

[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- γ 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. NKG2D is a type-II transmembrane protein that is expressed by essentially all natural killer cells where NKG2D serves as an activating receptor. NKG2D is also found on T cells where it acts as a costimulatory receptor. The ability to modulate NK cell function via NKG2D is useful in various therapeutic contexts including malignancy.

SUMMARY

[0008] ~~In one aspect, the present disclosure refers to a polypeptide comprising a single-chain variable fragment (scFv) linked to an antibody constant domain via a hinge comprising Ala-Ser, wherein the scFv comprises a heavy chain variable domain and a light chain variable domain.~~ In ~~another one~~ aspect, the present disclosure refers to a protein comprising (a) ~~the polypeptide as described herein, wherein the~~ a single-chain variable fragment (scFv) that binds a tumor-associated antigen, wherein the scFv comprises a heavy chain variable domain and a light chain variable domain of the polypeptide comprises a first antigen-binding site; (b) a Fab that binds NKG2Dsecond antigen-binding site; and (c) a first antibody constant domain and a second antibody constant domain that form a heterodimer binding CD16, wherein the scFv is linked to the N-terminus of the first antibody constant domain via a hinge comprising Ala-Ser sequence, and the Fab is linked to the N-terminus of the second antibody constant domain.

[0008a] In another aspect, the present disclosure refers to a protein comprising: (a) a single-chain variable fragment (scFv) that binds a tumor-associated antigen; a first antigen-binding site that binds a tumor-associated antigen; (b) a Fab that binds NKG2D; and a second antigen-binding site that binds the same tumor-associated antigen as the first antigen-binding site; (c) a first antibody constant domain and a second antibody constant domain that form a heterodimer binding CD16, a third antigen-binding site that binds NKG2D; and (d) an antibody constant region or a portion thereof sufficient to bind CD16, or a fourth antigen-binding site that binds CD16 wherein the scFv comprises a heavy chain variable domain and a light chain variable domain and is linked to the N-terminus of the first antibody constant domain via a hinge, and the Fab is linked to the N-terminus of the second antibody constant domain, wherein the tumor-associated antigen is selected from the group consisting of CCR4, CD123, CD25, DLL3, GD2, CXCR4, HLA-E, PD-L1, VLA4, CD44, CD13, CD15, CD47, CD81, CD23, CD79a, CD79b, CD80, CRLF2, SLAMF7, CD138, CA125, NaPi2b, ADAM8, ADAM9, SLC44A4, CA19-9, LILRB1, LILRB2, LILRB3, LILRB4, LILRB5, LILRA1, LILRA2, LILRA3, LILRA4, LILRA5, and LILRA6, CCR8, CD7, CTLA4, CX3CR1, ENTPD1, HAVCR2, IL-1R2, PDCD1LG2, TIGIT, TNFRSF4, TNFRSF8, TNFRSF9, GEM, NT5E, TNFRSF18, P-cadherin, Plexin-A1, TNFRSF10B, STEAP1, CDCP1, PTK7, Axl, erbB-3, EDNRB, Tyrp1, CD14, CD163, CSF3R, Siglec-9, ITGAM, VISTA, B7-H4 (VTCN1), CCR1, LRRC25, PTAFR, SIRPB1, TLR2, TLR4, CD300LB, ATP1A3, CCR5, Plexin-A1, TNFRSF10B, STEAP1, CDCP1, PTK7, Axl, EDNRB, OLR1, and Tyrp1.

[0008b] ~~In yet another aspect, the present disclosure refers to a protein comprising: (a) an antigen-binding site that binds NKG2D; (b) an antigen-binding T-cell receptor (TCR) fragment; and (c) an antibody constant region or a portion thereof sufficient to bind CD16, or an additional antigen-binding site that binds CD16.~~ In yet another aspect, the present

disclosure refers to a formulation comprising a protein as described herein and a pharmaceutically acceptable carrier. In yet another aspect, the present disclosure refers to a cell comprising one or more nucleic acids encoding a protein as described herein.

[0008c] In a further aspect, the present disclosure refers to the protein as described herein or the formulation as described herein for use in therapy. In a further aspect, the present disclosure refers to use of the protein as described herein or the formulation as described herein in the manufacture of a medicament for treating cancer.

