CLAIMS:

1. An isolated antibody or antigen-binding fragment specifically binding to TRAIL, comprising:

a V_H, wherein the V_H comprises

an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1,

an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 3, and

an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 5; and

a V_L, wherein the V_L comprises

an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 7,

an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 9, and

an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 11.

2. The isolated antibody or antigen-binding fragment specifically binding to TRAIL of claim 1, comprising:

(i) a V_H comprising the amino acid sequence of SEQ ID NO: 13, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 13; and a V_L comprising the amino acid sequence of SEQ ID NO: 22, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 22;

(ii) a V_H comprising the amino acid sequence of SEQ ID NO: 14, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 14; and a V_L comprising the amino acid sequence of SEQ ID NO: 23, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 23;

(iii) a V_H comprising the amino acid sequence of SEQ ID NO: 14, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 14; and a V_L comprising the amino acid sequence of SEQ ID NO: 24, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 24;

(iv) a V_H comprising the amino acid sequence of SEQ ID NO: 14, or a variant

thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 14; and a V_L comprising the amino acid sequence of SEQ ID NO: 25, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 25;

(v) a V_H comprising the amino acid sequence of SEQ ID NO: 14, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 14; and a V_L comprising the amino acid sequence of SEQ ID NO: 26, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 26; or

(vi) a V_H comprising the amino acid sequence of SEQ ID NO: 14, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 14; and a V_L comprising the amino acid sequence of SEQ ID NO: 27, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 27.

3. A bispecific antibody, comprising a first antigen-binding domain specifically binding to TRAIL, and a second antigen-binding domain specifically binding to FasL; and

wherein the first antigen-binding domain comprises:

a V_H, wherein the V_H comprises

an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 3, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 5; and

a V_L, wherein the V_L comprises

an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 7, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 9, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 11;

and/or,

wherein the first antigen-binding domain comprises:

(i) a V_H comprising the amino acid sequence of any one of SEQ ID NOs: 13

and 33, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 13 and 33; and a V_L comprising the amino acid sequence of any one of SEQ ID NOs: 22 and 41, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 22 and 41;

(ii) a V_H comprising the amino acid sequence of any one of SEQ ID NOs: 14 and 34, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 14 and 34; and a V_L comprising the amino acid sequence of any one of SEQ ID NOs: 23 and 42, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 23 and 42;

(iii) a V_H comprising the amino acid sequence of any one of SEQ ID NOs: 14 and 34, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 14 and 34; and a V_L comprising the amino acid sequence of any one of SEQ ID NOs: 24 and 43, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 24 and 43; or

(iv) a V_H comprising the amino acid sequence of SEQ ID NO: 164, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 164; and a V_L comprising the amino acid sequence of SEQ ID NO: 168, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 168.

4. The bispecific antibody of claim 3, wherein the second antigen-binding domain comprises:

(i) a V_H, wherein the V_H comprises

an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 51, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 53, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 55; and

a V_L, wherein the V_L comprises

an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 57, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 59, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 61;

(ii) a V_H, wherein the V_H comprises

an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 52, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 54, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 56; and

a V_L, wherein the V_L comprises

an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 58, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 60, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62; or

(iii) a V_H, wherein the V_H comprises

an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 52, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 54, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 56; and

a V_L, wherein the V_L comprises

an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 162, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 60, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62;

and/or,

wherein the second antigen-binding domain comprises:

(i) a V_H comprising the amino acid sequence of any one of SEQ ID NOs: 63 and 80, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 63 and 80; and a V_L comprising the amino acid sequence of any one of SEQ ID NOs: 73 and 89, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 73 and 89;

(ii) a V_H comprising the amino acid sequence of any one of SEQ ID NOs: 64 and 81, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 64 and 81; and a V_L comprising the amino acid sequence of any one of SEQ ID NOs: 74 and 90, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 74 and 90;

(iii) a V_H comprising the amino acid sequence of any one of SEQ ID NOs: 66 and 82, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 66 and 82; and a V_L comprising the amino acid sequence of any one of SEQ ID NOs: 76 and 92, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 76 and 92;

(iv) a V_H comprising the amino acid sequence of any one of SEQ ID NOs: 70 and 86, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 70 and 86; and a V_L comprising the amino acid sequence of any one of SEQ ID NOs: 78 and 94, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 78 and 94;

