, CTLA4, CD40, VISTA, ICOS, BTLA, Light, HVEM, CD73, CD39, etc.

An example tetra-specific molecules disclosed herein (FIGURE 1) target either human ROR1 (SEQIDs 33-48), human CD19 (SEQIDs 53-56) or EGFR vIII (SEQIDs 49-52) as tumor associated antigens. Each of these targeted tetra-specific proteins also carries an anti-human PD-L1 (SEQIDs 9-16), an anti-human 4-1BB (SEQIDs 21-32) and an anti-human CD3 binding domain (SEQIDs 1-8). These binding domains were converted to scFv, VLVH, for placement at the N-terminal Domain 1 (D1) or scFv, VHVL, for placement at the C-terminal Domains 3 (D3) and 4 (D4) of the peptide (FIGURE 1).

In some embodiments, scFv molecules described herein contain a 20 amino acid flexible gly-gly-gly-gly-ser (G4S) X4 linker that operably links the VH and VL, regardless of the V-region orientation (LH or HL). The remaining position in the tetra-specific protein, Domain 2 (D2), consists of an IgG1 heavy chain, VH-CH1-Hinge-CH2-CH3, and its corresponding light chain, VL-CL, which may be either a kappa or lambda chain. D1 and D2 are genetically linked through a 10 amino acid (G4S) x 2 linker, as are D2, D3 and D4 resulting in a contiguous ~150 kDa heavy chain monomer peptide. When co-transfected with the appropriate light chain, the final symmetric tetra-specific peptide may be purified through the IgG1 Fc (Protein A/Protein G) and assayed to assess functional activity. Heavy and light chain gene "cassettes" were previously constructed such that V-regions could be cloned using either restriction enzyme sites (HindIII/NheI for the heavy chain and HindIII/BsiWI for the light chain) or "restriction-free cloning" such as Gibson Assembly (SGI-DNA, La Jolla, CA), Infusion (Takara Bio USA) or NEBuilder (NEB, Ipswich, MA), the latter of which was used here.

Tetra-specific proteins are produced through a process that involves design of the intact molecule, synthesis and cloning of the nucleotide sequences for each domain, expression in mammalian cells and purification of the final product. Nucleotide sequences were assembled using the Geneious 10.2.3 software package (Biomatters, Auckland, NZ) and broken up into their component domains for gene synthesis (Genewiz, South Plainsfield, NJ).

In this example, SI-35E18 (SEQID 65 and 67) was split into its component domains where the anti-4-1BB scFv, VLVH, occupies D1, anti-human PD-L1 clone PL230C6 occupies D2 (Fab position), anti-human ROR1 Ig domain-specific clone 323H7 VHVL scFv occupies D3, and anti-human CD3 scFv, VHVL, occupies the C-terminal D4. Using NEBuilder web-based tools, 5' and 3' nucleotides were appended to each of the domains depending on their position in the larger protein so that each domain overlaps its flanking domains by 20-30 nucleotides which direct site-specific recombination, thus genetically fusing each domain in a single gene assembly step. Due to the high number of homologous regions in the tetra-specific nucleotide sequence, the N-terminal domains 1 and 2 are assembled separately from the C-terminal D3 and D4. The N- and C-terminal fragments were then assembled together in a second NEBuilder reaction.

A small aliquot was transformed into *E.coli* DH10b (Invitrogen, Carlsbad, CA) and plated on TB + carbenicillin 100ug/ml plates (Teknova, Hollister, CA) and incubated at 37C overnight. Resultant colonies were selected and 2ml overnight cultures inoculated in TB + carbenicillin. DNA was prepared (Thermo-Fisher, Carlsbad, CA) from overnight cultures and subsequently sequenced (Genewiz, South Plainsfield, NJ) using sequencing primers (Sigma,St. Louis, MO) flanking each domain. In some embodiments, DNA sequences were assembled and analyzed in Geneious.the

In another aspect, the application provides pharmaceutical compositions including the multi-specific antibody monomers, the multi-specific antibodies, the antigen-binding fragments, and the immuno-conjugates thereof, and methods of using the disclosed antibodies or pharmaceutical compositions for treatment of cancer.

The advantages of using the disclosed tetra-specific antibody monomers, multi-specific antibodies or compositions for treatment purpose over any existing therapies include, among others: 1) Inclusion of an IgG Fc domain may confer the characteristic of a longer half-life in serum compared to a bi-specific BiTe molecule; 2) Inclusion of two binding domains that are specific for immune checkpoint modulators, that may inhibit the suppressive pathways and engage the co-stimulatory pathways at the same time; and 3) Cross-link CD3 on T cells with tumor associated antigens thus "re-directing" T cells to kill the tumor without the need to remove T cells from the patient and genetically modify them to be specific for the tumor cell before re-introducing them back into the patient as done for chimeric antigen receptor T cells (CAR-T).

Formulation of the pharmaceutical composition may be accomplished according to standard methodology know to those of ordinary skill in the art.

In one embodiment, the antibodies and monomers according to the disclosure may be prepared in a physiologically acceptable formulation and may comprise a pharmaceutically acceptable carrier, diluent and/or excipient using known techniques. For example, the antibody according to the disclosure and as described herein including any functionally equivalent antibody or functional parts thereof, in particular, the monoclonal antibody including any functionally equivalent antibody or functional parts thereof is combined with a pharmaceutically acceptable carrier, diluent and/or excipient to form a therapeutic composition. Formulation of the pharmaceutical composition according to the disclosure may be accomplished according to standard methodology know to those of ordinary skill in the art.

With respect to the formulation of suitable compositions for administration to a subject such as a human patient in need of treatment, the antibodies disclosed herein may be mixed or combined with pharmaceutically acceptable carriers known in the art dependent upon the chosen route of administration. There are no particular limitations to the modes of application of the antibodies disclosed herein, and the choice of suitable administration routes and suitable compositions are known in the art without undue experimentation.

Suitable pharmaceutical carriers, diluents and/or excipients are well known in the art and include, for example, phosphate buffered saline solutions, water, emulsions such as oil/water emulsions.

"Pharmaceutically acceptable" refers to those compounds, materials, compositions, and dosage forms which are, within the scope of sound medical judgment, suitable for use contact with the tissues of human beings or animals without excessive toxicity, irritation, or other problem or complication, commensurate with a reasonable benefit/risk ratio.

In one embodiment, the pharmaceutical composition may include proteinaceous carriers such as, for example, serum albumin or immunoglobulin, particularly of human origin. Further biologically active agents may be present in the pharmaceutical composition of the disclosure dependent on the intended use. In one embodiment, the proteinaceous pharmaceutically active matter may be present in amounts between 1 ng and 10 mg per dose. Generally, the regime of administration should be in the range of between 0.1 μg and 10 mg of the antibody according to the disclosure, particularly in a range 1.0 μg to 1.0 mg, and more particularly in a range of between 1.0 μg and 100 μg, with all individual numbers

falling within these ranges also being part of the disclosure. If the administration occurs through continuous infusion a more proper dosage may be in the range of between 0.01 μg and 10 mg units per kilogram of body weight per hour with all individual numbers falling within these ranges also being part of the disclosure.

The compositions of the present disclosure may be administered to a subject in the form of a solid, liquid or aerosol at a suitable, pharmaceutically effective dose. Examples of solid compositions include pills, creams, and implantable dosage units. Pills may be administered orally. Therapeutic creams may be administered topically. Implantable dosage units may be administered locally, for example, at a tumor site, or may be implanted for systematic release of the therapeutic composition, for example, subcutaneously. Examples of liquid compositions include formulations adapted for injection intramuscularly, subcutaneously, intravenously, intra-arterially, and formulations for topical and intraocular administration. Examples of aerosol formulations include inhaler formulations for administration to the lungs.

It is well known to those of ordinary skill in the art that the dosage of the composition may depend on various factors such as, for example, the condition of being treated, the particular composition used, and other clinical factors such as weight, size, sex and general health condition of the patient, body surface area, the particular compound or composition to be administered, other drugs being administered concurrently, and the route of administration.

The term “therapeutically effective amount” or “effective amount” refers to the amount of antibody which, when administered to a human or animal, elicits a response which is sufficient to result in a therapeutic effect in said human or animal, e.g., to ameliorate disease in a subject. The effective amount is readily determined by one of ordinary skill in the art following routine procedures. Where the disease is a cancer, the effective amount of the drug may inhibit (for example, slow to some extent, inhibit or stop) one or more of the following example characteristics including, without limitation, cancer cell growth, cancer cell proliferation, cancer cell motility, cancer cell infiltration into peripheral organs, tumor metastasis, and tumor growth. Wherein the disease is a mayer, the effective amount of the drug may alternatively do one or more of the following when administered to a subject: slow or stop tumor growth, reduce tumor size (for example, volume or mass), relieve to some extent one or more of the symptoms associated with the cancer, extend progression free survival, result in an objective response (including, for example, a partial response or a complete response), and increase overall survival time. To the extent the drug may prevent growth and/or kill existing cancer cells, it is cytostatic and/or cytotoxic.

A person skilled in the art have the ability to determine the effective amount or concentration of the antibodies disclosed therein to effective treat a condition such as a cancer. Other parameters such as the proportions of the various components in the pharmaceutical composition, administration does and frequency may be obtained by a person skilled in the art without undue experimentation. For example, a suitable solution for injection may contain, without limitation, from about 1 to about 20, from about 1 to about 10 mg antibodies per ml. The example dose may be, without limitation, from about 0.1 to

about 20, from about 1 to about 5mg/Kg body weight. The example administration frequency could be, without limitation, once per day or three times per week.

The compositions may be administered by standard routes of administration. In general, the composition may be administered by topical, oral, rectal, nasal, intradermal, intraperitoneal, or parenteral (for example, intravenous, subcutaneous, or intramuscular) routes. In some embodiments, the composition may be incorporated into sustained release matrices such as biodegradable polymers, the polymers being implanted in the vicinity of where delivery is desired, for example, at the site of a tumor. The method includes administration of a single dose, administration of repeated doses at predetermined time intervals, and sustained administration for a predetermined period of time.

Although many forms of administration are possible, an example administration form would be a solution for injection, in particular for intravenous or intra-arterial injection. Usually, a suitable pharmaceutical composition for injection may include pharmaceutically suitable carriers or excipients such as, without limitation, a buffer, a surfactant, or a stabilizer agent. Example buffers may include, without limitation, acetate, phosphate or citrate buffer. Example surfactants may include, without limitation, polysorbate. Example stabilizer may include, without limitation, human albumin.

In one embodiment, the administration may be parenterally, e.g. intravenously. Preparations for parenteral administration include sterile aqueous or non-aqueous solutions, suspensions and emulsions. Non-aqueous solvents include without being limited to it, propylene glycol, polyethylene glycol, vegetable oil such as olive oil, and injectable organic esters such as ethyl oleate. Aqueous solvents may be chosen from the group consisting of water, alcohol/aqueous solutions, emulsions or suspensions including saline and buffered media. Parenteral vehicles include sodium chloride solution, Ringer's dextrose, dextrose and sodium chloride, lactated Ringer's, or fixed oils. Intravenous vehicles include fluid and nutrient replenishers, electrolyte replenishers (such as those based on Ringer's dextrose) and others. Preservatives may also be present such as, for example, antimicrobials, anti-oxidants, chelating agents, inert gases, etc.

The antibody monomers, antibodies, antigen-binding fragments and immuno-conjugates thereof may be used in combination with a therapeutic agent or a composition comprising a therapeutic agent for treatment purpose.

