PROTEINS BINDING BCMA, NKG2D AND CD16

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of and priority to U.S. Provisional Patent Application No. 62/457,780, filed February 10, 2017, the entire contents of which are incorporated by reference herein for all purposes.

SEQUENCE LISTING

[0002] The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on February 8, 2018, is named DFY-003PC_SL.txt and is 91,310 bytes in size.

FIELD OF THE INVENTION

[0003] The invention relates to multi-specific binding proteins that bind to B-cell maturation antigen (BCMA), the NKG2D receptor, and CD16.

BACKGROUND

[0004] Cancer continues to be a significant health problem despite the substantial research efforts and scientific advances reported in the literature for treating this disease. Blood and bone marrow cancers are frequently diagnosed cancer types, including multiple myelomas, leukemia, and lymphomas. Current treatment options for these cancers are not effective for all patients and/or can have substantial adverse side effects. Other types of cancer also remain challenging to treat using existing therapeutic options.

[0005] Cancer immunotherapies are desirable because they are highly specific and can facilitate destruction of cancer cells using the patient's own immune system. Fusion proteins such as bi-specific T-cell engagers are cancer immunotherapies described in the literature that bind to tumor cells and T-cells to facilitate destruction of tumor cells. Antibodies that bind to certain tumor-associated antigens and to certain immune cells have been described in the literature. See, for example WO 2016/134371 and WO 2015/095412.

[0006] Natural killer (NK) cells are a component of the innate immune system and make up approximately 15% of circulating lymphocytes. NK cells infiltrate virtually all tissues and were originally characterized by their ability to kill tumor cells effectively without the need for prior sensitization. Activated NK cells kill target cells by means similar to cytotoxic T

cells – *i.e.*, via cytolytic granules that contain perforin and granzymes as well as via death receptor pathways. Activated NK cells also secrete inflammatory cytokines such as IFN-gamma and chemokines that promote the recruitment of other leukocytes to the target tissue.

[0007] NK cells respond to signals through a variety of activating and inhibitory receptors on their surface. For example, when NK cells encounter healthy self-cells, their activity is inhibited through activation of the killer-cell immunoglobulin-like receptors (KIRs). Alternatively, when NK cells encounter foreign cells or cancer cells, they are activated via their activating receptors (*e.g.*, NKG2D, NCRs, DNAM1). NK cells are also activated by the constant region of some immunoglobulins through CD16 receptors on their surface. The overall sensitivity of NK cells to activation depends on the sum of stimulatory and inhibitory signals.

[0008] BCMA is a transmembrane protein belonging to the TNF-receptor superfamily. It specifically binds to the tumor necrosis factor (ligand) superfamily, member 13b (TNFSF13B/TALL-1/BAFF), leading to NF-κB and MAPK8/JNK activation. Its expression is restricted to the B-cell lineage and has been shown to be important for B cell development and autoimmune response. BCMA also binds to various TRAF family members, and thus may transduce signals for cell survival and proliferation. BCMA is implicated in a variety of cancers, such as multiple myeloma, lymphoma and leukemia. The present invention provides certain advantages to improve treatments for BCMA-expressing cancers.

SUMMARY

[0009] The invention provides multi-specific binding proteins that bind to BCMA on a cancer cell and the NKG2D receptor and CD16 receptor on natural killer cells. Such proteins can engage more than one kind of NK activating receptor, and may block the binding of natural ligands to NKG2D. In certain embodiments, the proteins can agonize NK cells in humans, and in other species such as rodents and cynomolgus monkeys. Various aspects and embodiments of the invention are described in further detail below.

[0010] Accordingly, one aspect of the invention provides a protein that incorporates a first antigen-binding site that binds NKG2D; a second antigen-binding site that binds to BCMA; and an antibody Fc domain, a portion thereof sufficient to bind CD16, or a third antigen-binding site that binds CD16. The antigen-binding sites may each incorporate an antibody heavy chain variable domain and an antibody light chain variable domain (*e.g.*, arranged as in an antibody, or fused together to from an scFv), or one or more of the antigen-

binding sites may be a single domain antibody, such as a V_HH antibody like a camelid antibody or a V_{NAR} antibody like those found in cartilaginous fish.

[0011] The first antigen-binding site that binds to NKG2D, in one embodiment, can incorporate a heavy chain variable domain related to SEQ ID NO:1, such as by having an amino acid sequence at least 90%, at least 95%, or 100% identical to SEQ ID NO:1, and/or incorporating amino acid sequences identical to the CDR1 (SEQ ID NO:64), CDR2 (SEQ ID NO:65), and CDR3 (SEQ ID NO:66) sequences of SEQ ID NO:1. Alternatively, the first antigen-binding site can incorporate a heavy chain variable domain related to SEQ ID NO:41 and a light chain variable domain related to SEQ ID NO:42. For example, the heavy chain variable domain of the first antigen-binding site can be at least 90%, at least 95%, or 100% identical to SEQ ID NO:41, and/or incorporate amino acid sequences identical to the CDR1 (SEQ ID NO:67), CDR2 (SEQ ID NO:68), and CDR3 (SEQ ID NO:69) sequences of SEQ ID NO:41. Similarly, the light chain variable domain of the second antigen-binding site can be at least 90%, at least 95%, or 100% identical to SEQ ID NO:42, and/or incorporate amino acid sequences identical to the CDR1 (SEQ ID NO:70), CDR2 (SEQ ID NO:71), and CDR3 (SEQ ID NO:72) sequences of SEQ ID NO:42. In other embodiments, the first antigen-binding site can incorporate a heavy chain variable domain related to SEQ ID NO:43 and a light chain variable domain related to SEQ ID NO:44. For example, the heavy chain variable domain of the first antigen-binding site can be at least 90%, at least 95%, or 100% identical to SEQ ID NO:43, and/or incorporate amino acid sequences identical to the CDR1 (SEQ ID NO:73), CDR2 (SEQ ID NO:74), and CDR3 (SEQ ID NO:75) sequences of SEQ ID NO:43. Similarly, the light chain variable domain of the second antigen-binding site can be at least 90%, at least 95%, or 100% identical to SEQ ID NO:44, and/or incorporate amino acid sequences identical to the CDR1 (SEQ ID NO:76), CDR2 (SEQ ID NO:77), and CDR3 (SEQ ID NO:78) sequences of SEQ ID NO:44.

[0012] Alternatively, the first antigen-binding site can incorporate a heavy chain variable domain related to SEQ ID NO:45 and a light chain variable domain related to SEQ ID NO:46, such as by having amino acid sequences at least 90%, at least 95%, or 100% identical to SEQ ID NO:45 and SEQ ID NO:46 respectively. In another embodiment, the first antigen-binding site can incorporate a heavy chain variable domain related to SEQ ID NO:47 and a light chain variable domain related to SEQ ID NO:48, such as by having amino acid sequences at least 90%, at least 95%, or 100% identical to SEQ ID NO:47 and SEQ ID NO:48 respectively.

[0013] The second antigen-binding site can optionally incorporate a heavy chain variable domain related to SEQ ID NO:49 and a light chain variable domain related to SEQ ID NO:53 or SEQ ID NO:54. For example, the heavy chain variable domain of the second antigen-binding site can be at least 90%, at least 95%, or 100% identical to SEQ ID NO:49, and/or incorporate amino acid sequences identical to the CDR1 (SEQ ID NO:50), CDR2 (SEQ ID NO:51), and CDR3 (SEQ ID NO:52) sequences of SEQ ID NO:49. Similarly, the light chain variable domain of the second antigen-binding site can be at least 90%, at least 95%, or 100% identical to SEQ ID NO:53 and/or incorporate amino acid sequences identical to the CDR1 (SEQ ID NO:55), CDR2 (SEQ ID NO:56), and CDR3 (SEQ ID NO:57) sequences of SEQ ID NO:53. Alternatively, the light chain variable domain of the second antigen-binding site can be at least 90%, at least 95%, or 100% identical to SEQ ID NO:54 and/or incorporate amino acid sequences identical to the CDR1 (SEQ ID NO:55), CDR2 (SEQ ID NO:56), and CDR3 (SEQ ID NO:58) sequences of SEQ ID NO:54.

[0014] Alternatively, the second antigen-binding site can incorporate a heavy chain variable domain related to SEQ ID NO:59 and a light chain variable domain related to SEQ ID NO:60. For example, the heavy chain variable domain of the second antigen-binding site can be at least 90%, at least 95%, or 100% identical to SEQ ID NO:59, and/or incorporate amino acid sequences identical to the CDR1 (SEQ ID NO:79), CDR2 (SEQ ID NO:80), and CDR3 (SEQ ID NO:81) sequences of SEQ ID NO:59. Similarly, the light chain variable domain of the second antigen-binding site can be at least 90%, at least 95%, or 100% identical to SEQ ID NO:60, and/or incorporate amino acid sequences identical to the CDR1 (SEQ ID NO:82), CDR2 (SEQ ID NO:83), and CDR3 (SEQ ID NO:84) sequences of SEQ ID NO:60.

[0015] In another embodiment, the second antigen-binding site can incorporate a heavy chain variable domain related to SEQ ID NO:61 and a light chain variable domain related to SEQ ID NO:62. For example, the heavy chain variable domain of the second antigen-binding site can be at least 90%, at least 95%, or 100% identical to SEQ ID NO:61, and/or incorporate amino acid sequences identical to the CDR1 (SEQ ID NO:85), CDR2 (SEQ ID NO:86), and CDR3 (SEQ ID NO:87) sequences of SEQ ID NO:61. Similarly, the light chain variable domain of the second antigen-binding site can be at least 90%, at least 95%, or 100% identical to SEQ ID NO:62, and/or incorporate amino acid sequences identical to the CDR1 (SEQ ID NO:88), CDR2 (SEQ ID NO:89), and CDR3 (SEQ ID NO:90) sequences of SEQ ID NO:62.

[0016] In some embodiments, the second antigen-binding site incorporates a light chain variable domain having an amino acid sequence identical to the amino acid sequence of the light chain variable domain present in the first antigen-binding site.

[0017] In some embodiments, the protein incorporates a portion of an antibody Fc domain sufficient to bind CD16, wherein the antibody Fc domain comprises hinge and CH2 domains, and/or amino acid sequences at least 90% identical to amino acid sequence 234-332 of a human IgG antibody.

[0018] Formulations containing one of these proteins; cells containing one or more nucleic acids expressing these proteins, and methods of enhancing tumor cell death using these proteins are also provided.

[0019] Another aspect of the invention provides a method of treating cancer in a patient. The method comprises administering to a patient in need thereof a therapeutically effective amount of the multi-specific binding protein described herein. Exemplary cancers for treatment using the multi-specific binding proteins include, for example, multiple myeloma, acute myelomonocytic leukemia, T cell lymphoma, acute monocytic leukemia, and follicular lymphoma.

BRIEF DESCRIPTION OF THE DRAWINGS

[0020] **FIG. 1** is a representation of a heterodimeric, multi-specific antibody. NKG2D-binding domain (right arm): tumor antigen-binding domain (left arm). The light chains that are common are represented with the same shade or pattern in the drawing.

[0021] **FIG. 2** is a representation of a heterodimeric, multi-specific antibody. NKG2D-binding domain - scFv (right arm); tumor antigen-binding domain (left arm).

[0022] **FIG. 3** is a representation of a TriNKET in the Triomab form, which is a trifunctional, bispecific antibody that maintains an IgG-like shape. This chimera consists of two half antibodies, each with one light and one heavy chain, that originate from two parental antibodies. Triomab form may be an heterodimeric construct containing ½ of rat antibody and ½ of mouse antibody.

[0023] **FIG. 4** is a representation of a TriNKET in the KiH Common Light Chain (LC) form, which involves the knobs-into-holes (KIHs) technology. KiH is a heterodimer containing 2 Fabs binding to target 1 and 2, and an Fc stabilized by heterodimerization mutations. TriNKET in the KiH format may be an heterodimeric construct with 2 fabs binding to target 1 and target 2, containing two different heavy chains and a common light chain that pairs with both heavy chains.

[0024] **FIG. 5** is a representation of a TriNKET in the dual-variable domain immunoglobulin (DVD-Ig™) form, which combines the target binding domains of two monoclonal antibodies via flexible naturally occurring linkers, and yields a tetravalent IgG -like molecule. DVD-Ig™ is an homodimeric construct where variable domain targeting antigen 2 is fused to the N terminus of variable domain of Fab targeting antigen 1 Construct contains normal Fc.

[0025] **FIG. 6** is a representation of a TriNKET in the Orthogonal Fab interface (Ortho-Fab) form, which is an heterodimeric construct that contains 2 Fabs binding to target1 and target 2 fused to Fc. LC-HC pairing is ensured by orthogonal interface. Heterodimerization is ensured by mutations in the Fc.

[0026] **FIG. 7** is a representation of a TrinKET in the 2-in-1 Ig format.

[0027] **FIG. 8** is a representation of a TriNKET in the ES form, which is an heterodimeric construct containing two different Fabs binding to target 1 and target 2 fused to the Fc. Heterodimerization is ensured by electrostatic steering mutations in the Fc.

[0028] **FIG. 9** is a representation of a TriNKET in the Fab Arm Exchange form: antibodies that exchange Fab arms by swapping a heavy chain and attached light chain (half-molecule) with a heavy-light chain pair from another molecule, resulting in bispecific antibodies. Fab Arm Exchange form (cFae) is a heterodimer containing 2 Fabs binding to target 1 and 2, and an Fc stabilized by heterodimerization mutations.

[0029] **FIG. 10** is a representation of a TriNKET in the SEED Body form, which is an heterodimer containing 2 Fabs binding to target 1 and 2, and an Fc stabilized by heterodimerization mutations.

[0030] **FIG. 11** is a representation of a TriNKET in the LuZ-Y form, in which leucine zipper is used to induce heterodimerization of two different HCs. LuZ-Y form is a heterodimer containing two different scFabs binding to target 1 and 2, fused to Fc. Heterodimerization is ensured through leucine zipper motifs fused to C-terminus of Fc.

[0031] **FIG. 12** is a representation of a TriNKET in the Cov-X-Body form.

[0032] **FIGs. 13A-13B** are representations of TriNKETs in the κλ-Body forms, which are an heterodimeric constructs with two different Fabs fused to Fc stabilized by heterodimerization mutations: Fab1 targeting antigen 1 contains kappa LC, while second Fab targeting antigen 2 contains lambda LC. FIG. 13A is an exemplary representation of one form of a κλ-Body; FIG. 13B is an exemplary representation of another κλ-Body.

[0033] **FIG. 14** are line graphs demonstrating the binding affinity of NKG2D-binding domains (listed as clones) to human recombinant NKG2D in an ELISA assay.

[0034] **FIG. 15** are line graphs demonstrating the binding affinity of NKG2D-binding domains (listed as clones) to cynomolgus recombinant NKG2D in an ELISA assay.

[0035] **FIG. 16** are line graphs demonstrating the binding affinity of NKG2D-binding domains (listed as clones) to mouse recombinant NKG2D in an ELISA assay.

[0036] **FIG. 17** are bar graphs demonstrating the binding of NKG2D-binding domains (listed as clones) to EL4 cells expressing human NKG2D by flow cytometry showing mean fluorescence intensity (MFI) fold over background.

[0037] **FIG. 18** are bar graphs demonstrating the binding of NKG2D-binding domains (listed as clones) to EL4 cells expressing mouse NKG2D by flow cytometry showing mean fluorescence intensity (MFI) fold over background.

[0038] **FIG. 19** are line graphs demonstrating specific binding affinity of NKG2D-binding domains (listed as clones) to recombinant human NKG2D-Fc by competing with natural ligand ULBP-6.

[0039] **FIG. 20** are line graphs demonstrating specific binding affinity of NKG2D-binding domains (listed as clones) to recombinant human NKG2D-Fc by competing with natural ligand MICA.

[0040] **FIG. 21** are line graphs demonstrating specific binding affinity of NKG2D-binding domains (listed as clones) to recombinant mouse NKG2D-Fc by competing with natural ligand Rae-1 delta.

[0041] **FIG. 22** are bar graphs showing activation of human NKG2D by NKG2D-binding domains (listed as clones) by quantifying the percentage of TNF-alpha positive cells, which express human NKG2D-CD3 zeta fusion proteins.

[0042] **FIG. 23** are bar graphs showing activation of mouse NKG2D by NKG2D-binding domains (listed as clones) by quantifying the percentage of TNF-alpha positive cells, which express mouse NKG2D-CD3 zeta fusion proteins.

[0043] **FIG. 24** are bar graphs showing activation of human NK cells by NKG2D-binding domains (listed as clones).

[0044] **FIG. 25** are bar graphs showing activation of human NK cells by NKG2D-binding domains (listed as clones).

[0045] **FIG. 26** are bar graphs showing activation of mouse NK cells by NKG2D-binding domains (listed as clones).

[0046] **FIG. 27** are bar graphs showing activation of mouse NK cells by NKG2D-binding domains (listed as clones).

