Claims

1. An anti-c-MET antibody or antigen-binding fragment thereof, comprising a heavy chain variable region and a light chain variable region, wherein the CDRs of the heavy chain variable region and/or the CDRs of the light chain variable region have sequences identical to the sequences of the CDRs of a sequence-defined antibody or have 1, 2, or 3 amino acid substitutions compared to the CDRs of the sequence-defined antibody, wherein the sequence-defined antibody comprises:

(1) the amino acid sequence of a heavy chain variable region set forth in SEQ ID NO: 2, 4, 6, 8, 10, or 12; and/or

(2) the amino acid sequence of a light chain variable region set forth in SEQ ID NO: 1, 3, 5, 7, 9, or 11.

2. The anti-c-MET antibody or antigen-binding fragment thereof according to claim 1,

comprising: the HCDR1, the HCDR2, and the HCDR3 comprised in the heavy chain variable region set forth in SEQ ID NO: 10; and the LCDR1, the LCDR2, and the LCDR3 comprised in the light chain variable region set forth in SEQ ID NO: 9;

the HCDR1, the HCDR2, and the HCDR3 comprised in the heavy chain variable region set forth in SEQ ID NO: 12; and the LCDR1, the LCDR2, and the LCDR3 comprised in the light chain variable region set forth in SEQ ID NO: 11;

the HCDR1, the HCDR2, and the HCDR3 comprised in the heavy chain variable region set forth in SEQ ID NO: 2; and the LCDR1, the LCDR2, and the LCDR3 comprised in the light chain variable region set forth in SEQ ID NO: 1;

the HCDR1, the HCDR2, and the HCDR3 comprised in the heavy chain variable region set forth in SEQ ID NO: 4; and the LCDR1, the LCDR2, and the LCDR3 comprised in the light chain variable region set forth in SEQ ID NO: 3;

the HCDR1, the HCDR2, and the HCDR3 comprised in the heavy chain variable region set forth in SEQ ID NO: 6; and the LCDR1, the LCDR2, and the LCDR3 comprised in the light chain variable region set forth in SEQ ID NO: 5; or

the HCDR1, the HCDR2, and the HCDR3 comprised in the heavy chain variable region set forth in SEQ ID NO: 8; and the LCDR1, the LCDR2, and the LCDR3 comprised in the light chain variable region set forth in SEQ ID NO: 7; wherein

preferably, the HCDRs 1-3 and the LCDRs 1-3 are determined according to the definition scheme of IMGT, Kabat, or Chothia.

3. An anti-c-MET antibody or antigen-binding fragment thereof, comprising a heavy chain variable region and a light chain variable region, wherein

a. the heavy chain variable region comprises the HCDR1, the HCDR2, and the HCDR3, which comprise the amino acid sequences set forth in SEQ ID NO: 13, SEQ ID NO: 14, and SEQ

ID NO: 15, respectively; and the light chain variable region comprises the LCDR1, the LCDR2, and the LCDR3, which comprise the amino acid sequences set forth in SEQ ID NO: 20, SEQ ID NO: 21, and SEQ ID NO: 22, respectively;

b. the heavy chain variable region comprises the HCDR1, the HCDR2, and the HCDR3, which comprise the amino acid sequences set forth in SEQ ID NO: 16, SEQ ID NO: 17, and SEQ ID NO: 19, respectively; and the light chain variable region comprises the LCDR1, the LCDR2, and the LCDR3, which comprise the amino acid sequences set forth in SEQ ID NO: 23, SEQ ID NO: 24, and SEQ ID NO: 22, respectively;

c. the heavy chain variable region comprises the HCDR1, the HCDR2, and the HCDR3, which comprise the amino acid sequences set forth in SEQ ID NO: 16, SEQ ID NO: 18, and SEQ ID NO: 19, respectively; and the light chain variable region comprises the LCDR1, the LCDR2, and the LCDR3, which comprise the amino acid sequences set forth in SEQ ID NO: 23, SEQ ID NO: 24, and SEQ ID NO: 22, respectively;

d. the heavy chain variable region comprises the HCDR1, the HCDR2, and the HCDR3, which comprise the amino acid sequences set forth in SEQ ID NO: 25, SEQ ID NO: 53, and SEQ ID NO: 19, respectively; and the light chain variable region comprises the amino acid sequences set forth in SEQ ID NO: 23, SEQ ID NO: 24, and SEQ ID NO: 22, respectively;

e. the heavy chain variable region comprises the HCDR1, the HCDR2, and the HCDR3, which comprise the amino acid sequences set forth in SEQ ID NO: 26, SEQ ID NO: 27, and SEQ ID NO: 28, respectively; and the light chain variable region comprises the LCDR1, the LCDR2, and the LCDR3, which comprise the amino acid sequences set forth in SEQ ID NO: 33, SEQ ID NO: 34, and SEQ ID NO: 35, respectively;

f. the heavy chain variable region comprises the HCDR1, the HCDR2, and the HCDR3, which comprise the amino acid sequences set forth in SEQ ID NO: 29, SEQ ID NO: 30, and SEQ ID NO: 32, respectively; and the light chain variable region comprises the LCDR1, the LCDR2, and the LCDR3, which comprise the amino acid sequences set forth in SEQ ID NO: 36, SEQ ID NO: 37, and SEQ ID NO: 35, respectively;

g. the heavy chain variable region comprises the HCDR1, the HCDR2, and the HCDR3, which comprise the amino acid sequences set forth in SEQ ID NO: 29, SEQ ID NO: 31, and SEQ ID NO: 32, respectively; and the light chain variable region comprises the LCDR1, the LCDR2, and the LCDR3, which comprise the amino acid sequences set forth in SEQ ID NO: 36, SEQ ID NO: 37, and SEQ ID NO: 35, respectively;

h. the heavy chain variable region comprises the HCDR1, the HCDR2, and the HCDR3, which comprise the amino acid sequences set forth in SEQ ID NO: 54, SEQ ID NO: 55, and SEQ ID NO: 32, respectively; and the light chain variable region comprises the LCDR1, the LCDR2, and the LCDR3, which comprise the amino acid sequences set forth in SEQ ID NO: 36, SEQ ID NO: 37, and SEQ ID NO: 35, respectively;

i. the heavy chain variable region comprises the HCDR1, the HCDR2, and the HCDR3, which comprise the amino acid sequences set forth in SEQ ID NO: 39, SEQ ID NO: 40, and SEQ ID NO: 41, respectively; and the light chain variable region comprises the LCDR1, the LCDR2, and the LCDR3, which comprise the amino acid sequences set forth in SEQ ID NO: 45, SEQ ID NO: 46, and SEQ ID NO: 47, respectively;

j. the heavy chain variable region comprises the HCDR1, the HCDR2, and the HCDR3, which comprise the amino acid sequences set forth in SEQ ID NO: 42, SEQ ID NO: 43, and SEQ ID NO: 44, respectively; and the light chain variable region comprises the LCDR1, the LCDR2, and the LCDR3, which comprise the amino acid sequences set forth in SEQ ID NO: 48, SEQ ID NO: 49, and SEQ ID NO: 50, respectively; or

