Claims:

1. An analytical method comprising:

(i) conjugation of unoccupied cysteine sites of a cysteine-conjugated antibody drug conjugate (ADC) using an isotopically-labeled cytotoxin containing a carbonyl group and a reductant to produce an isotopically-labeled ADC sample; and

(ii) peptide mapping the sample.

2. The method of claim 1, wherein the cytotoxin is MMAF or MMAE.

3. The method of claim 1 or 2, wherein the ADC is first reduced by the reductant and then conjugated with the isotopically-labeled cytotoxin.

4. The method of any one of claims 1 to 3, wherein excess isotopically-labeled cytotoxin is removed prior to the peptide mapping by eluting the sample through a size exclusion chromatography column.

5. The method of any one of claims 1 to 4, wherein the peptide mapping comprises using liquid chromatography tandem mass spectrometry (LC-MS/MS) analysis.

6. The method of any one of claims 1 to 5, wherein the peptide mapping comprises denaturing the sample, reducing all remaining disulfide bonds, and alkylating resulting free sulfhydryls.

7. The method of any one of claims 1 to 6, wherein the peptide mapping comprises enzymatically digesting the sample to produce isotopically-labeled conjugated peptides and optionally quenching the enzymatic digestion by addition of a strong acid.

8. The method of claim 7, wherein the isotopically-labeled conjugated peptides are ionized and mass-to-charge ratios are detected, and the mass-to-charge ratios detected for the isotopically-labeled conjugated peptides are compared to non-isotopically-labeled conjugated peptides.

9. The method of any one of claims 1 to 8, wherein the method comprises reacting cytotoxin with isotopically-labeled water to produce the isotopically-labeled cytotoxin.

10. The method of any one of claims 1 to 9, wherein the ADC is belantamab mafodotin.

11. A composition comprising an anti-BCMA antibody conjugated to a cytotoxic agent to form an antibody drug conjugate (ADC), wherein the antibody comprises a CDRH1 comprising the amino acid sequence according to SEQ ID NO:1; a CDRH2 comprising the amino acid sequence according to SEQ ID NO:2; a CDRH3 comprising the amino acid sequence according to SEQ ID NO:3; a CDRL1 comprising the amino acid sequence according to SEQ ID NO:4; a CDRL2 comprising the amino acid sequence according to SEQ ID NO:5; and a CDRL3 comprising the amino acid sequence according to SEQ ID NO:6; wherein the cytotoxic agent is MMAF or MMAE; and wherein the percentage drug load at LC C214 is between about 56% to about 80%, the percentage drug load at HC C224 is between about 58% to about 81%, the percentage drug load of HC hinge DL2 at HC C230 and C233 is between about 15% to about 46%, and/or the percentage drug load of HC hinge DL1 at HC C230 or HC C233 is between about 11% to about 15%.

12. The composition of claim 11, wherein the anti-BCMA antibody is belantamab.

13. The composition of claim 11, wherein the ADC is belantamab mafodotin.

14. A pharmaceutical composition comprising the composition of claim 11 and at least one pharmaceutically acceptable excipient.

15. A composition of claim 11 or the pharmaceutical composition of claim 14 for use in the treatment of cancer.

16. Use of a composition of claim 11 in the manufacture of a medicament for use in the treatment of cancer.

17. A method of determining conjugation levels of cysteine-conjugated antibody drug conjugates, the method comprising:

a) reducing the antibody drug conjugates to form reduced antibody drug conjugates;

b) conjugating the reduced antibody drug conjugates with an isotypically-labeled cytotoxin to form isotopically-labeled antibody drug conjugates;

c) producing isotopically-labeled conjugated peptides from the isotopically-labeled antibody drug conjugates and performing peptide mapping on the isotopically-labeled conjugated peptides;

d) detecting mass-to-charge ratios for the isotopically-labeled conjugated peptides; and

e) comparing the mass-to-charge ratios of the isotopically-labeled conjugated peptides to mass-to charge ratios for non-isotopically-labeled conjugated peptides to determine the conjugation levels of cysteine-conjugated antibody drug conjugates.

18. The method of claim 17, wherein the cytotoxin is MMAF or MMAE.

19. The method of claim 17 or 18, wherein the cysteine-conjugated antibody drug conjugates are first reduced by a reductant and then conjugated with the isotopically-labeled cytotoxin.

20. The method of claim 19, wherein excess reductant is removed prior to the peptide mapping by eluting the sample through a size exclusion chromatography column.

21. The method of any one of claims 17 to 20, wherein the peptide mapping comprises using liquid chromatography tandem mass spectrometry (LC-MS/MS) analysis.

22. The method of any one of claims 17 to 21, wherein the peptide mapping comprises denaturing the sample, reducing remaining disulfide bonds, and alkylating resulting free sulfhydryls.

23. The method of any one of claims 17 to 22, wherein the peptide mapping comprises enzymatically digesting the sample to produce isotopically-labeled conjugated peptides and optionally quenching the enzymatic digestion by addition of a strong acid.

24. The method of any one of claims 17 to 23, wherein the method comprises reacting cytotoxin with isotopically-labeled water to produce the isotopically-labeled cytotoxin.

25. The method of any one of claims 17 to 24, wherein the cysteine-conjugated antibody drug conjugates are belantamab mafodotin.