[0047] **FIG. 28** are bar graphs showing the cytotoxic effect of NKG2D-binding domains (listed as clones) on tumor cells.

[0048] **FIG. 29** are bar graphs showing the melting temperature of NKG2D-binding domains (listed as clones) measured by differential scanning fluorimetry.

[0049] **FIG. 30** are line graphs showing binding profile of BCMA-targeting TriNKETs to NKG2D expressed on EL4 cells.

[0050] **FIG. 31** are line graphs showing binding profile of BCMA-targeting TriNKETs to BCMA expressed on MM.1S human myeloma cells.

[0051] **FIG. 32** are bar graphs showing human NK activation in culture with BCMA-positive MM. 1S human myeloma cells.

[0052] **FIG. 33** are line graphs showing that BCMA targeting TriNKETs with different NKG2D-binding domains enhance human NK cell lysis of KMS12-PE myeloma cells.

[0053] **FIGs. 34A-34C** are bar graphs of synergistic activation of NK cells using CD16 and NKG2D. FIG. 34A demonstrates levels of CD107a; FIG. 34B demonstrates levels of IFNγ; FIG. 34C demonstrates levels of CD107a and IFNγ. Graphs indicate the mean (n = 2) ±SD. Data are representative of five independent experiments using five different healthy donors.

[0054] **FIG. 35** is an Oasc-Fab heterodimeric construct that includes Fab binding to target 1 and scFab binding to target 2 fused to Fc. Heterodimerization is ensured by mutations in the Fc.

[0055] **FIG. 36** is a DuetMab, which is an heterodimeric construct containing two different Fabs binding to antigens 1 and 2, and Fc stabilized by heterodimerization mutations. Fab 1 and 2 contain differential S-S bridges that ensure correct light chain (LC) and heavy chain (HC) pairing.

[0056] **FIG. 37** is a CrossmAb, which is an heterodimeric construct with two different Fabs binding to targets 1 and 2 fused to Fc stabilized by heterodimerization. CL and CH1 domains and VH and VL domains are switched, *e.g.*, CH1 is fused in-line with VL, while CL is fused in-line with VH.

[0057] **FIG. 38** is a Fit-Ig, which is an homodimeric constructs where Fab binding to antigen 2 is fused to the N terminus of HC of Fab that binds to antigen 1. The construct contains wild-type Fc.

[0058] **FIG. 39** is a graph showing that TriNKETs enhance human NK cell lysis of KMS12-PE myeloma cells.

DETAILED DESCRIPTION

[0059] The invention provides multi-specific binding proteins that bind BCMA on a cancer cell and the NKG2D receptor and CD16 receptor on natural killer cells to activate the natural killer cell, pharmaceutical compositions comprising such multi-specific binding proteins, and therapeutic methods using such multi-specific proteins and pharmaceutical compositions, including for the treatment of cancer. Various aspects of the invention are set forth below in sections; however, aspects of the invention described in one particular section are not to be limited to any particular section.

[0060] To facilitate an understanding of the present invention, a number of terms and phrases are defined below.

[0061] The terms “a” and “an” as used herein mean “one or more” and include the plural unless the context is inappropriate.

[0062] As used herein, the term "antigen-binding site" refers to the part of the immunoglobulin molecule that participates in antigen-binding. In human antibodies, the antigen-binding site is formed by amino acid residues of the N-terminal variable ("V") regions of the heavy ("H") and light ("L") chains. Three highly divergent stretches within the V regions of the heavy and light chains are referred to as "hypervariable regions" which are interposed between more conserved flanking stretches known as "framework regions," or "FRs". Thus the term "FR" refers to amino acid sequences which are naturally found between and adjacent to hypervariable regions in immunoglobulins. In a human antibody molecule, the three hypervariable regions of a light chain and the three hypervariable regions of a heavy chain are disposed relative to each other in three dimensional space to form an antigen-binding surface. The antigen-binding surface is complementary to the three-dimensional surface of a bound antigen, and the three hypervariable regions of each of the heavy and light chains are referred to as "complementarity-determining regions," or "CDRs." In certain animals, such as camels and cartilaginous fish, the antigen-binding site is formed by a single antibody chain providing a “single domain antibody.” Antigen-binding sites can exist in an intact antibody, in an antigen-binding fragment of an antibody that retains the antigen-binding surface, or in a recombinant polypeptide such as an scFv, using a peptide linker to connect the heavy chain variable domain to the light chain variable domain in a single polypeptide.

[0063] The term “tumor associated antigen” as used herein means any antigen including but not limited to a protein, glycoprotein, ganglioside, carbohydrate, lipid that is associated

with cancer. Such antigen can be expressed on malignant cells or in the tumor microenvironment such as on tumor-associated blood vessels, extracellular matrix, mesenchymal stroma, or immune infiltrates.

[0064] As used herein, the terms "subject" and "patient" refer to an organism to be treated by the methods and compositions described herein. Such organisms preferably include, but are not limited to, mammals (*e.g.*, murines, simians, equines, bovines, porcines, canines, felines, and the like), and more preferably include humans.

[0065] As used herein, the term "effective amount" refers to the amount of a compound (*e.g.*, a compound of the present invention) sufficient to effect beneficial or desired results. An effective amount can be administered in one or more administrations, applications or dosages and is not intended to be limited to a particular formulation or administration route. As used herein, the term "treating" includes any effect, *e.g.*, lessening, reducing, modulating, ameliorating or eliminating, that results in the improvement of the condition, disease, disorder, and the like, or ameliorating a symptom thereof.

[0066] As used herein, the term "pharmaceutical composition" refers to the combination of an active agent with a carrier, inert or active, making the composition especially suitable for diagnostic or therapeutic use *in vivo* or *ex vivo*.

[0067] As used herein, the term "pharmaceutically acceptable carrier" refers to any of the standard pharmaceutical carriers, such as a phosphate buffered saline solution, water, emulsions (*e.g.*, such as an oil/water or water/oil emulsions), and various types of wetting agents. The compositions also can include stabilizers and preservatives. For examples of carriers, stabilizers and adjuvants, s*ee e.g.*, Martin, Remington's Pharmaceutical Sciences, 15th Ed., Mack Publ. Co., Easton, PA [1975].

[0068] As used herein, the term "pharmaceutically acceptable salt" refers to any pharmaceutically acceptable salt (*e.g.*, acid or base) of a compound of the present invention which, upon administration to a subject, is capable of providing a compound of this invention or an active metabolite or residue thereof. As is known to those of skill in the art, "salts" of the compounds of the present invention may be derived from inorganic or organic acids and bases. Exemplary acids include, but are not limited to, hydrochloric, hydrobromic, sulfuric, nitric, perchloric, fumaric, maleic, phosphoric, glycolic, lactic, salicylic, succinic, toluene-p-sulfonic, tartaric, acetic, citric, methanesulfonic, ethanesulfonic, formic, benzoic, malonic, naphthalene-2-sulfonic, benzenesulfonic acid, and the like. Other acids, such as oxalic, while not in themselves pharmaceutically acceptable, may be employed in the preparation of salts

useful as intermediates in obtaining the compounds of the invention and their pharmaceutically acceptable acid addition salts.

[0069] Exemplary bases include, but are not limited to, alkali metal (*e.g.*, sodium) hydroxides, alkaline earth metal (*e.g.*, magnesium) hydroxides, ammonia, and compounds of formula NW_4^+, wherein W is C_{1-4} alkyl, and the like.

[0070] Exemplary salts include, but are not limited to: acetate, adipate, alginate, aspartate, benzoate, benzenesulfonate, bisulfate, butyrate, citrate, camphorate, camphorsulfonate, cyclopentanepropionate, digluconate, dodecylsulfate, ethanesulfonate, fumarate, flucoheptanoate, glycerophosphate, hemisulfate, heptanoate, hexanoate, hydrochloride, hydrobromide, hydroiodide, 2-hydroxyethanesulfonate, lactate, maleate, methanesulfonate, 2-naphthalenesulfonate, nicotinate, oxalate, palmoate, pectinate, persulfate, phenylpropionate, picrate, pivalate, propionate, succinate, tartrate, thiocyanate, tosylate, undecanoate, and the like. Other examples of salts include anions of the compounds of the present invention compounded with a suitable cation such as Na^+, NH_4^+, and NW_4^+ (wherein W is a C_{1-4} alkyl group), and the like.

[0071] For therapeutic use, salts of the compounds of the present invention are contemplated as being pharmaceutically acceptable. However, salts of acids and bases that are non-pharmaceutically acceptable may also find use, for example, in the preparation or purification of a pharmaceutically acceptable compound.

[0072] Throughout the description, where compositions are described as having, including, or comprising specific components, or where processes and methods are described as having, including, or comprising specific steps, it is contemplated that, additionally, there are compositions of the present invention that consist essentially of, or consist of, the recited components, and that there are processes and methods according to the present invention that consist essentially of, or consist of, the recited processing steps.

[0073] As a general matter, compositions specifying a percentage are by weight unless otherwise specified. Further, if a variable is not accompanied by a definition, then the previous definition of the variable controls.

I. PROTEINS

[0074] The invention provides multi-specific binding proteins that bind BCMA on a cancer cell and the NKG2D receptor and CD16 receptor on natural killer cells to activate the natural killer cell. The multi-specific binding proteins are useful in the pharmaceutical compositions and therapeutic methods described herein. Binding of the multi-specific binding

protein to the NKG2D receptor and CD16 receptor on natural killer cell enhances the activity of the natural killer cell toward destruction of a cancer cell. Binding of the multi-specific binding protein to BCMA on a cancer cell brings the cancer cell into proximity to the natural killer cell, which facilitates direct and indirect destruction of the cancer cell by the natural killer cell. Further description of exemplary multi-specific binding proteins is provided below.

[0075] The first component of the multi-specific binding proteins binds to NKG2D receptor-expressing cells, which can include but are not limited to NK cells, γδ T cells and $CD8^+$ αβ T cells. Upon NKG2D-binding, the multi-specific binding proteins may block natural ligands, such as ULBP6 and MICA, from binding to NKG2D.

[0076] The second component of the multi-specific binding proteins binds to BCMA-expressing cells, which can include but are not limited to multiple myeloma, acute myelomonocytic leukemia, T cell lymphoma, acute monocytic leukemia, and follicular lymphoma.

[0077] The third component for the multi-specific binding proteins binds to cells expressing CD16, an Fc receptor on the surface of leukocytes including natural killer cells, macrophages, neutrophils, eosinophils, mast cells, and follicular dendritic cells.

[0078] The multi-specific binding proteins can take several formats as shown in but not limited to the examples below. One format is a heterodimeric, multi-specific antibody that includes a first immunoglobulin heavy chain, a second immunoglobulin heavy chain and an immunoglobulin light chain. The first immunoglobulin heavy chain includes a first Fc (hinge-CH2-CH3) domain, a first variable heavy chain domain and an optional first CH1 heavy chain domain. The immunoglobulin light chain includes a variable light chain domain and a constant light chain domain; together with the first immunoglobulin heavy chain, the immunoglobulin light chain forms an antigen-binding site that binds NKG2D. The second immunoglobulin heavy chain comprises a second Fc (hinge-CH2-CH3) domain, a second variable heavy chain domain and a second CH1 heavy chain domain that may pair with an immunoglobulin light chain identical to the one that pairs with the first immunoglobulin heavy chain, except that when immunoglobulin light chain is paired with the second immunoglobulin heavy chain, the resulting antigen-binding site binds to BCMA. The first Fc domain and second Fc domain together are able to bind to CD16 (FIG.1).

[0079] Another exemplary format involves a heterodimeric, multi-specific antibody that includes a first immunoglobulin heavy chain, an immunoglobulin light chain and a second immunoglobulin heavy chain. The first immunoglobulin heavy chain includes a first Fc

(hinge-CH2-CH3) domain fused via either a linker or an antibody hinge to a single chain Fv (scFv) that binds NKG2D. A variety of linkers could be used for linking the scFv to the first Fc domain or within the scFv itself. In addition, the scFv can incorporate mutations that enable the formation of a disulfide bond to stabilize the overall scFv structure. The scFv can also incorporate mutations to modify the isoelectric point of the overall first immunoglobulin heavy chain and/or to enable more facile downstream purification. The second immunoglobulin heavy chain includes a second Fc (hinge-CH2-CH3) domain and a second variable heavy chain domain and a second optional CH1 heavy chain domain. The immunoglobulin light chain includes a variable light chain domain and a constant light chain domain. The second immunoglobulin heavy chain pairs with the immunoglobulin light chain and binds to BCMA. The first Fc domain and the second Fc domain together are able to bind to CD16 (FIG. 2).

[0080] One or more additional binding motifs may be fused to the C-terminus of the constant region CH3 domain, optionally via a linker sequence. In certain embodiments, the antigen-binding site could be a single-chain or disulfide-stabilized variable region (scFv) or could form a tetravalent or trivalent molecule.

[0081] In some embodiments, the multi-specific binding protein is in the Triomab form, which is a trifunctional, bispecific antibody that maintains an IgG-like shape. This chimera consists of two half antibodies, each with one light and one heavy chain, that originate from two parental antibodies.

[0082] In some embodiments, the multi-specific binding protein is the KiH Common Light Chain (LC) form, which involves the knobs-into-holes (KIHs) technology. The KIH involves engineering C_H3 domains to create either a "knob" or a "hole" in each heavy chain to promote heterodimerization. The concept behind the "Knobs-into-Holes (KiH)" Fc technology was to introduce a "knob" in one CH3 domain (CH3A) by substitution of a small residue with a bulky one (*i.e.*, $T366W_{CH3A}$ in EU numbering). To accommodate the "knob," a complementary "hole" surface was created on the other CH3 domain (CH3B) by replacing the closest neighboring residues to the knob with smaller ones (i.e., $T366S/L368A/Y407V_{CH3B}$). The "hole" mutation was optimized by structured-guided phage library screening (Atwell S, Ridgway JB, Wells JA, Carter P. Stable heterodimers from remodeling the domain interface of a homodimer using a phage display library. *J. Mol. Biol.* (1997) 270(1):26–35). X-ray crystal structures of KiH Fc variants (Elliott JM, Ultsch M, Lee J, Tong R, Takeda K, Spiess C, *et al.*, Antiparallel conformation of knob and hole aglycosylated half-antibody homodimers is mediated by a CH2-CH3 hydrophobic

interaction. *J. Mol. Biol.* (2014) 426(9):1947–57; Mimoto F, Kadono S, Katada H, Igawa T, Kamikawa T, Hattori K. Crystal structure of a novel asymmetrically engineered Fc variant with improved affinity for FcgammaRs. Mol Immunol (2014) 58(1):132–8) demonstrated that heterodimerization is thermodynamically favored by hydrophobic interactions driven by steric complementarity at the inter-CH3 domain core interface, whereas the knob–knob and the hole–hole interfaces do not favor homodimerization owing to steric hindrance and disruption of the favorable interactions, respectively.

[0083] In some embodiments, the multi-specific binding protein is in the dual-variable domain immunoglobulin (DVD-Ig™) form, which combines the target binding domains of two monoclonal antibodies via flexible naturally occurring linkers, and yields a tetravalent IgG-like molecule.

[0084] In some embodiments, the multi-specific binding protein is in the Orthogonal Fab interface (Ortho-Fab) form. In ortho-Fab IgG approach (Lewis SM, Wu X, Pustilnik A, Sereno A, Huang F, Rick HL, *et al.* Generation of bispecific IgG antibodies by structure-based design of an orthogonal Fab interface. *Nat. Biotechnol.* (2014) 32(2):191–8), structure-based regional design introduces complementary mutations at the LC and $HC_{VH\text{-}CH1}$ interface in only one Fab, without any changes being made to the other Fab.

[0085] In some embodiments, the multi-specific binding protein is in the 2-in-1 Ig format. In some embodiments, the multi-specific binding protein is in the ES form, which is an heterodimeric construct containing two different Fabs binding to targets 1 and target 2 fused to the Fc. Heterodimerization is ensured by electrostatic steering mutations in the Fc. In some embodiments, the multi-specific binding protein is in the κλ-Body form, which is an heterodimeric constructs with two different Fabs fused to Fc stabilized by heterodimerization mutations: Fab1 targeting antigen 1 contains kappa LC, while second Fab targeting antigen 2 contains lambda LC. FIG. 13A is an exemplary representation of one form of a κλ-Body; FIG. 13B is an exemplary representation of another κλ-Body.

[0086] In some embodiments, the multi-specific binding protein is in Fab Arm Exchange form (antibodies that exchange Fab arms by swapping a heavy chain and attached light chain (half-molecule) with a heavy-light chain pair from another molecule, which results in bispecific antibodies). In some embodiments, the multi-specific binding protein is in the SEED Body form. The strand-exchange engineered domain (SEED) platform was designed to generate asymmetric and bispecific antibody-like molecules, a capability that expands therapeutic applications of natural antibodies. This protein engineered platform is based on exchanging structurally related sequences of immunoglobulin within the conserved CH3

domains. The SEED design allows efficient generation of AG/GA heterodimers, while disfavoring homodimerization of AG and GA SEED CH3 domains. (Muda M. et al., *Protein Eng. Des. Sel.* (2011, 24(5):447-54)). In some embodiments, the multi-specific binding protein is in the LuZ-Y form, in which leucine zipper is used to induce heterodimerization of two different HCs. (Wranik, BJ. *et al.*, *J. Biol. Chem.* (2012), 287:43331-9).