[0008d] In one example, the current disclosure provides an improvement on a single-chain variable fragment (scFv) that is linked to an antibody constant domain via a hinge sequence. In some examples, the hinge comprises amino acids Ala-Ser. In some other examples, the hinge comprises amino acids Ala-Ser and Thr-Lys-Gly. The scFv may include a heavy chain variable domain and a light chain variable domain. In some examples, the scFv binds NKG2D or a tumor-associated antigen. The hinge sequence provides flexibility of binding to the target antigen.

[0009] In some examples of the scFv, the heavy chain variable domain forms a disulfide bridge with the light chain variable domain. For example, a disulfide bridge can be formed between the C44 residue of the heavy chain variable domain and the C100 residue of the light chain variable domain. In some examples, the heavy chain variable domain is linked to the light chain variable domain via a flexible linker, such as (G₄S)₄ (SEQ ID NO:427). In some examples of the scFv, the heavy chain variable domain is positioned at the N terminus of the light chain variable domain. In some examples of the scFv, the heavy chain variable domain is positioned at the C terminus of the light chain variable domain.

[0010] In some examples, the antibody constant domain linked to the scFv is able to bind to CD16. In some examples, the antibody constant domain comprises a CH2 domain and a CH3 domain of an IgG antibody, for example, a human IgG1 antibody. In some examples, mutations are introduced in the antibody constant domain to enable heterodimerization with another antibody constant domain. For example, if the antibody constant domain is derived

Claims:

1. ~~—A polypeptide comprising a single chain variable fragment (scFv) linked to an antibody constant domain via a hinge comprising Ala-Ser, wherein the scFv comprises a heavy chain variable domain and a light chain variable domain.~~

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2. ~~—The polypeptide according to claim 1, wherein the heavy chain variable domain forms a disulfide bridge with the light chain variable domain, optionally between C44 from the heavy chain variable domain and C100 from the light chain variable domain.~~

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3. ~~—A polypeptide according to claim 1 or 2, wherein the heavy chain variable domain is linked to the light chain variable domain via a flexible linker, optionally wherein the flexible linker comprises (G₄S)₄.~~

4. ~~—A polypeptide according to any one of claims 1-3, wherein the heavy chain variable domain is positioned at the N-terminus or the C-terminus of the light chain variable domain.~~

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5. ~~—A polypeptide according to any one of claims 1-4, wherein the hinge further comprises amino acid sequence Thr-Lys-Gly.~~

6. ~~—A polypeptide according to any one of claims 1-5, wherein the antibody constant domain comprises:~~

~~(a) an antibody Fc domain or a portion thereof sufficient to bind CD16;~~

~~(b) a CH2 and a CH3 domain of a human IgG1 antibody;~~

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~~(c) an amino acid sequence at least 90% identical to amino acids 234-332 of a human IgG1 antibody; and/or~~

~~(d) an amino acid sequence at least 90% identical to the Fc domain of human IgG1 and differing 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, and K439.~~

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7. — A polypeptide according to claim 6, wherein the antibody constant domain comprises amino acid sequence at least 90% identical to the Fc domain of human IgG1 and differing by one or more substitutions selected from the group consisting of Q347E, Q347R, Y349S, Y349K, Y349T, Y349D, Y349E, Y349C, 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, D399R, D399K, D399V, S400K, S400R, D401K, F405A, F405T, Y407A, Y407I, Y407V, K409F, K409W, K409D, T411D, T411E, K439D, and K439E.

8. — A polypeptide according to any one of claims 1-7, wherein the scFv binds NKG2D.

9. — A polypeptide according to claim 8, wherein:

(a) the heavy chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:94 and the light chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:98;

(b) the heavy chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:322 and the light chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:98;

(c) the heavy chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:325 and the light chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:98;

(d) the heavy chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:328 and the light chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:98;

(e) the heavy chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:331 and the light chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:98;

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- (f) ~~the heavy chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:334 and the light chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:98;~~
- (g) ~~the heavy chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:337 and the light chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:98;~~
- (h) ~~wherein the heavy chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:44 and the light chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:48;~~
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- (i) ~~the heavy chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:52 and the light chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:56.~~
- (j) ~~the heavy chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:60 and the light chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:61;~~
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- (k) ~~the heavy chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:62 and the light chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:66;~~
- (l) ~~the heavy chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:70 and the light chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:74;~~
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- (m) ~~the heavy chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:78 and the light chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:82;~~
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- (n) ~~the heavy chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:86 and the light chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:90;~~