In some embodiments, the multi-specific antibody molecule is used in combination with one or more additional therapeutic agents at an effective amount. The additional therapeutic agent includes an antibody, a chemotherapy agent, an enzyme, or a combination thereof. In some embodiment, the additional therapeutic agent may be an anti-estrogen agent, a receptor tyrosine kinase inhibitor, a kinase inhibitor, a cell cycle inhibitor, a DNA, RNA or protein synthesis inhibitor, a RAS inhibitor, or a combination thereof. In some embodiments, the additional therapeutic agent may be a check point inhibitor. In some embodiments, therapeutic agent comprises inhibitors of PD1, PDL1, CTLA4, 4-1BB, OX40, GITR, ICOS, LIGHT, TIM3, LAG3, TIGIT, CD40, CD27, HVEM, BTLA, VISTA, B7H4, CSF1R, NKG2D, CD73, a derivative or a combination thereof.

In one embodiment, the therapeutic agent may include capecitabine, cisplatin, trastuzumab, fulvestrant, tamoxifen, letrozole, exemestane, anastrozole, aminoglutethimide, testolactone, vorozole, formestane, fadrozole, letrozole, erlotinib, lafatinib, dasatinib, gefitinib, imatinib, pazopinib, lapatinib, sunitinib, nilotinib, sorafenib, nab-palitaxel, a derivative or a combination thereof. In one embodiment, the therapeutic agent may include capecitabine, cisplatin, Cyclophosphamide, methotrexate, 5-fluorouracil, Doxorubicin, cyclophosphamide, mustine, vincristine, procarbazine, prednisolone, bleomycin, vinblastine, dacarbazine, etoposide, Epirubicin, pemetrexed, folinic acid, gemicitabine, oxaliplatin, irinotemay, topotemay, camptothecin, docetaxel, paclitaxel, , fulvestrant, tamoxifen, letrozole, exemestane, anastrozole, aminoglutethimide, testolactone, vorozole, formestane, fadrozole, letrozole, erlotinib, lafatinib, dasatinib, gefitinib, osimertinib, vandertanib, afatinib, imatinib, pazopinib, lapatinib, sunitinib, nilotinib, sorafenib, nab-palitaxel, Everolimus, temsirolimus, Dabrafenib, vemurafenib, trametinib, vintafolide, apatinib, crizotinib, periforsine, olaparib, Bortezomib, tofacitinib, a derivative or a combination thereof.

Cancers, including breast cancer, colorectal cancer, pancreatic cancer, head and neck cancer, melanoma, ovarian cancer, prostate cancer, non-small lung cell cancer, glioma, esophageal cancer, nasopharyngeal cancer, anal cancer, rectal cancer, gastric cancer, bladder cancer, cervical cancer, or brain cancer, may express cancer-associated genes. Inhibition of cancer-associated activity with specific monoclonal antibodies or antigen-binding fragment may have therapeutic effect on cancers. Furthermore, administering a therapeutically effective amount of composition comprising monoclonal antibodies or antigen-binding fragment specific for cancer-associated protein may cure, prevent, ameliorate, and delay the development or metastasis of cancers, through the effect of the cytotoxic agent.

The present disclosure may be understood more readily by reference to the following detailed description of specific embodiments and examples included herein. Although the present disclosure has been described with reference to specific details of certain embodiments thereof, it is not intended that such details should be regarded as limitations upon the scope of the disclosure.

EXAMPLES

Example 1: Binding of tetra-specific antibodies to EGFRvIII antigen

Binding of tetra-specific antibodies listed in TABLE 1 to EGFRvIII antigen expressed on the surface of U87 cell line was assessed using FACS method. The tetra-specific antibodies were incubate with U87 cell line and then detected with secondary anti-human antibodies directly conjugated to Alexa Fluor 647 fluorochrome. Cellular binding of the tetra-specific antibodies was analyzed on a flow cytometer BD LSRFortessa. All tested antibodies bound to the antigen with a KD in a single digit and sub-nanomolar range (TABLE 2). Observed differences in binding were within 3-fold range and might be driven by the position of the binding domain within the molecule as well as by interactions with adjacent domains.

TABLE 1 shows example tetra-specific antibodies with EGFRvIII tumor antigen binding domain. TABLE 2 shows the binding to EGFRvIII antigen expressed in U87 cell line. Binding of tetra-specific antibodies listed in TABLE 1 to EGFRvIII antigen was assessed by flow cytometry.

TABLE 1. Tetra-specific antibodies with EGFRvIII tumor antigen binding domain.

Antibody ID	Antibody domain structure						
SI-39E29	806	X	284A10	X	PL221	X	420H5
SI-39E18	284A10	X	806	X	PL221	X	420H5
SI-39E13	420H5	X	PL230	X	284A10	X	806
SI-39E4	PL230	X	806	X	284A10	X	420H5
SI-39E10	420H5	X	PL230	X	806	X	284A10
SI-39E23	PL230	X	806	X	420H5	X	284A10

TABLE 2. Binding to EGFRvIII antigen expressed in CHO cell line.

	CHO-EGFRviii binding							
Antibody ID	Antibody domain structure							EC50 (nM)
SI-39E29	806	X	284A10	X	PL221	X	420H5	0.489
SI-39E18	284A10	X	806	X	PL221	X	420H5	0.7549
SI-39E13	420H5	X	PL230	X	284A10	X	806	1.244
SI-39E4	PL230	X	806	X	284A10	X	420H5	1.115
SI-39E10	420H5	X	PL230	X	806	X	284A10	1.542
SI-39E23	PL230	X	806	X	420H5	X	284A10	0.9222

Example 2: Binding of tetra-specific antibodies to EGFRvIII, 4-1BB, PD-L1 and CD3 protein antigens

Binding affinities and kinetics of tetra-specific antibodies listed in TABLE 1 to their respective antigens was assessed via Surface Plasmon Resonance on ForteBio Octet RED96 instrument. The antigens were immobilized on the sensor chip surface and the tested antibodies were flown over the immobilized antigens. All molecules showed high binding to the antigens (TABLE 3). SI-39E29, SI-39E18 and SI-39E23 showed lower binding to CD3 e/d antigen than other antibodies tested. TABLE 3 shows the binding of tetra-specific antibodies listed in TABLE 1 to EGFRvIII, 4-1BB, PD-L1 and CD3 antigens.

TABLE 3. Binding to EGFRvIII, 4-1BB, PD-L1 and CD3 antigens.

Table 3A.

								EGFRVIII binding				4-1BB binding			
Antibody ID	Antibody domain structure							Response	KD (M)	kon(1/Ms)	kdis(1/s)	Response	KD (M)	kon(1/Ms)	kdis(1/s)
SI-39E29	806	X	284A10	X	PL221	X	420H5	1.4113	<1.0E-12	1.38E+05	<1.0E-07	1.9181	5.94E-10	2.32E+05	1.38E-04
SI-39E18	284A10	X	806	X	PL221	X	420H5	1.4606	<1.0E-12	1.19E+05	<1.0E-07	2.0165	3.93E-10	2.35E+05	9.24E-05
SI-39E13	420H5	X	PL230	X	284A10	X	806	1.2317	<1.0E-12	9.90E+04	<1.0E-07	2.4703	1.17E-10	2.27E+05	2.65E-05
SI-39E4	PL230	X	806	X	284A10	X	420H5	1.4058	<1.0E-12	8.43E+04	<1.0E-07	2.417	3.54E-10	1.67E+05	5.91E-05
SI-39E10	420H5	X	PL230	X	806	X	284A10	1.1414	<1.0E-12	8.63E+04	<1.0E-07	2.6348	3.56E-11	2.09E+05	7.43E-06
SI-39E23	PL230	X	806	X	420H5	X	284A10	1.3408	<1.0E-12	1.41E+05	<1.0E-07	2.0159	6.96E-10	2.03E+05	1.41E-04

Table 3B.

								PD-L1 binding				CD3 e/d binding			
Antibody ID	Antibody domain structure							Response	KD (M)	kon(1/Ms)	kdis(1/s)	Response	KD (M)	kon(1/Ms)	kdis(1/s)
SI-39E29	806	X	284A10	X	PL221	X	420H5	1.7228	2.83E-10	3.76E+05	1.06E-04	1.8493	4.75E-10	1.66E+05	7.86E-05
SI-39E18	284A10	X	806	X	PL221	X	420H5	1.8256	1.68E-10	3.79E+05	6.37E-05	1.7586	6.32E-10	1.74E+05	1.10E-04
SI-39E13	420H5	X	PL230	X	284A10	X	806	1.9223	8.01E-11	4.15E+05	3.32E-05	1.8019	<1.0E-12	1.04E+05	<1.0E-07
SI-39E4	PL230	X	806	X	284A10	X	420H5	2.1532	7.23E-11	3.33E+05	2.41E-05	1.965	<1.0E-12	8.61E+04	<1.0E-07
SI-39E10	420H5	X	PL230	X	806	X	284A10	1.9364	6.85E-11	3.81E+05	2.61E-05	2.2404	<1.0E-12	1.10E+05	<1.0E-07
SI-39E23	PL230	X	806	X	420H5	X	284A10	1.9024	4.02E-11	4.83E+05	1.94E-05	2.6545	2.07E-10	1.23E+05	2.54E-05

Example 3: Redirected PBMC cytotoxicity against astrocytoma cell line U87 that was transfected with EGFRvIII

Tetra-specific antibodies listed in TABLE 1 were assessed for their ability to redirect PBMC to lyse U87 transfected with EGFRvIII tumor cell line (U87vIII). PBMC were isolated by ficoll gradient. U87vIII tumor cell line was stably expressing nucleus-localized Red Fluorescent Protein (RFP) delivered via lentiviral transduction (Sartorius). U87vIII tumor cells were co-cultured with PBMC. Lysis of tumor cells was assessed by counting RFP labeled tumor cell nuclei. Images were acquired on live cell imager IncuCyte (Sartorius). SI-39E18 and SI-39E13 tetra-specific antibodies showed the highest efficacy at 96 hours followed by SI-39E10. SI-39E4, SI-39E23 and SI-39E29 showed lower efficacy in this study than other antibodies listed in TABLE 1 (FIGURE 2).

Example 4: Redirected PBMC cytotoxicity against acute lymphoblastic leukemia cell line Kasumi-2

Tetra-specific antibodies listed in TABLE 4 were assessed for their ability to lyse leukemia cell line Kasumi-2. PBMC were isolated by ficoll gradient. Kasumi-2 tumor cells were co-cultured with PBMC. Tumor cell lysis was assessed on BD LSRFortessa flow cytometer via counting the number of live tumor cells present after 96 hours of co-culture. Tetra-specific antibody SI-38E14 showed the most potent activity in this study followed by SI-38E38 (FIGURE 3). TABLE 4 shows example tetra-specific antibodies with CD19 tumor antigen recognition domain.

Table 4. Tetraspecific antibodies with CD19 tumor antigen recognition domain.