[0087] In some embodiments, the multi-specific binding protein is in the Cov-X-Body form. In bispecific CovX-Bodies, two different peptides are joined together using a branched azetidinone linker and fused to the scaffold antibody under mild conditions in a site-specific manner. Whereas the pharmacophores are responsible for functional activities, the antibody scaffold imparts long half-life and Ig-like distribution. The pharmacophores can be chemically optimized or replaced with other pharmacophores to generate optimized or unique bispecific antibodies. (Doppalapudi VR *et al.*, *PNAS* (2010), 107(52);22611-22616).

[0088] In some embodiments, the multi-specific binding protein is in an Oasc-Fab heterodimeric form that includes Fab binding to target 1, and scFab binding to target 2 fused to Fc. Heterodimerization is ensured by mutations in the Fc.

[0089] In some embodiments, the multi-specific binding protein is in a DuetMab form, which is an heterodimeric construct containing two different Fabs binding to antigens 1 and 2, and Fc stabilized by heterodimerization mutations. Fab 1 and 2 contain differential S-S bridges that ensure correct LC and HC pairing.

[0090] In some embodiments, the multi-specific binding protein is in a CrossmAb form, which is an heterodimeric construct with two different Fabs binding to targets 1 and 2, fused to Fc stabilized by heterodimerization. CL and CH1 domains and VH and VL domains are switched, *e.g.*, CH1 is fused in-line with VL, while CL is fused in-line with VH.

[0091] In some embodiments, the multi-specific binding protein is in a Fit-Ig form, which is an homodimeric constructs where Fab binding to antigen 2 is fused to the N terminus of HC of Fab that binds to antigen 1. The construct contains wild-type Fc.

[0092] Table 1 lists peptide sequences of heavy chain variable domains and light chain variable domains that, in combination, can bind to NKG2D.

Table 1		
Clones	Heavy chain variable region amino acid sequence	Light chain variable region amino acid sequence
ADI-27705	QVQLQQWGAGLLKPSETLSLTCAVY GGSFSGYYWSWIRQPPGKGLEWIGEI DHSGSTNYNPSLKSRVTISVDTSKNQ FSLKLSSVTAADTAVYYCARARGPW SFDPWGQGTLVTVSS (SEQ ID NO:1) CDR1 (SEQ ID NO:64) – GSFSGYYWS CDR2 (SEQ ID NO:65) – EIDHSGSTNYNPSLKS CDR3 (SEQ ID NO:66) – ARARGPWSFDP	DIQMTQSPSTLSASVGDRVTITCR ASQSISSWLAWYQQKPGKAPKLL IYKASSLESGVPSRFSGSGSGTEFT LTISSLQPDDFATYYCQQYNSYPI TFGGGTKVEIK (SEQ ID NO:2)
ADI-27724	QVQLQQWGAGLLKPSETLSLTCAVY GGSFSGYYWSWIRQPPGKGLEWIGEI DHSGSTNYNPSLKSRVTISVDTSKNQ FSLKLSSVTAADTAVYYCARARGPW SFDPWGQGTLVTVSS (SEQ ID NO:3)	EIVLTQSPGTLSLSPGERATLSCRA SQSVSSSYLAWYQQKPGQAPRLL IYGASSRATGIPDRFSGSGSGTDFT LTISRLEPEDFAVYYCQQYGSSPIT FGGGTKVEIK (SEQ ID NO:4)
ADI-27740 (A40)	QVQLQQWGAGLLKPSETLSLTCAVY GGSFSGYYWSWIRQPPGKGLEWIGEI DHSGSTNYNPSLKSRVTISVDTSKNQ FSLKLSSVTAADTAVYYCARARGPW SFDPWGQGTLVTVSS (SEQ ID NO:5)	DIQMTQSPSTLSASVGDRVTITCR ASQSIGSWLAWYQQKPGKAPKLL IYKASSLESGVPSRFSGSGSGTEFT LTISSLQPDDFATYYCQQYHSFYT FGGGTKVEIK (SEQ ID NO:6)
ADI-27741	QVQLQQWGAGLLKPSETLSLTCAVY GGSFSGYYWSWIRQPPGKGLEWIGEI DHSGSTNYNPSLKSRVTISVDTSKNQ	DIQMTQSPSTLSASVGDRVTITCR ASQSIGSWLAWYQQKPGKAPKLL IYKASSLESGVPSRFSGSGSGTEFT

	FSLKLSSVTAADTAVYYCARARGPW SFDPWGQGTLVTVSS (SEQ ID NO:7)	LTISSLQPDDFATYYCQQSNSYYT FGGGTKVEIK (SEQ ID NO:8)
ADI-27743	QVQLQQWGAGLLKPSETLSLTCAVY GGSFSGYYWSWIRQPPGKGLEWIGEI DHSGSTNYNPSLKSRVTISVDTSKNQ FSLKLSSVTAADTAVYYCARARGPW SFDPWGQGTLVTVSS (SEQ ID NO:9)	DIQMTQSPSTLSASVGDRVTITCR ASQSISSWLAWYQQKPGKAPKLL IYKASSLESGVPSRFSGSGSGTEFT LTISSLQPDDFATYYCQQYNSYPT FGGGTKVEIK (SEQ ID NO:10)
ADI-28153	QVQLQQWGAGLLKPSETLSLTCAVY GGSFSGYYWSWIRQPPGKGLEWIGEI DHSGSTNYNPSLKSRVTISVDTSKNQ FSLKLSSVTAADTAVYYCARARGPW GFDPWGQGTLVTVSS (SEQ ID NO:11)	ELQMTQSPSSLSASVGDRVTITCR TSQSISSYLNWYQQKPGQPPKLLI YWASTRESGVPDRFSGSGSGTDF TLTISSLQPEDSATYYCQQSYDIPY TFGQGTKLEIK (SEQ ID NO:12)
ADI-28226 (C26)	QVQLQQWGAGLLKPSETLSLTCAVY GGSFSGYYWSWIRQPPGKGLEWIGEI DHSGSTNYNPSLKSRVTISVDTSKNQ FSLKLSSVTAADTAVYYCARARGPW SFDPWGQGTLVTVSS (SEQ ID NO:13)	DIQMTQSPSTLSASVGDRVTITCR ASQSISSWLAWYQQKPGKAPKLL IYKASSLESGVPSRFSGSGSGTEFT LTISSLQPDDFATYYCQQYGSFPIT FGGGTKVEIK (SEQ ID NO:14)
ADI-28154	QVQLQQWGAGLLKPSETLSLTCAVY GGSFSGYYWSWIRQPPGKGLEWIGEI DHSGSTNYNPSLKSRVTISVDTSKNQ FSLKLSSVTAADTAVYYCARARGPW SFDPWGQGTLVTVSS (SEQ ID NO:15)	DIQMTQSPSTLSASVGDRVTITCR ASQSISSWLAWYQQKPGKAPKLL IYKASSLESGVPSRFSGSGSGTDFT LTISSLQPDDFATYYCQQSKEVPW TFGQGTKVEIK (SEQ ID NO:16)
ADI-29399	QVQLQQWGAGLLKPSETLSLTCAVY GGSFSGYYWSWIRQPPGKGLEWIGEI DHSGSTNYNPSLKSRVTISVDTSKNQ FSLKLSSVTAADTAVYYCARARGPW SFDPWGQGTLVTVSS (SEQ ID NO:17)	DIQMTQSPSTLSASVGDRVTITCR ASQSISSWLAWYQQKPGKAPKLL IYKASSLESGVPSRFSGSGSGTEFT LTISSLQPDDFATYYCQQYNSFPT FGGGTKVEIK (SEQ ID NO:18)

ADI-29401	QVQLQQWGAGLLKPSETLSLTCAVY GGSFSGYYWSWIRQPPGKGLEWIGEI DHSGSTNYNPSLKSRVTISVDTSKNQ FSLKLSSVTAADTAVYYCARARGPW SFDPWGQGTLVTVSS (SEQ ID NO:19)	DIQMTQSPSTLSASVGDRVTITCR ASQSIGSWLAWYQQKPGKAPKLL IYKASSLESGVPSRFSGSGSGTEFT LTISSLQPDDFATYYCQQYDIYPT FGGGTKVEIK (SEQ ID NO:20)
ADI-29403	QVQLQQWGAGLLKPSETLSLTCAVY GGSFSGYYWSWIRQPPGKGLEWIGEI DHSGSTNYNPSLKSRVTISVDTSKNQ FSLKLSSVTAADTAVYYCARARGPW SFDPWGQGTLVTVSS (SEQ ID NO:21)	DIQMTQSPSTLSASVGDRVTITCR ASQSISSWLAWYQQKPGKAPKLL IYKASSLESGVPSRFSGSGSGTEFT LTISSLQPDDFATYYCQQYDSYPT FGGGTKVEIK (SEQ ID NO:22)
ADI-29405	QVQLQQWGAGLLKPSETLSLTCAVY GGSFSGYYWSWIRQPPGKGLEWIGEI DHSGSTNYNPSLKSRVTISVDTSKNQ FSLKLSSVTAADTAVYYCARARGPW SFDPWGQGTLVTVSS (SEQ ID NO:23)	DIQMTQSPSTLSASVGDRVTITCR ASQSISSWLAWYQQKPGKAPKLL IYKASSLESGVPSRFSGSGSGTEFT LTISSLQPDDFATYYCQQYGSFPT FGGGTKVEIK (SEQ ID NO:24)
ADI-29407	QVQLQQWGAGLLKPSETLSLTCAVY GGSFSGYYWSWIRQPPGKGLEWIGEI DHSGSTNYNPSLKSRVTISVDTSKNQ FSLKLSSVTAADTAVYYCARARGPW SFDPWGQGTLVTVSS (SEQ ID NO:25)	DIQMTQSPSTLSASVGDRVTITCR ASQSISSWLAWYQQKPGKAPKLL IYKASSLESGVPSRFSGSGSGTEFT LTISSLQPDDFATYYCQQYQSFPT FGGGTKVEIK (SEQ ID NO:26)
ADI-29419	QVQLQQWGAGLLKPSETLSLTCAVY GGSFSGYYWSWIRQPPGKGLEWIGEI DHSGSTNYNPSLKSRVTISVDTSKNQ FSLKLSSVTAADTAVYYCARARGPW SFDPWGQGTLVTVSS (SEQ ID NO:27)	DIQMTQSPSTLSASVGDRVTITCR ASQSISSWLAWYQQKPGKAPKLL IYKASSLESGVPSRFSGSGSGTEFT LTISSLQPDDFATYYCQQYSSFSTF GGGTKVEIK (SEQ ID NO:28)
ADI-29421	QVQLQQWGAGLLKPSETLSLTCAVY GGSFSGYYWSWIRQPPGKGLEWIGEI DHSGSTNYNPSLKSRVTISVDTSKNQ	DIQMTQSPSTLSASVGDRVTITCR ASQSISSWLAWYQQKPGKAPKLL IYKASSLESGVPSRFSGSGSGTEFT

	FSLKLSSVTAADTAVYYCARARGPW SFDPWGQGTLVTVSS (SEQ ID NO:29)	LTISSLQPDDFATYYCQQYESYST FGGGTKVEIK (SEQ ID NO:30)
ADI-29424	QVQLQQWGAGLLKPSETLSLTCAVY GGSFSGYYWSWIRQPPGKGLEWIGEI DHSGSTNYNPSLKSRVTISVDTSKNQ FSLKLSSVTAADTAVYYCARARGPW SFDPWGQGTLVTVSS (SEQ ID NO:31)	DIQMTQSPSTLSASVGDRVTITCR ASQSISSWLAWYQQKPGKAPKLL IYKASSLESGVPSRFSGSGSGTEFT LTISSLQPDDFATYYCQQYDSFITF GGGTKVEIK (SEQ ID NO:32)
ADI-29425	QVQLQQWGAGLLKPSETLSLTCAVY GGSFSGYYWSWIRQPPGKGLEWIGEI DHSGSTNYNPSLKSRVTISVDTSKNQ FSLKLSSVTAADTAVYYCARARGPW SFDPWGQGTLVTVSS (SEQ ID NO:33)	DIQMTQSPSTLSASVGDRVTITCR ASQSISSWLAWYQQKPGKAPKLL IYKASSLESGVPSRFSGSGSGTEFT LTISSLQPDDFATYYCQQYQSYPT FGGGTKVEIK (SEQ ID NO:34)
ADI-29426	QVQLQQWGAGLLKPSETLSLTCAVY GGSFSGYYWSWIRQPPGKGLEWIGEI DHSGSTNYNPSLKSRVTISVDTSKNQ FSLKLSSVTAADTAVYYCARARGPW SFDPWGQGTLVTVSS (SEQ ID NO:35)	DIQMTQSPSTLSASVGDRVTITCR ASQSIGSWLAWYQQKPGKAPKLL IYKASSLESGVPSRFSGSGSGTEFT LTISSLQPDDFATYYCQQYHSFPT FGGGTKVEIK (SEQ ID NO:36)
ADI-29429	QVQLQQWGAGLLKPSETLSLTCAVY GGSFSGYYWSWIRQPPGKGLEWIGEI DHSGSTNYNPSLKSRVTISVDTSKNQ FSLKLSSVTAADTAVYYCARARGPW SFDPWGQGTLVTVSS (SEQ ID NO:37)	DIQMTQSPSTLSASVGDRVTITCR ASQSIGSWLAWYQQKPGKAPKLL IYKASSLESGVPSRFSGSGSGTEFT LTISSLQPDDFATYYCQQYELYSY TFGGGTKVEIK (SEQ ID NO:38)
ADI-29447 (F47)	QVQLQQWGAGLLKPSETLSLTCAVY GGSFSGYYWSWIRQPPGKGLEWIGEI DHSGSTNYNPSLKSRVTISVDTSKNQ FSLKLSSVTAADTAVYYCARARGPW SFDPWGQGTLVTVSS (SEQ ID NO:39)	DIQMTQSPSTLSASVGDRVTITCR ASQSISSWLAWYQQKPGKAPKLL IYKASSLESGVPSRFSGSGSGTEFT LTISSLQPDDFATYYCQQYDTFITF GGGTKVEIK (SEQ ID NO:40)

ADI-27727	QVQLVQSGAEVKKPGSSVKVSCKAS GGTFSSYAISWVRQAPGQGLEWMGG IIPIFGTANYAQKFQGRVTITADESTS TAYMELSSLRSEDTAVYYCARGDSSI RHAYYYYGMDVWGQGTTVTVSS (SEQ ID NO:41) CDR1 (SEQ ID NO:67) – GTFSSYAIS CDR2 (SEQ ID NO:68) – GIIPIFGTANYAQKFQG CDR3 (SEQ ID NO:69) – ARGDSSIRHAYYYYGMDV	DIVMTQSPDSLAVSLGERATINCK SSQSVLYSSNNKNYLAWYQQKP GQPPKLLIYWASTRESGVPDRFSG SGSGTDFTLTISSLQAEDVAVYYC QQYYSTPITFGGGTKVEIK (SEQ ID NO:42) CDR1 (SEQ ID NO:70) – KSSQSVLYSSNNKNYLA CDR2 (SEQ ID NO:71) – WASTRES CDR3 (SEQ ID NO:72) – QQYYSTPIT
ADI-29443 (F43)	QLQLQESGPGLVKPSETLSLTCTVSG GSISSSSYYWGWIRQPPGKGLEWIGSI YYSGSTYYNPSLKSRVTISVDTSKNQ FSLKLSSVTAADTAVYYCARGSDRF HPYFDYWGQGTLVTVSS (SEQ ID NO:43) CDR1 (SEQ ID NO:73) – GSISSSSYYWG CDR2 (SEQ ID NO:74) – SIYYSGSTYYNPSLKS CDR3 (SEQ ID NO:75) – ARGSDRFHPYFDY	EIVLTQSPATLSLSPGERATLSCRA SQSVSRYLAWYQQKPGQAPRLLI YDASNRATGIPARFSGSGSGTDFT LTISSLEPEDFAVYYCQQFDTWPP TFGGGTKVEIK (SEQ ID NO:44) CDR1 (SEQ ID NO:76) – RASQSVSRYLA CDR2 (SEQ ID NO:77) – DASNRAT CDR3 (SEQ ID NO:78) – QQFDTWPPT
ADI-29404 (F04)	QVQLQQWGAGLLKPSETLSLTCAVY GGSFSGYYWSWIRQPPGKGLEWIGEI DHSGSTNYNPSLKSRVTISVDTSKNQ FSLKLSSVTAADTAVYYCARARGPW SFDPWGQGTLVTVSS (SEQ ID NO:95)	DIQMTQSPSTLSASVGDRVTITCR ASQSISSWLAWYQQKPGKAPKLL IYKASSLESGVPSRFSGSGSGTEFT LTISSLQPDDFATYYCEQYDSYPT FGGGTKVEIK (SEQ ID NO:96)
ADI-28200	QVQLVQSGAEVKKPGSSVKVSCKAS GGTFSSYAISWVRQAPGQGLEWMGG	DIVMTQSPDSLAVSLGERATINCE SSQSLLNSGNQKNYLTWYQQKPG