- (o) ~~the heavy chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:102 and the light chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:106;~~
- (p) ~~the heavy chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:110 and the light chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:111; or~~
- (q) ~~the heavy chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:112 and the light chain variable domain comprises an amino acid sequence at least 90% identical to SEQ ID NO:113.~~
10. — ~~A polypeptide according to any one of claims 1-7, wherein the scFv binds to a tumor-associated antigen, optionally wherein the tumor-associated antigen is selected from the group consisting of ANO1, CAIX, CCR4, CD2, CD123, CD133, CD20, CD22, CD25, CD30, CD37, CD38, CD40, CD52, CD70, CLAUDIN-18.2, DLL3, GD2, IGF1R, HER2, HER3/ERBB3, HER4/ERBB4, MUC1, SLAMF7, PSMA, mesothelin, MICA, MICB, TRAILR1, TRAILR2, TROP2, MAGE-A3, B7.1, B7.2, CTLA4, PD1, 5T4, GPNMB, FR-alpha, PAPP-A, GPC3, CXCR4, ROR1, ROR2, PD-L1, VLA4, CD44, CD13, CD15, CD47, CD81, CD23, CD79a, CD79b, CD80, CRLF2, SLAMF7, CD138, CA125, NaPi2b, ADAM8, ADAM9, SLC44A4, CA19-9, LILRB1, LILRB2, LILRB3, LILRB4, LILRB5, ULRA-1, LILRA2, LILRA3, ULRA4, LILRA5, and ULRA6, CCR8, CD7, CTLA4, CX3CR1, ENTPD1, HAVCR2, IL-1R2, PDCD1LG2, TIGIT, TNFRSF4, TNFRSF8, TNFRSF9, GEM, NT5E, TNFRSF18, P-cadherin, Plexin-A1, TNFRSF10B, STEAP1, CDCP1, PTK7, Axl, erbB-3, EDNRB, Tyrp1, CD14, CD163, CSF3R, Siglec-9, ITGAM, VISTA, B7-H4 (VTCN1), CCR1, LRRC25, PTAFR, SIRPB1, TLR2, TLR4, CD300LB, ATP1A3, CCR5, Plexin-A1, TNFRSF10B, STEAP1, CDCP1, PTK7, AXL, EDNRB, OLR1, and TYRP1.~~
11. A protein comprising:
- (a) the polypeptide according to any one of claims 1-10, wherein thea single-chain variable fragment (scFv) that binds a tumor-associated antigen, wherein the scFv

comprises a heavy chain variable domain and a light chain variable domain of the polypeptide comprises a first antigen-binding site;

(b) a second antigen-binding site Fab that binds NKG2D; and

(c) a first antibody constant domain and a second antibody constant domain that form a heterodimer binding CD16,

wherein the scFv is linked to the N-terminus of the first antibody constant domain via a hinge comprising Ala-Ser sequence, and the Fab is linked to the N-terminus of the second antibody constant domain.

2. A protein according to claim 1, wherein the tumor-associated antigen is selected from the group consisting of ANO1, CAIX, CCR4, CD2, CD123, CD133, CD20, CD22, CD25, CD30, CD37, CD38, CD40, CD52, CD70, CLAUDIN-18.2, DLL3, GD2, IGF1R, HER2, HER3/ERBB3, HER4/ERBB4, MUC1, SLAMF7, PSMA, mesothelin, MICA, MICB, TRAILR1, TRAILR2, TROP2, MAGE-A3, B7.1, B7.2, CTLA4, PD1, 5T4, GPNMB, FR-alpha, PAPP-A, GPC3, CXCR4, ROR1, ROR2, PD-L1, VLA4, CD44, CD13, CD15, CD47, CD81, CD23, CD79a, CD79b, CD80, CRLF2, SLAMF7, CD138, CA125, NaPi2b, ADAM8, ADAM9, SLC44A4, CA19-9, LILRB1, LILRB2, LILRB3, LILRB4, LILRB5, LILRA1, LILRA2, LILRA3, LILRA4, LILRA5, LILRA6, CCR8, CD7, CTLA4, CX3CR1, ENTPD1, HAVCR2, IL-1R2, PDCD1LG2, TIGIT, TNFRSF4, TNFRSF8, TNFRSF9, GEM, NT5E, TNFRSF18, P-cadherin, Plexin-A1, TNFRSF10B, STEAP1, CDCP1, PTK7, Axl, erbB-3, EDNRB, Tyrp1, CD14, CD163, CSF3R, Siglec-9, ITGAM, VISTA, B7-H4 (VTCN1), CCR1, LRRC25, PTAFR, SIRPB1, TLR2, TLR4, CD300LB, ATP1A3, CCR5, Plexin-A1, TNFRSF10B, STEAP1, CDCP1, PTK7, AXL, EDNRB, OLR1, and TYRP1.