Antibody ID	Antibody domain structure
SI-38E14	PL230 x 466F6 x 21D4 x 284A10
SI-38E38	PD224 x 466F6 x 21D4 x 284A10
SI-38E5	466F6 x PL230 x 284A10 x 21D4
SI-38E20	466F6 x 21D4 x 284A10 x PL221
SI-38E35	21D4 x 284A10 x 466F6 x PL221

Example 5: Redirected PBMC cytotoxicity against astrocytoma cell line U87 that was transfected with EGFRvIII, functional activity of different 4-1BB domains and functional impact of PD-L1 and 4-1BB domains

Tetra-specific antibodies listed in TABLE 5 were assessed for their ability to redirect PBMC to lyse U87 transfected with EGFRvIII tumor cell line (U87vIII). PBMC were isolated by ficoll gradient. U87vIII tumor cell line was stably expressing nucleus-localized Red Fluorescent Protein (RFP) delivered via lentiviral transduction (Sartorius). U87vIII tumor cells were co-cultured with PBMC. Lysis of tumor cells was

assessed by counting RFP labeled tumor cell nuclei. Images were acquired on live cell imager IncuCyte (Sartorius). Activity of the antibodies was assessed after 96 hours of incubation. Antibodies with different 4-1BB domains – SI-39E4, SI-39E2 and SI-39E3 showed similar activity (FIGURE 4). Antibodies with PD-L1 and 4-1BB domains replaced by silent (not functional) FITC domains, SI-39E1 and SI-39E5, showed reduction in lysis activity. This observation confirms functional contribution of 4-1BB and PD-L1 domains. TABLE 5 shows example tetra-specific antibodies with EGFRvIII tumor antigen binding domain. FITC control antibodies.

Table 5. Tetraspecific antibodies with EGFRvIII tumor antigen binding domain. FITC control antibodies.

Antibody ID	Antibody domain structure						
SI-39E4	PL230	X	806	X	284A10	X	420H5
SI-39E3	PL230	X	806	X	284A10	X	466F6
SI-39E2	PL230	X	806	X	284A10	X	460C3
SI-39E5	FITC	X	806	X	284A10	X	420H5
SI-39E1	PL230	X	806	X	284A10	X	FITC

Example 6: FACS analysis of tetra-specific specific antibody binding to human ROR1 transfected CHO cells

The tetra-specific -specific antibodies listed in TABLEs 1 and 2 were tested for binding to Chinese hamster ovary cells (CHO) cells stably expressing full length human ROR1. Antibodies were prepared at 2X final concentration and titrated 1:5 across 3 wells of a 96 well plate in 50 ul of PBS/2% FBS and then 5,000 ROR1-CHO cells in 50ul PBS/2%FBS were added. This mixture was incubated for 30 minutes on ice, washed once with 200 ul PBS/2%FBS, and then the secondary antibody PE Goat anti-Human IgG Fc at 1:1000 dilution of stock was added, and this mixture was incubated for 30 minutes on ice. Cells were washed 2 x 200 ul PBS/2%FBS, resuspended in 50 ul PBS/2%FBS and analyzed on a BD LSRFORTESSA and the binding profile is shown in FIGURE 5. The tetra-specific antibodies SI-35E18, 19, and 20, with the 323H7 binding domain specific for the Ig domain of ROR1, showed higher binding than the tetra-specific antibodies SI-3521, 22, and 23, with the 338H4 binding domain specific for the frizzled domain of ROR1, and the tetra-specific antibodies SI-3524, 25, and 26, with the 330F11 binding domain specific for the kringle domain of ROR1, did not bind.

Example 7: FACS analysis of tetra-specific specific antibody binding to human 41BB transfected CHO cells

The tetra-specific -specific antibodies listed in TABLE 6 were tested for binding to Chinese hamster ovary cells (CHO) cells stably expressing full length human ROR1. Antibodies were prepared at 2X final concentration and titrated 1:5 across 3 wells of a 96 well plate in 50 ul of PBS/2% FBS and then 5,000 ROR1-CHO cells in 50ul PBS/2%FBS were added. This mixture was incubated for 30 minutes on ice, washed once with 200 ul PBS/2%FBS, and then the secondary antibody PE Goat anti-Human IgG Fc at 1:1000 dilution of stock was added, and this mixture was incubated for 30 minutes on ice. Cells were washed 2 x 200 ul PBS/2%FBS, resuspended in 50 ul PBS/2%FBS and analyzed on a BD LSRFortessa and the binding profile is shown in FIGURE 6. All of the tetra-specific antibodies except for the control SI-

27E12 contain a 41BB binding domain, 460C3, 420H5, or 466F6 and bound to 41BB expressing CHO cells with varying intensity. TABLE 6 shows the example tetra-specific antibody list.

TABLE 6. Tetraspecific antibody list.

		Domain 1		Domain 2			Domain 3		Domain 4	
ID = SI-xx		LH-scFv	Humanized Variant	Fab	Humanized Variant	Fc	HL-scFv	Humanized Variant	HL-scFv	Humanized Variant
39	E02	PL230C6	L2H3	806	-		284A10	H1L1	460C3	H1L1
39	E03	PL230C6	L2H3	806	-		284A10	H1L1	466F6	H2L5
39	E18	284A10	L1H1	806	-	n2	PL221G5	H1L1	420H5	H3L3
39	E13	420H5	L3H3	PL230C6	H3L2	n2	284A10	H1L1	806	
39	E10	420H5	L3H3	PL230C6	H3L2	n2	806	-	284A10	H1L1
39	E29	806	-	284A10	H1L1	n2	PL221G5	H1L1	420H5	H3L3
39	E04	PL230C6	L2H3	806	-	n2	284A10	H1L1	420H5	H3L3
39	E23	PL230C6	L2H3	806	-	n2	420H5	H3L3	284A10	H1L1
38	E14	PL230C6	L2H3	466F6	H2L5	n2	21D4	-	284A10	H1L1
38	E38	PD224D1	L2H2	466F6	H2L5	n2	21D4	-	284A10	H1L1
38	E05	466F6	L5H2	PL230C6	H3L2	n2	284A10	H1L1	21D4	-
38	E20	466F6	L5H2	21D4	-	n2	284A10	H1L1	PL221G5	H1L1
39	E05	4-4-20 (FITC)	-	806	-	n2	284A10	H1L1	420H5	H3L3
39	E01	PL230C6	L2H3	806	-	n2	284A10	H1L1	4-4-20 (FITC)	-
35	E02	460C3	L1H1	PL230C6	H3L2	n2	324C6	H2L1	4-4-20 (FITC)	-
35	E12	4-4-20 (FITC)	-	PL230C6	H3L2	n2	324C6	H2L1	480C8	H1L1
35	E13	460C3	L1H1	PL230C6	H3L2	n2	4-4-20 (FITC)	-	480C8	H1L1
35	E15	460C3	L1H1	4-4-20 (FITC)	-	n2	324C6	H2L1	480C8	H1L1
35	E18	460C3	L1H1	PL230C6	H3L2	n2	323H7	H4L1	284A10	H1L1
35	E19	420H5	L3H3	PL230C6	H3L2	n2	323H7	H4L1	284A10	H1L1
35	E20	466F6	L5H2	PL230C6	H3L2	n2	323H7	H4L1	284A10	H1L1
35	E21	460C3	L1H1	PL230C6	H3L2	n2	338H4	H3L4	284A10	H1L1
35	E22	420H5	L3H3	PL230C6	H3L2	n2	338H4	H3L4	284A10	H1L1
35	E23	466F6	L5H2	PL230C6	H3L2	n2	338H4	H3L4	284A10	H1L1
35	E24	460C3	L1H1	PL230C6	H3L2	n2	330F11	H1L1	284A10	H1L1
35	E25	420H5	L3H3	PL230C6	H3L2	n2	330F11	H1L1	284A10	H1L1
35	E26	466F6	L5H2	PL230C6	H3L2	n2	330F11	H1L1	284A10	H1L1
35	E36	4-4-20 (FITC)	-	PL230C6	H3L2	n2	338H4	H3L4	284A10	H1L1
35	E37	460C3	L1H1	4-4-20 (FITC)	-	n2	338H4	H3L4	284A10	H1L1
35	E38	460C3	L1H1	PL230C6	H3L2	n2	4-4-20 (FITC)	-	284A10	H1L1
35	E39	460C3	L1H1	PL230C6	H3L2	n2	338H4	H3L4	4-4-20 (FITC)	-

Example 8: FACS analysis of tetra-specific specific antibody binding to human PD-L1 transfected CHO cells

The tetra-specific -specific antibodies listed in TABLE 6 were tested for binding to Chinese hamster ovary cells (CHO) cells stably expressing full length human ROR1. Antibodies were prepared at 2X final concentration and titrated 1:5 across 3 wells of a 96 well plate in 50 ul of PBS/2% FBS and then 5,000 ROR1-CHO cells in 50ul PBS/2%FBS were added. This mixture was incubated for 30 minutes on ice, washed once with 200 ul PBS/2%FBS, and then the secondary antibody PE Goat anti-Human IgG Fc at 1:1000 dilution of stock was added, and this mixture was incubated for 30 minutes on ice. Cells were washed 2 x 200 ul PBS/2%FBS, resuspended in 50 ul PBS/2%FBS and analyzed on a BD LSRFORTESSA and the binding profile is shown in FIGURE 7. All of the tetra-specific antibodies except for the control SI-27E15 contain the same PD-L1 binding domain, PL230C6, and showed very similar binding intensity to PD-L1 expressing CHO cells.

Example 9: Re-directed T cell cytotoxicity (RTCC) assay with peripheral blood mononuclear cells as effectors and B-Acute Lymphoblastic Leukemia (B-ALL) cell line Kasumi-2 as targets

The tetra-specific-specific antibodies listed in TABLE 6 were tested for RTCC activity against the B-ALL cell line Kasumi 2 using human peripheral blood mononuclear cells (PBMC) as effectors. The Kasumi 2 target cells, 5 x 10e6, were labeled with CFSE (Invitrogen, #C34554) at 0.5 uM in 10 ml of culture media

for 20 minutes at 37C. The cells were washed 3 times with 50 ml of culture media before resuspending in 10 ml then counted again. Antibodies were prepared at 2X final concentration and titrated 1:3 across 10 wells of a 96 well plate in 200 ul of RPMI + 10%FBS. Human PBMC were purified by standard ficoll density gradient from a "leukopak" which is an enriched leukapheresis product collected from normal human peripheral blood. In the final destination 96 well plate the target cells, PBMC, and serially titrated antibodies were combined by adding 100 ul of target cells (5,000), 50 ul of PBMC (25,000), and 100 ul of each antibody dilution to each well of the assay. The assay plate was incubated at 37C for approximately 72 hours and then the contents of each assay well were harvested and analyzed for the number of CFSE-labeled target cells remaining. As shown on FIGURE 8, the tetra-specific antibodies all contain the same PD-L1 binding domain PL230C6, the same ROR1 binding domain 323H7, and the same CD3 binding domain 284A10, but have one of the 41BB binding domains 460C3, 420H5, and 466F6 and showed greater RTCC activity compared to the controls except for the control SI-27E12 which does not have a 41BB binding domain but appeared to be similarly potent at the tetra-specific antibodies SI-35E18, 19, and 20.