k. the heavy chain variable region comprises the HCDR1, the HCDR2, and the HCDR3, which comprise the amino acid sequences set forth in SEQ ID NO: 62, SEQ ID NO: 60, and SEQ ID NO: 44, respectively; and the light chain variable region comprises the LCDR1, the LCDR2, and the LCDR3, which comprise the amino acid sequences set forth in SEQ ID NO: 48, SEQ ID NO: 49, and SEQ ID NO: 50, respectively; wherein

preferably,

a. the heavy chain variable region comprises the HCDR1, the HCDR2, and the HCDR3 set forth in SEQ ID NO: 13, SEQ ID NO: 14, and SEQ ID NO: 15, respectively; and the light chain variable region comprises the LCDR1, the LCDR2, and the LCDR3 set forth in SEQ ID NO: 20, SEQ ID NO: 21, and SEQ ID NO: 22, respectively; wherein

the foregoing HCDRs 1-3 and LCDRs 1-3 are determined according to the definition scheme of IMGT;

b. the heavy chain variable region comprises the HCDR1, the HCDR2, and the HCDR3 set forth in SEQ ID NO: 16, SEQ ID NO: 17, and SEQ ID NO: 19, respectively; and the light chain variable region comprises the LCDR1, the LCDR2, and the LCDR3 set forth in SEQ ID NO: 23, SEQ ID NO: 24, and SEQ ID NO: 22, respectively; wherein

the foregoing HCDRs 1-3 and LCDRs 1-3 are determined according to the definition scheme of Kabat;

c. the heavy chain variable region comprises the HCDR1, the HCDR2, and the HCDR3 set forth in SEQ ID NO: 16, SEQ ID NO: 18, and SEQ ID NO: 19, respectively; and the light chain variable region comprises the LCDR1, the LCDR2, and the LCDR3 set forth in SEQ ID NO: 23, SEQ ID NO: 24, and SEQ ID NO: 22, respectively; wherein

the foregoing HCDRs 1-3 and LCDRs 1-3 are determined according to the definition scheme of Kabat;

d. the heavy chain variable region comprises the HCDR1, the HCDR2, and the HCDR3 set forth in SEQ ID NO: 25, SEQ ID NO: 53, and SEQ ID NO: 19, respectively; and the light chain variable region comprises the LCDR1, the LCDR2, and the LCDR3 set forth in SEQ ID NO: 23, SEQ ID NO: 24, and SEQ ID NO: 22, respectively; wherein

the foregoing HCDRs 1-3 and LCDRs 1-3 are determined according to the definition scheme of Chothia;

e. the heavy chain variable region comprises the HCDR1, the HCDR2, and the HCDR3 set forth in SEQ ID NO: 26, SEQ ID NO: 27, and SEQ ID NO: 28, respectively; and the light chain variable region comprises the LCDR1, the LCDR2, and the LCDR3 set forth in SEQ ID NO: 33, SEQ ID NO: 34, and SEQ ID NO: 35, respectively; wherein

the foregoing HCDRs 1-3 and LCDRs 1-3 are determined according to the definition scheme of IMGT;

f. the heavy chain variable region comprises the HCDR1, the HCDR2, and the HCDR3 set forth in SEQ ID NO: 29, SEQ ID NO: 30, and SEQ ID NO: 32, respectively; and the light chain variable region comprises the LCDR1, the LCDR2, and the LCDR3 set forth in SEQ ID NO: 36, SEQ ID NO: 37, and SEQ ID NO: 35, respectively; wherein

the foregoing HCDRs 1-3 and LCDRs 1-3 are determined according to the definition scheme of Kabat;

g. the heavy chain variable region comprises the HCDR1, the HCDR2, and the HCDR3 set forth in SEQ ID NO: 29, SEQ ID NO: 31, and SEQ ID NO: 32, respectively; and the light chain variable region comprises the LCDR1, the LCDR2, and the LCDR3 set forth in SEQ ID NO: 36, SEQ ID NO: 37, and SEQ ID NO: 35, respectively; wherein

the foregoing HCDRs 1-3 and LCDRs 1-3 are determined according to the definition scheme of Kabat;

h. the heavy chain variable region comprises the HCDR1, the HCDR2, and the HCDR3 set forth in SEQ ID NO: 54, SEQ ID NO: 55, and SEQ ID NO: 32, respectively; and the light chain variable region comprises the LCDR1, the LCDR2, and the LCDR3 set forth in SEQ ID NO: 36, SEQ ID NO: 37, and SEQ ID NO: 35, respectively; wherein

the foregoing HCDRs 1-3 and LCDRs 1-3 are determined according to the definition scheme of Chothia;

i. the heavy chain variable region comprises the HCDR1, the HCDR2, and the HCDR3 set forth in SEQ ID NO: 39, SEQ ID NO: 40, and SEQ ID NO: 41, respectively; and the light chain variable region comprises the LCDR1, the LCDR2, and the LCDR3 set forth in SEQ ID NO: 45, SEQ ID NO: 46, and SEQ ID NO: 47, respectively; wherein

the foregoing HCDRs 1-3 and LCDRs 1-3 are determined according to the definition scheme of IMGT;

j. the heavy chain variable region comprises the HCDR1, the HCDR2, and the HCDR3 set forth in SEQ ID NO: 42, SEQ ID NO: 43, and SEQ ID NO: 44, respectively; and the light chain variable region comprises the LCDR1, the LCDR2, and the LCDR3 set forth in SEQ ID NO: 48, SEQ ID NO: 49, and SEQ ID NO: 50, respectively; wherein

the foregoing HCDRs 1-3 and LCDRs 1-3 are determined according to the definition scheme of Kabat; or

k. the heavy chain variable region comprises the HCDR1, the HCDR2, and the HCDR3 set forth in SEQ ID NO: 62, SEQ ID NO: 60, and SEQ ID NO: 44, respectively; and the light chain variable region comprises the LCDR1, the LCDR2, and the LCDR3 set forth in SEQ ID NO: 48, SEQ ID NO: 49, and SEQ ID NO: 50, respectively; wherein

the foregoing HCDRs 1-3 and LCDRs 1-3 are determined according to the definition scheme of Chothia.

4. The anti-c-MET antibody or antigen-binding fragment thereof according to any one of claims 1-3, comprising the heavy chain variable region and the light chain variable region, wherein 4, 3, 2, or 1 CDR(s) of 6 CDRs of the HCDRs 1-3 and the LCDRs 1-3 comprised in the heavy chain variable region and the light chain variable region comprise to 1, 2, or 3 amino acid substitutions; wherein

preferably, the substitutions are conservative substitutions.

5. The anti-c-MET antibody or antigen-binding fragment thereof according to any one of claims 1-4, comprising the heavy chain variable region and the light chain variable region, wherein

(1) the heavy chain variable region has at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 10, and/or the light chain variable region has at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 9;

(2) the heavy chain variable region has at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 12, and/or the light chain variable region has at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 11;

(3) the heavy chain variable region has at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 2, and/or the light chain variable region has at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 1;

(4) the heavy chain variable region has at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 4, and/or the light chain variable region has at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 3;

(5) the heavy chain variable region has at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 6, and/or the light chain variable region has at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 5; or

(6) the heavy chain variable region has at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 8, and/or the light chain variable region has

at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 7.