3. A protein comprising:

(a) a single-chain variable fragment (scFv) that binds a tumor-associated antigen;

(b) a Fab that binds NKG2D; and

(c) a first antibody constant domain and a second antibody constant domain that form a heterodimer binding CD16,

wherein the scFv comprises a heavy chain variable domain and a light chain variable domain and is linked to the N-terminus of the first antibody constant domain via a hinge, and the Fab is linked to the N-terminus of the second antibody constant domain, and

wherein the tumor-associated antigen is selected from the group consisting of CCR4, CD123, CD25, DLL3, GD2, CXCR4, HLA-E, PD-L1, VLA4, CD44, CD13, CD15, CD47, CD81, CD23, CD79a, CD79b, CD80, CRLF2, SLAMF7, CD138, CA125, NaPi2b, ADAM8, ADAM9, SLC44A4, CA19-9, LILRB1, LILRB2, LILRB3, LILRB4, LILRB5, LILRA1, LILRA2, LILRA3, LILRA4, LILRA5, and LILRA6, CCR8, CD7, CTLA4, CX3CR1, ENTPD1, HAVCR2, IL-1R2, PDCD1LG2, TIGIT, TNFRSF4, TNFRSF8, TNFRSF9, GEM, NT5E, TNFRSF18, P-cadherin, Plexin-A1, TNFRSF10B, STEAP1, CDCP1, PTK7, Axl, erbB-3, EDNRB, Tyrp1, CD14, CD163, CSF3R, Siglec-9, ITGAM, VISTA, B7-H4 (VTCN1), CCR1, LRRC25, PTAFR, SIRPB1, TLR2, TLR4, CD300LB, ATP1A3, CCR5, Plexin-A1, TNFRSF10B, STEAP1, CDCP1, PTK7, Axl, EDNRB, OLR1, and Tyrp1.

4. The protein according to any one of claims 1-3, wherein the heavy chain variable domain forms a disulfide bridge with the light chain variable domain, optionally between C44 from the heavy chain variable domain and C100 from the light chain variable domain.

5. A protein according to any one of claims 1-4, wherein the heavy chain variable domain of the scFv is linked to the light chain variable domain via a flexible linker, optionally wherein the flexible linker comprises (G₄S)₄.

6. A protein according to any one of claims 1-5, wherein the heavy chain variable domain of the scFv is positioned at the N-terminus of the light chain variable domain.

~~12. The protein of claim 11, wherein the first antigen-binding site binds NKG2D, and the second antigen-binding site binds an tumor-associated antigen.~~

~~13. The protein of claim 11, wherein the first antigen-binding site binds an tumor-associated antigen, and the second antigen-binding site binds NKG2D.~~

~~14. A protein according to any one of claims 11-13, wherein the second antigen binding site comprises a Fab.~~

157. A protein according to any one of claims ~~11-14~~ 6, wherein the first antibody constant domain and/or the second antibody constant domain comprises:

(a) a hinge and a CH2 domain of a human IgG1 antibody;

(b) ~~an amino acid sequence at least 90% identical to amino acids 234-332 of a human IgG1 antibody; and/or~~

(b) ~~an amino acid sequence at least 90% identical to the Fc domain of human IgG1 and differing 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, and K439.~~

8. The protein according to any one of claims 1-7, wherein the first antibody constant domain and/or the second antibody constant domain comprises an amino acid sequence at least 90% identical to amino acids 234-332 of a human IgG1 antibody.

9. The protein according to any one of claims 1-8, wherein the first antibody constant domain and/or the second antibody constant domain comprises an amino acid sequence at least 90% identical to the Fc domain of human IgG1 and differing 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, and K439.