	IIPIFGTANYAQKFQGRVTITADESTS TAYMELSSLRSEDTAVYYCARRGRK ASGSFYYYYGMDVWGQGTTVTVSS (SEQ ID NO:97)	QPPKPLIYWASTRESGVPDRFSGS GSGTDFTLTISSLQAEDVAVYYCQ NDYSYPYTFGQGTKLEIK (SEQ ID NO:98)
ADI-27744 (A44)	EVQLLESGGGLVQPGGSLRLSCAASG FTFSSYAMSWVRQAPGKGLEWVSAI SGSGGSTYYADSVKGRFTISRDNSKN TLYLQMNSLRAEDTAVYYCAKDGG YYDSGAGDYWGQGTLVTVSS (SEQ ID NO:99) CDR1 (SEQ ID NO:105) - FTFSSYAMS CDR2 (SEQ ID NO:106) - AISGSGGSTYYADSVKG CDR3 (SEQ ID NO:107) - AKDGGYYDSGAGDY	DIQMTQSPSSVSASVGDRVTITCR ASQGIDSWLAWYQQKPGKAPKL LIYAASSLQSGVPSRFSGSGSGTD FTLTISSLQPEDFATYYCQQGVSY PRTFGGGTKVEIK (SEQ ID NO:100) CDR1 (SEQ ID NO:108) - RASQGIDSWLA CDR2 (SEQ ID NO:109) - AASSLQS CDR3 (SEQ ID NO:110) - QQGVSYPRT
ADI-27749 (A49)	EVQLVESGGGLVKPGGSLRLSCAAS GFTFSSYSMNWVRQAPGKGLEWVSS ISSSSSYIYYADSVKGRFTISRDNAKN SLYLQMNSLRAEDTAVYYCARGAP MGAAAGWFDPWGQGTLVTVSS (SEQ ID NO:101) CDR1 (SEQ ID NO:111) - FTFSSYSMN CDR2 (SEQ ID NO:112) - SISSSSSYIYYADSVKG CDR3 (SEQ ID NO:113) - ARGAPMGAAAGWFDP	DIQMTQSPSSVSASVGDRVTITCR ASQGISSWLAWYQQKPGKAPKLL IYAASSLQSGVPSRFSGSGSGTDF TLTISSLQPEDFATYYCQQGVSFP RTFGGGTKVEIK (SEQ ID NO:102) CDR1 (SEQ ID NO:114) - RASQGISSWLA CDR2 (SEQ ID NO:115) - AASSLQS CDR3 (SEQ ID NO:116) - QQGVSFPRT
ADI-29463 (F63)	QVQLVQSGAEVKKPGASVKVSCKAS GYTFTGYYMHWVRQAPGQGLEWM	EIVLTQSPGTLSLSPGERATLSCRA SQSVSSNLAWYQQKPGQAPRLLI

	GWINPNSGGTNYAQKFQGRVTMTR DTSISTAYMELSRLRSDDTAVYYCAR DTGEYYDTDDHGMDVWGQGTTVTV SS (SEQ ID NO:103) CDR1 (SEQ ID NO:117) - YTFTGYYMH CDR2 (SEQ ID NO:118) - WINPNSGGTNYAQKFQG CDR3 (SEQ ID NO:119) - ARDTGEYYDTDDHGMDV	YGASTRATGIPARFSGSGSGTEFT LTISSLQSEDFAVYYCQQDDYWP PTFGGGTKVEIK (SEQ ID NO:104) CDR1 (SEQ ID NO:120) - RASQSVSSNLA CDR2 (SEQ ID NO:121) - GASTRAT CDR3 (SEQ ID NO:122) - QQDDYWPPT

[0093] Alternatively, a heavy chain variable domain defined by SEQ ID NO:45 can be paired with a light chain variable domain defined by SEQ ID NO:46 to form an antigen-binding site that can bind to NKG2D, as illustrated in US 9,273,136.

QVQLVESGGGLVKPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIRYDGS NKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDRGLGDGTYFDYW GQGTTVTVSS (SEQ ID NO:45)

QSALTQPASVSGSPGQSITISCSGSSSNIGNNAVNWYQQLPGKAPKLLIYYDDLLPSG VSDRFSGSKSGTSAFLAISGLQSEDEADYYCAAWDDSLNGPVFGGGTKLTVL (SEQ ID NO:46)

[0094] Alternatively, a heavy chain variable domain defined by SEQ ID NO:47 can be paired with light chain variable domain defined by SEQ ID NO:48 to form an antigen-binding site that can bind to NKG2D, as illustrated in US 7,879,985.

QVHLQESGPGLVKPSETLSLTCTVSDDSISSYYWSWIRQPPGKGLEWIGHISYSGSAN YNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCANWDDAFNIWGQGTMVTVS S (SEQ ID NO:47)

EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGI PDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK (SEQ ID NO:48)

[0095] Table 2 lists peptide sequences of heavy chain variable domains and light chain variable domains that, in combination, can bind to BCMA.

Table 2		
Clones	Heavy chain variable domain peptide sequence	Light chain variable domain peptide sequence
1 (US14,776,649)	QVQLVQSGAEVKKPGASVKVS CKASGYSFPDYYINWVRQAPGQ GLEWMGWIYFASGNSEYNQKF TGRVTMTRDTSSSTAYMELSSL RSEDTAVYFCASLYDYDWYFD VWGQGTMVTVSS (SEQ ID NO:49) CDR1(SEQ ID NO:50) - DYYIN CDR2 (SEQ ID NO:51) - WIYFASGNSEYNQKFTG CDR3 (SEQ ID NO:52) - LYDYDWYFDV	DIVMTQTPLSLSVTPGEPASIS CKSSQSLVHSNGNTYLHWYL QKPGQSPQLLIYKVSNRFSGVP DRFSGSGSGADFTLKISRVEAE DVGVYYCAETSHVPWTFGQG TKLEIK (SEQ ID NO:53) or DIVMTQTPLSLSVTPGQPASIS CKSSQSLVHSNGNTYLHWYL QKPGQSPQLLIYKVSNRFSGVP DRFSGSGSGTDFTLKISRVEAE DVGIYYCSQSSIYPWTFGQGT KLEIK (SEQ ID NO:54) CDR1(SEQ ID NO:55) - KSSQSLVHSNGNTYLH CDR2 (SEQ ID NO:56) - KVSNRFS CDR3 - AETSHVPWT (SEQ ID NO:57) or SQSSIYPWT (SEQ ID NO:58)
2	QIQLVQSGPELKKPGETVKISCK ASGYTFTDYSINWVKRAPGKGL	DIVLTQSPPSLAMSLGKRATIS CRASESVTILGSHLIHWYQQK

Table 2		
Clones	Heavy chain variable domain peptide sequence	Light chain variable domain peptide sequence
(PCT/US15/64269)	KWMGWINTETREPAYAYDFRGRFAFSLETSASTAYLQINNLKYEDTATYFCALDYSYAMDYWGQGTSVTVSS (SEQ ID NO:59) CDR1 (SEQ ID NO:79) - DYSIN CDR2 (SEQ ID NO:80) - WINTETREPAYAYDFR CDR3 (SEQ ID NO:81) - DYSYAMDY	PGQPPTLLIQLASNVQTGVPARFSGSGSRTDFTLTIDPVEEDDVAVYYCLQSRTIPRTFGGGTKLEIK (SEQ ID NO:60) CDR1 (SEQ ID NO:82) - RASESVTILGSHLIH CDR2 (SEQ ID NO:83) - LASNVQT CDR3 (SEQ ID NO:84) - LQSRTIPRT
3 (US14,122,391)	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSNYWMHWVRQAPGQGLEWMGATYRGHSDTYYNQKFKGRVTITADKSTSTAYMELSSLRSEDTAVYYCARGAIYNGYDVLDNWGQGTLVTVSS (SEQ ID NO:61) CDR1 (SEQ ID NO:85) - NYWMH CDR2 (SEQ ID NO:86) - ATYRGHSDTYYNQKFKG CDR3 (SEQ ID NO:87) - GAIYNGYDVLDN	DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKLLIYYTSNLHSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYRKLPWTFGQGTKLEIKR (SEQ ID NO:62) CDR1 (SEQ ID NO:88) - SASQDISNYLN CDR2 (SEQ ID NO:89) - YTSNLHS CDR3 (SEQ ID NO:90) - QQYRKLPWT
4 (US20170051068)	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYFWGWIRQPPGKGLEWIGSIYYSGITYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADT	SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQPPGQAPVVVVYDDSDRPSGIPERFSGSNSGNTATLTISRVEAGDEAVYYCQVWDSSSDHVVFGGGTKLTVL (SEQ ID NO:124)

Table 2		
Clones	Heavy chain variable domain peptide sequence	Light chain variable domain peptide sequence
	AVYYCARHDGATAGLFDYWG QGTLVTVSS (SEQ ID NO:123) CDR1: SSSYFWG (SEQ ID NO:125) CDR2: SIYYSGITYYNPSLKS (SEQ ID NO:126) CDR3: HDGATAGLFDY (SEQ ID NO:127)	CDR1: GGNNIGSKSVH (SEQ ID NO:128) CDR2: DDSDRPS (SEQ ID NO:129) CDR3: QVWDSSSDHVV (SEQ ID NO:130)
5 (WO2017021450)	EVQLLESGGGLVQPGGSLRLSC AASGFTFSDNAMGWVRQAPGK GLEWVSAISGPGSSTYYADSVK GRFTISRDNSKNTLYLQMNSLR AEDTAVYYCAKVLGWFDYWG QGTLVTVSS (SEQ ID NO:93) CDR1: RASQSVSDEYLS (SEQ ID NO:131) CDR2: SASTRAT (SEQ ID NO:132) CDR3: QQYGYPPDFT (SEQ ID NO:133)	EIVLTQSPGTLSLSPGERATLS CRASQSVSDEYLSWYQQKPG QAPRLLIHSASTRATGIPDRFS GSGSGTDFTLAISRLEPEDFAV YYCQQYGYPPDFTFGQGTKV EIK (SEQ ID NO:94) CDR1: RASQSVSDEYLS (SEQ ID NO:134) CDR2: SASTRAT (SEQ ID NO:135) CDR3: QQYGYPPDFT (SEQ ID NO:136)

[0096] Alternatively, novel antigen-binding sites that can bind to BCMA can be identified by screening for binding to the amino acid sequence defined by SEQ ID NO:63.

SEQ ID NO:63

MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAIL WTCLGLSLIISLAVFVLMFLLRKINSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILP RGLEYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSA TEIEKSISAR

[0097] Within the Fc domain, CD16 binding is mediated by the hinge region and the CH2 domain. For example, within human IgG1, the interaction with CD16 is primarily focused on

amino acid residues Asp 265 – Glu 269, Asn 297 – Thr 299, Ala 327 – Ile 332, Leu 234 – Ser 239, and carbohydrate residue N-acetyl-D-glucosamine in the CH2 domain (see, Sondermann *et al.*, Nature, 406 (6793):267-273). Based on the known domains, mutations can be selected to enhance or reduce the binding affinity to CD16, such as by using phage-displayed libraries or yeast surface-displayed cDNA libraries, or can be designed based on the known three-dimensional structure of the interaction.

[0098] The assembly of heterodimeric antibody heavy chains can be accomplished by expressing two different antibody heavy chain sequences in the same cell, which may lead to the assembly of homodimers of each antibody heavy chain as well as assembly of heterodimers. Promoting the preferential assembly of heterodimers can be accomplished by incorporating different mutations in the CH3 domain of each antibody heavy chain constant region as shown in US13/494870, US16/028850, US11/533709, US12/875015, US13/289934, US14/773418, US12/811207, US13/866756, US14/647480, and US14/830336. For example, mutations can be made in the CH3 domain based on human IgG1 and incorporating distinct pairs of amino acid substitutions within a first polypeptide and a second polypeptide that allow these two chains to selectively heterodimerize with each other. The positions of amino acid substitutions illustrated below are all numbered according to the EU index as in Kabat.

[0099] In one scenario, an amino acid substitution in the first polypeptide replaces the original amino acid with a larger amino acid, selected from arginine (R), phenylalanine (F), tyrosine (Y) or tryptophan (W), and at least one amino acid substitution in the second polypeptide replaces the original amino acid(s) with a smaller amino acid(s), chosen from alanine (A), serine (S), threonine (T), or valine (V), such that the larger amino acid substitution (a protuberance) fits into the surface of the smaller amino acid substitutions (a cavity). For example, one polypeptide can incorporate a T366W substitution, and the other can incorporate three substitutions including T366S, L368A, and Y407V.

[00100] An antibody heavy chain variable domain of the invention can optionally be coupled to an amino acid sequence at least 90% identical to an antibody constant region, such as an IgG constant region including hinge, CH2 and CH3 domains with or without CH1 domain. In some embodiments, the amino acid sequence of the constant region is at least 90% identical to a human antibody constant region, such as an human IgG1 constant region, an IgG2 constant region, IgG3 constant region, or IgG4 constant region. In some other embodiments, the amino acid sequence of the constant region is at least 90% identical to an antibody constant region from another mammal, such as rabbit, dog, cat, mouse, or horse.

One or more mutations can be incorporated into the constant region as compared to human IgG1 constant region, for example at Q347, Y349, L351, S354, E356, E357, K360, Q362, S364, T366, L368, K370, N390, K392, T394, D399, S400, D401, F405, Y407, K409, T411 and/or K439. Exemplary substitutions include, for example, Q347E, Q347R, Y349S, Y349K, Y349T, Y349D, Y349E, Y349C, T350V, L351K, L351D, L351Y, S354C, E356K, E357Q, E357L, E357W, K360E, K360W, Q362E, S364K, S364E, S364H, S364D, T366V, T366I, T366L, T366M, T366K, T366W, T366S, L368E, L368A, L368D, K370S, N390D, N390E, K392L, K392M, K392V, K392F, K392D, K392E, T394F, T394W, D399R, D399K, D399V, S400K, S400R, D401K, F405A, F405T, Y407A, Y407I , Y407V, K409F, K409W, K409D, T411D, T411E, K439D, and K439E.

[00101] In certain embodiments, mutations that can be incorporated into the CH1 of a human IgG1 constant region may be at amino acid V125, F126, P127, T135, T139, A140, F170, P171, and/or V173. In certain embodiments, mutations that can be incorporated into the Cκ of a human IgG1 constant region may be at amino acid E123, F116, S176, V163, S174, and/or T164.

[00102] Amino acid substitutions could be selected from the following sets of substitutions shown in Table 3.

Table 3		
	First Polypeptide	Second Polypeptide
Set 1	S364E/F405A	Y349K/T394F
Set 2	S364H/D401K	Y349T/T411E
Set 3	S364H/T394F	Y349T/F405A
Set 4	S364E/T394F	Y349K/F405A
Set 5	S364E/T411E	Y349K/D401K
Set 6	S364D/T394F	Y349K/F405A
Set 7	S364H/F405A	Y349T/T394F
Set 8	S364K/E357Q	L368D/K370S
Set 9	L368D/K370S	S364K
Set 10	L368E/K370S	S364K
Set 11	K360E/Q362E	D401K
Set 12	L368D/K370S	S364K/E357L
Set 13	K370S	S364K/E357Q
Set 14	F405L	K409R

Set 15	K409R	F405L

[00103] Alternatively, amino acid substitutions could be selected from the following sets of substitutions shown in Table 4.

Table 4		
	First Polypeptide	Second Polypeptide
Set 1	K409W	D399V/F405T
Set 2	Y349S	E357W
Set 3	K360E	Q347R
Set 4	K360E/K409W	Q347R/D399V/F405T
Set 5	Q347E/K360E/K409W	Q347R/D399V/F405T
Set 6	Y349S/K409W	E357W/D399V/F405T

[00104] Alternatively, amino acid substitutions could be selected from the following set of substitutions shown in Table 5.

Table 5		
	First Polypeptide	Second Polypeptide
Set 1	T366K/L351K	L351D/L368E
Set 2	T366K/L351K	L351D/Y349E
Set 3	T366K/L351K	L351D/Y349D
Set 4	T366K/L351K	L351D/Y349E/L368E
Set 5	T366K/L351K	L351D/Y349D/L368E
Set 6	E356K/D399K	K392D/K409D

[00105] Alternatively, at least one amino acid substitution in each polypeptide chain could be selected from Table 6.