6. The anti-c-MET antibody or antigen-binding fragment thereof according to any one of claims 1-5, comprising the heavy chain variable region and the light chain variable region, wherein:

(1) the heavy chain variable region comprises or consists of the amino acid sequence set forth in SEQ ID NO: 10; and the light chain variable region comprises or consists of the amino acid sequence set forth in SEQ ID NO: 9;

(2) the heavy chain variable region comprises or consists of the amino acid sequence set forth in SEQ ID NO: 12; and the light chain variable region comprises or consists of the amino acid sequence set forth in SEQ ID NO: 11;

(3) the heavy chain variable region comprises or consists of the amino acid sequence set forth in SEQ ID NO: 2; and the light chain variable region comprises or consists of the amino acid sequence set forth in SEQ ID NO: 1;

(4) the heavy chain variable region comprises or consists of the amino acid sequence set forth in SEQ ID NO: 4; and the light chain variable region comprises or consists of the amino acid sequence set forth in SEQ ID NO: 3;

(5) the heavy chain variable region comprises or consists of the amino acid sequence set forth in SEQ ID NO: 6; and the light chain variable region comprises or consists of the amino acid sequence set forth in SEQ ID NO: 5; or

(6) the heavy chain variable region comprises or consists of the amino acid sequence set forth in SEQ ID NO: 8; and the light chain variable region comprises or consists of the amino acid sequence set forth in SEQ ID NO: 7.

7. The anti-c-MET antibody or antigen-binding fragment thereof according to any one of claims 1-6, further comprising a heavy chain constant region and a light chain constant region of the antibody; wherein

preferably, the heavy chain constant region is selected from a human IgG1, IgG2, IgG3, or IgG4 constant region, and the light chain constant region is selected from a human antibody κ or λ chain constant region; and

more preferably, the antibody comprises a heavy chain constant region set forth in SEQ ID NO: 51 and a light chain constant region set forth in SEQ ID NO: 52.

8. The anti-c-MET antibody or antigen-binding fragment thereof according to any one of claims 1-7, comprising:

a. a heavy chain having at least 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 56, and/or a light chain having at least 85%, 90%,

91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 57; wherein

preferably, the anti-c-MET antibody comprises: a heavy chain comprising or consisting of the amino acid sequence set forth in SEQ ID NO: 56 and a light chain comprising or consisting of the amino acid sequence set forth in SEQ ID NO: 57; or

b. a heavy chain having at least 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 58, and/or a light chain having at least 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 59; wherein

preferably, the anti-c-MET antibody comprises: a heavy chain comprising or consisting of the amino acid sequence set forth in SEQ ID NO: 58 and a light chain comprising or consisting of the amino acid sequence set forth in SEQ ID NO: 59.

9. An anti-c-MET antibody or antigen-binding fragment thereof, wherein the antibody competes for binding to a human c-MET with the anti-c-MET antibody or antigen-binding fragment thereof according to any one of claims 1-8.

10. A multispecific antibody, comprising the anti-c-MET antibody or antigen-binding fragment thereof according to any one of claims 1-9, wherein

preferably, the multispecific antibody is a bispecific antibody, or a trispecific antibody, or a tetraspecific antibody.

11. A nucleic acid molecule, encoding the anti-c-MET antibody or antigen-binding fragment thereof according to any one of claims 1-9, or the multispecific antibody according to claim 10.

12. A host cell, comprising the nucleic acid molecule according to claim 11.

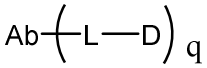
13. An immunoconjugate, comprising: the anti-c-MET antibody or antigen-binding fragment thereof according to any one of claims 1-9 and an effector molecule, wherein the effector molecule is conjugated to the anti-c-MET antibody; and

preferably, the effector molecule is selected from an anti-tumor agent, an immunomodulatory agent, a biological response modifier, a lectin, a cytotoxic drug, a chromophore, a fluorophore, a chemiluminescent compound, an enzyme, a metal ion, and any combination thereof.

14. A method for *in-vitro* immune detection or assay of c-MET, comprising a step of contacting the anti-c-MET antibody according to any one of claims 1-10 with a subject or a sample from the subject.

15. An antibody-drug conjugate, a stereoisomer thereof, a prodrug thereof, a pharmaceutically acceptable salt thereof, a tautomer thereof, or a pharmaceutically acceptable solvate thereof, comprising the antibody or antigen-binding fragment thereof according to any one of claims 1-9, or the multispecific antibody according to claim 10.

16. The antibody-drug conjugate, the stereoisomer thereof, the prodrug thereof, the pharmaceutically acceptable salt thereof, the tautomer thereof, or the pharmaceutically acceptable solvate thereof according to claim 15, wherein the antibody-drug conjugate has a structure as represented in Formula (I):



Formula (I)

wherein:

Ab is the antibody or antigen-binding fragment thereof according to any one of claims 1-9, or the multispecific antibody according to claim 10;

D is an active drug unit;

q is an integer selected from 1-20, for example, selected from 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, or 14;

L is a linking group covalently attached to the antibody or antigen-binding fragment thereof Ab and the active drug unit D, respectively;

the L is covalently attached to an amino residue or a sulfhydryl residue on the antibody Ab;

preferably, the L is covalently attached to the sulfhydryl residue on the antibody Ab; and more preferably, the L is covalently attached to a sulfhydryl residue formed after an interchain disulfide bond on the antibody Ab being opened up; and

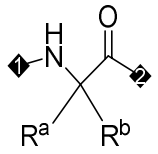
preferably, the active drug unit is selected from a cytotoxic agent; and more preferably, the active drug unit is selected from a DNA topoisomerase inhibitor (for example, a camptothecin-based biologically active molecule, such as camptothecin, DXD, camptothecin with a substitutent modified or DXD with a substitutent modified, hydroxycamptothecin, 9-aminocamptothecin, SN-38, irinotecan, topotecan, belotecan, and rubitecan) or a tubulin inhibitor (for example, an MMAF-like tubulin inhibitor, and an MMAE-like tubulin inhibitor).