(v) a V_H comprising the amino acid sequence of any one of SEQ ID NOs: 69 and 85, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 69 and 85; and a V_L comprising the amino acid sequence of any one of SEQ ID NOs: 79 and 95, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 79 and 95;

(vi) a V_H comprising the amino acid sequence of SEQ ID NO: 163, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 163; and a V_L comprising the amino acid sequence of SEQ ID NO: 167, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 167; or

(vii)a V_H comprising the amino acid sequence of SEQ ID NO: 165, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 165; and a V_L comprising the amino acid sequence of SEQ ID NO: 169, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 169.

5. The bispecific antibody of any one of claims 3-4,

a) wherein the first antigen-binding domain comprises: a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 3, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 5; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 7, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 9, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 11;

and wherein the second antigen-binding domain comprises: a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 51, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 53, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 55; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 57, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 59, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 61; or

b) wherein the first antigen-binding domain comprises: a VH comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 3, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 5; and a VL comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 7, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 9, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO:

11;

and wherein the second antigen-binding domain comprises: a VH comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 52, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 54, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 56; and a VL comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 58, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 60, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62.

6. The bispecific antibody of any one of claims 3-5,

a) wherein the first antigen-binding domain comprises: a VH comprising the amino acid sequence of any one of SEQ ID NOs: 14 and 34, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 14 and 34; and a VL comprising the amino acid sequence of any one of SEQ ID NOs: 23 and 42, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 23 and 42;

and wherein the second antigen-binding domain comprises: a VH comprising the amino acid sequence of any one of SEQ ID NOs: 64 and 81, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 64 and 81; and a VL comprising the amino acid sequence of any one of SEQ ID NOs: 74 and 90, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 74 and 90;

b) wherein the first antigen-binding domain comprises: a VH comprising the amino acid sequence of any one of SEQ ID NOs: 14 and 34, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 14 and 34; and a VL comprising the amino acid sequence of any one of SEQ ID NOs: 24 and 43, or a variant

thereof having at least about 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 24 and 43;

and wherein the second antigen-binding domain comprises: a VH comprising the amino acid sequence of any one of SEQ ID NOs: 64 and 81, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 64 and 81; and a VL comprising the amino acid sequence of any one of SEQ ID NOs: 74 and 90, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 74 and 90;

c) wherein the first antigen-binding domain comprises: a VH comprising the amino acid sequence of SEQ ID NO: 164, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 164; and a VL comprising the amino acid sequence of SEQ ID NO: 168, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 168;

and wherein the second antigen-binding domain comprises: a VH comprising the amino acid sequence of SEQ ID NO: 163, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 163; and a VL comprising the amino acid sequence of SEQ ID NO: 167, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 167; or

d) wherein the first antigen-binding domain comprises: a V_H comprising the amino acid sequence of any one of SEQ ID NOs: 14 and 34, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 14 and 34; and a V_L comprising the amino acid sequence of any one of SEQ ID NOs: 23 and 42, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 23 and 42;

and wherein the second antigen-binding domain comprises: a V_H comprising the amino acid sequence of SEQ ID NO:163, or a variant

thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 163; and a V_L comprising the amino acid sequence of SEQ ID NO: 167, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 167.

7. The bispecific antibody of any one of claims 3-6, which comprises an Fc region, wherein

(i) the Fc region is selected from the group consisting of an Fc region of an IgGl, IgG2, IgG3, IgG4, IgA, IgM, IgE, and IgD; and/or

(ii) the Fc region comprises a variant Fc region; and/or,

(iii) the variant Fc region comprises a substitution at one or more of positions 228, 239, 282, 289, 297, 312, 324, 330, 335, 337, 339, 356, 359, 361, 383, 384, 398, 400, 440, 422, and 442, as numbered by the EU index; and/or,

(iv) the Fc region is aglycosylated; or,

(v) the Fc region is deglycosylated; or,

(vi) the Fc region has reduced fucosylation or is afucosylated.

8. The bispecific antibody of any one of claims 3-7, wherein the bispecific antibody has a format selected from the group consisting of DVD-IgG, Bs4Ab, Hetero H, CrossMab, IgG-(scFv)2, and scFv-Fab IgG.