Table 6	
First Polypeptide	Second Polypeptide
L351Y, D399R, D399K, S400K, S400R, Y407A, Y407I, Y407V	T366V, T366I, T366L, T366M, N390D, N390E, K392L, K392M, K392V, K392F K392D, K392E, K409F, K409W, T411D and T411E

[00106] Alternatively, at least one amino acid substitution could be selected from the following set of substitutions in Table 7, where the position(s) indicated in the First Polypeptide column is replaced by any known negatively-charged amino acid, and the position(s) indicated in the Second Polypeptide Column is replaced by any known positively-charged amino acid.

Table 7	
First Polypeptide	Second Polypeptide
K392, K370, K409, or K439	D399, E356, or E357

[00107] Alternatively, at least one amino acid substitution could be selected from the following set of in Table 8, where the position(s) indicated in the First Polypeptide column is replaced by any known positively-charged amino acid, and the position(s) indicated in the Second Polypeptide Column is replaced by any known negatively-charged amino acid.

Table 8	
First Polypeptide	Second Polypeptide
D399, E356, or E357	K409, K439, K370, or K392

[00108] Alternatively, or in addition, the structural stability of a heteromultimer protein may be increased by introducing S354C on either of the first or second polypeptide chain, and Y349C on the opposing polypeptide chain, which forms an artificial disulfide bridge within the interface of the two polypeptides.

[00109] The multispecific proteins described above can be made using recombinant DNA technology well known to a skilled person in the art. For example, a first nucleic acid sequence encoding the first immunoglobulin heavy chain can be cloned into a first expression vector; a second nucleic acid sequence encoding the second immunoglobulin heavy chain can be cloned into a second expression vector; a third nucleic acid sequence encoding the immunoglobulin light chain can be cloned into a third expression vector; the first, second, and third expression vectors can be stably transfected together into host cells to produce the multimeric proteins.

[00110] To achieve the highest yield of the multi-specific protein, different ratios of the first, second, and third expression vector can be explored to determine the optimal ratio for transfection into the host cells. After transfection, single clones can be isolated for cell bank

generation using methods known in the art, such as limited dilution, ELISA, FACS, microscopy, or Clonepix.

[00111] Clones can be cultured under conditions suitable for bio-reactor scale-up and maintained expression of the multi-specific protein. The multispecific proteins can be isolated and purified using methods known in the art including centrifugation, depth filtration, cell lysis, homogenization, freeze-thawing, affinity purification, gel filtration, ion exchange chromatography, hydrophobic interaction exchange chromatography, and mixed-mode chromatography.

II. Characteristics of TriNKETs

[00112] In certain embodiments, TriNKETs described herein, which include an NKG2D-binding domain and a binding domain for a tumor associated antigen, bind to cells expressing human NKG2D. In certain embodiments, TriNKETs, which include an NKG2D-binding domain and a binding domain for a tumor associated antigen, bind to the tumor associated antigen at a comparable level to that of a monoclonal antibody having the same tumor associated antigen-binding domain.

[00113] The TriNKETs described herein are more effective in reducing tumor growth and killing cancer cells.

[00114] In certain embodiments, TriNKETs described herein, which include an NKG2D-binding domain and a binding domain for tumor associated antigen, activate primary human NK cells when culturing with tumor cells expressing the antigen. NK cell activation is marked by the increase in CD107a degranulation and IFNγ cytokine production. Furthermore, compared to a monoclonal antibody that includes the tumor associated antigen-binding domain, TriNKETs show superior activation of human NK cells in the presence of tumor cells expressing the antigen. For example, compared to an anti-BCMA monoclonal antibody, TriNKETs of the present disclosure having a BCMA-binding domain, have a superior activation of human NK cells in the presence of BCMA-expressing cancer cells.

[00115] In certain embodiments, TriNKETs described herein, which include an NKG2D-binding domain and a binding domain for a tumor associated antigen, enhance the activity of rested and IL-2-activated human NK cells in the presence of tumor cells expressing the antigen. Rested NK cells showed less background IFNγ production and CD107a degranulation than IL-2-activated NK cells. In certain embodiments, rested NK cells show a

greater change in IFNγ production and CD107a degranulation compared to IL-2-activated NK cells. In certain embodiments, IL-2-activated NK cells show a greater percentage of cells becoming IFNγ+; CD107a+ after stimulation with TriNKETs.

[00116] In certain embodiments, TriNKETs described herein, which include an NKG2D-binding domain and a binding domain for tumor associated antigen BCMA, enhance the cytotoxic activity of rested and IL-2-activated human NK cells in the presence of tumor cells expressing the antigen. Furthermore, TriNKETs (*e.g.*, A40-TriNKET, A44-TriNKET, A49-TriNKET, C26-TriNKET, F04-TriNKET, F43-TriNKET, F47-TriNKET, and F63-TriNKET), which include a binding domain for tumor associated antigen BCMA more potently direct activated and rested NK cell responses against the tumor cells, compared to a monoclonal antibody that includes the same tumor associated antigen-binding site. In certain embodiments, TriNKETs offer advantage against tumor cells expressing medium and low BCMA compared to monoclonal antibodies that include the BCMA-binding site. Therefore, a therapy including TriNKETs can be superior to an anti-BCMA monoclonal antibody therapy.

[00117] In certain embodiments, compared to monoclonal antibodies, TriNKETs described herein (*e.g.*, A40-TriNKET, A44-TriNKET, A49-TriNKET, C26-TriNKET, F04-TriNKET, F43-TriNKET, F47-TriNKET, and F63-TriNKET), which include a binding domain for tumor associated antigen BCMA are advantageous in treating cancers with high expression of Fc receptor (FcR), or cancers residing in a tumor microenvironment with high levels of FcR. Monoclonal antibodies exert their effects on tumor growth through multiple mechanisms including ADCC, CDC, phagocytosis, and signal blockade amongst others. Amongst FcγRs, CD16 has the lowest affinity for IgG Fc; FcγRI (CD64) is the high-affinity FcR, which binds about 1000 times more strongly to IgG Fc than CD16. CD64 is normally expressed on many hematopoietic lineages such as the myeloid lineage, and can be expressed on tumors derived from these cell types, such as acute myeloid leukemia (AML). Immune cells infiltrating into the tumor, such as MDSCs and monocytes, also express CD64 and are known to infiltrate the tumor microenvironment. Expression of CD64 by the tumor or in the tumor microenvironment can have a detrimental effect on monoclonal antibody therapy. Expression of CD64 in the tumor microenvironment makes it difficult for these antibodies to engage CD16 on the surface of NK cells, as the antibodies prefer to bind the high-affinity receptor. TriNKETs, through targeting two activating receptors on the surface of NK cells, can overcome the detrimental effect of CD64 expression (either on tumor or tumor microenvironment) on monoclonal antibody therapy. Regardless of CD64 expression on the tumor cells, TriNKETs are able to mediate human NK cell responses against all tumor cells,

because dual targeting of two activating receptors on NK cells provides stronger specific binding to NK cells.

[00118] In some embodiments, TriNKETs described herein (*e.g.*, A40-TriNKET, A44-TriNKET, A49-TriNKET, C26-TriNKET, F04-TriNKET, F43-TriNKET, F47-TriNKET, and F63-TriNKET), which include a binding domain for tumor associated antigen BCMA, provide a better safety profile through reduced on-target off-tumor side effects. Natural killer cells and CD8 T cells are both able to directly lyse tumor cells, although the mechanisms through which NK cells and CD8 T cell recognize normal self from tumor cells differ. The activity of NK cells is regulated by the balance of signals from activating (NCRs, NKG2D, CD16, *etc.*) and inhibitory (KIRs, NKG2A, *etc.*) receptors. The balance of these activating and inhibitory signals allow NK cells to determine healthy self-cells from stressed, virally infected, or transformed self-cells. This 'built-in' mechanism of self-tolerance will help protect normal heathy tissue from NK cell responses. To extend this principle, the self-tolerance of NK cells will allow TriNKETs to target antigens expressed both on self and tumor without off tumor side effects, or with an increased therapeutic window. Unlike natural killer cells, T cells require recognition of a specific peptide presented by MHC molecules for activation and effector functions. T cells have been the primary target of immunotherapy, and many strategies have been developed to redirect T cell responses against the tumor. T cell bispecifics, checkpoint inhibitors, and CAR-T cells have all been approved by the FDA, but often suffer from dose-limiting toxicities. T cell bispecifics and CAR-T cells work around the TCR-MHC recognition system by using binding domains to target antigens on the surface of tumor cells, and using engineered signaling domains to transduce the activation signals into the effector cell. Although effective at eliciting an anti-tumor immune response these therapies are often coupled with cytokine release syndrome (CRS), and on-target off-tumor side effects. TriNKETs are unique in this context as they will not 'override' the natural systems of NK cell activation and inhibition. Instead, TriNKETs are designed to sway the balance, and provide additional activation signals to the NK cells, while maintaining NK tolerance to healthy self.

[00119] In some embodiments, TriNKETs described herein including an NKG2D-binding domain (*e.g.*, A40-TriNKET, A44-TriNKET, A49-TriNKET, C26-TriNKET, F04-TriNKET, F43-TriNKET, F47-TriNKET, and F63-TriNKET and a binding domain for tumor associated antigen BCMA delay progression of the tumor more effectively than monoclonal antibodies that include the same tumor antigen-binding domain. In some embodiments, TriNKETs including an NKG2D-binding domain and tumor antigen BCMA-binding domain

are more effective against cancer metastases than monoclonal antibodies that include the anti-BCMA-binding domain.

III. THERAPEUTIC APPLICATIONS

[00120] The invention provides methods for treating cancer using a multi-specific binding protein described herein and/or a pharmaceutical composition described herein. The methods may be used to treat a variety of cancers which express BCMA by administering to a patient in need thereof a therapeutically effective amount of a multi-specific binding protein described herein.

[00121] The therapeutic method can be characterized according to the cancer to be treated. For example, in certain embodiments, the cancers are blood or bone marrow derived. Exemplary ones include multiple myeloma, acute myelomonocytic leukemia, T cell lymphoma, acute monocytic leukemia and follicular lymphoma. T-cell lymphomas can include precursor T-lymphoblastic lymphoma, peripheral T-cell lymphoma, cutaneous T-cell lymphoma, angioimmunoblastic T-cell lymphoma, extranodal natural killer/T-cell lymphoma, enteropathy type T-cell lymphoma, subcutaneous panniculitis-like T-cell lymphoma, anaplastic large cell lymphoma, or peripheral T-cell lymphoma.

[00122] In certain embodiments, the cancer is a B-cell lymphoma, such as a diffuse large B-cell lymphoma, primary mediastinal B-cell lymphoma, follicular lymphoma, small lymphocytic lymphoma, mantle cell lymphoma, marginal zone B-cell lymphoma, extranodal marginal zone B-cell lymphoma, nodal marginal zone B-cell lymphoma, splenic marginal zone B-cell lymphoma, Burkitt lymphoma, lymphoplasmacytic lymphoma, hairy cell leukemia, or primary central nervous system (CNS) lymphoma.

[00123] In certain other embodiments, the cancer is a solid tumor, such as brain cancer, bladder cancer, breast cancer, cervical cancer, colon cancer, colorectal cancer, endometrial cancer, esophageal cancer, leukemia, lung cancer, liver cancer, melanoma, ovarian cancer, pancreatic cancer, prostate cancer, rectal cancer, renal cancer, stomach cancer, testicular cancer, or uterine cancer. In yet other embodiments, the cancer is a vascularized tumor, squamous cell carcinoma, adenocarcinoma, small cell carcinoma, melanoma, glioma, neuroblastoma, sarcoma (*e.g.*, an angiosarcoma or chondrosarcoma), larynx cancer, parotid cancer, bilary tract cancer, thyroid cancer, acral lentiginous melanoma, actinic keratoses, acute lymphocytic leukemia, acute myeloid leukemia, adenoid cycstic carcinoma, adenomas, adenosarcoma, adenosquamous carcinoma, anal canal cancer, anal cancer, anorectum cancer, astrocytic tumor, bartholin gland carcinoma, basal cell carcinoma, biliary cancer, bone

cancer, bone marrow cancer, bronchial cancer, bronchial gland carcinoma, carcinoid, cholangiocarcinoma, chondosarcoma, choriod plexus papilloma/carcinoma, chronic lymphocytic leukemia, chronic myeloid leukemia, clear cell carcinoma, connective tissue cancer, cystadenoma, digestive system cancer, duodenum cancer, endocrine system cancer, endodermal sinus tumor, endometrial hyperplasia, endometrial stromal sarcoma, endometrioid adenocarcinoma, endothelial cell cancer, ependymal cancer, epithelial cell cancer, Ewing's sarcoma, eye and orbit cancer, female genital cancer, focal nodular hyperplasia, gallbladder cancer, gastric antrum cancer, gastric fundus cancer, gastrinoma, glioblastoma, glucagonoma, heart cancer, hemangiblastomas, hemangioendothelioma, hemangiomas, hepatic adenoma, hepatic adenomatosis, hepatobiliary cancer, hepatocellular carcinoma, Hodgkin's disease, ileum cancer, insulinoma, intaepithelial neoplasia, interepithelial squamous cell neoplasia, intrahepatic bile duct cancer, invasive squamous cell carcinoma, jejunum cancer, joint cancer, Kaposi's sarcoma, pelvic cancer, large cell carcinoma, large intestine cancer, leiomyosarcoma, lentigo maligna melanomas, lymphoma, male genital cancer, malignant melanoma, malignant mesothelial tumors, medulloblastoma, medulloepithelioma, meningeal cancer, mesothelial cancer, metastatic carcinoma, mouth cancer, mucoepidermoid carcinoma, multiple myeloma, muscle cancer, nasal tract cancer, nervous system cancer, neuroepithelial adenocarcinoma nodular melanoma, non-epithelial skin cancer, non-Hodgkin's lymphoma, oat cell carcinoma, oligodendroglial cancer, oral cavity cancer, osteosarcoma, papillary serous adenocarcinoma, penile cancer, pharynx cancer, pituitary tumors, plasmacytoma, pseudosarcoma, pulmonary blastoma, rectal cancer, renal cell carcinoma, respiratory system cancer, retinoblastoma, rhabdomyosarcoma, sarcoma, serous carcinoma, sinus cancer, skin cancer, small cell carcinoma, small intestine cancer, smooth muscle cancer, soft tissue cancer, somatostatin-secreting tumor, spine cancer, squamous cell carcinoma, striated muscle cancer, submesothelial cancer, superficial spreading melanoma, T cell leukemia, tongue cancer, undifferentiated carcinoma, ureter cancer, urethra cancer, urinary bladder cancer, urinary system cancer, uterine cervix cancer, uterine corpus cancer, uveal melanoma, vaginal cancer, verrucous carcinoma, VIPoma, vulva cancer, well differentiated carcinoma, or Wilms tumor.

[00124] The cancer to be treated can be characterized according to the presence of a particular antigen expressed on the surface of the cancer cell. In certain embodiments, the cancer cell can expresses one or more of the following in addition to BCMA: CD2, CD19, CD20, CD30, CD38, CD40, CD52, CD70, EGFR/ERBB1, IGF1R, HER3/ERBB3,

HER4/ERBB4, MUC1, cMET, SLAMF7, PSCA, MICA, MICB, TRAILR1, TRAILR2, MAGE-A3, B7.1, B7.2, CTLA4, and PD1.

IV. COMBINATION THERAPY

[00125] Another aspect of the invention provides for combination therapy. Multi-specific binding proteins described herein be used in combination with additional therapeutic agents to treat the cancer.

[00126] Exemplary therapeutic agents that may be used as part of a combination therapy in treating cancer, include, for example, radiation, mitomycin, tretinoin, ribomustin, gemcitabine, vincristine, etoposide, cladribine, mitobronitol, methotrexate, doxorubicin, carboquone, pentostatin, nitracrine, zinostatin, cetrorelix, letrozole, raltitrexed, daunorubicin, fadrozole, fotemustine, thymalfasin, sobuzoxane, nedaplatin, cytarabine, bicalutamide, vinorelbine, vesnarinone, aminoglutethimide, amsacrine, proglumide, elliptinium acetate, ketanserin, doxifluridine, etretinate, isotretinoin, streptozocin, nimustine, vindesine, flutamide, drogenil, butocin, carmofur, razoxane, sizofilan, carboplatin, mitolactol, tegafur, ifosfamide, prednimustine, picibanil, levamisole, teniposide, improsulfan, enocitabine, lisuride, oxymetholone, tamoxifen, progesterone, mepitiostane, epitiostanol, formestane, interferon-alpha, interferon-2 alpha, interferon-beta, interferon-gamma, colony stimulating factor-1, colony stimulating factor-2, denileukin diftitox, interleukin-2, luteinizing hormone releasing factor and variations of the aforementioned agents that may exhibit differential binding to its cognate receptor, and increased or decreased serum half-life.