17. The antibody-drug conjugate, the stereoisomer thereof, the prodrug thereof, the pharmaceutically acceptable salt thereof, the tautomer thereof, or the pharmaceutically acceptable solvate thereof according to claim 16, wherein the L is a cleavable linker or a non-cleavable linker,

preferably, the cleavable linker comprises a peptide unit comprising 2-10 amino acid residues selected from natural amino acid residues, non-natural amino acid residues, or amino acid residues set forth in AA_1 or stereoisomers thereof;

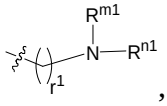
more preferably, the peptide unit is a dipeptide, tripeptide, tetrapeptide, pentapeptide, hexapeptide, heptapeptide, octapeptide, nonapeptide, or decapeptide comprising at least 1 (for example, 1, 2, or 3) amino acid residues set forth in AA_1 or stereoisomers thereof;

The amino acid residue set forth in AA^1 has a structure as follows,



AA^1

wherein:

either of R^a and R^b is H, and the other is , and r^1 is 4;

or R^a and R^b, taken together with the carbon atom to which they are attached, form a 5-6-membered heterocycle substituted with R^0;

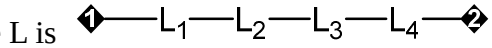
R^{m1} and R^{n1} are each independently selected from hydrogen, C_{1-6} alkyl, and C_{3-6} cycloalkyl;

R^0 is selected from C_{1-6} alkyl, C_{3-6} cycloalkyl, $-NR^{m2}R^{n2}$, and a 5-6-membered heterocyclyl optionally substituted with C_{1-6} alkyl; and

R^{m2} and R^{n2} are each independently selected from hydrogen and C_{1-6} alkyl;

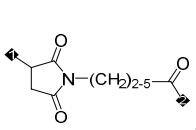
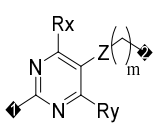
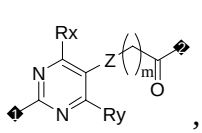
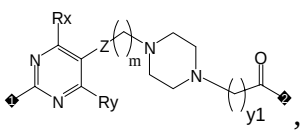
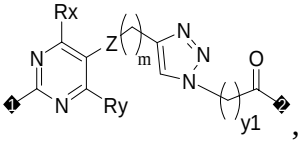
preferably, the amino acid residue is selected from -Val-, -Ala-, -Gly-, -Cit-, $-AA^1-$, -Arg-, -Phe-, -Lys-, and -Asn-; and

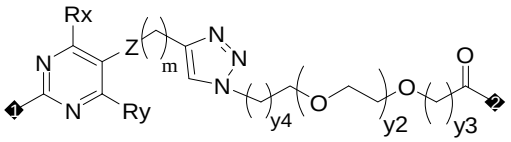
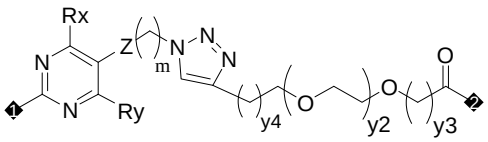
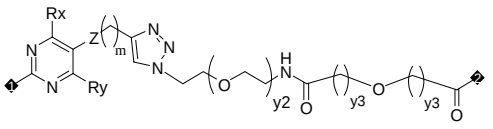
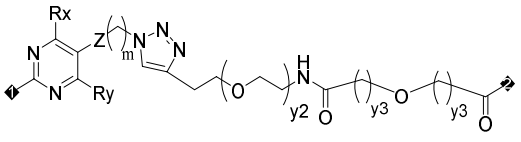
preferably, the peptide unit is selected from -valine-citrulline- (-Val-Cit-), -valine-alanine- (-Val-Ala-), -valine-lysine- (-Val-Lys-), -valine-arginine- (-Val-Arg-), -phenylalanine-citrulline- (-Phe-Cit-), -phenylalanine-lysine- (-Phe-Lys-), -phenylalanine-arginine- (-Phe-Arg-)-, -alanine-alanine-alanine- (-Ala-Ala-Ala-), -alanine-alanine-asparagine- (-Ala-Ala-Asn-), -valine-AA^1-glycine- (-Val-AA^1-Gly-), -valine-AA^1-alanine- (-Val-AA^1-Ala-), -glycine-glycine-phenylalanine-glycine- (-Gly-Gly-Phe-Gly-), and -glycine-glycine-valine-alanine- (-Gly-Gly-Val-Ala-).

18. The antibody-drug conjugate, the stereoisomer thereof, the prodrug thereof, the pharmaceutically acceptable salt thereof, the tautomer thereof, or the pharmaceutically acceptable solvate thereof according to claim 16 or 17, wherein the L is ,

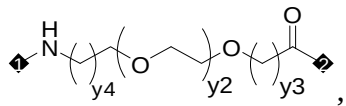
wherein,

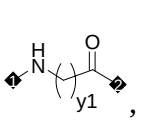
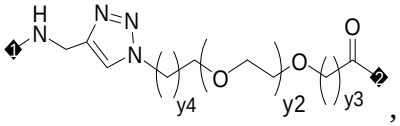
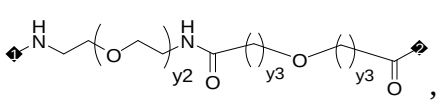
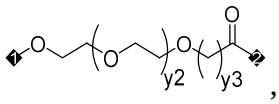
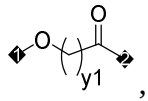
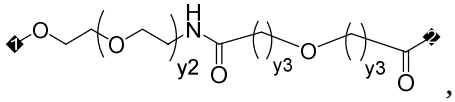
L_1 is selected from:

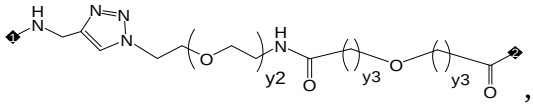
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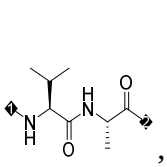





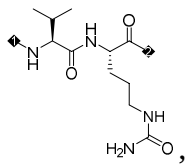
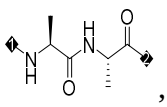
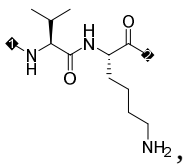
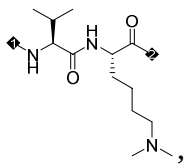
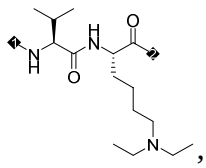
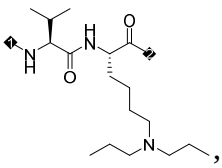
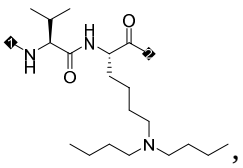
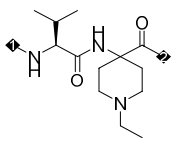
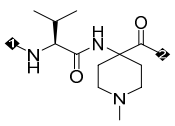
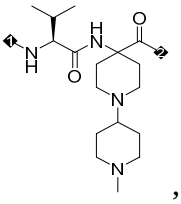
, and , each Z is independently selected from a direct bond, a carbon-carbon triple bond, a carbon-carbon double bond, C_{6-10} aryl, a 5-10-membered heteroaryl, and acylamino (preferably selected from a direct bond, a carbon-carbon triple bond, and a carbon-carbon double bond); Rx and Ry are independently selected from H and C_{1-4} alkyl; each m is independently selected from 0, 1, 2, 3, 4, 5, and 6; y1 is selected from any integer from 1 to 6 (such as 4, 5, or 6); each y2 is independently selected from any integer from 0 to 15 (such as from 6 to 15); each y3 is independently selected from 1, 2, and 3; each y4 is independently selected from 0 and 1; the position 1 is attached to the antibody or antigen-binding fragment thereof via an S atom, and the position 2 is attached to L_2 or L_3;