10. A protein according to claim 9, wherein the first antibody constant domain and the second antibody constant domain comprise an amino acid sequence at least 90% identical to the Fc domain of human IgG1 and differ by one or more substitutions selected from the group consisting of Q347E, Q347R, Y349S, Y349K, Y349T, Y349D, Y349E, Y349C, 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, D399R, D399K, D399V, S400K, S400R, D401K, F405A, F405T, Y407A, Y407I, Y407V, K409F, K409W, K409D, T411D, T411E, K439D, and K439E.

16. ~~A protein comprising:~~

~~(a) a first antigen-binding site that binds a tumor-associated antigen;~~

~~(b) a second antigen-binding site that binds the same tumor-associated antigen as the first antigen-binding site;~~

~~(c) a third antigen-binding site that binds NKG2D; and~~

(d) ~~an antibody constant region or a portion thereof sufficient to bind CD16, or a fourth antigen-binding site that binds CD16.~~

17. ~~A protein according to claim 16, wherein the first antigen-binding site and the second antigen-binding site each comprises a Fab.~~

5 18. ~~A protein according to claim 16 or 17, wherein the third antigen-binding site comprises an scFv.~~

19. ~~A protein according to any one of claims 16-18, wherein the tumor-associated antigen is selected from the group consisting of ANO1, CAIX, CCR4, CD2, CD123, CD133, CD20, CD22, CD25, CD30, CD37, CD38, CD40, CD52, CD70, CLAUDIN 18.2, DLL3, GD2, IGF1R, HER2, HER3/ERBB3, HER4/ERBB4, MUC1, SLAMF7, PSMA, mesothelin, MICA, MICB, TRAILR1, TRAILR2, TROP2, MAGE-A3, B7.1, B7.2, CTLA4, PD1, 5T4, GPNMB, FR-alpha, PAPP-A, GPC3, CXCR4, ROR1, ROR2, PD-L1, VLA4, CD44, CD13, CD15, CD47, CD81, CD23, CD79a, CD79b, CD80, CRLF2, SLAMF7, CD138, CA125, NaPi2b, ADAM8, ADAM9, SLC44A4, CA19-9, LILRB1, LILRB2, LILRB3, LILRB4, LILRB5, ULRA-1, LILRA2, LILRA3, ULRA4, LILRA5, and ULRA6, CCR8, CD7, CTLA4, CX3CR1, ENTPD1, HAVCR2, IL-1R2, PDCD1LG2, TIGIT, TNFRSF4, TNFRSF8, TNFRSF9, GEM, NT5E, TNFRSF18, P-cadherin, Plexin-A1, TNFRSF10B, STEAP1, CDCP1, PTK7, Axl, erbB-3, EDNRB, Tyrp1, CD14, CD163, CSF3R, Siglec-9, ITGAM, VISTA, B7-H4 (VTCN1), CCR1, LRRC25, PTAFR, SIRPB1, TLR2, TLR4, CD300LB, ATP1A3, CCR5, Plexin-A1, TNFRSF10B, STEAP1, CDCP1, PTK7, AXL, EDNRB, OLR1, and TYRP1.~~

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2011. A protein according to any one of claims ~~16-19~~1-10, wherein the ~~third antigen-binding site~~Fab that binds NKG2D comprises:

(a) a heavy chain variable domain (VH) comprising an amino acid sequence at least 90% identical to SEQ ID NO:94, wherein the VH comprises a complementarity determining region (CDR) 1 sequence identical to the amino acid sequence of SEQ ID NO:319, a CDR2 sequence identical to the amino acid sequence of SEQ ID NO:96, and a CDR3 sequence identical to the amino acid sequence of SEQ ID NO:320; and a light chain variable domain (VL) comprising an amino acid

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sequence at least 90% identical to SEQ ID NO:98, wherein the VL comprises a CDR1 sequence identical to the amino acid sequence of SEQ ID NO:99, a CDR2 sequence identical to the amino acid sequence of SEQ ID NO:100, and a CDR3 sequence identical to the amino acid sequence of SEQ ID NO:101;

