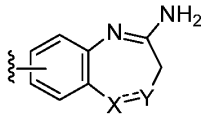
We claim:

1. An aqueous formulation comprising a conjugate comprising a compound linked to a polypeptide, wherein the compound comprises the structure:



wherein ≡ is a double bond or a single bond;

wherein when ≡ is a double bond, X and Y are each CH; and

when ≡ is a single bond, one of X and Y is CH_2 and the other is CH_2, O, or NH; and the structure is optionally substituted at any position other than the -NH_2;

wherein the pH of the formulation is from 4 to 5.2 or from 4.4 to 5.4.

2. The aqueous formulation of claim 1, wherein the pH of the formulation is from 4.4 to 5.4, 4.5 to 5.3, 4.6 to 5.2, 4.7 to 5.1, 4.8 to 5.1, 4.9 to 5.1, 4.4 to 5.0, 4.5 to 5.0, 4.6 to 5.0, 4.7 to 5.0, 4.8 to 5.0, or 4.9 to 5.0.

3. The aqueous formulation of claim 1, wherein the pH of the formulation is from 4.4 to 5.4.

4. The aqueous formulation of claim 1, wherein the pH of the formulation is from 4.4 to 5.3.

5. The aqueous formulation of claim 1, wherein the pH of the formulation is from 4.4 to 5.2.

6. The aqueous formulation of claim 1, wherein the pH of the formulation is from 4.4 to 5.1.

7. The aqueous formulation of claim 1, wherein the pH of the formulation is from 4.5 to 5.1.

8. The aqueous formulation of claim 1, wherein the pH of the formulation is from 4.6 to 5.0.

9. The aqueous formulation of claim 1, wherein the pH of the formulation is from 4.7 to 4.9.

10. The aqueous formulation of claim 1, wherein the pH of the formulation is 4.8.

11. The aqueous formulation of claim 1, wherein the pH of the formulation is 4.9.

12. The aqueous formulation of claim 1, wherein the pH of the formulation is 5.0.

13. The aqueous formulation of any one of claims 1-12, wherein the formulation comprises at least one buffering agent.

14. The aqueous formulation of claim 13, wherein the at least one buffering agent is selected from histidine, citrate, aspartate, acetate, phosphate, lactate, tromethamine, gluconate, glutamate, tartrate, succinate, malic acid, fumarate, α-ketoglutarate, and combinations thereof.

15. The aqueous formulation of claim 14, wherein the at least one buffering agent is histidine and aspartate.

16. The aqueous formulation of any one of claims 13-15, wherein the total concentration of buffering agents in the formulation is about 15mM to about 25mM.

17. The aqueous formulation of any one of claims 1-16, wherein the aqueous formulation comprises at least one lyoprotectant selected from sucrose, arginine, glycine, sorbitol, glycerol, trehalose, dextrose, alpha-cyclodextrin, hydroxypropyl beta-cyclodextrin, hydroxypropyl gamma-cyclodextrin, proline, methionine, albumin, mannitol, maltose, dextran, and combinations thereof.

18. The aqueous formulation of claim 17, wherein the at least one lyoprotectant is sucrose.

19. The aqueous formulation of claim 17 or claim 18, wherein the total concentration of the at least one lyoprotectant is about 7% to about 9%.

20. The aqueous formulation of any one of claims 1-19, wherein the aqueous formulation comprises at least one surfactant.

21. The aqueous formulation of claim 20, wherein the at least one surfactant is selected from polysorbate 80, polysorbate 20, poloxamer 88, and combinations thereof.

22. The aqueous formulation of claim 21, wherein the at least one surfactant is polysorbate 80.

23. The aqueous formulation of any one of claims 20-22, wherein the total concentration of the at least one surfactant is about 0.01% to about 0.05%.

24. The aqueous formulation of any one of claims 1-23, wherein the concentration of the conjugate in the aqueous formulation is about 70 mg/mL to about 100 mg/mL.

25. The aqueous formulation of any one of claims 1-24, wherein the polypeptide is an antibody.

26. The aqueous formulation of claim 25, wherein the antibody comprises an antigen binding domain and an Fc domain.

27. The aqueous formulation of claim 26, wherein the Fc domain exhibits the same or substantially similar binding affinity to Fcgamma and/or FcRn receptors as compared to a wild-type Fc domain from an IgG1 antibody.