9. The bispecific antibody of any one of claims 3-8, comprising four polypeptide chains selected from (i) and (ii):

(i) wherein two of the polypeptide chains comprise V_H1-L-V_H2-C_H1 structure from the N-terminal to the C-terminal, wherein V_H1 is a heavy chain variable domain specifically binding to TRAIL, V_H2 is a heavy chain variable domain specifically binding to FasL; L is a linker; C_H1 is a heavy chain constant domain 1; wherein the polypeptide chain further comprises Fc that comprises C_H2 and C_H3 domains; and

the other two of the polypeptide chains comprise the structure of V_L1-L-V_L2-CL, wherein V_L1 is a light chain variable domain specifically binding

to TRAIL; V_L2 is a light chain variable domain specifically binding to FasL; L is a linker; C_L is a light chain constant domain; or

(ii) wherein two of the polypeptide chains comprise V_H1-L-V_H2-C_H1 structure from the N-terminal to the C-terminal, wherein V_H1 is a heavy chain variable domain specifically binding to FasL, V_H2 is a heavy chain variable domain specifically binding to TRAIL; L is a linker; C_H1 is a heavy chain constant domain 1; wherein the polypeptide chain further comprises Fc that comprises C_H2 and C_H3 domains; and

the other two of the polypeptide chains comprise the structure of V_L1-L-V_L2-C_L, wherein V_L1 is a light chain variable domain specifically binding to FasL; V_L2 is a light chain variable domain specifically binding to TRAIL; L is a linker; C_L is a light chain constant domain.

10. The bispecific antibody of claim 9, wherein the bispecific antibody comprises:

a) the amino acid sequence of SEQ ID NO: 104, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 104; and/or

the amino acid sequence of SEQ ID NO: 105, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 105;

b) the amino acid sequence of SEQ ID NO: 104, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 104; and/or

the amino acid sequence of SEQ ID NO: 106, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 106;

c) the amino acid sequence of SEQ ID NO: 107, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 107; and/or

the amino acid sequence of SEQ ID NO: 108, or a variant thereof having

at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 108; or

d) the amino acid sequence of SEQ ID NO: 107, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 107; and/or

the amino acid sequence of SEQ ID NO: 109, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 109.

11. The bispecific antibody of claim 9, wherein the bispecific antibody comprises:

a) the amino acid sequence of SEQ ID NO: 131, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 131; and/or

the amino acid sequence of SEQ ID NO: 105, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 105;

b) the amino acid sequence of SEQ ID NO: 131, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 131; and/or

the amino acid sequence of SEQ ID NO: 106, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 106;

c) the amino acid sequence of SEQ ID NO: 132, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 132; and/or

the amino acid sequence of SEQ ID NO: 108, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 108; or

d) the amino acid sequence of SEQ ID NO: 132, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 132; and/or

the amino acid sequence of SEQ ID NO: 109, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 109.

12. The bispecific antibody of any one of claims 3-8, comprising four polypeptide chains selected from (i) and (ii):

(i) wherein two of the polypeptide chains comprise V_H1-C_H1-L1-V_H2-L3-V_L2 or V_H1-C_H1-L1-V_L2-L3-V_H2 structure from the N-terminal to the C-terminal, wherein V_H1 is a heavy chain variable domain specifically binding to TRAIL; V_H2 is a heavy chain variable domain specifically binding to FasL, V_L2 is a light chain variable domain specifically binding to FasL; L1 and L3 are the linker; C_H1 is a heavy chain constant domain 1; wherein the polypeptide chain further comprises Fc that comprises C_H2 and C_H3 domains; and

the other two of the polypeptide chains comprise V_L1-C_L structure from the N-terminal to the C-terminal, wherein V_L1 is a light chain variable domain specifically binding to TRAIL, C_L is a light chain constant domain; or

(ii) wherein two of the polypeptide chains comprise V_H1-C_H1-L1-V_H2-L3-V_L2 or V_H1-C_H1-L1-V_L2-L3-V_H2 structure from the N-terminal to the C-terminal, wherein V_H1 is a heavy chain variable domain specifically binding to FasL; V_H2 is a heavy chain variable domain specifically binding to TRAIL, V_L2 is a light chain variable domain specifically binding to TRAIL; L1 and L3 are a linker; C_H1 is a heavy chain constant domain 1; wherein the polypeptide chain further comprises Fc that comprises C_H2 and C_H3 domains; and

the other two of the polypeptide chains comprise V_L1-C_L structure from the N-terminal to the C-terminal, wherein V_L1 is a light chain variable domain specifically binding to FasL, C_L is a light chain constant domain.

