[0008a] According to an aspect, there is provided an antibody conjugate comprising an antibody that specifically binds to CD74 linked site-specifically to at least one payload moiety, wherein the antibody comprises a non-natural amino acid at a site selected from the group consisting of HC-F404, HC-K121, HC-Y180, HC-F241, HC-221, LC-T22, LC-S7, LC-N152, LC-K42, LC-E161, LC-D170, HC-S136, HC-S25, HC-A40, HC-S119, HC-S190, HC-K222, HC-R19, HC-Y52, or HC-S70, according to the Kabat, Chothia, or EU numbering scheme, and wherein the payload is conjugated to the non-natural amino acid either directly or indirectly, and wherein the antibody further comprises:

a. a V_H comprising: a CDR-H1 comprising at least one of SEQ ID NOs: 1 and 33; a CDR-H2 comprising at least one of SEQ ID NOs: 65 and 97; and a CDR-H3 comprising SEQ ID NO: 129;

b. a V_H comprising: a CDR-H1 comprising at least one of SEQ ID NOs: 2 and 34; a CDR-H2 comprising at least one of SEQ ID NOs: 66 and 98; and a CDR-H3 comprising SEQ ID NO: 130;

c. a V_H comprising: a CDR-H1 comprising at least one of SEQ ID NOs: 3 and 35; a CDR-H2 comprising at least one of SEQ ID NOs: 67 and 99; and a CDR-H3 comprising SEQ ID NO: 131;

d. a V_H comprising: a CDR-H1 comprising at least one of SEQ ID NOs: 4 and 36; a CDR-H2 comprising at least one of SEQ ID NOs: 68 and 100; and a CDR-H3 comprising SEQ ID NO: 132;

e. a V_H comprising: a CDR-H1 comprising at least one of SEQ ID NOs: 5 and 37; a CDR-H2 comprising at least one of SEQ ID NOs: 69 and 101; and a CDR-H3 comprising SEQ ID NO: 133;

f. a V_H comprising: a CDR-H1 comprising at least one of SEQ ID NOs: 6 and 38; a CDR-H2 comprising at least one of SEQ ID NOs: 70 and 102; and a CDR-H3 comprising SEQ ID NO: 134;

g. a V_H comprising: a CDR-H1 comprising at least one of SEQ ID NOs: 7 and 39; a CDR-H2 comprising at least one of SEQ ID NOs: 71 and 103; and a CDR-H3 comprising SEQ ID NO: 135;

WHAT IS CLAIMED IS:

1. An antibody conjugate comprising an antibody that specifically binds to CD74 linked site-specifically to at least one payload moiety, wherein the antibody comprises a non-natural amino acid at a site selected from the group consisting of HC-F404, HC-K121, HC-Y180, HC-F241, HC-221, LC-T22, LC-S7, LC-N152, LC-K42, LC-E161, LC-D170, HC-S136, HC-S25, HC-A40, HC-S119, HC-S190, HC-K222, HC-R19, HC-Y52, or HC-S70, according to the Kabat, Chothia, or EU numbering scheme, and wherein the payload is conjugated to the non-natural amino acid either directly or indirectly, and wherein the antibody further comprises:

a. a V_H comprising: a CDR-H1 comprising at least one of SEQ ID NOs: 1 and 33; a CDR-H2 comprising at least one of SEQ ID NOs: 65 and 97; and a CDR-H3 comprising SEQ ID NO: 129;

b. a V_H comprising: a CDR-H1 comprising at least one of SEQ ID NOs: 2 and 34; a CDR-H2 comprising at least one of SEQ ID NOs: 66 and 98; and a CDR-H3 comprising SEQ ID NO: 130;

c. a V_H comprising: a CDR-H1 comprising at least one of SEQ ID NOs: 3 and 35; a CDR-H2 comprising at least one of SEQ ID NOs: 67 and 99; and a CDR-H3 comprising SEQ ID NO: 131;