28. The aqueous formulation of any one of claims 25-27, wherein the antibody binds a tumor associated antigen.

29. The aqueous formulation of claim 28, wherein the tumor associated antigen is selected from HER2, Nectin-4, ASGR1, mesothelin, PSMA, rsPSMA, TROP2, LIV-1, MUC16, CEACAM1, CEACAM3, CEACAM4, CEACAM5, CEACAM6, CEACAM7, CEACAM8, CEACAM16, CEACAM18, CEACAM19, CEACAM20, CEACAM21, URLC10, NY-ESO-1, GAA, OFA, cyclin B1, WT-1, CEF, VEGRR1, VEGFR2, TTK, MUC1, HPV16E7, CEA, IMA910, KOC1, SL-701, MART-1, gp100, tyrosinase, GSK2302050A, survivin, MAGE-3.1, MAGE-10.A2, OVA BiP, gp209-2M, melan-A, NA17.A2, KOC1, CO16, DEPDC1, MPHOSPH1, MAGE12, ONT-10, GD2L, GD3L, GSK2302032A, URLC10, CDCA1, TF, PSA, MUC-2, TERT, HPV16, HPV18, STF-II, G17DT, ICT-107, Dex2, hTERT, PAP, tyrosinase related peptide 2 (TRP2), and LRRC15.

30. The aqueous formulation of claim 28, wherein the tumor associated antigen is selected from:

a) an antigen present on lung cancer, wherein the antigen is optionally selected from mesothelin, HER2, EGFR, PD-L1, MSLN, LY6K, CD56, PTK7, FOLR1, DLL3, SLC34A2, CECAM5, MUC16, LRRC15, ADAM12, EGFRvIII, LYPD3, EFNA4, and MUC1;
b) an antigen present on liver cancer, wherein the antigen is optionally selected from GPC3, EPCAM, and CECAM5;
c) an antigen present on kidney cancer, wherein the antigen is optionally selected from HAVCR1, ENPP3, CDH6, CD70, and cMET;
d) an antigen present on pancreatic cancer, wherein the antigen is optionally selected from PTK7, MUC16, MSLN, LRRC15, ADAM12, EFNA4, MUC5A, and MUC1;
e) an antigen present on colorectal cancer, wherein the antigen is optionally selected from EPHB2, TMEM238, CECAM5, LRRC15, ADAM12, EFNA4, and GPA33;
f) an antigen present on ovarian cancer, wherein the antigen is optionally selected from MUC16, MUC1, MSLN, FOLR1, sTN, VTCN1, HER2, PTK7, FAP, TMEM238, LRRC15, CLDN6, SLC34A2, and EFNA4;
g) an antigen present on head and neck cancer, wherein the antigen is optionally selected from LY6K, PTK7, LRRC15, ADAM12, LYPD3, EFNA4 and TNC;
h) an antigen present on bone cancer, wherein the antigen is optionally selected from EPHA2, LRRC15, ADAM12, GPNMB, TP-3, and CD248;
i) an antigen present on mesothelioma, wherein the antigen is optionally MSLN;

j) an antigen present on bladder cancer, wherein the antigen is optionally selected from LY6K, PTK7, UPK1B, UPK2, TNC, Nectin4, SLITRK6, LYPD3, EFNA4, and HER2;

k) an antigen present on stomach cancer, wherein the antigen is optionally selected from HER2, EPHB2, TMEM238, CECAM5, and EFNA4;

l) an antigen present on prostate cancer, wherein the antigen is optionally selected from PSMA, FOLH1, PTK7, STEAP, TMEFF2 (TENB2), OR51E2, SLC30A4, and EFNA4;

m) an antigen present on thyroid cancer, wherein the antigen is optionally PTK7;

n) an antigen present on uterine cancer, wherein the antigen is optionally selected from LY6K, PTK7, EPHB2, FOLR1, ALPPL2, MUC16, and EFNA4;

o) an antigen present on cervical/endometrial cancer, wherein the antigen is optionally selected from LY6K, PTK7, MUC16, LYPD3, EFNA4, and MUC1; and

p) an antigen present on breast cancer, wherein the antigen is optionally selected from HER2, TROP2, LIV-1, CDH3 (p-cadherin), MUC1, Sialo-epitope CA6, PTK7, GPNMB, LAMP-1, LRRC15, ADAM12, EPHA2, TNC, LYPD3, EFNA4, and CLDN6.