[00127] An additional class of agents that may be used as part of a combination therapy in treating cancer is immune checkpoint inhibitors. Exemplary immune checkpoint inhibitors include agents that inhibit one or more of (i) cytotoxic T‑lymphocyte-associated antigen 4 (CTLA4), (ii) programmed cell death protein 1 (PD1), (iii) PDL1, (iv) LAG3, (v) B7-H3, (vi) B7-H4, and (vii) TIM3. The CTLA4 inhibitor ipilimumab has been approved by the United States Food and Drug Administration for treating melanoma.

[00128] Yet other agents that may be used as part of a combination therapy in treating cancer are monoclonal antibody agents that target non-checkpoint targets (*e.g.*, herceptin) and non-cytotoxic agents (*e.g.*, tyrosine-kinase inhibitors).

[00129] Yet other categories of anti-cancer agents include, for example: (i) an inhibitor selected from an ALK Inhibitor, an ATR Inhibitor, an A2A Antagonist, a Base Excision Repair Inhibitor, a Bcr-Abl Tyrosine Kinase Inhibitor, a Bruton's Tyrosine Kinase Inhibitor, a CDC7 Inhibitor, a CHK1 Inhibitor, a Cyclin-Dependent Kinase Inhibitor, a DNA-PK

Inhibitor, an Inhibitor of both DNA-PK and mTOR, a DNMT1 Inhibitor, a DNMT1 Inhibitor plus 2-chloro-deoxyadenosine, an HDAC Inhibitor, a Hedgehog Signaling Pathway Inhibitor, an IDO Inhibitor, a JAK Inhibitor, a mTOR Inhibitor, a MEK Inhibitor, a MELK Inhibitor, a MTH1 Inhibitor, a PARP Inhibitor, a Phosphoinositide 3-Kinase Inhibitor, an Inhibitor of both PARP1 and DHODH, a Proteasome Inhibitor, a Topoisomerase-II Inhibitor, a Tyrosine Kinase Inhibitor, a VEGFR Inhibitor, and a WEE1 Inhibitor; (ii) an agonist of OX40, CD137, CD40, GITR, CD27, HVEM, TNFRSF25, or ICOS; and (iii) a cytokine selected from IL-12, IL-15, GM-CSF, and G-CSF.

[00130] Proteins of the invention can also be used as an adjunct to surgical removal of the primary lesion.

[00131] The amount of multi-specific binding protein and additional therapeutic agent and the relative timing of administration may be selected in order to achieve a desired combined therapeutic effect. For example, when administering a combination therapy to a patient in need of such administration, the therapeutic agents in the combination, or a pharmaceutical composition or compositions comprising the therapeutic agents, may be administered in any order such as, for example, sequentially, concurrently, together, simultaneously and the like. Further, for example, a multi-specific binding protein may be administered during a time when the additional therapeutic agent(s) exerts its prophylactic or therapeutic effect, or *vice versa*.

V. PHARMACEUTICAL COMPOSITIONS

[00132] The present disclosure also features pharmaceutical compositions that contain a therapeutically effective amount of a protein described herein. The composition can be formulated for use in a variety of drug delivery systems. One or more physiologically acceptable excipients or carriers can also be included in the composition for proper formulation. Suitable formulations for use in the present disclosure are found in Remington's Pharmaceutical Sciences, Mack Publishing Company, Philadelphia, Pa., 17th ed., 1985. For a brief review of methods for drug delivery, *see, e.g.*, Langer (Science 249:1527-1533, 1990).

[00133] The intravenous drug delivery formulation of the present disclosure may be contained in a bag, a pen, or a syringe. In certain embodiments, the bag may be connected to a channel comprising a tube and/or a needle. In certain embodiments, the formulation may be a lyophilized formulation or a liquid formulation. In certain embodiments, the formulation may freeze-dried (lyophilized) and contained in about 12-60 vials. In certain embodiments, the formulation may be freeze-dried and 45 mg of the freeze-dried formulation may be

contained in one vial. In certain embodiments, the about 40 mg – about 100 mg of freeze-dried formulation may be contained in one vial. In certain embodiments, freeze dried formulation from 12, 27, or 45 vials are combined to obtained a therapeutic dose of the protein in the intravenous drug formulation. In certain embodiments, the formulation may be a liquid formulation and stored as about 250 mg/vial to about 1000 mg/vial. In certain embodiments, the formulation may be a liquid formulation and stored as about 600 mg/vial. In certain embodiments, the formulation may be a liquid formulation and stored as about 250 mg/vial.

[00134] This present disclosure could exist in a liquid aqueous pharmaceutical formulation including a therapeutically effective amount of the protein in a buffered solution forming a formulation.

[00135] These compositions may be sterilized by conventional sterilization techniques, or may be sterile filtered. The resulting aqueous solutions may be packaged for use as-is, or lyophilized, the lyophilized preparation being combined with a sterile aqueous carrier prior to administration. The pH of the preparations typically will be between 3 and 11, more preferably between 5 and 9 or between 6 and 8, and most preferably between 7 and 8, such as 7 to 7.5. The resulting compositions in solid form may be packaged in multiple single dose units, each containing a fixed amount of the above-mentioned agent or agents. The composition in solid form can also be packaged in a container for a flexible quantity.

[00136] In certain embodiments, the present disclosure provides a formulation with an extended shelf life including the protein of the present disclosure, in combination with mannitol, citric acid monohydrate, sodium citrate, disodium phosphate dihydrate, sodium dihydrogen phosphate dihydrate, sodium chloride, polysorbate 80, water, and sodium hydroxide.

[00137] In certain embodiments, an aqueous formulation is prepared including the protein of the present disclosure in a pH-buffered solution. The buffer of this invention may have a pH ranging from about 4 to about 8, *e.g.*, from about 4.5 to about 6.0, or from about 4.8 to about 5.5, or may have a pH of about 5.0 to about 5.2. Ranges intermediate to the above recited pH's are also intended to be part of this disclosure. For example, ranges of values using a combination of any of the above recited values as upper and/or lower limits are intended to be included. Examples of buffers that will control the pH within this range include acetate (*e.g.* sodium acetate), succinate (such as sodium succinate), gluconate, histidine, citrate and other organic acid buffers.

[00138] In certain embodiments, the formulation includes a buffer system which contains citrate and phosphate to maintain the pH in a range of about 4 to about 8. In certain embodiments the pH range may be from about 4.5 to about 6.0, or from about pH 4.8 to about 5.5, or in a pH range of about 5.0 to about 5.2. In certain embodiments, the buffer system includes citric acid monohydrate, sodium citrate, disodium phosphate dihydrate, and/or sodium dihydrogen phosphate dihydrate. In certain embodiments, the buffer system includes about 1.3 mg/ml of citric acid (*e.g.*, 1.305 mg/ml), about 0.3 mg/ml of sodium citrate (*e.g.*, 0.305 mg/ml), about 1.5 mg/ml of disodium phosphate dihydrate (*e.g.*, 1.53 mg/ml), about 0.9 mg/ml of sodium dihydrogen phosphate dihydrate (*e.g.*, 0.86), and about 6.2 mg/ml of sodium chloride (*e.g.*, 6.165 mg/ml). In certain embodiments, the buffer system includes 1-1.5 mg/ml of citric acid, 0.25 to 0.5 mg/ml of sodium citrate, 1.25 to 1.75 mg/ml of disodium phosphate dihydrate, 0.7 to 1.1 mg/ml of sodium dihydrogen phosphate dihydrate, and 6.0 to 6.4 mg/ml of sodium chloride. In certain embodiments, the pH of the formulation is adjusted with sodium hydroxide.

[00139] A polyol, which acts as a tonicifier and may stabilize the antibody, may also be included in the formulation. The polyol is added to the formulation in an amount which may vary with respect to the desired isotonicity of the formulation. In certain embodiments, the aqueous formulation may be isotonic. The amount of polyol added may also be altered with respect to the molecular weight of the polyol. For example, a lower amount of a monosaccharide (*e.g.*, mannitol) may be added, compared to a disaccharide (such as trehalose). In certain embodiments, the polyol which may be used in the formulation as a tonicity agent is mannitol. In certain embodiments, the mannitol concentration may be about 5 to about 20 mg/ml. In certain embodiments, the concentration of mannitol may be about 7.5 to 15 mg/ml. In certain embodiments, the concentration of mannitol may be about 10-14 mg/ml. In certain embodiments, the concentration of mannitol may be about 12 mg/ml. In certain embodiments, the polyol sorbitol may be included in the formulation.

[00140] A detergent or surfactant may also be added to the formulation. Exemplary detergents include nonionic detergents such as polysorbates (*e.g.*, polysorbates 20, 80 etc.) or poloxamers (*e.g.*, poloxamer 188). The amount of detergent added is such that it reduces aggregation of the formulated antibody and/or minimizes the formation of particulates in the formulation and/or reduces adsorption. In certain embodiments, the formulation may include a surfactant which is a polysorbate. In certain embodiments, the formulation may contain the detergent polysorbate 80 or Tween 80. Tween 80 is a term used to describe polyoxyethylene (20) sorbitanmonooleate (*see* Fiedler, Lexikon der Hifsstoffe, Editio Cantor Verlag

Aulendorf, 4th ed., 1996). In certain embodiments, the formulation may contain between about 0.1 mg/mL and about 10 mg/mL of polysorbate 80, or between about 0.5 mg/mL and about 5 mg/mL. In certain embodiments, about 0.1% polysorbate 80 may be added in the formulation.

[00141] In embodiments, the protein product of the present disclosure is formulated as a liquid formulation. The liquid formulation may be presented at a 10 mg/mL concentration in either a USP / Ph Eur type I 50R vial closed with a rubber stopper and sealed with an aluminum crimp seal closure. The stopper may be made of elastomer complying with USP and Ph Eur. In certain embodiments vials may be filled with 61.2 mL of the protein product solution in order to allow an extractable volume of 60 mL. In certain embodiments, the liquid formulation may be diluted with 0.9% saline solution.

[00142] In certain embodiments, the liquid formulation of the disclosure may be prepared as a 10 mg/mL concentration solution in combination with a sugar at stabilizing levels. In certain embodiments the liquid formulation may be prepared in an aqueous carrier. In certain embodiments, a stabilizer may be added in an amount no greater than that which may result in a viscosity undesirable or unsuitable for intravenous administration. In certain embodiments, the sugar may be disaccharides, *e.g.*, sucrose. In certain embodiments, the liquid formulation may also include one or more of a buffering agent, a surfactant, and a preservative.

[00143] In certain embodiments, the pH of the liquid formulation may be set by addition of a pharmaceutically acceptable acid and/or base. In certain embodiments, the pharmaceutically acceptable acid may be hydrochloric acid. In certain embodiments, the base may be sodium hydroxide.

[00144] In addition to aggregation, deamidation is a common product variant of peptides and proteins that may occur during fermentation, harvest/cell clarification, purification, drug substance/drug product storage and during sample analysis. Deamidation is the loss of NH_3 from a protein forming a succinimide intermediate that can undergo hydrolysis. The succinimide intermediate results in a 17 daltons mass decrease of the parent peptide. The subsequent hydrolysis results in an 18 daltons mass increase. Isolation of the succinimide intermediate is difficult due to instability under aqueous conditions. As such, deamidation is typically detectable as 1 dalton mass increase. Deamidation of an asparagine results in either aspartic or isoaspartic acid. The parameters affecting the rate of deamidation include pH, temperature, solvent dielectric constant, ionic strength, primary sequence, local polypeptide conformation and tertiary structure. The amino acid residues adjacent to Asn in the peptide

chain affect deamidation rates. Gly and Ser following an Asn in protein sequences results in a higher susceptibility to deamidation.

[00145] In certain embodiments, the liquid formulation of the present disclosure may be preserved under conditions of pH and humidity to prevent deamination of the protein product.

[00146] The aqueous carrier of interest herein is one which is pharmaceutically acceptable (safe and non-toxic for administration to a human) and is useful for the preparation of a liquid formulation. Illustrative carriers include sterile water for injection (SWFI), bacteriostatic water for injection (BWFI), a pH buffered solution (*e.g.*, phosphate-buffered saline), sterile saline solution, Ringer's solution or dextrose solution.

[00147] A preservative may be optionally added to the formulations herein to reduce bacterial action. The addition of a preservative may, for example, facilitate the production of a multi-use (multiple-dose) formulation.

[00148] Intravenous (IV) formulations may be the preferred administration route in particular instances, such as when a patient is in the hospital after transplantation receiving all drugs via the IV route. In certain embodiments, the liquid formulation is diluted with 0.9% Sodium Chloride solution before administration. In certain embodiments, the diluted drug product for injection is isotonic and suitable for administration by intravenous infusion.

[00149] In certain embodiments, a salt or buffer components may be added in an amount of 10 mM - 200 mM. The salts and/or buffers are pharmaceutically acceptable and are derived from various known acids (inorganic and organic) with “base forming” metals or amines. In certain embodiments, the buffer may be phosphate buffer. In certain embodiments, the buffer may be glycinate, carbonate, citrate buffers, in which case, sodium, potassium or ammonium ions can serve as counterion.

[00150] A preservative may be optionally added to the formulations herein to reduce bacterial action. The addition of a preservative may, for example, facilitate the production of a multi-use (multiple-dose) formulation.

[00151] The aqueous carrier of interest herein is one which is pharmaceutically acceptable (safe and non-toxic for administration to a human) and is useful for the preparation of a liquid formulation. Illustrative carriers include sterile water for injection (SWFI), bacteriostatic water for injection (BWFI), a pH buffered solution (*e.g.*, phosphate-buffered saline), sterile saline solution, Ringer's solution or dextrose solution.

[00152] This present disclosure could exist in a lyophilized formulation including the proteins and a lyoprotectant. The lyoprotectant may be sugar, *e.g.*, disaccharides. In certain embodiments, the lyoprotectant may be sucrose or maltose. The lyophilized formulation may

also include one or more of a buffering agent, a surfactant, a bulking agent, and/or a preservative.

[00153] The amount of sucrose or maltose useful for stabilization of the lyophilized drug product may be in a weight ratio of at least 1:2 protein to sucrose or maltose. In certain embodiments, the protein to sucrose or maltose weight ratio may be of from 1:2 to 1:5.

[00154] In certain embodiments, the pH of the formulation, prior to lyophilization, may be set by addition of a pharmaceutically acceptable acid and/or base. In certain embodiments the pharmaceutically acceptable acid may be hydrochloric acid. In certain embodiments, the pharmaceutically acceptable base may be sodium hydroxide.

[00155] Before lyophilization, the pH of the solution containing the protein of the present disclosure may be adjusted between 6 to 8. In certain embodiments, the pH range for the lyophilized drug product may be from 7 to 8.

[00156] In certain embodiments, a salt or buffer components may be added in an amount of 10 mM - 200 mM. The salts and/or buffers are pharmaceutically acceptable and are derived from various known acids (inorganic and organic) with "base forming" metals or amines. In certain embodiments, the buffer may be phosphate buffer. In certain embodiments, the buffer may be glycinate, carbonate, citrate buffers, in which case, sodium, potassium or ammonium ions can serve as counterion.

[00157] In certain embodiments, a "bulking agent" may be added. A "bulking agent" is a compound which adds mass to a lyophilized mixture and contributes to the physical structure of the lyophilized cake (*e.g.*, facilitates the production of an essentially uniform lyophilized cake which maintains an open pore structure). Illustrative bulking agents include mannitol, glycine, polyethylene glycol and sorbitol. The lyophilized formulations of the present invention may contain such bulking agents.

[00158] A preservative may be optionally added to the formulations herein to reduce bacterial action. The addition of a preservative may, for example, facilitate the production of a multi-use (multiple-dose) formulation.

[00159] In certain embodiments, the lyophilized drug product may be constituted with an aqueous carrier. The aqueous carrier of interest herein is one which is pharmaceutically acceptable (*e.g.*, safe and non-toxic for administration to a human) and is useful for the preparation of a liquid formulation, after lyophilization. Illustrative diluents include sterile water for injection (SWFI), bacteriostatic water for injection (BWFI), a pH buffered solution (*e.g.*, phosphate-buffered saline), sterile saline solution, Ringer's solution or dextrose solution.

[00160] In certain embodiments, the lyophilized drug product of the current disclosure is reconstituted with either Sterile Water for Injection, USP (SWFI) or 0.9% Sodium Chloride Injection, USP. During reconstitution, the lyophilized powder dissolves into a solution.

[00161] In certain embodiments, the lyophilized protein product of the instant disclosure is constituted to about 4.5 mL water for injection and diluted with 0.9% saline solution (sodium chloride solution).

[00162] Actual dosage levels of the active ingredients in the pharmaceutical compositions of this invention may be varied so as to obtain an amount of the active ingredient which is effective to achieve the desired therapeutic response for a particular patient, composition, and mode of administration, without being toxic to the patient.