d. a V_H comprising: a CDR-H1 comprising at least one of SEQ ID NOs: 4 and 36; a CDR-H2 comprising at least one of SEQ ID NOs: 68 and 100; and a CDR-H3 comprising SEQ ID NO: 132;

e. a V_H comprising: a CDR-H1 comprising at least one of SEQ ID NOs: 5 and 37; a CDR-H2 comprising at least one of SEQ ID NOs: 69 and 101; and a CDR-H3 comprising SEQ ID NO: 133;

f. a V_H comprising: a CDR-H1 comprising at least one of SEQ ID NOs: 6 and 38; a CDR-H2 comprising at least one of SEQ ID NOs: 70 and 102; and a CDR-H3 comprising SEQ ID NO: 134;

g. a V_H comprising: a CDR-H1 comprising at least one of SEQ ID NOs: 7 and 39; a CDR-H2 comprising at least one of SEQ ID NOs: 71 and 103; and a CDR-H3 comprising SEQ ID NO: 135;

z. a V_H comprising: a CDR-H1 comprising at least one of SEQ ID NOs: 26 and 58; a CDR-H2 comprising at least one of SEQ ID NOs: 90 and 122; and a CDR-H3 comprising SEQ ID NO: 154;

aa. a V_H comprising: a CDR-H1 comprising at least one of SEQ ID NOs: 27 and 59; a CDR-H2 comprising at least one of SEQ ID NOs: 91 and 123; and a CDR-H3 comprising SEQ ID NO: 155; or

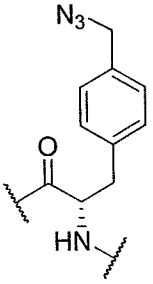
bb. a V_H comprising: a CDR-H1 comprising at least one of SEQ ID NOs: 28 and 60; a CDR-H2 comprising at least one of SEQ ID NOs: 92 and 124; and a CDR-H3 comprising SEQ ID NO: 156.

2. The antibody conjugate of claim 1 or 2, wherein the non-natural amino acid is selected from the group consisting of p-acetyl-L-phenylalanine, O-methyl-L-tyrosine, an -3-(2-naphthyl)alanine, 3-methyl-phenylalanine, O-4-allyl-L-tyrosine, 4-propyl-L-tyrosine, a tri-O-acetyl-GlcNAcβ-serine, L-Dopa, fluorinated phenylalanine, isopropyl-L-phenylalanine, p-azido-L-phenylalanine, p-azidomethyl-L-phenylalanine, compound 56, p-acyl-L-phenylalanine, p-benzoyl-L-phenylalanine, L-phosphoserine, phosphonoserine, phosphonotyrosine, p-iodo-phenylalanine, p-bromophenylalanine, p-amino-L-phenylalanine, isopropyl-L-phenylalanine, and p-propargyloxy-phenylalanine.

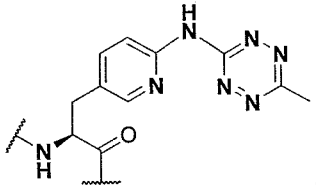
3. The antibody conjugate of claim 2, wherein the antibody is linked to the payload moiety via a linker that is hydrolytically stable.

4. The antibody conjugate of claim 2, wherein the antibody is linked to the payload moiety via a linker that is cleavable.

5. The antibody conjugate of any one of claims 2 to 4 wherein the non-natural amino acid residue is according to formula 30:



or formula 56:



6. The antibody conjugate of any of the preceding claims according to any of formulas 101a-104b:

l. a V_L comprising: a CDR-L1 comprising SEQ ID NO: 172; a CDR-L2 comprising SEQ ID NO: 192; and a CDR-L3 comprising SEQ ID NO: 212;

m. a V_L comprising: a CDR-L1 comprising SEQ ID NO: 173; a CDR-L2 comprising SEQ ID NO: 193; and a CDR-L3 comprising SEQ ID NO: 213;

n. a V_L comprising: a CDR-L1 comprising SEQ ID NO: 174; a CDR-L2 comprising SEQ ID NO: 194; and a CDR-L3 comprising SEQ ID NO: 214;

o. a V_L comprising: a CDR-L1 comprising SEQ ID NO: 175; a CDR-L2 comprising SEQ ID NO: 195; and a CDR-L3 comprising SEQ ID NO: 215;

p. a V_L comprising: a CDR-L1 comprising SEQ ID NO: 176; a CDR-L2 comprising SEQ ID NO: 196; and a CDR-L3 comprising SEQ ID NO: 216;

q. a V_L comprising: a CDR-L1 comprising SEQ ID NO: 177; a CDR-L2 comprising SEQ ID NO: 197; and a CDR-L3 comprising SEQ ID NO: 217;

r. a V_L comprising: a CDR-L1 comprising SEQ ID NO: 178; a CDR-L2 comprising SEQ ID NO: 198; and a CDR-L3 comprising SEQ ID NO: 218; or

s. a V_L comprising: a CDR-L1 comprising SEQ ID NO: 179; a CDR-L2 comprising SEQ ID NO: 199; and a CDR-L3 comprising SEQ ID NO: 219.

10. The antibody conjugate of any of the preceding claims, wherein the antibody comprises:

a. the V_H region is SEQ ID NO: 236, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 256, or the conservative modified variants, glycosylation variants, or Fc variants thereof;

b. the V_H region is SEQ ID NO: 236, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 257, or the conservative modified variants, glycosylation variants, or Fc variants thereof;

c. the V_H region is SEQ ID NO: 236, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 265, or the conservative modified variants, glycosylation variants, or Fc variants thereof;

d. the V_H region is SEQ ID NO: 236, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 264, or the conservative modified variants, glycosylation variants, or Fc variants thereof;

e. the V_H region is SEQ ID NO: 236, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 267, or the conservative modified variants, glycosylation variants, or Fc variants thereof;

f. the V_H region is SEQ ID NO: 236, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 268, or the conservative modified variants, glycosylation variants, or Fc variants thereof;

g. the V_H region is SEQ ID NO: 236, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 269, or the conservative modified variants, glycosylation variants, or Fc variants thereof;

h. the V_H region is SEQ ID NO: 236, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 270, or the conservative modified variants, glycosylation variants, or Fc variants thereof;

i. the V_H region is SEQ ID NO: 237, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 256, or the conservative modified variants, glycosylation variants, or Fc variants thereof;

j. the V_H region is SEQ ID NO: 237, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 257, or the conservative modified variants, glycosylation variants, or Fc variants thereof;

k. the V_H region is SEQ ID NO: 237, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 265, or the conservative modified variants, glycosylation variants, or Fc variants thereof;

l. the V_H region is SEQ ID NO: 237, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 264, or the conservative modified variants, glycosylation variants, or Fc variants thereof;

m. the V_H region is SEQ ID NO: 237, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 267, or the conservative modified variants, glycosylation variants, or Fc variants thereof;

n. the V_H region is SEQ ID NO: 237, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 268, or the conservative modified variants, glycosylation variants, or Fc variants thereof;

o. the V_H region is SEQ ID NO: 237, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 269, or the conservative modified variants, glycosylation variants, or Fc variants thereof;

p. the V_H region is SEQ ID NO: 237, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 270, or the conservative modified variants, glycosylation variants, or Fc variants thereof;

q. the V_H region is SEQ ID NO: 238, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 256, or the conservative modified variants, glycosylation variants, or Fc variants thereof;

r. the V_H region is SEQ ID NO: 238, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 257, or the conservative modified variants, glycosylation variants, or Fc variants thereof;

s. the V_H region is SEQ ID NO: 238, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 265, or the conservative modified variants, glycosylation variants, or Fc variants thereof;

t. the V_H region is SEQ ID NO: 238, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 264, or the conservative modified variants, glycosylation variants, or Fc variants thereof;