5 (b) a ~~heavy chain variable domain-VH~~ comprising an amino acid sequence at least 90% identical to SEQ ID NO:322, wherein the VH comprises a CDR1 sequence identical to the amino acid sequence of SEQ ID NO:319, a CDR2 sequence identical to the amino acid sequence of SEQ ID NO:96, and a CDR3 sequence identical to the amino acid sequence of SEQ ID NO:324; and a ~~light chain variable domain-VL~~ comprising an amino acid sequence at least 90% identical to SEQ ID NO:98; wherein the VL comprises a CDR1 sequence identical to the amino acid sequence of SEQ ID NO:99, a CDR2 sequence identical to the amino acid sequence of SEQ ID NO:100, and a CDR3 sequence identical to the amino acid sequence of SEQ ID NO:101;

15 (c) a ~~heavy chain variable domain-VH~~ comprising an amino acid sequence at least 90% identical to SEQ ID NO:325, wherein the VH comprises a CDR1 sequence identical to the amino acid sequence of SEQ ID NO:319, a CDR2 sequence identical to the amino acid sequence of SEQ ID NO:96, and a CDR3 sequence identical to the amino acid sequence of SEQ ID NO:327; and a ~~light chain variable domain-VL~~ comprising an amino acid sequence at least 90% identical to SEQ ID NO:98, wherein the VL comprises a CDR1 sequence identical to the amino acid sequence of SEQ ID NO:99, a CDR2 sequence identical to the amino acid sequence of SEQ ID NO:100, and a CDR3 sequence identical to the amino acid sequence of SEQ ID NO:101;

25 (d) a ~~heavy chain variable domain-VH~~ comprising an amino acid sequence at least 90% identical to SEQ ID NO:328, wherein the VH comprises a CDR1 sequence identical to the amino acid sequence of SEQ ID NO:319, a CDR2 sequence identical to the amino acid sequence of SEQ ID NO:96, and a CDR3 sequence identical to the amino acid sequence of SEQ ID NO:330; and a ~~light chain~~

~~variable domain-VL~~ comprising an amino acid sequence at least 90% identical to SEQ ID NO:98, wherein the VL comprises a CDR1 sequence identical to the amino acid sequence of SEQ ID NO:99, a CDR2 sequence identical to the amino acid sequence of SEQ ID NO:100, and a CDR3 sequence identical to the amino acid sequence of SEQ ID NO:101;

- (e) a ~~heavy chain variable domain-VH~~ comprising an amino acid sequence at least 90% identical to SEQ ID NO:331, wherein the VH comprises a CDR1 sequence identical to the amino acid sequence of SEQ ID NO:319, a CDR2 sequence identical to the amino acid sequence of SEQ ID NO:96, and a CDR3 sequence identical to the amino acid sequence of SEQ ID NO:333; and a ~~light chain variable domain-VL~~ comprising an amino acid sequence at least 90% identical to SEQ ID NO:98, wherein the VL comprises a CDR1 sequence identical to the amino acid sequence of SEQ ID NO:99, a CDR2 sequence identical to the amino acid sequence of SEQ ID NO:100, and a CDR3 sequence identical to the amino acid sequence of SEQ ID NO:101;

- (f) a ~~heavy chain variable domain-VH~~ comprising an amino acid sequence at least 90% identical to SEQ ID NO:334, wherein the VH comprises a CDR1 sequence identical to the amino acid sequence of SEQ ID NO:319, a CDR2 sequence identical to the amino acid sequence of SEQ ID NO:96, and a CDR3 sequence identical to the amino acid sequence of SEQ ID NO:336; and a ~~light chain variable domain-VL~~ comprising an amino acid sequence at least 90% identical to SEQ ID NO:98, wherein the VL comprises a CDR1 sequence identical to the amino acid sequence of SEQ ID NO:99, a CDR2 sequence identical to the amino acid sequence of SEQ ID NO:100, and a CDR3 sequence identical to the amino acid sequence of SEQ ID NO:101;

- (g) a ~~heavy chain variable domain-VH~~ comprising an amino acid sequence at least 90% identical to SEQ ID NO:337, wherein the VH comprises a CDR1 sequence identical to the amino acid sequence of SEQ ID NO:319, a CDR2 sequence identical to the amino acid sequence of SEQ ID NO:96, and a CDR3 sequence

identical to the amino acid sequence of SEQ ID NO:339; and a ~~light chain~~
~~variable domain-VL~~ comprising an amino acid sequence at least 90% identical to
SEQ ID NO:98, wherein the VL comprises a light chain CDR1 sequence identical
to the amino acid sequence of SEQ ID NO:99, a light chain CDR2 sequence
identical to the amino acid sequence of SEQ ID NO:100, and a light chain CDR3
sequence identical to the amino acid sequence of SEQ ID NO:101;