13. The bispecific antibody of claim 12, wherein the bispecific antibody comprises:

a) the amino acid sequence of SEQ ID NO: 116, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 116; and/or the amino acid sequence of SEQ ID NO: 119, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 119;

b) the amino acid sequence of SEQ ID NO: 117, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 117; and/or the amino acid sequence of SEQ ID NO: 119, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 119;

c) the amino acid sequence of SEQ ID NO: 118, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 118; and/or the amino acid sequence of SEQ ID NO: 119, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 119;

d) the amino acid sequence of SEQ ID NO: 120, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 120; and/or the amino acid sequence of SEQ ID NO: 121, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 121;

e) the amino acid sequence of SEQ ID NO: 120, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 120; and/or the amino acid sequence of SEQ ID NO: 122, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 122; or

f) the amino acid sequence of SEQ ID NO: 171, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 171; and/or the amino acid sequence of SEQ ID NO: 173, or a

variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 173.

14. The bispecific antibody of claim 12, wherein the bispecific antibody comprises:

a) the amino acid sequence of SEQ ID NO: 138, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 138; and/or the amino acid sequence of SEQ ID NO: 119, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 119;

b) the amino acid sequence of SEQ ID NO: 139, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 139; and/or the amino acid sequence of SEQ ID NO: 119, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 119;

c) the amino acid sequence of SEQ ID NO: 140, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 140; and/or the amino acid sequence of SEQ ID NO: 119, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 119;

d) the amino acid sequence of SEQ ID NO: 141, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 141; and/or the amino acid sequence of SEQ ID NO: 121, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 121;

e) the amino acid sequence of SEQ ID NO: 141, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 141; and/or the amino acid sequence of SEQ ID NO: 122, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 122;

f) the amino acid sequence of SEQ ID NO: 175, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 175; and/or the amino acid sequence of SEQ ID NO: 173, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 173;

g) the amino acid sequence of SEQ ID NO: 193, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 193; and/or the amino acid sequence of SEQ ID NO: 177, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 177;

h) the amino acid sequence of SEQ ID NO: 194, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 194; and/or the amino acid sequence of SEQ ID NO: 178, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 178;

i) the amino acid sequence of SEQ ID NO: 195, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 195; and/or the amino acid sequence of SEQ ID NO: 179, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 179;

j) the amino acid sequence of SEQ ID NO: 196, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 196; and/or the amino acid sequence of SEQ ID NO: 180, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 180;

k) the amino acid sequence of SEQ ID NO: 197, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 197; and/or the amino acid sequence of SEQ ID NO: 181, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 181;

l) the amino acid sequence of SEQ ID NO: 198, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 198; and/or the amino acid sequence of SEQ ID NO: 182, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 182;

m) the amino acid sequence of SEQ ID NO: 199, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 199; and/or the amino acid sequence of SEQ ID NO: 183 or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 183; or

n) the amino acid sequence of SEQ ID NO: 200, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 200; and/or the amino acid sequence of SEQ ID NO: 184, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 184.

15. A pharmaceutical composition comprising the antibody or antigen-binding fragment specifically binding to TRAIL of claim 1 or 2, the bispecific antibody of any one of claims 3-14, and a pharmaceutically acceptable carrier or excipient.

16. A pharmaceutical composition, comprising the antibody or antigen-binding fragment specifically binding to TRAIL of claim 1 or 2 and an antibody or antigen-binding fragment specifically binding to FasL,

and/or,

wherein the antibody or antigen-binding fragment specifically binding to TRAIL comprises:

(i) a V_H comprising the amino acid sequence of SEQ ID NO: 13, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 13; and a V_L comprising the amino acid sequence of SEQ ID NO: 22, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 22;

(ii) a V_H comprising the amino acid sequence of SEQ ID NO: 14, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 14; and a V_L comprising the amino acid sequence of SEQ ID NO: 23, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 23;

(iii) a V_H comprising the amino acid sequence of SEQ ID NO: 14, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 14; and a V_L comprising the amino acid sequence of SEQ ID NO: 24, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 24;

(iv) a V_H comprising the amino acid sequence of SEQ ID NO: 15, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 15; and a V_L comprising the amino acid sequence of SEQ ID NO: 28, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 28;

(v) a V_H comprising the amino acid sequence of SEQ ID NO: 20, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 20; and a V_L comprising the amino acid sequence of SEQ ID NO: 30, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 30; or

(vi) a V_H comprising the amino acid sequence of SEQ ID NO: 16, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 16; and a V_L comprising the amino acid sequence of SEQ ID NO: 31, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 31.