31. The aqueous formulation of any one of claims 25-30, wherein the antibody is an anti-HER2 antibody.

32. The aqueous formulation of claim 31, wherein the anti-HER2 antibody comprises heavy chain (HC)-CDR1, HC-CDR2, HC-CDR3, light chain (LC)-CDR1, LC-CDR2, and LC-CDR3 of SEQ ID NOS:1-6, respectively.

33. The aqueous formulation of claim 32, wherein the anti-HER2 antibody comprises a heavy chain variable region (V_H) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_H amino acid sequence of SEQ ID NO:7 and a light chain variable region (V_L) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_L amino acid sequence of SEQ ID NO:8.

34. The aqueous formulation of claim 31 or claim 32, wherein the anti-HER2 antibody comprises a V_H comprising or consisting of the amino acid sequence of SEQ ID NO:7 and a V_L comprising or consisting of the amino acid sequence of SEQ ID NO:8.

35. The aqueous formulation of any one of claims 32-34, wherein the anti-HER2 antibody comprises a heavy chain and light chain, wherein the heavy chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the heavy chain amino acid sequence of SEQ ID NO:9; and the light chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the light chain amino acid sequence of SEQ ID NO:10.

36. The aqueous formulation of claim 31 or claim 32, wherein the anti-HER2 antibody comprises a heavy chain comprising or consisting of the amino acid sequence of SEQ ID NO:9 and a light chain comprising or consisting of the amino acid sequence of SEQ ID NO:10.

37. The aqueous formulation of any one of claims 25-30, wherein the antibody is an anti-Nectin-4 antibody.

38. The aqueous formulation of claim 37, wherein the anti-Nectin-4 antibody comprises heavy chain (HC)-CDR1, HC-CDR2, HC-CDR3 of SEQ ID NOS: 11-13, respectively, and light chain (LC)-CDR1 of SEQ ID NO:14 or 15, LC-CDR2 of SEQ ID NO:16, and LC-CDR3 of SEQ ID NO:17.

39. The aqueous formulation of claim 38, wherein the anti-Nectin-4 antibody comprises a heavy chain variable region (V_H) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_H amino acid sequence of SEQ ID NO:18 and a light chain variable region (V_L) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_L amino acid sequence of SEQ ID NO:19 or 20.

40. The aqueous formulation of claim 37 or claim 38, wherein the anti-Nectin-4 antibody comprises a V_H comprising or consisting of the amino acid sequence of SEQ ID NO:18 and a V_L comprising or consisting of the amino acid sequence of SEQ ID NO:19 or 20.

41. The aqueous formulation of any one of claims 38-40, wherein the anti-Nectin-4 antibody comprises a heavy chain and light chain, wherein the heavy chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the heavy chain amino acid sequence of SEQ ID NO:21; and the light chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%,

at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the light chain amino acid sequence of SEQ ID NO:22 or 23.

42. The aqueous formulation of claim 37 or claim 38, wherein the anti-Nectin-4 antibody comprises a heavy chain comprising or consisting of the amino acid sequence of SEQ ID NO:21 and a light chain comprising or consisting of the amino acid sequence of SEQ ID NO:22 or 23.

43. The aqueous formulation of any one of claims 25-30, wherein the antibody is an anti-ASGR1 antibody.

44. The aqueous formulation of claim 43, wherein the anti-ASGR1 antibody comprises heavy chain (HC)-CDR1 of SEQ ID NO: 24 or 25, HC-CDR2 of SEQ ID NO:26, 27, or 28, HC-CDR3 of SEQ ID NO:29 or 30, light chain (LC)-CDR1 of SEQ ID NO:31 or 32, LC-CDR2 of SEQ ID NO:33, 34, 35 or 36, and LC-CDR3 of SEQ ID NO:37 or 38.

45. The aqueous formulation of claim 43, wherein the anti-ASGR1 antibody comprises (a) heavy chain (HC)-CDR1 of SEQ ID NO: 24, HC-CDR2 of SEQ ID NO:26, HC-CDR3 of SEQ ID NO:29, light chain (LC)-CDR1 of SEQ ID NO:31, LC-CDR2 of SEQ ID NO:33 or 34, and LC-CDR3 of SEQ ID NO:37; or (b) heavy chain (HC)-CDR1 of SEQ ID NO: 25, HC-CDR2 of SEQ ID NO:27 or 28, HC-CDR3 of SEQ ID NO:30, light chain (LC)-CDR1 of SEQ ID NO:32, LC-CDR2 of SEQ ID NO:35 or 36, and LC-CDR3 of SEQ ID NO:38.