Example 10: Re-directed T cell cytotoxicity (RTCC) assay with CD8+, CD45RO+ memory T cells as effectors and B-Acute Lymphoblastic Leukemia (B-ALL) cell line Kasumi-2 as targets

The tetra-specific-specific antibodies listed in TABLE 6 were tested for RTCC activity against the B-ALL cell line Kasumi 2 using human CD8+, CD45RO+ memory T cells as effectors. The Kasumi 2 target cells, 5 x 10e6, were labeled with CFSE (Invitrogen, #C34554) at 0.5 uM in 10 ml of culture media for 20 minutes at 37C. The cells were washed 3 times with 50 ml of culture media before resuspending in 10 ml then counted again. Antibodies were prepared at 2X final concentration and titrated 1:3 across 10 wells of a 96 well plate in 200 ul of RPMI + 10%FBS. Human CD8+, CD45RO+ memory T cells were enriched from peripheral blood mononuclear cells from a normal donor using the EasySep™ Human Memory CD8+ T Cell Enrichment Kit (Stemcell Technologies, #19159) as per the manufacturers protocol. The final cell population was determined to be 98% CD8+, CD45RO+ T cells by FACS analysis (data not shown). In the final destination 96 well plate the target cells, T cells, and serially titrated antibodies were combined by adding 100 ul of target cells (5,000), 50 ul of CD8+, CD45RO+ memory T cells (25,000), and 100 ul of each antibody dilution to each well of the assay. The assay plate was incubated at 37C for approximately 72 hours and then the contents of each assay well were harvested and analyzed for the number of CFSE-labeled target cells remaining. As shown on FIGURE 9, the tetra-specific antibodies all contain the same PD-L1 binding domain PL230C6, the same ROR1 binding domain 323H7, and the same CD3 binding domain 284A10, but have one of the 41BB binding domains 460C3, 420H5, and 466F6 and showed greater RTCC activity compared to the controls that do not contain one of the 41BB, PD-L1, ROR1, or CD3 binding domains.

Example 11: Re-directed T cell cytotoxicity (RTCC) assay with CD8+, CD45RA+ naive T cells as effectors and B-Acute Lymphoblastic Leukemia (B-ALL) cell line Kasumi-2 as targets

The tetra-specific-specific antibodies listed in TABLE 6 were tested for RTCC activity against the B-ALL cell line Kasumi 2 using human CD8+, CD45RA+ memory T cells as effectors. The Kasumi 2 target cells, 5 x 10e6, were labeled with CFSE (Invitrogen, #C34554) at 0.5 uM in 10 ml of culture media for 20 minutes

at 37C. The cells were washed 3 times with 50 ml of culture media before resuspending in 10 ml then counted again. Antibodies were prepared at 2X final concentration and titrated 1:3 across 10 wells of a 96 well plate in 200 ul of RPMI + 10%FBS. Human CD8+, CD45RA+ memory T cells were enriched from peripheral blood mononuclear cells from a normal donor using the EasySep™ Human Naïve CD8+ T Cell Isolation Kit (Stemcell Technologies, #19258) as per the manufacturers protocol. The final cell population was determined to be 98% CD8+, CD45RA+ T cells by FACS analysis (data not shown). In the final destination 96 well plate the target cells, T cells, and serially titrated antibodies were combined by adding 100 ul of target cells (5,000), 50 ul of CD8+, CD45RO+ T cells (25,000), and 100 ul of each antibody dilution to each well of the assay. The assay plate was incubated at 37C for approximately 72 hours and then the contents of each assay well were harvested and analyzed for the number of CFSE-labeled target cells remaining. As shown on FIGURE 10, the tetra-specific antibodies all contain the same PD-L1 binding domain PL230C6, the same ROR1 binding domain 323H7, and the same CD3 binding domain 284A10, but have one of the 41BB binding domains 460C3, 420H5, and 466F6 and showed greater RTCC activity compared to the controls that do not contain one of the 41BB, PD-L1, ROR1, or CD3 binding domains.

Example 12: Re-directed T cell cytotoxicity (RTCC) assay with peripheral blood mononuclear cells as effectors and B-Acute Lymphoblastic Leukemia (B-ALL) cell line Kasumi-2 as targets.

The tetra-specific-specific antibodies listed in TABLE 6 were tested for RTCC activity against the B-ALL cell line Kasumi 2 using human peripheral blood mononuclear cells (PBMC) as effectors. The Kasumi 2 target cells, 5 x 10e6, were labeled with CFSE (Invitrogen, #C34554) at 0.5 uM in 10 ml of culture media for 20 minutes at 37C. The cells were washed 3 times with 50 ml of culture media before resuspending in 10 ml then counted again. Antibodies were prepared at 2X final concentration and titrated 1:3 across 10 wells of a 96 well plate in 200 ul of RPMI + 10%FBS. Human PBMC were purified by standard ficoll density gradient from a "leukopak" which is an enriched leukapheresis product collected from normal human peripheral blood. In the final destination 96 well plate the target cells, PBMC, and serially titrated antibodies were combined by adding 100 ul of target cells (5,000), 50 ul of PBMC (25,000), and 100 ul of each antibody dilution to each well of the assay. The assay plate was incubated at 37C for approximately 72 hours and then the contents of each assay well were harvested and analyzed for the number of CFSE-labeled target cells remaining. As shown on FIGURE 11, the tetra-specific antibodies all contain the same PD-L1 binding domain PL230C6, the same ROR1 binding domain 338H4, and the same CD3 binding domain 284A10, but have one of the 41BB binding domains 460C3, 420H5, and 466F6 and showed greater RTCC activity compared to the controls except for the control SI-35E36 which does not have a 41BB binding domain but appeared to be similarly potent at the tetra-specific antibodies SI-35E18, 19, and 20.

Example 13: Re-directed T cell cytotoxicity (RTCC) assay with CD8+, CD45RO+ memory T cells as effectors and B-Acute Lymphoblastic Leukemia (B-ALL) cell line Kasumi-2 as targets

The tetra-specific-specific antibodies listed in TABLE 6 were tested for RTCC activity against the B-ALL cell line Kasumi 2 using human CD8+, CD45RO+ memory T cells as effectors. The Kasumi 2 target cells, 5 x 10e6, were labeled with CFSE (Invitrogen, #C34554) at 0.5 uM in 10 ml of culture media for 20 minutes

at 37C. The cells were washed 3 times with 50 ml of culture media before resuspending in 10 ml then counted again. Antibodies were prepared at 2X final concentration and titrated 1:3 across 10 wells of a 96 well plate in 200 ul of RPMI + 10%FBS. Human CD8+, CD45RO+ memory T cells were enriched from peripheral blood mononuclear cells from a normal donor using the EasySep™ Human Memory CD8+ T Cell Enrichment Kit (Stemcell Technologies, #19159) as per the manufacturers protocol. The final cell population was determined to be 98% CD8+, CD45RO+ T cells by FACS analysis (data not shown). In the final destination 96 well plate the target cells, T cells, and serially titrated antibodies were combined by adding 100 ul of target cells (5,000), 50 ul of CD8+, CD45RO+ memory T cells (25,000), and 100 ul of each antibody dilution to each well of the assay. The assay plate was incubated at 37C for approximately 72 hours and then the contents of each assay well were harvested and analyzed for the number of CFSE-labeled target cells remaining. As shown on FIGURE 12, the tetra-specific antibodies all contain the same PD-L1 binding domain PL230C6, the same ROR1 binding domain 338H4, and the same CD3 binding domain 284A10, but have one of the 41BB binding domains 460C3, 420H5, and 466F6 and showed greater RTCC activity compared to the controls that do not contain one of the 41BB, PD-L1, ROR1, or CD3 binding domains.

Example 14: Re-directed T cell cytotoxicity (RTCC) assay with CD8+, CD45RA+ naive T cells as effectors and B-Acute Lymphoblastic Leukemia (B-ALL) cell line Kasumi-2 as targets

The tetra-specific-specific antibodies listed in TABLE 6 were tested for RTCC activity against the B-ALL cell line Kasumi 2 using human CD8+, CD45RA+ memory T cells as effectors. The Kasumi 2 target cells, 5 x 10e6, were labeled with CFSE (Invitrogen, #C34554) at 0.5 uM in 10 ml of culture media for 20 minutes at 37C. The cells were washed 3 times with 50 ml of culture media before resuspending in 10 ml then counted again. Antibodies were prepared at 2X final concentration and titrated 1:3 across 10 wells of a 96 well plate in 200 ul of RPMI + 10%FBS. Human CD8+, CD45RA+ memory T cells were enriched from peripheral blood mononuclear cells from a normal donor using the EasySep™ Human Naïve CD8+ T Cell Isolation Kit (Stemcell Technologies, #19258) as per the manufacturers protocol. The final cell population was determined to be 98% CD8+, CD45RA+ T cells by FACS analysis (data not shown). In the final destination 96 well plate the target cells, T cells, and serially titrated antibodies were combined by adding 100 ul of target cells (5,000), 50 ul of CD8+, CD45RO+ T cells (25,000), and 100 ul of each antibody dilution to each well of the assay. The assay plate was incubated at 37C for approximately 72 hours and then the contents of each assay well were harvested and analyzed for the number of CFSE-labeled target cells remaining. As shown on FIGURE 13, the tetra-specific antibodies all contain the same PD-L1 binding domain PL230C6, the same ROR1 binding domain 338H4, and the same CD3 binding domain 284A10, but have one of the 41BB binding domains 460C3, 420H5, and 466F6 but did not show greater RTCC activity compared to the controls that do not contain one of the 41BB, PD-L1, ROR1, or CD3 binding domains. This is in contrast to the tetra-specific antibodies described in example 6 and shown in FIGURE 10 that do show RTCC activity with CD8+, CD45RA+ naïve T cells.

While the present disclosure has been described with reference to particular embodiments or examples, it may be understood that the embodiments are illustrative and that the disclosure scope is not so limited. Alternative embodiments of the present disclosure may become apparent to those having ordinary skill in the art to which the present disclosure pertains. Such alternate embodiments are

considered to be encompassed within the scope of the present disclosure. Accordingly, the scope of the present disclosure is defined by the appended claims and is supported by the foregoing description. . All references cited or referred to in this disclosure are hereby incorporated by reference in their entireties.

SEQUENCE LISTING

CDR's underlined in amino acid sequences

>SEQ ID:01 anti-CD3 284A10 VHv1 nt

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTC
TGGATTCACCATCAGTACCAATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAG
TCATTACTGGTCGTGATATCACATACTACGCGAGCTGGGCGAAAGGCAGATTCACCATCTCCAGAGACAATTCCAA
GAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGCGCGACGGTGG
ATCATCTGCTATTACTAGTAACAACATTTGGGGCCAAGGAACTCTGGTCACCGTTTCTTCA

>SEQ ID:02 anti-CD3 284A10 VHv1 aa

EVQLVESGGGLVQPGGSLRLSCAASGFTISTNAMSWVRQAPGKGLEWIGVITGRDITYYASWAKGRFTISRDNSKNTLY
LQMNSLRAEDTAVYYCARDGGSSAITSNNIWGQGTLVTVSS

>SEQ ID:03 anti-CD3 284A10 VLv1 nt

GACGTCGTGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAAGCCA
GTGAGAGCATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGAAG
CATCCAAACTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCA
GCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAAGGCTATTTTTATTTTATTAGTCGTACTTATGTAAATT
CTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

>SEQ ID:04 anti-CD3 284A10 VLv1 aa

DVVMTQSPSTLSASVGDRVTINCQASESISSWLAWYQQKPGKAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISSLQPD
DFATYYCQGYFYFISRTYVNSFGGGTKVEIK

>SEQ ID:05 anti-CD3 480C8 VHv1 nt

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTC
TGGAATCGACCTCAGTAGCAATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAG
TCATTACTGGTCGTGATATCACATACTACGCGAGCTGGGCGAAAGGCAGATTCACCATCTCCAGAGACAATTCCAA
GAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGCGCGACGGTGG
ATCATCTGCTATTAATAGTAAGAACATTTGGGGCCAAGGAACTCTGGTCACCGTTTCTTCA