L_2 is absent or present, when L_2 is present, L_2 is selected from ,

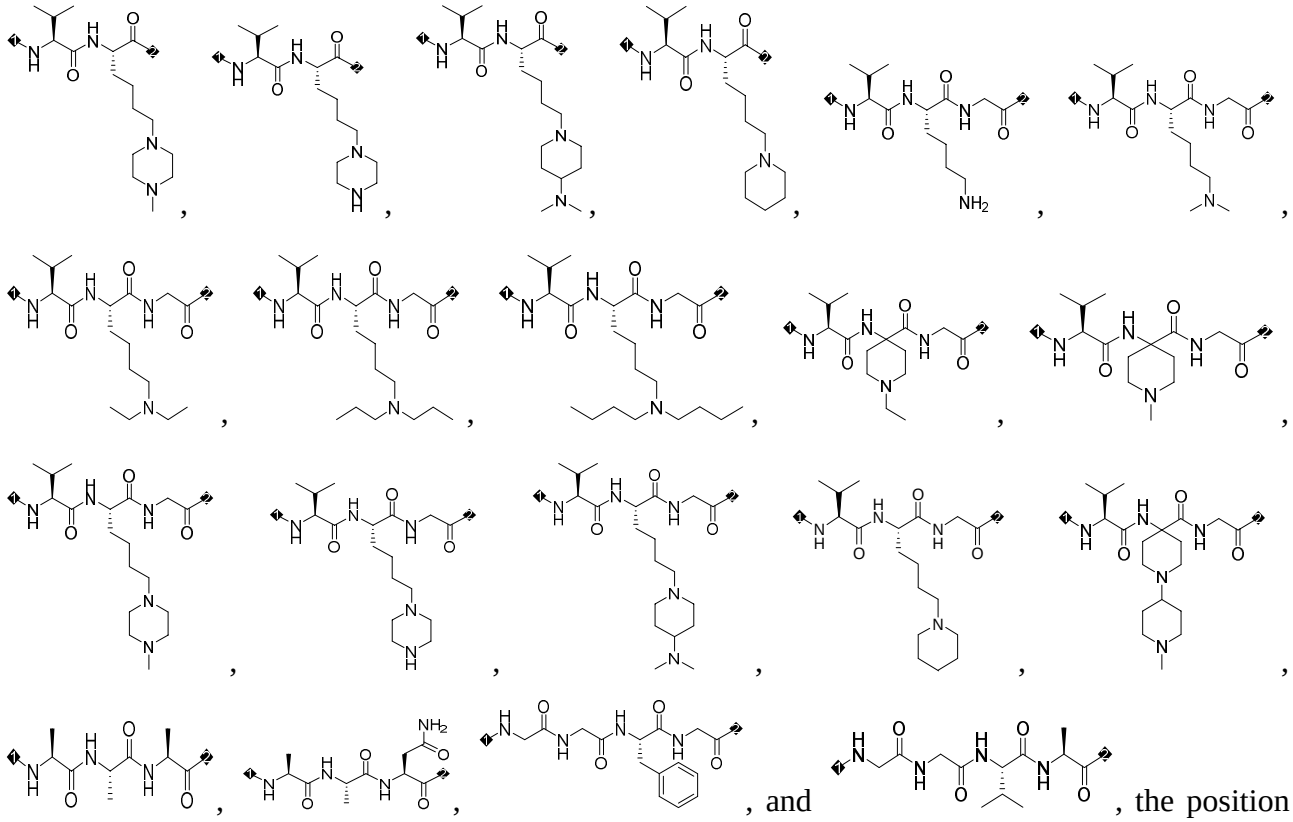







, and , each y1 is selected from any integer from 1 to 6 (such as 4, 5, 6), each y2 is independently selected from any integer from 0 to 10 (such as from 6 to 10), each y3 is independently selected from 1 or 2, each y4 is independently selected from 0 or 1, the position 1 is attached to L_1, and the position 2 is attached to L_3;

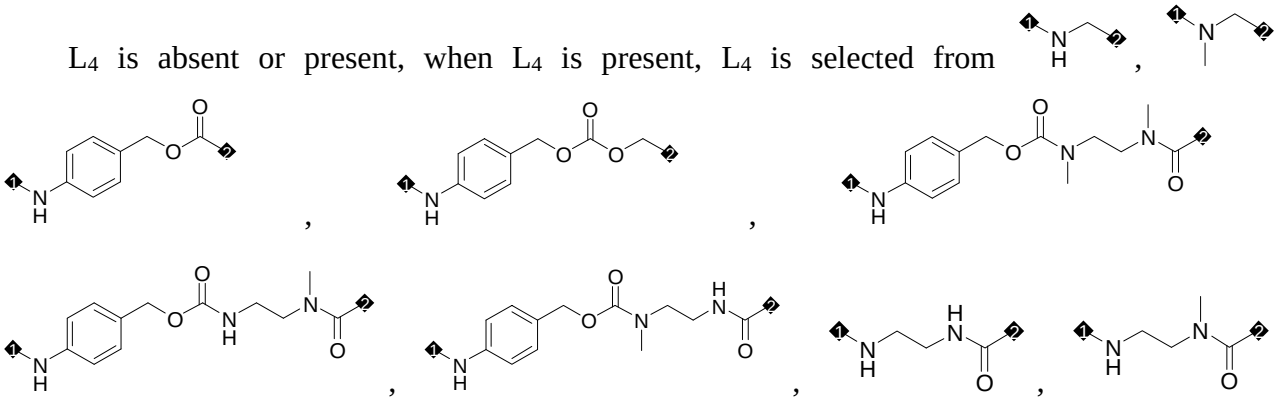
L_3 is selected from ,

,

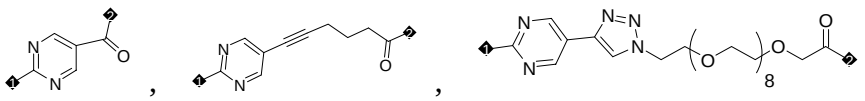


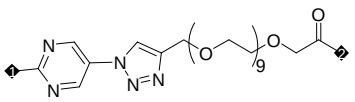
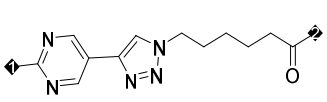
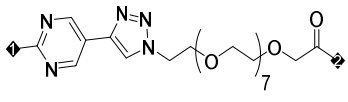
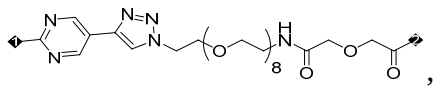
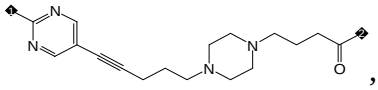
, the position 1 is attached to L_1 or L_2, and the position 2 is attached to L_4 or D; and

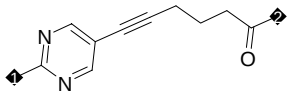
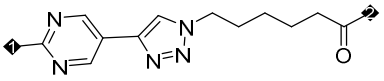
L_4 is absent or present, when L_4 is present, L_4 is selected from 

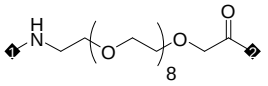
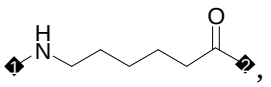
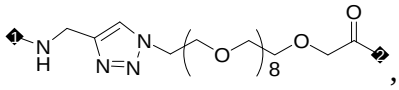
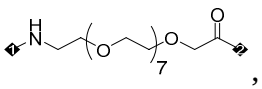
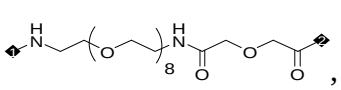
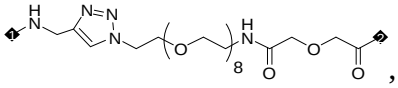
, the position 1 is attached to L_3, and the position 2 is attached to D.