(h) a ~~heavy chain variable domain-VH~~ comprising an amino acid sequence at least
90% identical to SEQ ID NO:44, wherein the VH comprises a CDR1 sequence
identical to the amino acid sequence of SEQ ID NO:309, a CDR2 sequence
identical to the amino acid sequence of SEQ ID NO:46, and a CDR3 sequence
identical to the amino acid sequence of SEQ ID NO:310; and a ~~light chain~~
~~variable domain-VL~~ comprising an amino acid sequence at least 90% identical to
SEQ ID NO:48, wherein the VL comprises a CDR1 sequence identical to the
amino acid sequence of SEQ ID NO:49, a CDR2 sequence identical to the amino
acid sequence of SEQ ID NO:50, and a CDR3 sequence identical to the amino
acid sequence of SEQ ID NO:51;

(i) a ~~heavy chain variable domain-VH~~ comprising an amino acid sequence at least
90% identical to SEQ ID NO:52, wherein the VH comprises a CDR1 sequence
identical to the amino acid sequence of SEQ ID NO:311, a CDR2 sequence
identical to the amino acid sequence of SEQ ID NO:54, and a CDR3 sequence
identical to the amino acid sequence of SEQ ID NO:312; and a ~~light chain~~
~~variable domain-VL~~ comprising an amino acid sequence at least 90% identical to
SEQ ID NO:56, wherein the VL comprises a CDR1 sequence identical to the
amino acid sequence of SEQ ID NO:57, a CDR2 sequence identical to the amino
acid sequence of SEQ ID NO:58, and a CDR3 sequence identical to the amino
acid sequence of SEQ ID NO:59;

(j) a ~~heavy chain variable domain-VH~~ comprising an amino acid sequence ~~at least~~
~~90%~~ identical to SEQ ID NO:60; and a ~~light chain variable domain-VL~~
comprising an amino acid sequence ~~at least 90%~~ identical to SEQ ID NO:61;

- (k) a ~~heavy chain variable domain~~ VH comprising an amino acid sequence at least 90% identical to SEQ ID NO:62, wherein the VH comprises a CDR1 sequence identical to the amino acid sequence of SEQ ID NO:63, a CDR2 sequence identical to the amino acid sequence of SEQ ID NO:64, and a CDR3 sequence identical to the amino acid sequence of SEQ ID NO:65; and a ~~light chain variable domain~~ VL comprising an amino acid sequence at least 90% identical to SEQ ID NO:66, wherein the VL comprises a CDR1 sequence identical to the amino acid sequence of SEQ ID NO:67, a CDR2 sequence identical to the amino acid sequence of SEQ ID NO:68, and a CDR3 sequence identical to the amino acid sequence of SEQ ID NO:69;
- (l) a ~~heavy chain variable domain~~ VH comprising an amino acid sequence at least 90% identical to SEQ ID NO:70, wherein the VH comprises a CDR1 sequence identical to the amino acid sequence of SEQ ID NO:313, a CDR2 sequence identical to the amino acid sequence of SEQ ID NO:72, and a CDR3 sequence identical to the amino acid sequence of SEQ ID NO:314; and a ~~light chain variable domain~~ VL comprising an amino acid sequence at least 90% identical to SEQ ID NO:74, wherein the VL comprises a CDR1 sequence identical to the amino acid sequence of SEQ ID NO:75, a CDR2 sequence identical to the amino acid sequence of SEQ ID NO:76, and a CDR3 sequence identical to the amino acid sequence of SEQ ID NO:77;
- (m) a ~~heavy chain variable domain~~ VH comprising an amino acid sequence at least 90% identical to SEQ ID NO:78, wherein the VH comprises a CDR1 sequence identical to the amino acid sequence of SEQ ID NO:315, a CDR2 sequence identical to the amino acid sequence of SEQ ID NO:80, and a CDR3 sequence identical to the amino acid sequence of SEQ ID NO:316; and a ~~light chain variable domain~~ VL comprising an amino acid sequence at least 90% identical to SEQ ID NO:82, wherein the VL comprises a CDR1 sequence identical to the amino acid sequence of SEQ ID NO:83, a CDR2 sequence identical to the amino acid sequence of SEQ ID NO:84, and a CDR3 sequence identical to the amino acid sequence of SEQ ID NO:85;