>SEQ ID:06 anti-CD3 480C8 VHv1 aa

EVQLVESGGGLVQPGGSLRLSCAASGIDLSSNAMSWVRQAPGKGLEWIGVITGRDITYYASWAKGRFTISRDNSKNTLY
LQMNSLRAEDTAVYYCARDGGSSAINSKNIWGQGTLVTVSS

>SEQ ID:07 anti-CD3 480C8 VLv1 nt

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAAGCCA
GTGAGAGCATTAGCAGTTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGAAG
CATCCAAACTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCA
GCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAAGGCTATTTTTATTTTATTAGTCGTACTTATGTAAATG
CTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

>**SEQ ID:08 anti-CD3 480C8 VLv1 aa**

DIQMTQSPSTLSASVGDRVTITCQASESISSWLAWYQQKPGKAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISSLQPD
DFATYYCQGYFYFISRTYVNAFGGGTKVEIK

>**SEQ ID:09 anti-PD-L1 PL230C6 VHv3 nt**

CAGTCGGTGGAGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAGCCTCTGG
AATCGACCTTAATACCTACGACATGATCTGGGTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGTTGGAATCAT
TACTTATAGTGGTAGTAGATACTACGCGAACTGGGCGAAAGGCCGATTCACCATCTCCAAAGACAATACCAAGAA
CACGGTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCCAGAGATTATATGAG
TGGTTCCCACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCTAGT

>**SEQ ID:10 anti-PD-L1 PL230C6 VHv3 aa**

QSVEESGGGLVQPGGSLRLSCTASGIDLNTYDMIWVRQAPGKGLEWVGIITYSGSRYYANWAKGRFTISKDNTKNTVY
LQMNSLRAEDTAVYYCARDYMSGSHLWGQGTLVTVSS

>**SEQ ID:11 anti-PD-L1 PL230C6 VLv2 nt**

GCCTATGATATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCAAGTGTCAGGCCA
GTGAGGACATTTATAGCTTCTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCCATTCTGC
ATCCTCTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGC
AGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGGTTATGGTAAAAATAATGTTGATAATGCTTTCG
GCGGAGGGACCAAGGTGGAGATCAAA

>**SEQ ID:12 anti-PD-L1 PL230C6 VLv2 aa**

AYDMTQSPSSVSASVGDRVTIKCQASEDIYSFLAWYQQKPGKAPKLLIHSASSLASGVPSRFSGSGSGTDFTLTISSLQPE
DFATYYCQQGYGKNNVDNAFGGGTKVEIK

>**SEQ ID:13 anti-PD-L1 PL221G5 VHv1 nt**

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCT
GGATTCTCCTTCAGTAGCGGGTACGACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGC
ATGCATTGCTGCTGGTAGTGCTGGTATCACTTACGACGCGAACTGGGCGAAAGGCCGGTTCACCATCTCCAGAGA
CAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAG
ATCGGCGTTTTCGTTCGACTACGCCATGGACCTCTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

>**SEQ ID:14 anti-PD-L1 PL221G5 VHv1 aa**

EVQLLESGGGLVQPGGSLRLSCAASGFSFSSGYDMCWVRQAPGKGLEWIACIAAGSAGITYDANWAKGRFTISRDNSK
NTLYLQMNSLRAEDTAVYYCARSAFSFDYAMDLWGQGTLVTVSS

>SEQ ID:15 anti-PD-L1 PL221G5 VLv1 nt

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCA
GTCAGAGCATTAGTTCCCACTTAAACTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATAAGGC
ATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTTACTCTCACCATCAGC
AGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAACAGGGTTATAGTTGGGGTAATGTTGATAATGTTTTCG
GCGGAGGGACCAAGGTGGAGATCAAA

>SEQ ID:16 anti-PD-L1 PL221G5 VLv1 aa

DIQMTQSPSTLSASVGDRVTITCQASQSISSHLNWYQQKPGKAPKLLIYKASTLASGVPSRFSGSGSGTEFTLTISSLQPD
DFATYYCQQGYSWGNVDNVFGGGTKVEIK

>SEQ ID:17 anti-PD-1 PD224D1 VHv2 nt

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAGCCTC
TGGATTCTCCCTAAGTAGCTATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTACATCGGCTA
CATTGGTGATACTACTGGCATAGCCTACGCGAGCTGGGCGAATGGCAGATTCACCATCTCCAAAGACAATACCAA
GAACACGGTGGATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGCTGGT
CCTACTTAGACATCTGGGGCCAAGGGACCCTGGTCACCGTCTCGAGC

>SEQ ID:18 anti-PD-1 PD224D1 VHv2 aa

EVQLVESGGGLVQPGGSLRLSCTASGFSLSSYAMSWVRQAPGKGLEYIGYIGDTTGIAYASWANGRFTISKDNTKNTVD
LQMNSLRAEDTAVYYCARGWSYLDIWGQGTLVTVSS

>SEQ ID:19 anti-PD-1 PD224D1 VLv2 nt

GCCCTTGTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCA
GTCAGAACATTTACAGCAATTTAGCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTATCAGGC
CTCCACTCTGGCATCTGGGGTCCCATCTCGGTTCAGTGGCAGTGGATATGGGACAGATTTCACTCTCACCATCAGC
AGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCAAGGCGGTTATTATAGTGCTGCCCTTAATACTTTCGGCG
GAGGGACCAAGGTGGAGATCAAA

>SEQ ID:20 anti-PD-1 PD224D1 VLv2 aa

ALVMTQSPSSLSASVGDRVTITCQASQNIYSNLAWYQQKPGKVPKLLIYQASTLASGVPSRFSGSGYGTDFTLTISSLQPE
DVATYYCQGGYYSAALNTFGGGTKVEIK

>SEQ ID:21 anti-4-1BB 420H5 VHv3 nt

CAGTCGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGG
ATTCTCCTTCAGTAGCAACTACTGGATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATG
CATTTATGTTGGTAGTAGTGGTGACACTTACTACGCGAGCTCCGCGAAAGGCCGGTTCACCATCTCCAGAGACAAT

TCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGAGAT
AGTAGTAGTTATTATATGTTTAACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

>SEQ ID:22 anti-4-1BB 420H5 VHv3 aa

QSLVESGGGLVQPGGSLRLSCAASGFSFSSNYWICWVRQAPGKGLEWIACIYVGSSGDTYYASSAKGRFTISRDNSKNT
LYLQMNSLRAEDTAVYYCARDSSSYYMFNLWGQGTLVTVSS

>SEQ ID:23 anti-4-1BB 420H5 VLv3 nt

GCCCTTGTGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAGGCCA
GTGAGGACATTGATACCTATTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTTTTATGC
ATCCGATCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGC
AGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAAGGCGGTTACTATACTAGTAGTGCTGATACGAGGGGTG
CTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

>SEQ ID:24 anti-4-1BB 420H5 VLv3 aa

ALVMTQSPSTLSASVGDRVTINCQASEDIDTYLAWYQQKPGKAPKLLIFYASDLASGVPSRFSGSGSGTEFTLTISSLQPD
DFATYYCQGGYYTSSADTRGAFGGGTKVEIK

>SEQ ID:25 anti-4-1BB 466F6 VHv2 nt

CGGTCGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAGCCTCTGGA
TTCACCATCAGTAGCTACCACATGCAGTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTACATCGGAACCATT
AGTAGTGGTGGTAATGTATACTACGCGAGCTCCGCGAGAGGCAGATTCACCATCTCCAGACCCTCGTCCAAGAAC
ACGGTGGATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACTCTGGTTAT
AGTGATCCTATGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

>SEQ ID:26 anti-4-1BB 466F6 VHv2 aa

RSLVESGGGLVQPGGSLRLSCTASGFTISSYHMQWVRQAPGKGLEYIGTISSGGNVYYASSARGRFTISRPSSKNTVDLQ
MNSLRAEDTAVYYCARDSGYSDPMWGQGTLVTVSS

>SEQ ID:27 anti-4-1BB 466F6 VLv5 nt

GACGTTGTGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACCTGTCAGGCCA
GTCAGAACATTAGGACTTACTTATCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCTGC
AGCCAATCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGC
GACCTGGAGCCTGGCGATGCTGCAACTTACTATTGTCAGTCTACCTATCTTGGTACTGATTATGTTGGCGGTGCTTT
CGGCGGAGGGACCAAGGTGGAGATCAAA

>SEQ ID:28 anti-4-1BB 466F6 VLv5 aa

DVVMTQSPSSVSASVGDRVTITCQASQNIRTYLSWYQQKPGKAPKLLIYAAANLASGVPSRFSGSGSGTDFTLTISDLEP
GDAATYYCQSTYLGTDYVGGAFGGGTKVEIK

>SEQ ID:29 anti-4-1BB 460C3 VHv1 nt

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCT
GGAATCGACTTCAGTAGGAGATACTACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGC
ATGCATATATACTGGTAGCCGCGATACTCCTCACTACGCGAGCTCCGCGAAAGGCCGGTTCACCATCTCCAGAGAC
AATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGA
GAAGGTAGCCTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

>SEQ ID:30 anti-4-1BB 460C3 VHv1 aa

EVQLLESGGGLVQPGGSLRLSCAASGIDFSRRYYMCWVRQAPGKGLEWIACIYTGSRDTPHYASSAKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAREGSLWGQGTLVTVSS

>SEQ ID:31 anti-4-1BB 460C3 VLv1 nt

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCA
GTCAGAGTGTTTATAGTAACTGGTTCTCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATTC
TGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATC
AGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCGCAGGCGGTTACAATACTGTTATTGATACTTTTGCTTT
CGGCGGAGGGACCAAGGTGGAGATCAAA

>SEQ ID:32 anti-4-1BB 460C3 VLv1 aa

DIQMTQSPSTLSASVGDRVTITCQSSQSVYSNWFSWYQQKPGKAPKLLIYSASTLASGVPSRFSGSGSGTEFTLTISSLQP
DDFATYYCAGGYNTVIDTFAFGGGTKVEIK

>SEQ ID:33 anti-ROR1 324C6 VHv2 nt

CAGTCGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACTGCCTCTGGA
TTCTCCCTCAGTAGGTACTACATGACCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAACCATT
TATACTAGTGGTAGTACATGGTACGCGAGCTGGACAAAAGGCAGATTCACCATCTCCAAAGACAATACCAAGAAC
ACGGTGGATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGATCCTATTATGGC
GGTGATAAGACTGGTTTAGGCATCTGGGGCCAGGGAACTCTGGTTACCGTCTCTTCA

>SEQ ID:34 anti-ROR1 324C6 VHv2 nt

QSLVESGGGLVQPGGSLRLSCTASGFSLSRYYMTWVRQAPGKGLEWIGTIYTSGSTWYASWTKGRFTISKDNTKNTVD
LQMNSLRAEDTAVYYCARSYYGGDKTGLGIWGQGTLVTVSS

>SEQ ID:35 anti-ROR1 324C6 VLv1 nt

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCA
GTCAGAGCATTGATAGTTGGTTATCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATCAGGC
ATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGC
AGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAATCTGCTTATGGTGTTAGTGGTACTAGTAGTTATTTATA
TACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