19. The antibody-drug conjugate, the stereoisomer thereof, the prodrug thereof, the pharmaceutically acceptable salt thereof, the tautomer thereof, or the pharmaceutically acceptable solvate thereof according to claim 18, wherein,

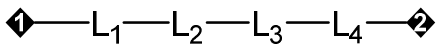
L_1 is selected from 

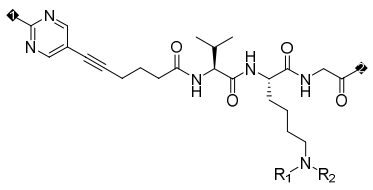
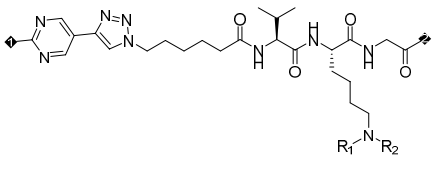
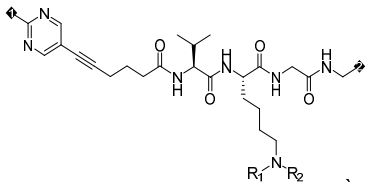
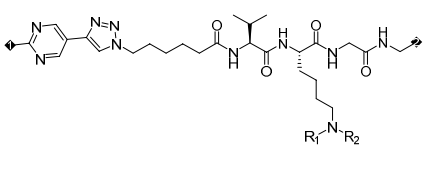
, , , , and , the position 1 is attached to Ab via an S atom, and the position 2 is attached to L_2 or L_3;

preferably, L_1 is selected from  and , the position 1 is attached to Ab via an S atom, and the position 2 is attached to L_2 or L_3; and

L_2 is absent or present, when L_2 is present, L_2 is selected from , , , , , and , the position 1 is attached to L_1, and the position 2 is attached to L_3; and

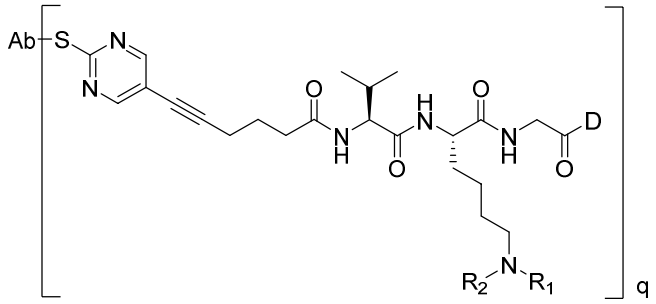
preferably, L_2 is absent.

20. The antibody-drug conjugate, the stereoisomer thereof, the prodrug thereof, the pharmaceutically acceptable salt thereof, the tautomer thereof, or the pharmaceutically acceptable solvate thereof according to claim 19, wherein the  has a structure as follows:

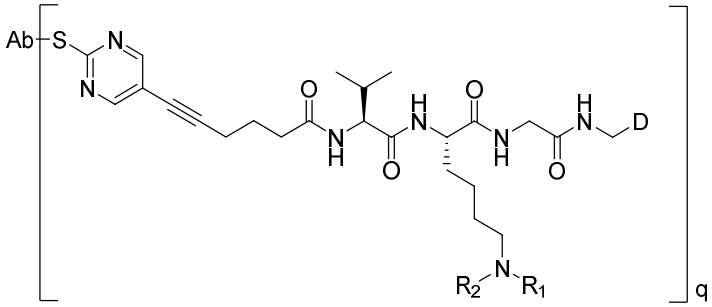
	
	

wherein R_1 and R_2 are independently selected from C_{1-6} alkyl and H; and is preferably C_{1-4} alkyl; and the position 1 is attached to the antibody or antigen-binding fragment thereof via an S atom, and the position 2 is attached to D.

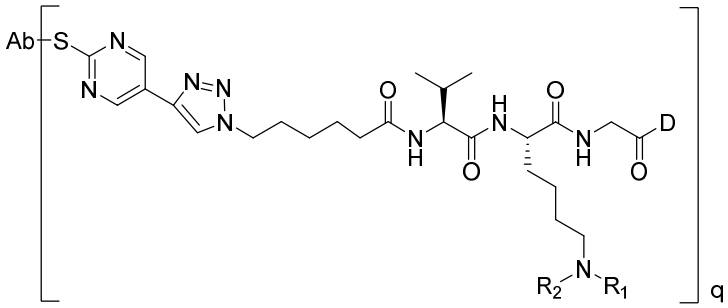
21. The antibody-drug conjugate, the stereoisomer thereof, the prodrug thereof, the pharmaceutically acceptable salt thereof, the tautomer thereof, or the pharmaceutically acceptable solvate thereof according to any one of claims 17-20, wherein the antibody-drug conjugate is a compound of Formula (IIA-1), Formula (IIA-2), Formula (IIB-1), or Formula (IIB-2):



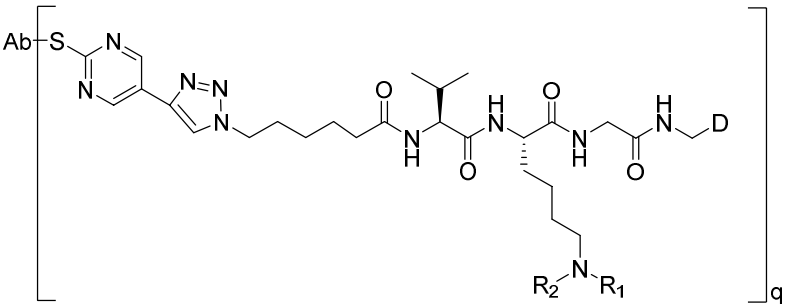
(IIA-1)



(IIA-2)



(IIB-1)