46. The aqueous formulation of claim 44 or claim 45, wherein the anti-ASGR1 antibody comprises a heavy chain variable region (V_H) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_H amino acid sequence of SEQ ID NO:39 and a light chain variable region (V_L) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_L amino acid sequence of SEQ ID NO:42 or 43.

47. The aqueous formulation of claim 44 or claim 45, wherein the anti-ASGR1 antibody comprises a heavy chain variable region (V_H) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_H amino acid sequence of SEQ ID NO:40 or 41 and a light chain variable region (V_L) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_L amino acid sequence of SEQ ID NO:44 or 45.

48. The aqueous formulation of any one of claims 43-45, wherein the anti-ASGR1 antibody comprises a V_H comprising or consisting of the amino acid sequence of SEQ ID NO:39 and a V_L comprising or consisting of the amino acid sequence of SEQ ID NO:42 or 43.

49. The aqueous formulation of any one of claims 43-45, wherein the anti-ASGR1 antibody comprises a V_H comprising or consisting of the amino acid sequence of SEQ ID NO:40 or 41 and a V_L comprising or consisting of the amino acid sequence of SEQ ID NO:44 or 45.

50. The aqueous formulation of any one of claims 44-46 and 48, wherein the anti-ASGR1 antibody comprises a heavy chain and light chain, wherein the heavy chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the heavy chain amino acid sequence of SEQ ID NO:46; and the light chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the light chain amino acid sequence of SEQ ID NO:49 or 50.

51. The aqueous formulation of any one of claims 43-45, wherein the anti-ASGR1 antibody comprises a heavy chain comprising or consisting of the amino acid sequence of SEQ ID NO:46 and a light chain comprising or consisting of the amino acid sequence of SEQ ID NO:49 or 50.

52. The aqueous formulation of any one of claims 44-45, 47, and 49, wherein the anti-ASGR1 antibody comprises a heavy chain and light chain, wherein the heavy chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the heavy chain amino acid sequence of SEQ ID NO:47 or 48; and the light chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the light chain amino acid sequence of SEQ ID NO:51 or 52.

53. The aqueous formulation of any one of claims 43-45, wherein the anti-ASGR1 antibody comprises a heavy chain comprising or consisting of the amino acid sequence of SEQ ID NO:47 or 48 and a light chain comprising or consisting of the amino acid sequence of SEQ ID NO:51 or 52.

54. The aqueous formulation of any one of claims 25-30, wherein the antibody is an anti-mesothelin antibody.

55. The aqueous formulation of claim 54, wherein the anti-mesothelin antibody comprises heavy chain (HC)-CDR1, HC-CDR2, HC-CDR3, light chain (LC)-CDR1, LC-CDR2, and LC-CDR3 of SEQ ID NOS:53-58, respectively.

56. The aqueous formulation of claim 55, wherein the anti-mesothelin antibody comprises a heavy chain variable region (V_H) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_H amino acid sequence of SEQ ID NO:59 and a light chain variable region (V_L) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_L amino acid sequence of SEQ ID NO:60.

57. The aqueous formulation of claim 54 or claim 55, wherein the anti-mesothelin antibody comprises a V_H comprising or consisting of the amino acid sequence of SEQ ID NO:59 and a V_L comprising or consisting of the amino acid sequence of SEQ ID NO:60.

58. The aqueous formulation of any one of claims 55-57, wherein the anti-mesothelin antibody comprises a heavy chain and light chain, wherein the heavy chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the heavy chain amino acid sequence of SEQ ID NO:70; and the light chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the light chain amino acid sequence of SEQ ID NO:71.

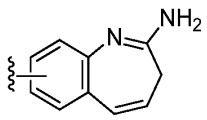
59. The aqueous formulation of claim 54 or claim 55, wherein the anti-mesothelin antibody comprises a heavy chain comprising or consisting of the amino acid sequence of SEQ ID NO:70 and a light chain comprising or consisting of the amino acid sequence of SEQ ID NO:71.

60. The aqueous formulation of claim 31, wherein the antibody is pertuzumab, trastuzumab, sacituzumab, or ladiratuzumab or comprises an antigen binding fragment of pertuzumab, trastuzumab, sacituzumab, or ladiratuzumab.