[00163] The specific dose can be a uniform dose for each patient, for example, 50-5000 mg of protein. Alternatively, a patient's dose can be tailored to the approximate body weight or surface area of the patient. Other factors in determining the appropriate dosage can include the disease or condition to be treated or prevented, the severity of the disease, the route of administration, and the age, sex and medical condition of the patient. Further refinement of the calculations necessary to determine the appropriate dosage for treatment is routinely made by those skilled in the art, especially in light of the dosage information and assays disclosed herein. The dosage can also be determined through the use of known assays for determining dosages used in conjunction with appropriate dose-response data. An individual patient's dosage can be adjusted as the progress of the disease is monitored. Blood levels of the targetable construct or complex in a patient can be measured to see if the dosage needs to be adjusted to reach or maintain an effective concentration. Pharmacogenomics may be used to determine which targetable constructs and/or complexes, and dosages thereof, are most likely to be effective for a given individual (Schmitz *et al*., *Clinica Chimica Acta* 308: 43-53, 2001; Steimer *et al*., *Clinica Chimica Acta* 308: 33-41, 2001).

[00164] In general, dosages based on body weight are from about 0.01 μg to about 100 mg per kg of body weight, such as about 0.01 μg to about 100 mg/kg of body weight, about 0.01 μg to about 50 mg/kg of body weight, about 0.01 μg to about 10 mg/kg of body weight, about 0.01 μg to about 1 mg/kg of body weight, about 0.01 μg to about 100 μg/kg of body weight, about 0.01 μg to about 50 μg/kg of body weight, about 0.01 μg to about 10 μg/kg of body weight, about 0.01 μg to about 1 μg/kg of body weight, about 0.01 μg to about 0.1 μg/kg of body weight, about 0.1 μg to about 100 mg/kg of body weight, about 0.1 μg to about 50 mg/kg of body weight, about 0.1 μg to about 10 mg/kg of body weight, about 0.1 μg to about 1 mg/kg of body weight, about 0.1 μg to about 100 μg/kg of body weight, about 0.1 μg to

about 10 μg/kg of body weight, about 0.1 μg to about 1 μg/kg of body weight, about 1 μg to about 100 mg/kg of body weight, about 1 μg to about 50 mg/kg of body weight, about 1 μg to about 10 mg/kg of body weight, about 1 μg to about 1 mg/kg of body weight, about 1 μg to about 100 μg/kg of body weight, about 1 μg to about 50 μg/kg of body weight, about 1 μg to about 10 μg/kg of body weight, about 10 μg to about 100 mg/kg of body weight, about 10 μg to about 50 mg/kg of body weight, about 10 μg to about 10 mg/kg of body weight, about 10 μg to about 1 mg/kg of body weight, about 10 μg to about 100 μg/kg of body weight, about 10 μg to about 50 μg/kg of body weight, about 50 μg to about 100 mg/kg of body weight, about 50μg to about 50 mg/kg of body weight, about 50 μg to about 10 mg/kg of body weight, about 50 μg to about 1 mg/kg of body weight, about 50 μg to about 100 μg/kg of body weight, about 100 μg to about 100 mg/kg of body weight, about 100 μg to about 50 mg/kg of body weight, about 100 μg to about 10 mg/kg of body weight, about 100 μg to about 1 mg/kg of body weight, about 1 mg to about 100 mg/kg of body weight, about 1 mg to about 50 mg/kg of body weight, about 1 mg to about 10 mg/kg of body weight, about 10 mg to about 100 mg/kg of body weight, about 10 mg to about 50 mg/kg of body weight, about 50 mg to about 100 mg/kg of body weight.

[00165] Doses may be given once or more times daily, weekly, monthly or yearly, or even once every 2 to 20 years. Persons of ordinary skill in the art can easily estimate repetition rates for dosing based on measured residence times and concentrations of the targetable construct or complex in bodily fluids or tissues. Administration of the present invention could be intravenous, intraarterial, intraperitoneal, intramuscular, subcutaneous, intrapleural, intrathecal, intracavitary, by perfusion through a catheter or by direct intralesional injection. This may be administered once or more times daily, once or more times weekly, once or more times monthly, and once or more times annually.

EXAMPLES

[00166] The invention now being generally described, will be more readily understood by reference to the following examples, which are included merely for purposes of illustration of certain aspects and embodiments of the present invention, and is not intended to limit the invention.

Example 1 – NKG2D-binding domains bind to NKG2D

NKG2D-binding domains bind to purified recombinant NKG2D

[00167] The nucleic acid sequences of human, mouse or cynomolgus NKG2D ectodomains were fused with nucleic acid sequences encoding human IgG1 Fc domains and introduced into mammalian cells to be expressed. After purification, NKG2D-Fc fusion proteins were adsorbed to wells of microplates. After blocking the wells with bovine serum albumin to prevent non-specific binding, NKG2D-binding domains were titrated and added to the wells pre-adsorbed with NKG2D-Fc fusion proteins. Primary antibody binding was detected using a secondary antibody which was conjugated to horseradish peroxidase and specifically recognizes a human kappa light chain to avoid Fc cross-reactivity. 3,3',5,5'-Tetramethylbenzidine (TMB), a substrate for horseradish peroxidase, was added to the wells to visualize the binding signal, whose absorbance was measured at 450 nM and corrected at 540 nM. An NKG2D-binding domain clone, an isotype control or a positive control (selected from SEQ ID NO: 45-48, or anti-mouse NKG2D clones MI-6 and CX-5 available at eBioscience) was added to each well.

[00168] The isotype control showed minimal binding to recombinant NKG2D-Fc proteins, while the positive control bound strongest to the recombinant antigens. NKG2D-binding domains produced by all clones demonstrated binding across human (FIG. 14), mouse (FIG. 16), and cynomolgus (FIG. 15) recombinant NKG2D-Fc proteins, although with varying affinities from clone to clone. Generally, each anti-NKG2D clone bound to human (FIG. 14) and cynomolgus (FIG. 15) recombinant NKG2D-Fc with similar affinity, but with lower affinity to mouse (FIG. 16) recombinant NKG2D-Fc.

NKG2D-binding domains bind to cells expressing NKG2D

[00169] EL4 mouse lymphoma cell lines were engineered to express human or mouse NKG2D - CD3 zeta signaling domain chimeric antigen receptors. An NKG2D-binding clone, an isotype control or a positive control was used at a 100 nM concentration to stain extracellular NKG2D expressed on the EL4 cells. The antibody binding was detected using fluorophore conjugated anti-human IgG secondary antibodies. Cells were analyzed by flow cytometry, and fold-over-background (FOB) was calculated using the mean fluorescence intensity (MFI) of NKG2D-expressing cells compared to parental EL4 cells.

[00170] NKG2D-binding domains produced by all clones bound to EL4 cells expressing human and mouse NKG2D. Positive control antibodies (selected from SEQ ID NO:45-48, or anti-mouse NKG2D clones MI-6 and CX-5 available at eBioscience) gave the best FOB binding signal. The NKG2D binding affinity for each clone was similar between cells expressing human NKG2D (FIG. 17) and mouse NKG2D (FIG. 18).

Example 2 – NKG2D-binding domains block natural ligand binding to NKG2D

Competition With ULBP-6

[00171] Recombinant human NKG2D-Fc proteins were adsorbed to wells of a microplate, and the wells were blocked with bovine serum albumin reduce non-specific binding. A saturating concentration of ULBP-6-His-biotin was added to the wells, followed by addition of the NKG2D-binding domain clones. After a 2-hour incubation, wells were washed and ULBP-6-His-biotin that remained bound to the NKG2D-Fc coated wells was detected by streptavidin conjugated to horseradish peroxidase and TMB substrate. Absorbance was measured at 450 nM and corrected at 540 nM. After subtracting background, specific binding of NKG2D-binding domains to the NKG2D-Fc proteins was calculated from the percentage of ULBP-6-His-biotin that was blocked from binding to the NKG2D-Fc proteins in wells. The positive control antibody (selected from SEQ ID NO:45-48) and various NKG2D-binding domains blocked ULBP-6 binding to NKG2D, while isotype control showed little competition with ULBP-6 (FIG. 19).

Competition With MICA

[00172] Recombinant human MICA-Fc proteins were adsorbed to wells of a microplate, and the wells were blocked with bovine serum albumin to reduce non-specific binding. NKG2D-Fc-biotin was added to wells followed by NKG2D-binding domains. After incubation and washing, NKG2D-Fc-biotin that remained bound to MICA-Fc coated wells was detected using streptavidin-HRP and TMB substrate. Absorbance was measured at 450 nM and corrected at 540 nM. After subtracting background, specific binding of NKG2D-binding domains to the NKG2D-Fc proteins was calculated from the percentage of NKG2D-Fc-biotin that was blocked from binding to the MICA-Fc coated wells. The positive control antibody (selected from SEQ ID NO:45-48) and various NKG2D-binding domains blocked MICA binding to NKG2D, while isotype control showed little competition with MICA (FIG. 20).

Competition With Rae-1 delta

[00173] Recombinant mouse Rae-1delta-Fc (purchased from R&D Systems) was adsorbed to wells of a microplate, and the wells were blocked with bovine serum albumin to reduce non-specific binding. Mouse NKG2D-Fc-biotin was added to the wells followed by NKG2D-binding domains. After incubation and washing, NKG2D-Fc-biotin that remained bound to

Rae-1delta-Fc coated wells was detected using streptavidin-HRP and TMB substrate. Absorbance was measured at 450 nM and corrected at 540 nM. After subtracting background, specific binding of NKG2D-binding domains to the NKG2D-Fc proteins was calculated from the percentage of NKG2D-Fc-biotin that was blocked from binding to the Rae-1delta-Fc coated wells. The positive control (selected from SEQ ID NO: 45-48, or anti-mouse NKG2D clones MI-6 and CX-5 available at eBioscience) and various NKG2D-binding domain clones blocked Rae-1delta binding to mouse NKG2D, while the isotype control antibody showed little competition with Rae-1delta (FIG. 21).

Example 3 – NKG2D-binding domain clones activate NKG2D

[00174] Nucleic acid sequences of human and mouse NKG2D were fused to nucleic acid sequences encoding a CD3 zeta signaling domain to obtain chimeric antigen receptor (CAR) constructs. The NKG2D-CAR constructs were then cloned into a retrovirus vector using Gibson assembly and transfected into expi293 cells for retrovirus production. EL4 cells were infected with viruses containing NKG2D-CAR together with 8 μg/mL polybrene. 24 hours after infection, the expression levels of NKG2D-CAR in the EL4 cells were analyzed by flow cytometry, and clones which express high levels of the NKG2D-CAR on the cell surface were selected.

[00175] To determine whether NKG2D-binding domains activate NKG2D, they were adsorbed to wells of a microplate, and NKG2D-CAR EL4 cells were cultured on the antibody fragment-coated wells for 4 hours in the presence of brefeldin-A and monensin. Intracellular TNF-alpha production, an indicator for NKG2D activation, was assayed by flow cytometry. The percentage of TNF-alpha positive cells was normalized to the cells treated with the positive control. All NKG2D-binding domains activated both human NKG2D (FIG. 22) and mouse (FIG. 23) NKG2D.

Example 4 – NKG2D-binding domains activate NK cells

Primary human NK cells

[00176] Peripheral blood mononuclear cells (PBMCs) were isolated from human peripheral blood buffy coats using density gradient centrifugation. NK cells ($CD3^-$ $CD56^+$) were isolated using negative selection with magnetic beads from PBMCs, and the purity of the isolated NK cells was typically >95%. Isolated NK cells were then cultured in media containing 100 ng/mL IL-2 for 24-48 hours before they were transferred to the wells of a microplate to which the NKG2D-binding domains were adsorbed, and cultured in the media

containing fluorophore-conjugated anti-CD107a antibody, brefeldin-A, and monensin. Following culture, NK cells were assayed by flow cytometry using fluorophore-conjugated antibodies against CD3, CD56 and IFN-gamma. CD107a and IFN-gamma staining were analyzed in $CD3^-$ $CD56^+$ cells to assess NK cell activation. The increase in CD107a/IFN-gamma double-positive cells is indicative of better NK cell activation through engagement of two activating receptors rather than one receptor. NKG2D-binding domains and the positive control (selected from SEQ ID NO:45-48) showed a higher percentage of NK cells becoming $CD107a^+$ and IFN-$gamma^+$ than the isotype control (FIG. 24 & FIG. 25 represent data from two independent experiments, each using a different donor's PBMC for NK cell preparation).

Primary mouse NK cells

[00177] Spleens were obtained from C57Bl/6 mice and crushed through a 70 µm cell strainer to obtain single cell suspension. Cells were pelleted and resuspended in ACK lysis buffer (purchased from Thermo Fisher Scientific #A1049201; 155mM ammonium chloride, 10mM potassium bicarbonate, 0.01mM EDTA) to remove red blood cells. The remaining cells were cultured with 100 ng/mL hIL-2 for 72 hours before being harvested and prepared for NK cell isolation. NK cells ($CD3^-NK1.1^+$) were then isolated from spleen cells using a negative depletion technique with magnetic beads with typically >90% purity. Purified NK cells were cultured in media containing 100 ng/mL mIL-15 for 48 hours before they were transferred to the wells of a microplate to which the NKG2D-binding domains were adsorbed, and cultured in the media containing fluorophore-conjugated anti-CD107a antibody, brefeldin-A, and monensin. Following culture in NKG2D-binding domain-coated wells, NK cells were assayed by flow cytometry using fluorophore-conjugated antibodies against CD3, NK1.1 and IFN-gamma. CD107a and IFN-gamma staining were analyzed in $CD3^-$ $NK1.1^+$ cells to assess NK cell activation. The increase in CD107a/IFN-gamma double-positive cells is indicative of better NK cell activation through engagement of two activating receptors rather than one receptor. NKG2D-binding domains and the positive control (selected from anti-mouse NKG2D clones MI-6 and CX-5 available at eBioscience) showed a higher percentage of NK cells becoming $CD107a^+$ and IFN-$gamma^+$ than the isotype control (FIG. 26 & FIG. 27 represent data from two independent experiments, each using a different mouse for NK cell preparation**).**

Example 5 – NKG2D-binding domains enable cytotoxicity of target tumor cells

[00178] Human and mouse primary NK cell activation assays demonstrate increased cytotoxicity markers on NK cells after incubation with NKG2D-binding domains. To address whether this translates into increased tumor cell lysis, a cell-based assay was utilized where each NKG2D-binding domain was developed into a monospecific antibody. The Fc region was used as one targeting arm, while the Fab region (NKG2D-binding domain) acted as another targeting arm to activate NK cells. THP-1 cells, which are of human origin and express high levels of Fc receptors, were used as a tumor target and a Perkin Elmer DELFIA Cytotoxicity Kit was used. THP-1 cells were labeled with BATDA reagent, and resuspended at 10^5/mL in culture media. Labeled THP-1 cells were then combined with NKG2D antibodies and isolated mouse NK cells in wells of a microtiter plate at 37ºC for 3 hours. After incubation, 20 µl of the culture supernatant was removed, mixed with 200 µl of Europium solution and incubated with shaking for 15 minutes in the dark. Fluorescence was measured over time by a PheraStar plate reader equipped with a time-resolved fluorescence module (Excitation 337nm, Emission 620nm) and specific lysis was calculated according to the kit instructions.

[00179] The positive control, ULBP-6 - a natural ligand for NKG2D, showed increased specific lysis of THP-1 target cells by mouse NK cells. NKG2D antibodies also increased specific lysis of THP-1 target cells, while isotype control antibody showed reduced specific lysis. The dotted line indicates specific lysis of THP-1 cells by mouse NK cells without antibody added (FIG. 28).

Example 6 – NKG2D antibodies show high thermostability

[00180] Melting temperatures of NKG2D-binding domains were assayed using differential scanning fluorimetry. The extrapolated apparent melting temperatures are high relative to typical IgG1 antibodies (FIG. 29).

Example 7 – Multi-specific binding proteins bind to NKG2D

[00181] EL4 mouse lymphoma cell lines were engineered to express human NKG2D. Trispecific binding proteins (TriNKETs) that each contain an NKG2D-binding domain, a tumor-associated antigen-binding domain (BCMA-binding domain), and an Fc domain that binds to CD16 as shown in FIG. 1, were tested for their affinity to extracellular NKG2D expressed on EL4 cells. The binding of the multi-specific binding proteins to NKG2D was detected using fluorophore-conjugated anti-human IgG secondary antibodies. Cells were

analyzed by flow cytometry, and fold-over-background (FOB) was calculated using the mean fluorescence intensity (MFI) of NKG2D-expressing cells compared to parental EL4 cells.

[00182] TriNKETs tested include BCMA-TriNKET-C26 (ADI-28226 and a BCMA-binding domain), BCMA-TriNKET-F04 (ADI-29404 and a BCMA-binding domain), BCMA-TriNKET-F43 (ADI-29443 and a BCMA-binding domain), and BCMA-TriNKET-F47 (ADI-29447 and a BCMA-binding domain).

[00183] The BCMA-binding domain used in the tested molecules was composed of a heavy chain variable domain and light chain variable domain as listed below.