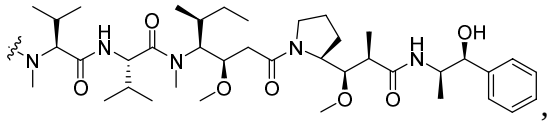
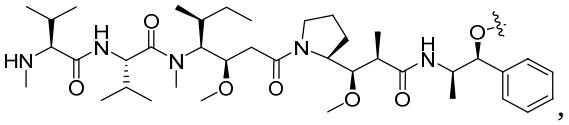
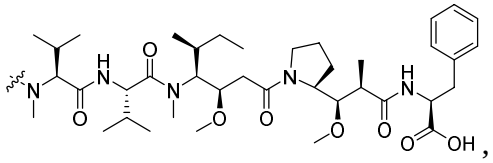
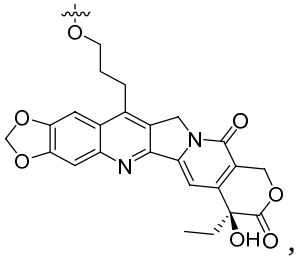
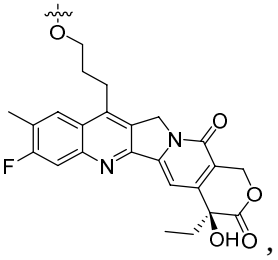
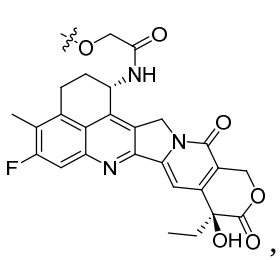
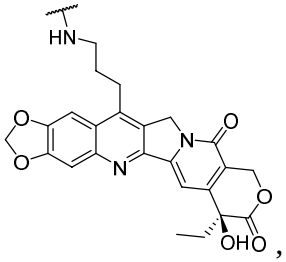
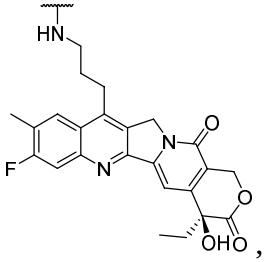
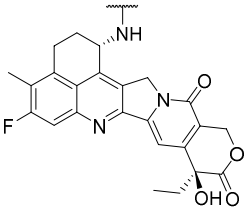


(IIB-2)

wherein,

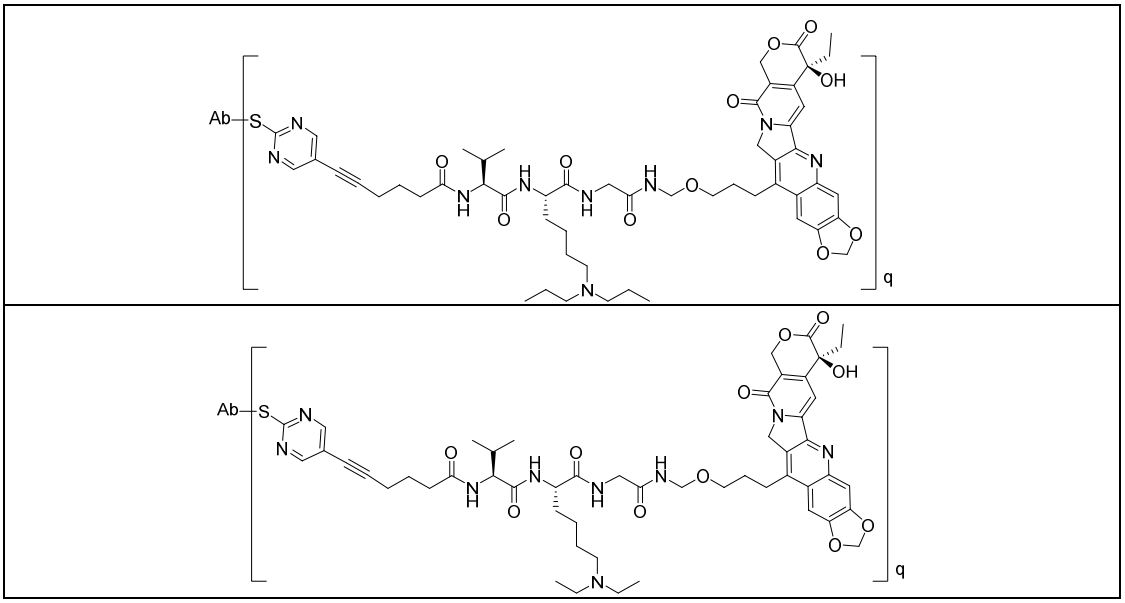
Ab is the antibody or antigen-binding fragment thereof according to any one of claims 1-9, or the multispecific antibody according to claim 10;

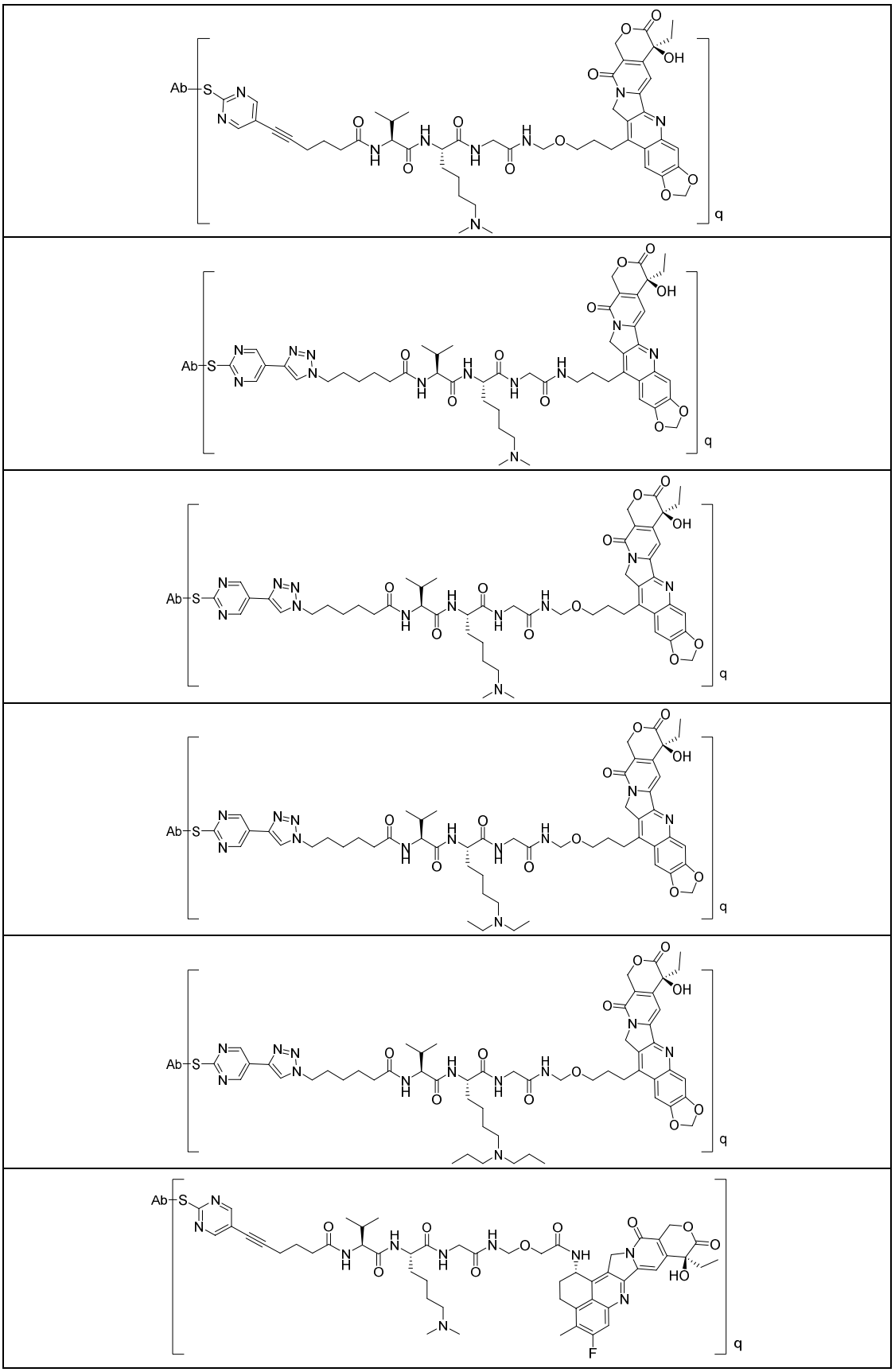
R_1 and R_2 are independently selected from C_{1-6} alkyl and H; and is preferably C_{1-4} alkyl;