>SEQ ID:36 anti-ROR1 324C6 VLv1 aa

DIQMTQSPSTLSASVGDRVTITCQASQSIDSWLSWYQQKPGKAPKLLIYQASTLASGVPSRFSGSGSGTEFTLTISSLQPD
DFATYYCQSAYGVSGTSSYLYTFGGGTKVEIK

>SEQ ID:37 anti-ROR1 323H7 VHv4 nt

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCT
GGATTCACCATCAGTCGCTACCACATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGACAT
ATTTATGTTAATAATGATGACACAGACTACGCGAGCTCCGCGAAAGGCCGGTTCACCATCTCCAGAGACAATTCCA
AGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCACCTATTTCTGTGCGAGATTGGATG
TTGGTGGTGGTGGTGCTTATATTGGGGACATCTGGGGCCAGGGAACTCTGGTTACCGTCTCTTCA

>SEQ ID:38 anti-ROR1 323H7 VHv4 aa

EVQLLESGGGLVQPGGSLRLSCAASGFTISRYHMTWVRQAPGKGLEWIGHIYVNNDDTDYASSAKGRFTISRDNSKNT
LYLQMNSLRAEDTATYFCARLDVGGGGAYIGDIWGQGTLVTVSS

>SEQ ID:39 anti-ROR1 323H7 VLv1 nt

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCA
GTCAGAGTGTTTATAACAACAACGACTTAGCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTA
TTATGCTTCCACTCTGGCATCTGGGGTCCCATCTCGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCA
TCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTGCAGGCGGTTATGATACGGATGGTCTTGATACGTT
TGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

>SEQ ID:40 anti-ROR1 323H7 VLv1 aa

DIQMTQSPSSLSASVGDRVTITCQSSQSVYNNNDLAWYQQKPGKVPKLLIYYASTLASGVPSRFSGSGSGTDFTLTISSL
QPEDVATYYCAGGYDTDGLDTFAFGGGTKVEIK

>SEQ ID:41 anti-ROR1 338H4 VHv3 nt

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACTGCCTCT
GGATTCTCCCTCAGTAGCTATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGAGGGGGCTGGAGTGGATCGGAAT
CATTTATGCTAGTGGTAGCACATACTACGCGAGCTCGGCGAAAGGCAGATTCACCATCTCCAAAGACAATACCAAG
AACACGGTGGATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAATTTATGAC
GGCATGGACCTCTGGGGCCAGGGAACTCTGGTTACCGTCTCTTCA

>SEQ ID:42 anti-ROR1 338H4 VHv3 aa

EVQLVESGGGLVQPGGSLRLSCTASGFSLSSYAMSWVRQAPGRGLEWIGIIYASGSTYYASSAKGRFTISKDNTKNTVDL
QMNSLRAEDTAVYYCARIYDGMDLWGQGTLVTVSS

>SEQ ID:43 anti-ROR1 338H4 VLv4 nt

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAGGCCA
GTCAGAACATTTACAGCTACTTATCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCGCCTGATCTATCTGGC
ATCTACTCTGGCATCTGGGGTCCCATCTCGGTTCAGTGGCAGTGGATCTGGGACAGATTACACTCTCACCATCAGC
AGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCAAAGCAATTATAACGGTAATTATGGTTTCGGCGGAGGGA
CCAAGGTGGAGATCAAA

>SEQ ID:44 anti-ROR1 338H4 VLv4 aa

DIQMTQSPSSLSASVGDRVTINCQASQNIYSYLSWYQQKPGKVPKRLIYLASTLASGVPSRFSGSGSGTDYTLTISSLQPE
DVATYYCQSNYNGNYGFGGGTKVEIK

>SEQ ID:45 anti-ROR1 330F11 VHv1 nt

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTC
TGGATTCTCCCTCAATAACTACTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAA
CCATTAGTAGTGGTGCGTATACATGGTTCGCCACCTGGGCGACAGGCAGATTCACCATCTCCAGAGACAATTCCAA
GAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGATATTCTTCT
ACTACTGATTGGACCTACTTTAACATCTGGGGCCAGGGAACTCTGGTTACCGTCTCTTCA

>SEQ ID:46 anti-ROR1 330F11 VHv1 aa

EVQLVESGGGLVQPGGSLRLSCAASGFSLNNYWMSWVRQAPGKGLEWIGTISSGAYTWFATWATGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCARYSSTTDWTYFNIWGQGTLVTVSS

>SEQ ID:47 anti-ROR1 330F11 VLv1 nt

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCA
GTCAGAGCATTAATAACTACTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATAGGGC
ATCCACTCTGGAATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGC
AGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAAAGCTATAATGGTGTTGGTAGGACTGCTTTCGGCGGAG
GGACCAAGGTGGAGATCAAA

>SEQ ID:48 anti-ROR1 330F11 VLv1 aa

DIQMTQSPSTLSASVGDRVTITCQASQSINNYLAWYQQKPGKAPKLLIYRASTLESGVPSRFSGSGSGTEFTLTISSLQPD
DFATYYCQSYNGVGRTAFGGGTKVEIK

>SEQ ID:49 anti-EGFRvIII mAb 806 VH nt

GATGTGCAGCTTCAGGAGTCGGGACCTAGCCTGGTGAAACCTTCTCAGTCTCTGTCCCTCACCTGCACTGTCACTG
GCTACTCAATCACCAGTGATTTTGCCTGGAACTGGATTCGGCAGTTTCCAGGAAACAAGCTGGAGTGGATGGGCT
ACATAAGTTATAGTGGTAACACTAGGTACAACCCATCTCTCAAAAGTCGAATCTCTATCACTCGCGACACATCCAAG
AACCAATTCTTCCTGCAGTTGAACTCTGTGACTATTGAGGACACAGCCACATATTACTGTGTAACGGCGGGACGCG
GGTTTCCTTATTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCA

>SEQ ID:50 anti-EGFRvIII mAb 806 VH aa

DVQLQESGPSLVKPSQSLSLTCTVTGYSITSDFAWNWIRQFPGNKLEWMGYISYSGNTRYNPSLKSRISITRDTSKNQFF
LQLNSVTIEDTATYYCVTAGRGFPYWGQGTLVTVSA

>SEQ ID:51 anti-EGFRvIII mAb 806 VL nt

GACATCCTGATGACCCAATCTCCATCCTCCATGTCTGTATCTCTGGGAGACACAGTCAGCATCACTTGCCATTCAAG
TCAGGACATTAACAGTAATATAGGGTGGTTGCAGCAGAGACCAGGGAAATCATTTAAGGGCCTGATCTATCATGG
AACCAACTTGGACGATGAAGTTCCATCAAGGTTCAGTGGCAGTGGATCTGGAGCCGATTATTCTCTCACCATCAGC
AGCCTGGAATCTGAAGATTTTGCAGACTATTACTGTGTACAGTATGCTCAGTTTCCGTGGACGTTCGGTGGAGGCA
CCAAGCTGGAAATCAAA

>SEQ ID:52 anti-EGFRvIII mAb 806 VL aa

DILMTQSPSSMSVSLGDTVSITCHSSQDINSNIGWLQQRPGKSFKGLIYHGTNLDDEVPSRFSGSGSGADYSLTISSLESE
DFADYYCVQYAQFPWTFGGGTKLEIK

>SEQ ID:53 anti-CD19 21D4 VH nt

GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAGAAACCAGGAGAGTCTCTGAAGATCTCCTGTAAGGGTTC
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TCATCTATCCTGATGACTCTGATACCAGATACAGTCCATCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCC
ATCAGGACTGCCTACCTGCAGTGGAGTAGCCTGAAGGCCTCGGACACCGCTATGTATTACTGTGCGAGACATGTT
ACTATGATTTGGGGAGTTATTATTGACTTCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

>SEQ ID:54 anti-CD19 21D4 VH aa

EVQLVQSGAEVKKPGESLKISCKGSGYSFSSSWIGWVRQAPGKGLEWMGIIYPDDSDTRYSPSFQGQVTISADKSIRTA
YLQWSSLKASDTAMYYCARHVTMIWGVIIDFWGQGTLVTVSS

>SEQ ID:55 anti-CD19 21D4 VL nt

GCCATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCAA
GTCAGGGCATTAGCAGTGCTTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCTCCTAAGCTCCTGATCTATGATG
CCTCCAGTTTGGAAAGTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAG
CAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCAACAGTTTAATAGTTACCCATTCACTTTCGGCCCTGGGA
CCAAAGTGGATATCAAA

>SEQ ID:56 anti-CD19 21D4 VL aa

AIQLTQSPSSLSASVGDRVTITCRASQGISSALAWYQQKPGKAPKLLIYDASSLESGVPSRFSGSGSGTDFTLTISSLQPED
FATYYCQQFNSYPFTFGPGTKVDIK

>SEQ ID:57 anti-FITC 4-4-20 VH nt

GAGGTGAAGCTGGATGAGACTGGAGGAGGCTTGGTGCAACCTGGGAGGCCCATGAAACTCTCCTGTGTTGCCTCT
GGATTCACTTTTAGTGACTACTGGATGAACTGGGTCCGCCAGTCTCCAGAGAAAGGACTGGAGTGGGTAGCACAA
ATTAGAAACAAACCTTATAATTATGAAACATATTATTCAGATTCTGTGAAAGGCAGATTCACCATCTCAAGAGATG

ATTCCAAAAGTAGTGTCTACCTGCAAATGAACAACTTAAGAGTTGAAGACATGGGTATCTATTACTGTACGGGTTC
TTACTATGGTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCA

>SEQ ID:58 anti-FITC 4-4-20 VH aa

EVKLDETGGGLVQPGRPMKLSCVASGFTFSDYWMNWVRQSPEKGLEWVAQIRNKPYNYETYYSDSVKGRFTISRDDS
KSSVYLQMNNLRVEDMGIYYCTGSYYGMDYWGQGTSVTVSS

>SEQ ID:59 anti-FITC 4-4-20 VL nt

GATGTCGTGATGACCCAAACTCCACTCTCCCTGCCTGTCAGTCTTGGAGATCAAGCCTCCATCTCTTGCAGATCTAG
TCAGAGCCTTGTACACAGTAATGGAAACACCTATTTACGTTGGTACCTGCAGAAGCCAGGCCAGTCTCCAAAGGTC
CTGATCTACAAAGTTTCCAACCGATTTTCTGGGGTCCCAGACAGGTTCAGTGGCAGTGGATCAGGGACAGATTTCA
CACTCAAGATCAGCAGAGTGGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAAGTACACATGTTCCGTGGAC
GTTCGGTGGAGGCACCAAGCTGGAAATCAAA

>SEQ ID:60 anti-FITC 4-4-20 VL aa

DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLRWYLQKPGQSPKVLIYKVSNRFSGVPDRFSGSGSGTDFTLKI
SRVEAEDLGVYFCSQSTHVPWTFGGGTKLEIK

>SEQ ID:61 human IgG1 null (G1m-fa with ADCC/CDC null mutations) nt

GCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTG
GGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTG
CACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTT
GGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCA
AATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTT
CCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCA
CGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGG
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AGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGC
CCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCC
TGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAG
ACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGC
AGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCT
GTCTCCGGGT

>SEQ ID:62 human IgG1 null (G1m-fa with ADCC/CDC null mutations) aa

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY
ICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN
HYTQKSLSLSPG

>SEQ ID:63 human Ig Kappa nt

CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGT
GTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAA
CTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCA
AAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGA
GCTTCAACAGGGGAGAGTGT