[00184] EM-801 heavy chain variable domain (SEQ ID NO:91):

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGG
CDR1 CDR2
STYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKVLGWFDYWGQGTL
VTVSS CDR3

[00185] EM-801 light chain variable domain (SEQ ID NO:92):

EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGI
CDR1 CDR2
PDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGYPPDFTFGQGTKVEIK
CDR3

[00186] EM-901 heavy chain variable domain (SEQ ID NO:93)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSDNAMGWVRQAPGKGLEWVSAISGPGS
ST CDR1 CDR2
YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKVLGWFDYWGQGTLVT
VSS CDR3

[00187] EM-901 light chain variable domain (SEQ ID NO:94)

EIVLTQSPGTLSLSPGERATLSCRASQSVSDEYLSWYQQKPGQAPRLLIHSASTRATGI
PD CDR1 CDR2
RFSGSGSGTDFTLAISRLEPEDFAVYYCQQYGYPPDFTFGQGTKVEIK
CDR3

Example 8 – Multi-specific binding proteins bind to human tumor antigens

Trispecific binding proteins bind to BCMA

[00188] MM.1S human myeloma cells expressing BCMA were used to assay the binding of TriNKETs to the tumor associated antigen BCMA. TriNKETs were diluted, and were incubated with the respective cells. TriNKETs and optionally the parental anti-BCMA monoclonal antibody (EM-801) were incubated with the cells, and the binding was detected using fluorophore-conjugated anti-human IgG secondary antibodies. Cells were analyzed by flow cytometry, and fold-over-background (FOB) was calculated using the mean fluorescence intensity (MFI) from TriNKETs and EM-801 normalized to secondary antibody controls. C26-TriNKET-BCMA, F04-TriNKET-BCMA, F43-TriNKET-BCMA, and F47-TriNKET-BCMA show comparable levels of binding to BCMA expressed on MM.1S cells as compared with EM-801 (FIG. 31).

Example 9 – Multi-specific binding proteins activate NK cells

Primary human NK cells are activated by TriNKETs in co-culture with target expressing human cancer cell lines

[00189] Co-culturing primary human NK cells with BCMA-positive MM.1S myeloma cells resulted in TriNKET-mediated activation of the primary human NK cells. TriNKETs targeting BCMA (*e.g.*, C26-TriNKET-BMCA and F04-TriNKET-BMCA) mediated activation of human NK cells co-cultured with MM.1S myeloma cells, as indicated by an increase in CD107a degranulation and IFNγ cytokine production (FIG. 32). Compared to isotype TriNKET, TriNKETs targeting BCMA (*e.g.*, A44-TriNKET-BMCA, A49-TriNKET-BMCA, C26-TriNKET-BMCA, F04-TriNKET-BMCA, F43-TriNKET-BMCA, F43-TriNKET-BMCA, F47-TriNKET-BMCA, and F63-TriNKET-BMCA) showed increased NK cell activity (FIG. 32).

Example 10 – Trispecific binding proteins enable cytotoxicity of target cancer cells

[00190] Peripheral blood mononuclear cells (PBMCs) were isolated from human peripheral blood buffy coats using density gradient centrifugation. NK cells ($CD3^-$ $CD56^+$) were isolated using negative selection with magnetic beads from PBMCs, and the purity of the isolated NK cells was typically >90%. Isolated NK cells were cultured in media

containing 100ng/mL IL-2 for activation or rested overnight without cytokine. IL-2-activated or rested NK cells were used the following day in cytotoxicity assays.

DELFIA cytotoxicity assay:

[00191] Human cancer cell lines expressing a target of interest were harvested from culture, cells were washed with PBS, and were resuspended in growth media at 10^6/mL for labeling with BATDA reagent (Perkin Elmer AD0116). Manufacturer instructions were followed for labeling of the target cells. After labeling cells were washed 3x with PBS, and were resuspended at 0.5-1.0x10^5/mL in culture media. To prepare the background wells an aliquot of the labeled cells was put aside, and the cells were spun out of the media. 100 µl of the media was carefully added to wells in triplicate to avoid disturbing the pelleted cells. 100 µl of BATDA labeled cells were added to each well of the 96-well plate. Wells were saved for spontaneous release from target cells, and wells were prepared for max lysis of target cells by addition of 1% Triton-X. Monoclonal antibodies or TriNKETs against the tumor target of interest were diluted in culture media, 50 µl of diluted mAb or TriNKET was added to each well. Rested and/or activated NK cells were harvested from culture, cells were washed, and were resuspended at 10^5-2.0x10^6/mL in culture media depending on the desired E:T ratio. 50 µl of NK cells was added to each well of the plate to make a total of 200 µl culture volume. The plate was incubated at 37 ºC with 5%CO2 for 2-3 hours before developing the assay.

[00192] After culturing for 2-3 hours, the plate was removed from the incubator and the cells were pelleted by centrifugation at 200g for 5 minutes. 20 µl of culture supernatant was transferred to a clean microplate provided from the manufacturer and 200 µl of room temperature europium solution was added to each well. The plate was protected from the light and incubated on a plate shaker at 250rpm for 15 minutes. The plate was read using either Victor 3 or SpectraMax i3X instruments. % Specific lysis was calculated as follows: % Specific lysis = ((Experimental release – Spontaneous release) / (Maximum release – Spontaneous release)) * 100%.

[00193] TriNKET-mediated lysis of BCMA-positive myeloma cells was assayed. FIG. 39 shows TriNKET-mediated lysis of BCMA-positive KMS12-PE myeloma cells by rested human NK effector cells. Two TriNKETs (cFAE-A49.801 and cFAE-A49.901) using the same NKG2D-binding domain (A49), but different BCMA targeting domains were tested for efficacy *in vitro*. Both TriNKETs enhanced NK cell lysis of KMS12-PE cells to a similar extent, but TriNKETs using the EM-901 targeting domain provided increased potency (FIG. 39).

[00194] FIG. 33 shows cytotoxic activity of several TriNKETs using different NKG2D-binding domains (A40, A44, A49, C26, and F47), but the same BCMA targeting domain. Changing the NKG2D-binding domain of the BCMA-targeted TriNKET produced variations in maximal killing as well as potency of the TriNKETs. All TriNKETs demonstrated increased killing of KMS12-PE target cells compared to EM-901 monoclonal antibody (FIG. 33).

Example 11

[00195] Synergistic activation of human NK cells by cross-linking NKG2D and CD16 was investigated.

Primary human NK cell activation assay

[00196] Peripheral blood mononuclear cells (PBMCs) were isolated from peripheral human blood buffy coats using density gradient centrifugation. NK cells were purified from PBMCs using negative magnetic beads (StemCell # 17955). NK cells were >90% $CD3^-$ $CD56^+$ as determined by flow cytometry. Cells were then expanded 48 hours in media containing 100 ng/mL hIL-2 (Peprotech #200-02) before use in activation assays. Antibodies were coated onto a 96-well flat-bottom plate at a concentration of 2 µg/ml (anti-CD16, Biolegend # 302013) and 5 µg/mL (anti-NKG2D, R&D #MAB139) in 100 µl sterile PBS overnight at 4 °C followed by washing the wells thoroughly to remove excess antibody. For the assessment of degranulation IL-2-activated NK cells were resuspended at 5×10^5 cells/ml in culture media supplemented with 100 ng/mL hIL2 and 1 µg/mL APC-conjugated anti-CD107a mAb (Biolegend # 328619). 1×10^5 cells/well were then added onto antibody coated plates. The protein transport inhibitors Brefeldin A (BFA, Biolegend # 420601) and Monensin (Biolegend # 420701) were added at a final dilution of 1:1000 and 1:270 respectively. Plated cells were incubated for 4 hours at 37 °C in 5% CO_2. For intracellular staining of IFN-γ NK cells were labeled with anti-CD3 (Biolegend #300452) and anti-CD56 mAb (Biolegend # 318328) and subsequently fixed and permeabilized and labeled with anti-IFN-γ mAb (Biolegend # 506507). NK cells were analyzed for expression of CD107a and IFN-γ by flow cytometry after gating on live $CD56^+CD3^-$cells.

[00197] To investigate the relative potency of receptor combination, crosslinking of NKG2D or CD16 and co-crosslinking of both receptors by plate-bound stimulation was

performed. As shown in Figure 34 (FIGs. 34A-3C), combined stimulation of CD16 and NKG2D resulted in highly elevated levels of CD107a (degranulation) (FIG. 3A) and/or IFN-γ production (FIG. 34B). Dotted lines represent an additive effect of individual stimulations of each receptor.

[00198] CD107a levels and intracellular IFN-γ production of IL-2-activated NK cells were analyzed after 4 hours of plate-bound stimulation with anti-CD16, anti-NKG2D or a combination of both monoclonal antibodies. Graphs indicate the mean (n = 2) ± SD. FIG. 34A demonstrates levels of CD107a; FIG. 34B demonstrates levels of IFNγ; FIG. 34C demonstrates levels of CD107a. Data shown in FIGs. 34A-34C are representative of five independent experiments using five different healthy donors.

INCORPORATION BY REFERENCE

[00199] The entire disclosure of each of the patent documents and scientific articles referred to herein is incorporated by reference for all purposes.

EQUIVALENTS

[00200] The invention may be embodied in other specific forms without departing from the spirit or essential characteristics thereof. The foregoing embodiments are therefore to be considered in all respects illustrative rather than limiting the invention described herein. Scope of the invention is thus indicated by the appended claims rather than by the foregoing description, and all changes that come within the meaning and range of equivalency of the claims are intended to be embraced therein.

WHAT IS CLAIMED IS:

1. A protein comprising:

(a) a first antigen-binding site that binds NKG2D;

(b) a second antigen-binding site that binds BCMA; and

(c) an antibody Fc domain or a portion thereof sufficient to bind CD16, or a third antigen-binding site that binds CD16.

2. The protein of claim 1, wherein the first antigen-binding site binds to NKG2D in humans, non-human primates, and rodents.

3. The protein of claim 1 or 2, wherein the first antigen-binding site comprises a heavy chain variable domain and a light chain variable domain.

4. A protein according to claim 3, wherein the heavy chain variable domain and the light chain variable domain are present on the same polypeptide.

5. A protein according to any one of claims 3-4, wherein the second antigen-binding site comprises a heavy chain variable domain and a light chain variable domain.

6. A protein according to claim 5, wherein the heavy chain variable domain and the light chain variable domain of the second antigen-binding site are present on the same polypeptide.

7. A protein according to claim 5 or 6, wherein the light chain variable domain of the first antigen-binding site has an amino acid sequence identical to the amino acid sequence of the light chain variable domain of the second antigen-binding site.

8. A protein according to any one of the preceding claims, wherein the first antigen-binding site comprises a heavy chain variable domain at least 90% identical to SEQ ID NO:1.

9. A protein according to any of claims 1-7, wherein the first antigen-binding site comprises a heavy chain variable domain at least 90% identical to SEQ ID NO:41 and a light chain variable domain at least 90% identical to SEQ ID NO:42.

10. A protein according to any of claims 1-7, wherein the first antigen-binding site comprises a heavy chain variable domain at least 90% identical to SEQ ID NO:43 and a light chain variable domain at least 90% identical to SEQ ID NO:44.

11. A protein according to any of claims 1-7, wherein the first antigen-binding site comprises a heavy chain variable domain at least 90% identical to SEQ ID NO:45 and a light chain variable domain at least 90% identical to SEQ ID NO:46.

12. A protein according to any of claims 1-7, wherein the first antigen-binding site comprises a heavy chain variable domain at least 90% identical to SEQ ID NO:47 and a light chain variable domain at least 90% identical to SEQ ID NO:48.

13. The protein of claim 1 or 2, wherein the first antigen-binding site is a single-domain antibody.

14. The protein of claim 13, wherein the single-domain antibody is a V_HH fragment or a V_{NAR} fragment.

15. A protein according to any one of claims 1-2 or 13-14, wherein the second antigen-binding site comprises a heavy chain variable domain and a light chain variable domain.

16. A protein according to claim 15, wherein the heavy chain variable domain and the light chain variable domain of the second antigen-binding site are present on the same polypeptide.

17. A protein according to any of the preceding claims, wherein the heavy chain variable domain of the second antigen-binding site comprises an amino acid sequence at least 90% identical to SEQ ID NO:49 and the light chain variable domain of the second antigen-binding site comprises an amino acid sequence at least 90% identical to SEQ ID NO:53 or SEQ ID NO:54.

18. A protein according to any of the preceding claims, wherein the heavy chain variable domain of the second antigen-binding site comprises an amino acid sequence including:

a heavy chain CDR1 sequence identical to the amino acid sequence of SEQ ID NO:50;

a heavy chain CDR2 sequence identical to the amino acid sequence of SEQ ID NO:51; and

a heavy chain CDR3 sequence identical to the amino acid sequence of SEQ ID NO:52.

19. A protein according to claim 18, wherein the light chain variable domain of the second antigen-binding site comprises an amino acid sequence including:

a light chain CDR1 sequence identical to the amino acid sequence of SEQ ID NO:55;

a light chain CDR2 sequence identical to the amino acid sequence of SEQ ID NO:56; and

a light chain CDR3 sequence identical to the amino acid sequence of SEQ ID NO:57 or SEQ ID NO:57.

20. A protein according to any one of claims 1-16, wherein the heavy chain variable domain of the second antigen-binding site comprises an amino acid sequence at least 90% identical to SEQ ID NO:59 and the light chain variable domain of the second antigen-binding site comprises an amino acid sequence at least 90% identical to SEQ ID NO:60.

21. A protein according to any one of claims 1-16 or 20, wherein the heavy chain variable domain of the second antigen-binding site comprises an amino acid sequence including:

a heavy chain CDR1 sequence identical to the amino acid sequence of SEQ ID NO:79;

a heavy chain CDR2 sequence identical to the amino acid sequence of SEQ ID NO:80; and

a heavy chain CDR3 sequence identical to the amino acid sequence of SEQ ID NO:81.

22. A protein according to claim 21, wherein the light chain variable domain of the second antigen-binding site comprises an amino acid sequence including:

a light chain CDR1 sequence identical to the amino acid sequence of SEQ ID NO:82;

a light chain CDR2 sequence identical to the amino acid sequence of SEQ ID NO:83; and

a light chain CDR3 sequence identical to the amino acid sequence of SEQ ID NO:84.

23. A protein according to any one of claims 1-16, wherein the heavy chain variable domain of the second antigen-binding site comprises an amino acid sequence at least 90% identical to SEQ ID NO:61 and the light chain variable domain of the second antigen-binding site comprises an amino acid sequence at least 90% identical to SEQ ID NO:62.

24. A protein according to any one of claims 1-16 or 23, wherein the heavy chain variable domain of the second antigen-binding site comprises an amino acid sequence including:

a heavy chain CDR1 sequence identical to the amino acid sequence of SEQ ID NO:85;

a heavy chain CDR2 sequence identical to the amino acid sequence of SEQ ID NO:86; and

a heavy chain CDR3 sequence identical to the amino acid sequence of SEQ ID NO:87.

25. A protein according to any one of claim 24, wherein the light chain variable domain of the second antigen-binding site comprises an amino acid sequence including:

a light chain CDR1 sequence identical to the amino acid sequence of SEQ ID NO:88;

a light chain CDR2 sequence identical to the amino acid sequence of SEQ ID NO:89; and

a light chain CDR3 sequence identical to the amino acid sequence of SEQ ID NO:90.

26. A protein according to any one of claims 1-4 or 8-14, wherein the second antigen-binding site is a single-domain antibody.

27. The protein of claim 26, wherein the second antigen-binding site is a V_HH fragment or a V_{NAR} fragment.

28. A protein according to any one of the preceding claims, wherein the protein comprises a portion of an antibody Fc domain sufficient to bind CD16, wherein the antibody Fc domain comprises hinge and CH2 domains.

29. A protein according to claim 28, wherein the antibody Fc domain comprises hinge and CH2 domains of a human IgG1 antibody.

30. A protein according to claim 28 or 29, wherein the Fc domain comprises an amino acid sequence at least 90% identical to amino acids 234-332 of a human IgG1 antibody.

31. A protein according to any one of claims 28-30, wherein the Fc domain comprises amino acid sequence at least 90% identical to the Fc domain of human IgG1 and differs at one or more positions selected from the group consisting of Q347, Y349, L351, S354, E356, E357, K360, Q362, S364, T366, L368, K370, N390, K392, T394, D399, S400, D401, F405, Y407, K409, T411, K439.

32. A formulation comprising a protein according to any one of the preceding claims and a pharmaceutically acceptable carrier.

33. A cell comprising one or more nucleic acids expressing a protein according to any one of claims 1-31.

34. A method of directly and/or indirectly enhancing tumor cell death, the method comprising exposing a tumor and natural killer cells to a protein according to any one of claims 1-31.

35. A method of treating cancer, wherein the method comprises administering a protein according to any one of claims 1-31 or a formulation according to claim 32 to a patient.

36. The method of claim 35, wherein the cancer is selected from the group consisting of multiple myeloma, acute myelomonocytic leukemia, T cell lymphoma, acute monocytic leukemia, and follicular lymphoma.