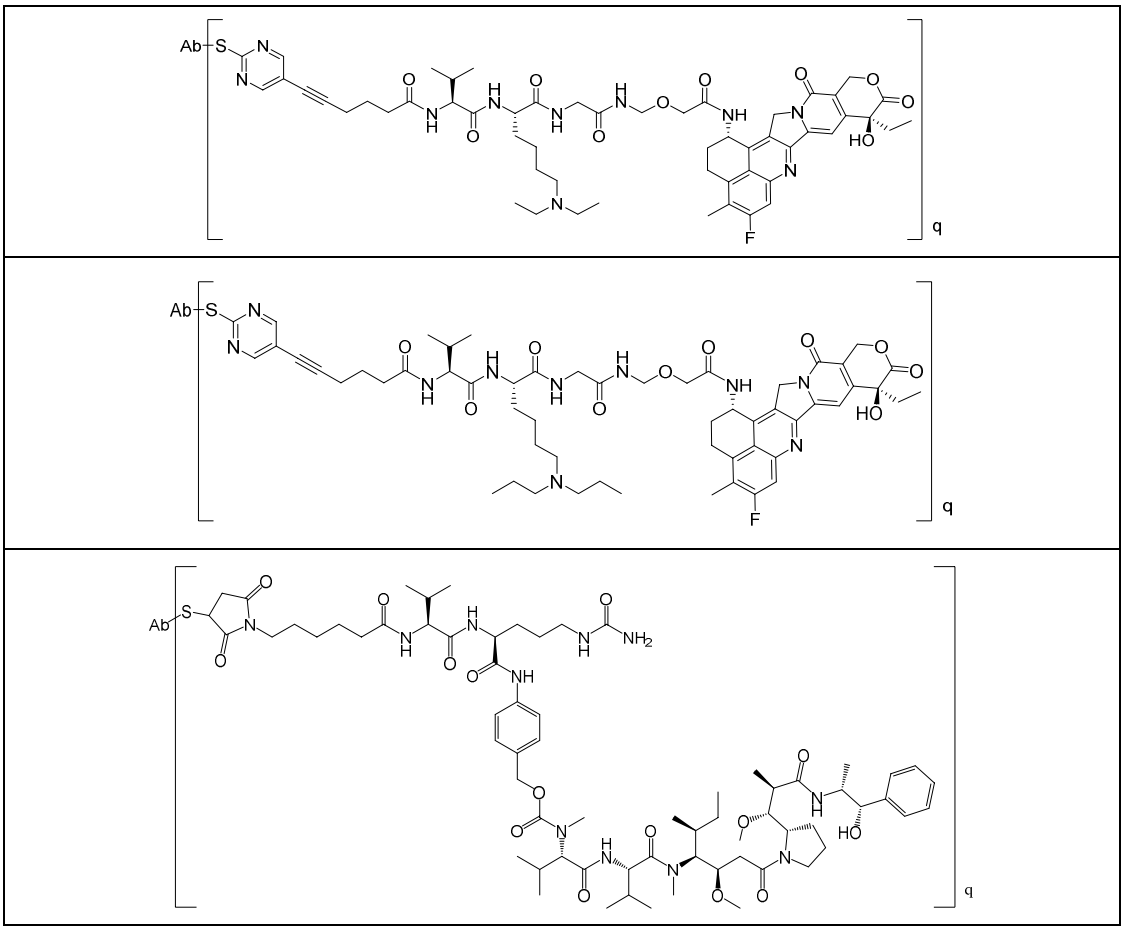
D is , , , , , , , , ; and

q is as defined in claim 16, and is preferably 2, 4, 6, or 8.

22. The antibody-drug conjugate, the stereoisomer thereof, the prodrug thereof, the pharmaceutically acceptable salt thereof, the tautomer thereof, or the pharmaceutically acceptable solvate thereof according to claim 16, wherein the antibody-drug conjugate has a structure as follows:







wherein,

q is as defined in claim 16; and is preferably 2, 4, 6 or, 8;

Ab is the antibody or antigen-binding fragment thereof according to any one of claims 1-9, or the multispecific antibody according to claim 10; and

preferably, Ab comprises: a heavy chain set forth in SEQ ID NO: 56 and a light chain set forth in SEQ ID NO: 57, or a heavy chain set forth in SEQ ID NO: 58 and a light chain set forth in SEQ ID NO: 59.

23. A population of antibody-drug conjugates, comprising or consisting of the antibody-drug conjugate, the stereoisomer thereof, the prodrug thereof, the pharmaceutically acceptable salt thereof, the tautomer thereof, or the pharmaceutically acceptable solvate thereof according to any one of claims 15-22, wherein the antibody-drug conjugate has one, two, or more q values;

preferably, an average DAR of the population of antibody-drug conjugates is selected from an integer or a decimal from 1 to 16, for example, selected from 1.5 to 2.5, 3.5 to 4.5, 5.5 to 6.5, or 7.5 to 8.5; and

more preferably, the average DAR of the population of antibody-drug conjugates is selected from about 2.0, 4.0, 6.0, or 8.0.

24. A pharmaceutical composition, comprising the antibody or antigen-binding fragment

thereof according to any one of claims 1-9, the multispecific antibody according to claim 10, the antibody-drug conjugate, the stereoisomer thereof, the prodrug thereof, the pharmaceutically acceptable salt thereof, the tautomer thereof, or the pharmaceutically acceptable solvate thereof according to any one of claims 15-22, the nucleic acid molecule according to claim 11, the immunoconjugate according to claim 13 or the population of antibody-drug conjugates according to claim 23, and optionally one or more pharmaceutically acceptable excipients.

25. Use of the antibody-drug conjugate, the stereoisomer thereof, the prodrug thereof, the pharmaceutically acceptable salt thereof, the tautomer thereof, or the pharmaceutically acceptable solvate thereof according to any one of claims 15-22, the anti-c-MET antibody or antigen-binding fragment thereof according to any one of claims 1-9, the multispecific antibody according to claim 10, the nucleic acid molecule according to claim 11, the immunoconjugate according to claim 13 or the population of antibody-drug conjugates according to claim 23, or the pharmaceutical composition according to claim 24, in the preparation of a medicine for treatment or prophylaxis of a disease related to c-MET activity;

preferably, the disease related to the c-MET activity is a tumor related to the c-MET activity; and

preferably, the tumor is selected from: lung cancer (for example, non-small cell lung cancer, small cell lung cancer, or lung adenocarcinoma), colon cancer (for example, human colon adenocarcinoma), rectal cancer, gastric cancer, colorectal cancer (for example, colorectal adenocarcinoma).