>SEQ ID:64 human Ig Kappa aa

RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE
KHKVYACEVTHQGLSSPVTKSFNRGEC

>SEQ ID:65 SI-35E18 (60C3-L1H1-scFv x PL230C6-Fab x 323H7-H4L1-scFv x 284A10-H1L1-scFv) heavy chain nt

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCA
GTCAGAGTGTTTATAGTAACTGGTTCTCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATTC
TGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATC
AGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCGCAGGCGGTTACAATACTGTTATTGATACTTTTGCTTT
CGGCGGAGGGACCAAGGTGGAGATCAAAGGCGGTGGCGGTAGTGGGGGAGGCGGTTCTGGCGGCGGAGGGTC
CGGCGGTGGAGGATCAGAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGA
CTCTCCTGTGCAGCCTCTGGAATCGACTTCAGTAGGAGATACTACATGTGCTGGGTCCGCCAGGCTCCAGGGAAG
GGGCTGGAGTGGATCGCATGCATATATACTGGTAGCCGCGATACTCCTCACTACGCGAGCTCCGCGAAAGGCCGG
TTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCC
GTATATTACTGTGCGAGAGAAGGTAGCCTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGCGGTGGAGG
GTCCGGCGGTGGTGGATCCCAGTCGGTGGAGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGA
CTCTCCTGTACAGCCTCTGGAATCGACCTTAATACCTACGACATGATCTGGGTCCGCCAGGCTCCAGGCAAGGGGC
TAGAGTGGGTTGGAATCATTACTTATAGTGGTAGTAGATACTACGCGAACTGGGCGAAAGGCCGATTCACCATCT
CCAAAGACAATACCAAGAACACGGTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACT
GTGCCAGAGATTATATGAGTGGTTCCCACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCTAGTGCTAGCACCA
AGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGG
TCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCC
CGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA
GACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGA
CAAAACTCACACATGCCCACCGTGCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAA
CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCT
GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT
ACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGT
GCGCGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAAC
CACAGGTGTATACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG
GCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT
CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG

AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGG
GTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCC
TGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCATCAGTCGCTACCACATGACTTGGGTCCGCCAG
GCTCCAGGGAAGGGGCTGGAGTGGATCGGACATATTTATGTTAATAATGATGACACAGACTACGCGAGCTCCGCG
AAAGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAG
GACACGGCCACCTATTTCTGTGCGAGATTGGATGTTGGTGGTGGTGGTGCTTATATTGGGGACATCTGGGGCCAG
GGAACTCTGGTTACCGTCTCTTCAGGCGGTGGCGGTAGTGGGGGAGGCGGTTCTGGCGGCGGAGGGTCCGGCG
GTGGAGGATCAGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC
TTGCCAGTCCAGTCAGAGTGTTTATAACAACAACGACTTAGCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAG
CTCCTGATCTATTATGCTTCCACTCTGGCATCTGGGGTCCCATCTCGGTTCAGTGGCAGTGGATCTGGGACAGATTT
CACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTGCAGGCGGTTATGATACGGATGGT
CTTGATACGTTTGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAAGGCGGTGGAGGGTCCGGCGGTGGTGGATC
CGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCT
CTGGATTCACCATCAGTACCAATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGA
GTCATTACTGGTCGTGATATCACATACTACGCGAGCTGGGCGAAAGGCAGATTCACCATCTCCAGAGACAATTCCA
AGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGCGCGACGGTG
GATCATCTGCTATTACTAGTAACAACATTTGGGGCCAAGGAACTCTGGTCACCGTTTCTTCAGGCGGTGGCGGTAG
TGGGGGAGGCGGTTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCAGACGTCGTGATGACCCAGTCTCCTTCCA
CCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAAGCCAGTGAGAGCATTAGCAGTTGGTTAGCCTG
GTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGAAGCATCCAAACTGGCATCTGGGGTCCCATC
AAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACT
TATTACTGCCAAGGCTATTTTTATTTTATTAGTCGTACTTATGTAAATTCTTTCGGCGGAGGGACCAAGGTGGAGAT
CAAA

>SEQ ID:66 SI-35E18 (460C3-L1H1-scFv x PL230C6-Fab x 323H7-H4L1-scFv x 284A10-H1L1-scFv) heavy chain aa

DIQMTQSPSTLSASVGDRVTITCQSSQSVYSNWFSWYQQKPGKAPKLLIYSASTLASGVPSRFSGSGSGTEFTLTISSLQP
DDFATYYCAGGYNTVIDTFAFGGGTKVEIK (anti-4-1BB 460C3 VLv1)

GGGGSGGGGSGGGGSGGGGS (Gly_4Ser)x4 linker

EVQLLESGGGLVQPGGSLRLSCAASGIDFSRRYYMCWVRQAPGKGLEWIACIYTGSRDTPHYASSAKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAREGSLWGQGTLVTVSS (anti-4-1BB 460C3 VHv1)

GGGGSGGGGS (Gly_4Ser)x2 linker

QSVEESGGGLVQPGGSLRLSCTASGIDLNTYDMIWVRQAPGKGLEWVGIITYSGSRYYANWAKGRFTISKDNTKNTVY
LQMNSLRAEDTAVYYCARDYMSGSHLWGQGTLVTVSS (anti-PD-L1 PL230C6 VHv3)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY
ICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD

ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPG (human IgG1 null)

GGGGSGGGGS (Gly_4Ser)x2 linker

EVQLLESGGGLVQPGGSLRLSCAASGFTISRYHMTWVRQAPGKGLEWIGHIYVNNDDTDYASSAKGRFTISRDNSKNT LYLQMNSLRAEDTATYFCARLDVGGGGAYIGDIWGQGTLVTVSS (anti-ROR1 323H7 VHv4)

GGGGSGGGGSGGGGSGGGGS (Gly_4Ser)x4 linker

DIQMTQSPSSLSASVGDRVTITCQSSQSVYNNNDLAWYQQKPGKVPKLLIYYASTLASGVPSRFSGSGSGTDFTLTISSL QPEDVATYYCAGGYDTDGLDTFAFGGGTKVEIK (anti-ROR1 323H7 VLv1)

GGGGSGGGGS (Gly_4Ser)x2 linker

EVQLVESGGGLVQPGGSLRLSCAASGFTISTNAMSWVRQAPGKGLEWIGVITGRDITYYASWAKGRFTISRDNSKNTLY LQMNSLRAEDTAVYYCARDGGSSAITSNNIWGQGTLVTVSS (anti-CD3 284A10 VHv1)

GGGGSGGGGSGGGGSGGGGS (Gly_4Ser)x4 linker

DVVMTQSPSTLSASVGDRVTINCQASESISSWLAWYQQKPGKAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISSLQPD DFATYYCQGYFYFISRTYVNSFGGGTKVEIK (anti-CD3 284A10 VLv1)

>SEQ ID:67 SI-35E18 (460C3-L1H1-scFv x PL230C6-Fab x 323H7-H4L1-scFv x 284A10-H1L1-scFv) light chain nt

GCCTATGATATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCAAGTGTCAGGCCA GTGAGGACATTTATAGCTTCTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCCATTCTGC ATCCTCTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGC AGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGGTTATGGTAAAAATAATGTTGATAATGCTTTCG GCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGC AGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAA GGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACA GCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATC AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

>SEQ ID:68 SI-35E18 (460C3-L1H1-scFv x PL230C6-Fab x 323H7-H4L1-scFv x 284A10-H1L1-scFv) light chain aa

AYDMTQSPSSVSASVGDRVTIKCQASEDIYSFLAWYQQKPGKAPKLLIHSASSLASGVPSRFSGSGSGTDFTLTISSLQPE DFATYYCQQGYGKNNVDNAFGGGTKVEIK (anti-PD-L1 PL230C6 VLv2)

RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC (human Ig Kappa)

Other sequences:

antigen	antibody	VH/VL	organism	patent	seq ID	Company
FITC	4-4-20	VH	artificial	US 2009/0042291 A1	14	Xencor
FITC	4-4-20	VL	artificial	US 2009/0042291 A1	13	Xencor
CD19	21D4	VH	human	US 2009/0142349 A1	1	Medarex
CD19	21D4	VL	human	US 2009/0142349 A1	9	Medarex
EGFRvIII	mAb 806	VH	mouse	US 2009/0137782 A1	11	Ludwig Institute
EGFRvIII	mAb 806	VL	mouse	US 2009/0137782 A1	12	Ludwig Institute

NOTE: EGFRvIII Systimmune sequence missing C-terminal Arginine.

Sequence index:

SEQ ID	Description
1	anti-CD3 284A10 VHv1 nt
2	anti-CD3 284A10 VHv1 aa
3	anti-CD3 284A10 VLv1 nt
4	anti-CD3 284A10 VLv1 aa
5	anti-CD3 480C8 VHv1 nt
6	anti-CD3 480C8 VHv1 aa
7	anti-CD3 480C8 VLv1 nt
8	anti-CD3 480C8 VLv1 aa
9	anti-PD-L1 PL230C6 VHv3 nt
10	anti-PD-L1 PL230C6 VHv3 aa
11	anti-PD-L1 PL230C6 VLv2 nt
12	anti-PD-L1 PL230C6 VLv2 aa
13	anti-PD-L1 PL221G5 VHv1 nt
14	anti-PD-L1 PL221G5 VHv1 aa
15	anti-PD-L1 PL221G5 VLv1 nt
16	anti-PD-L1 PL221G5 VLv1 aa
17	anti-PD-1 PD224D1 VHv2 nt
18	anti-PD-1 PD224D1 VHv2 aa
19	anti-PD-1 PD224D1 VLv2 nt
20	anti-PD-1 PD224D1 VLv2 aa
21	anti-4-1BB 420H5 VHv3 nt
22	anti-4-1BB 420H5 VHv3 aa
23	anti-4-1BB 420H5 VLv3 nt
24	anti-4-1BB 420H5 VHLv3 aa
25	anti-4-1BB 466F6 VHv2 nt
26	anti-4-1BB 466F6 VHv2 aa
27	anti-4-1BB 466F6 VLv5 nt
28	anti-4-1BB 466F6 VLv5 aa
29	anti-4-1BB 460C3 VHv1 nt
30	anti-4-1BB 460C3 VHv1 aa
31	anti-4-1BB 460C3 VLv1 nt
32	anti-4-1BB 460C3 VLv1 aa
33	anti-ROR1 324C6 VHv2 nt
34	anti-ROR1 324C6 VHv2 aa
35	anti-ROR1 324C6 VLv1 nt
36	anti-ROR1 324C6 VLv1 aa
37	anti-ROR1 323H7 VHv4 nt
38	anti-ROR1 323H7 VHv4 aa
39	anti-ROR1 323H7 VLv1 nt
40	anti-ROR1 323H7 VLv1 aa
41	anti-ROR1 338H4 VHv3 nt
42	anti-ROR1 338H4 VHv3 aa
43	anti-ROR1 338H4 VLv4 nt
44	anti-ROR1 338H4 VLv4 aa
45	anti-ROR1 330F11 VHv1 nt
46	anti-ROR1 330F11 VHv1 aa
47	anti-ROR1 330F11 VLv1 nt
48	anti-ROR1 330F11 VLv1 aa
49	anti-EGFRvIII mAb 806 VH nt
50	anti-EGFRvIII mAb 806 VH aa
51	anti-EGFRvIII mAb 806 VL nt
52	anti-EGFRvIII mAb 806 VL aa
53	anti-CD19 21D4 VH nt
54	anti-CD19 21D4 VH aa
55	anti-CD19 21D4 VL nt
56	anti-CD19 21D4 VL aa
57	anti-FITC 4-4-20 VH nt
58	anti-FITC 4-4-20 VH aa
59	anti-FITC 4-4-20 VL nt
60	anti-FITC 4-4-20 VL aa
61	human IgG1 null (G1m-fa with ADCC/CDC null mutations) nt
62	human IgG1 null (G1m-fa with ADCC/CDC null mutations) aa
63	human Ig Kappa nt
64	human Ig Kappa aa
65	SI-35E18 (60C3-L1H1-scFv x PL230C6-Fab x 323H7-H4L1-scFv x 284A10-H1L1-scFv) heavy chain nt
66	SI-35E18 (60C3-L1H1-scFv x PL230C6-Fab x 323H7-H4L1-scFv x 284A10-H1L1-scFv) heavy chain aa
67	SI-35E18 (60C3-L1H1-scFv x PL230C6-Fab x 323H7-H4L1-scFv x 284A10-H1L1-scFv) light chain nt
68	SI-35E18 (60C3-L1H1-scFv x PL230C6-Fab x 323H7-H4L1-scFv x 284A10-H1L1-scFv) light chain aa