- (n) a ~~heavy chain variable domain~~ VH comprising an amino acid sequence at least 90% identical to SEQ ID NO:86, wherein the VH comprises a CDR1 sequence identical to the amino acid sequence of SEQ ID NO:317, a CDR2 sequence identical to the amino acid sequence of SEQ ID NO:88, and a CDR3 sequence identical to the amino acid sequence of SEQ ID NO:318; and a ~~light chain variable domain~~ VL comprising an amino acid sequence at least 90% identical to SEQ ID NO:90, wherein the VL comprises a CDR1 sequence identical to the amino acid sequence of SEQ ID NO:91, a CDR2 sequence identical to the amino acid sequence of SEQ ID NO:92, and a CDR3 sequence identical to the amino acid sequence of SEQ ID NO:93;
- (o) a ~~heavy chain variable domain~~ VH comprising an amino acid sequence at least 90% identical to SEQ ID NO:102, wherein the VH comprises a CDR1 sequence identical to the amino acid sequence of SEQ ID NO:313, a CDR2 sequence identical to the amino acid sequence of SEQ ID NO:104, and a CDR3 sequence identical to the amino acid sequence of SEQ ID NO:321; and a ~~light chain variable domain~~ VL comprising an amino acid sequence at least 90% identical to SEQ ID NO:106, wherein the VL comprises a CDR1 sequence identical to the amino acid sequence of SEQ ID NO:107, a CDR2 sequence identical to the amino acid sequence of SEQ ID NO:108, and a CDR3 sequence identical to the amino acid sequence of SEQ ID NO:109;
- (p) a ~~heavy chain variable domain~~ VH comprising an amino acid sequence ~~at least 90%~~ identical to SEQ ID NO:110; and a ~~light chain variable domain~~ VL comprising an amino acid sequence ~~at least 90%~~ identical to SEQ ID NO:111; or
- (p) a ~~heavy chain variable domain~~ VH comprising an amino acid sequence ~~at least 90%~~ identical to SEQ ID NO:112; and a ~~light chain variable domain~~ VL comprising an amino acid sequence ~~at least 90%~~ identical to SEQ ID NO:113.
- (q)

21. — A protein according to any one of claims 16-20, wherein the antibody constant region or the portion thereof sufficient to bind CD16 comprises:

(a) — hinge and CH2 domain of a human IgG1 antibody;

(b) — an amino acid sequence at least 90% identical to amino acids 234-332 of a human IgG1 antibody; and/or

(c) — an amino acid sequence at least 90% identical to the Fc domain of human IgG1 and differing 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, and K439.

22. — A protein comprising:

an antigen-binding site that binds NKG2D;

an antigen-binding T cell receptor (TCR) fragment; and

an antibody constant region or a portion thereof sufficient to bind CD16, or an additional antigen-binding site that binds CD16.

2312. A formulation comprising a protein according to any one of claims 11-221-11 and a pharmaceutically acceptable carrier.

2413. A cell comprising one or more nucleic acids encoding a protein according to any one of claims 11-221-11.

2514. The protein according to any one of claims 11-221-11 or the formulation of claim 23-12 for use in therapy.

2615. Use of the protein according to any one of claims 11-221-11 or the formulation of claim 23-12 in the manufacture of a medicament for treating cancer.

2716. The use of claim 2615, wherein the cancer is selected from the group consisting of acute myeloid leukemia, acute myelomonocytic leukemia, B cell lymphoma, bladder cancer, breast cancer, colorectal cancer, diffuse large B cell lymphoma esophageal cancer, Ewing's sarcoma,

follicular lymphoma, gastric cancer, gastrointestinal cancer, gastrointestinal stromal tumors, glioblastoma, head and neck cancer, melanoma, mesothelioma, multiple myeloma, myelodysplastic syndrome, renal cell carcinoma, neuroblastoma, non-small cell lung cancer, neuroendocrine tumors, ovarian cancer, and pancreatic cancer, prostate cancer, sarcomas, small
5 cell lung cancer, T cell lymphoma, testis cancer, thymic carcinoma, thyroid cancer, urothelial cancer, cancers infiltrated by myeloid-derived suppressor cells, cancers with extracellular matrix deposition, cancers with high levels of reactive stroma, and cancers with neoangiogenesis.