17. The pharmaceutical composition of claim 16, wherein the antibody or antigen-binding fragment specifically binding to FasL comprises:

a) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 51, an HC-CDR2 comprising the amino acid sequence of

SEQ ID NO: 53, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 55; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 57, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 59, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 61; or

b) a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 52, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 54, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 56; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 58, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 60, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62;

and/or,

wherein the antibody or antigen-binding fragment specifically binding to FasL comprises:

(i) a V_H comprising the amino acid sequence of SEQ ID NO: 63, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO:63; and a V_L comprising the amino acid sequence of SEQ ID NO: 73, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 73;

(ii) a V_H comprising the amino acid sequence of SEQ ID NO: 64, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO:64; and a V_L comprising the amino acid sequence of SEQ ID NO: 74, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 74;

(iii) a V_H comprising the amino acid sequence of SEQ ID NO:66, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 66; and a V_L comprising the amino acid sequence of SEQ ID NO: 76, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 76;

(iv) V_H comprising the amino acid sequence of SEQ ID NO: 70, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 70; and a V_L comprising the amino acid sequence of SEQ ID NO: 78, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 78; or

(v) a V_H comprising the amino acid sequence of SEQ ID NO: 69, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 69; and a V_L comprising the amino acid sequence of SEQ ID NO: 79, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 79.

18. The pharmaceutical composition of claim 16,

a) wherein the antibody or antigen-binding fragment specifically binding to TRAIL comprises a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 3, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 5; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 7, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 9, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 11;

and wherein the antibody or antigen-binding fragment specifically binding to FasL comprises a V_H comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 51, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 53, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 55,; and a V_L comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 57, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 59, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 61; or

b) wherein the antibody or antigen-binding fragment specifically binding to TRAIL comprises a VH comprising an HC-CDR1 comprising the amino

acid sequence of SEQ ID NO: 1, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 3, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 5; and a VL comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 7, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 9, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 11;

and wherein the antibody or antigen-binding fragment specifically binding to FasL comprises a VH comprising an HC-CDR1 comprising the amino acid sequence of SEQ ID NO: 52, an HC-CDR2 comprising the amino acid sequence of SEQ ID NO: 54, and an HC-CDR3 comprising the amino acid sequence of SEQ ID NO: 56; and a VL comprising an LC-CDR1 comprising the amino acid sequence of SEQ ID NO: 58, an LC-CDR2 comprising the amino acid sequence of SEQ ID NO: 60, and an LC-CDR3 comprising the amino acid sequence of SEQ ID NO: 62.

19. The pharmaceutical composition of claim 16,

a) wherein the antibody or antigen-binding fragment specifically binding to TRAIL comprises a VH comprising the amino acid sequence of SEQ ID NO: 14, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 14; and a VL comprising the amino acid sequence of SEQ ID NO: 23, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 23;

and wherein the antibody or antigen-binding fragment specifically binding to FasL comprises a VH comprising the amino acid sequence of SEQ ID NO: 64, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO:64; and a VL comprising the amino acid sequence of SEQ ID NO: 74, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 74; or

b) wherein the antibody or antigen-binding fragment specifically binding to

TRAIL comprises a VH comprising the amino acid sequence of SEQ ID NO: 14, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 14; and a VL comprising the amino acid sequence of SEQ ID NO: 24, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 24; and wherein the antibody or antigen-binding fragment specifically binding to FasL comprises: a VH comprising the amino acid sequence of SEQ ID NO: 64, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO:64; and a VL comprising the amino acid sequence of SEQ ID NO: 74, or a variant thereof having at least about 80% sequence identity to the amino acid sequence of SEQ ID NO: 74.