u. the V_H region is SEQ ID NO: 238, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 267, or the conservative modified variants, glycosylation variants, or Fc variants thereof;

v. the V_H region is SEQ ID NO: 238, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 268, or the conservative modified variants, glycosylation variants, or Fc variants thereof;

w. the V_H region is SEQ ID NO: 238, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 269, or the conservative modified variants, glycosylation variants, or Fc variants thereof;

x. the V_H region is SEQ ID NO: 238, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 270, or the conservative modified variants, glycosylation variants, or Fc variants thereof;

y. the V_H region is SEQ ID NO: 239, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 256, or the conservative modified variants, glycosylation variants, or Fc variants thereof;

z. the V_H region is SEQ ID NO: 239, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 257, or the conservative modified variants, glycosylation variants, or Fc variants thereof;

aa. the V_H region is SEQ ID NO: 239, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 265, or the conservative modified variants, glycosylation variants, or Fc variants thereof;

bb. the V_H region is SEQ ID NO: 239, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 264, or the conservative modified variants, glycosylation variants, or Fc variants thereof;

cc. the V_H region is SEQ ID NO: 239, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 267, or the conservative modified variants, glycosylation variants, or Fc variants thereof;

dd. the V_H region is SEQ ID NO: 239, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 268, or the conservative modified variants, glycosylation variants, or Fc variants thereof;

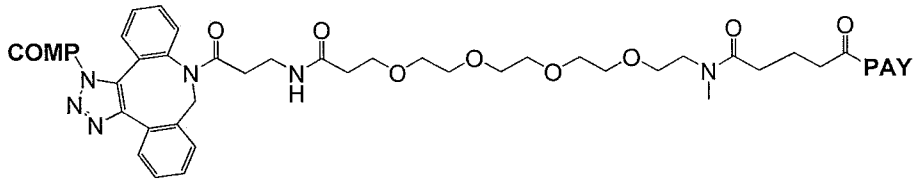
ee. the V_H region is SEQ ID NO: 239, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 269, or the conservative modified variants, glycosylation variants, or Fc variants thereof; or

ff. the V_H region is SEQ ID NO: 239, or the conservative modified variants, glycosylation variants, or Fc variants thereof, and the V_L region is SEQ ID NO: 270, or the conservative modified variants, glycosylation variants, or Fc variants thereof.

11. The antibody conjugate of claim 10, wherein the antibody comprises a non-natural amino acid at site HC-F404 according to the EU numbering scheme of Kabat.

12. The antibody conjugate of claim 11, wherein the non-natural amino acid is para-azidomethylphenylalanine or p-azidomethyl-L-phenylalanine.

13. The antibody conjugate of claim 12, wherein the antibody conjugate has the formula of (102b):



wherein **COMP** is the non-natural amino acid residue of the antibody bearing the indicated bond and **PAY** is DM1.

14. The antibody conjugate of claim 13, wherein the antibody conjugate has the structure of **Conjugate A**:

37. An antibody conjugate of any one of claims 1 to 32, or a pharmaceutical composition of claim 36 for use in treating or preventing a disease or condition in a subject.

38. An antibody conjugate of any one of claims 1 to 32, or a pharmaceutical composition of claim 36 for use in diagnosing a disease or condition in a subject.

39. The antibody conjugate or pharmaceutical composition of any of claims 37 or 38, wherein the disease or condition involves an upregulation of CD74 in a cancer, an autoimmune disease, an inflammatory disease, or an infection.

40. The antibody conjugate or pharmaceutical composition of claim 39, wherein the cancer is selected from multiple myeloma or pancreatic cancer.

41. The antibody conjugate or pharmaceutical composition of claim 39, wherein the disease or condition is B-cell lymphoma.

42. The antibody conjugate or pharmaceutical composition of claim 39, wherein the disease or condition is non-Hodgkin's lymphoma.

43. The antibody conjugate or pharmaceutical composition of claim 39, wherein the disease or condition is leukemia.