CLAIMS

What is claimed is:

1. A tetra-specific antibody monomer having a N-terminal and a C-terminal, comprising in tandem from the N-terminal to the C-terminal,

a first scFv domain at the N-terminal,

a Fab domain,

a Fc domain,

a second scFv domain, and

a third scFv domain at the C-terminal,

wherein the first scFv domain, the Fab domain, the second scFv domain, and the third scFv domain each has a binding specificity against a different antigen, wherein the first scFv domain, the Fab domain, the second scFv domain, and the third scFv domain each independently has a binding specificity against:

(i) an antigen selected from CD3, PD-L1, 4-1BB, and ROR1; or
(ii) an antigen selected from CD3, PD-L1, 4-1 BB, and CD19; or
(iii) an antigen selected from CD3, PD-L1, 4-1 BB, and EGFRvIII; and

wherein the monomer comprises:

(a) 3 complementarity determining regions (CDRs) of SEQ ID NO: 30, 3 CDRs of SEQ NO: 32, 3 CDRs of SEQ NO: 10, 3 CDRs of SEQ NO: 12, 3 CDRs of SEQ NO: 38, 3 CDRs of SEQ NO: 40, 3 CDRs of SEQ NO: 2, and 3 CDRs of SEQ NO: 4; or

(b) 3 CDRs of SEQ ID NO: 26, 3 CDRs of SEQ NO:28, 3 CDRs of SEQ NO:10, 3 CDRs of SEQ NO:12, 3 CDRs of SEQ NO:38, 3 CDRs of SEQ NO:40, 3 CDRs of SEQ NO:2, and 3 CDRs of SEQ NO:4; or

(c) 3 CDRs of SEQ ID NO:2, 3 CDRs of SEQ NO:4, 3 CDRs of SEQ NO:54, 3 CDRs of SEQ NO:56, 3 CDRs of SEQ NO:14, 3 CDRs of SEQ NO:16, 3 CDRs of SEQ NO:26, and 3 CDRs of SEQ NO:28; or

(d) 3 CDRs of SEQ ID NO: 2, 3 CDRs of SEQ NO: 4, 3 CDRs of SEQ NO: 50, 3 CDRs of SEQ NO: 52, 3 CDRs of SEQ NO: 14, 3 CDRs of SEQ NO: 16, 3 CDRs of SEQ NO: 22, and 3 CDRs of SEQ NO: 24.

2. A tetra-specific antibody monomer having a N-terminal and a C-terminal, comprising in tandem from the N-terminal to the C-terminal,

a first scFv domain at the N-terminal,

a Fab domain,

a Fc domain,

a second scFv domain, and

a third scFv domain at the C-terminal,

wherein the first scFv domain, the Fab domain, the second scFv domain, and the third scFv domain each has a binding specificity against a different antigen, wherein the first scFv domain, the Fab domain, the second scFv domain, and the third scFv domain each independently has a binding specificity against:

(i) an antigen selected from CD3, PD-L1, 4-1BB, and ROR1; or
(ii) an antigen selected from CD3, PD-L1, 4-1 BB, and CD19; or
(iii) an antigen selected from CD3, PD-L1, 4-1 BB, and EGFRvIII; and

wherein the monomer comprises:

a) an amino acid sequence having a percentage homology to SEQ ID NO: 30, an amino acid sequence having a percentage homology to SEQ ID NO: 32, an amino acid sequence having a percentage homology to SEQ ID NO: 10, an amino acid sequence having a percentage homology to SEQ ID NO: 12, an amino acid sequence having a percentage homology to SEQ ID NO: 38, an amino acid sequence having a percentage homology to SEQ ID NO: 40, an amino acid sequence having a percentage homology to SEQ ID NO: 2 and an amino acid sequence having a percentage homology to SEQ ID NO: 4, wherein the percentage homology is not less than 98%; or

b) an amino acid sequence having a percentage homology to SEQ ID NO: 26, an amino acid sequence having a percentage homology to SEQ ID NO: 28, an amino acid sequence having a percentage homology to SEQ ID NO: 10, an amino acid sequence having a percentage homology to SEQ ID NO: 12, an amino acid sequence having a percentage homology to SEQ ID NO: 38, an amino acid sequence having a percentage homology to SEQ ID NO: 40, an amino acid sequence having a percentage homology to SEQ ID NO: 2 and an amino acid sequence having a percentage homology to SEQ ID NO: 4, wherein the percentage homology is not less than 98%; or

c) an amino acid sequence having a percentage homology to SEQ ID NO: 2, an amino acid sequence having a percentage homology to SEQ ID NO: 4, an amino acid sequence having a percentage homology to SEQ ID NO: 54, an amino acid sequence having a percentage homology to SEQ ID NO: 56, an amino acid sequence having a percentage homology to SEQ ID NO: 14, an amino acid sequence having a percentage homology to SEQ ID NO: 16, an amino acid sequence having a percentage homology to SEQ ID NO: 26 and an amino acid sequence having a percentage homology to SEQ ID NO: 28, wherein the percentage homology is not less than 98%; or

d) an amino acid sequence having a percentage homology to SEQ ID NO: 2, an amino acid sequence having a percentage homology to SEQ ID NO: 4, an amino acid sequence having a percentage homology to SEQ ID NO: 50, an amino acid sequence having a percentage homology to SEQ ID NO: 52, an amino acid sequence having a percentage homology to SEQ ID NO: 14, an amino acid sequence having a percentage homology to SEQ ID NO: 16, an amino acid sequence having a percentage homology to SEQ ID NO: 22 and an amino acid sequence having a percentage homology to SEQ ID NO: 24, wherein the percentage homology is not less than 98%.

3. The tetra-specific antibody monomer of Claim 1 or 2, wherein the first scFv domain has a binding specificity against CD3.

4. The tetra-specific antibody monomer of Claim 1 or 2, wherein the Fab domain has a binding specificity against EGFRvIII.

5. The tetra-specific antibody monomer of Claim 1 or 2, wherein the second scFv domain has a binding specificity against PD-L1.

6. The tetra-specific antibody monomer of Claim 1 or 2, wherein the third scFv domain has a binding specificity against 4-1BB.

7. The tetra-specific antibody monomer of Claim 1 or 2, wherein the first scFv domain has a binding specificity against CD3, wherein the Fab domain has a binding specificity against EGFRvIII, and wherein the second scFv domain has a binding specificity against PD-L1, and wherein the third scFv domain has a binding specificity against 4-1BB.

8. The tetra-specific antibody monomer of Claim 1 or 2, wherein the first scFv domain, the second scFv domain, or the third scFv domain comprises a gly-gly-gly-gly-ser $(G4S)_n$ linker, wherein n is 2, 3 or 4.

9. The tetra-specific antibody monomer of Claim 1, wherein the tetra-specific antibody monomer comprises a scFv domain comprising an amino acid sequence having a percentage homology to SEQ ID NO. 02, 04, 10, 12, 14, 16, 22, 24, 26, 28, 30, 32, 38, 40, 50, 52, 54 or 56, wherein the percentage homology is not less than 98%.

10. The tetra-specific antibody monomer of Claim 1, wherein the tetra-specific antibody monomer comprises a Fab domain comprising an amino acid sequence having a percentage homology to SEQ ID NO. 02, 04, 10, 12, 14, 16, 22, 24, 26, 28, 30, 32, 38, 40, 50, 52, 54 or 56, wherein the percentage homology is not less than 98%.

11. A tetra-specific antibody comprising a tetra-specific antibody monomer having a N-terminal and a C-terminal, comprising in tandem from the N-terminal to the C-terminal,

a first scFv domain at the N-terminal,

a Fab domain,

a Fc domain,

a second scFv domain, and

a third scFv domain at the C-terminal,

wherein the first scFv domain, the Fab domain, the second scFv domain, and the third scFv domain each has a binding specificity against a different antigen, wherein the first scFv domain, the Fab domain, the second scFv domain, and the third scFv domain each independently has a binding specificity against:

an antigen selected from CD3, PD-L1, 4-1BB, and ROR1; and

wherein the tetra-specific antibody comprises an amino acid sequence having a percentage homology to SEQ ID NO. 66, and an amino acid sequence having a percentage homology to SEQ ID NO. 68, wherein the percentage homology is not less than 98%.

12. A tetra-specific antibody, comprising a tetra-specific antibody monomer of any one of Claims 1 to 10.

13. An isolated nucleic acid sequence encoding a tetra-specific antibody monomer of Claim 1 or 2.

14. The isolated nucleic acid sequence of Claim 13 encoding a tetra-specific antibody monomer of Claim 1 and comprising a nucleic acid sequence encoding an amino acid sequence having a percentage homology to SEQ ID NO. 02, 04, 10, 12, 14, 16, 22, 24, 26, 28, 30, 32, 38, 40, 50, 52, 54, 56, 66 or 68 wherein the percentage homology is not less than 98%.

15. An expression vector, comprising the isolated nucleic acid sequence of Claim 13 or 14.

16. A host cell comprising the isolated nucleic acid sequence of Claim 13 or 14.

17. A host cell according to claim 16 wherein the host cell comprises an isolated nucleic acid sequence encoding an amino acid sequence having a percentage homology to SEQ ID NO. 66 and an isolated nucleic acid sequence encoding an amino acid sequence having a percentage homology to SEQ ID NO. 68, wherein the percentage homology is not less than 98%.

18. A host cell according to Claim 16 or 17 wherein the host cell is a prokaryotic cell.

19. A host cell according to Claim 16 or 17, wherein the host cell is a eukaryotic cell.

20. A method for producing a tetra-specific antibody according to Claim 11 or 12 or a tetra-specific antibody monomer according to Claim 1 or 2, wherein the method comprises culturing a host cell capable of expressing the antibody or the monomer such that the tetra-specific antibody or monomer is expressed, and purifying said tetra-specific antibody or monomer, wherein the host cell capable of expressing the antibody or monomer is a host cell according to any one of Claims 16 to 19.

21. A pharmaceutical composition, comprising a pharmaceutically acceptable carrier and a tetra-specific antibody according to Claim 11 or 12.

22. Use of the tetra-specific antibody according to Claim 11 or 12 in the manufacture of a medicament for treating cancer.