61. The aqueous formulation of any one of claims 1-60, wherein the compound is a myeloid agonist.

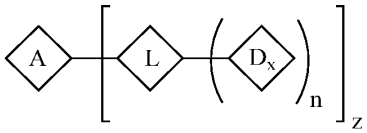
62. The aqueous formulation of any one of claims 1-61, wherein the compound is a TLR8 agonist.

63. The aqueous formulation of any one of claims 1-62, wherein the compound comprises the structure:



wherein the structure is optionally substituted at any position other than the $-NH_2$.

64. The aqueous formulation of any one of claims 1-63, wherein the conjugate is represented by Formula (I):



(I);

wherein:

A is the polypeptide,

L is a linker;

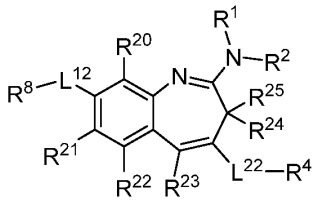
D_x is the compound;

n is selected from 1 to 20; and

z is selected from 1 to 20.

65. The aqueous formulation of claim 64, wherein n is 1 and z is from 1 to 8.

66. The aqueous formulation of any one of claims 1-63, wherein the conjugate comprises the compound linked to the polypeptide through a linker, wherein the compound and the linker together are a compound of Formula (IVB), or the aqueous formulation of claim 64 or claim 65, wherein L and Dx together are a compound of Formula (IVB):



(IVB)

wherein:

L^{12} is selected from $-X^3-$, $-X^3-C_{1-6}$ alkylene-X^3-, $-X^3-C_{2-6}$ alkenylene-X^3-, and $-X^3-C_{2-6}$ alkynylene-X^3-, each of which is optionally substituted on alkylene, alkenylene, or alkynylene with one or more substituents independently selected from R^{12};

L^{22} is independently selected from $-X^4-$, $-X^4-C_{1-6}$ alkylene-X^4-, $-X^4-C_{2-6}$ alkenylene-X^4-, and $-X^4-C_{2-6}$ alkynylene-X^4-, each of which is optionally substituted on alkylene, alkenylene, or alkynylene with one or more substituents independently selected from R^{10};

X^3 and X^4 are independently selected at each occurrence from a bond, -O-, -S-, $-N(R^{10})-$, -C(O)-, -C(O)O-, -OC(O)-, -OC(O)O-, $-C(O)N(R^{10})-$, $-C(O)N(R^{10})C(O)-$, $-C(O)N(R^{10})C(O)N(R^{10})-$,

-N(R^{10})C(O)-, -N(R^{10})C(O)N(R^{10})-, -N(R^{10})C(O)O-, -OC(O)N(R^{10})-, -C(NR^{10})-, -N(R^{10})C(NR^{10})-, -C(NR^{10})N(R^{10})-, -N(R^{10})C(NR^{10})N(R^{10})-, -S(O)$_2$-, -OS(O)-, -S(O)O-, -S(O)-, -OS(O)$_2$-, -S(O)$_2$O-, -N(R^{10})S(O)$_2$-, -S(O)$_2$N(R^{10})-, -N(R^{10})S(O)-, -S(O)N(R^{10})-, -N(R^{10})S(O)$_2$N(R^{10})-, and -N(R^{10})S(O)N(R^{10})-;

R^1 and R^2 are each hydrogen;

R^4 and R^8 are independently selected from: -OR^{10}, -N(R^{10})$_2$, -C(O)N(R^{10})$_2$, -C(O)R^{10}, -C(O)OR^{10}, -S(O)R^{10}, and -S(O)$_2$$R^{10}$; C_{1-10} alkyl, C_{2-10} alkenyl, C_{2-10} alkynyl, each of which is optionally bound to L^3 and each of which is optionally substituted with one or more substituents independently selected from halogen, -OR^{10}, -SR^{10}, -C(O)N(R^{10})$_2$, -N(R^{10})C(O)R^{10}, -N(R^{10})C(O)N(R^{10})$_2$, -N(R^{10})$_2$, -C(O)R^{10}, -C(O)OR^{10}, -OC(O)R^{10}, -NO$_2$, =O, =S, =N(R^{10}), -CN, C_{3-12} carbocycle, and 3- to 12-membered heterocycle; and C_{3-12} carbocycle and 3- to 12-membered heterocycle, wherein each C_{3-12} carbocycle and 3- to 12-membered heterocycle in R^4 and R^8 is optionally bound to L^3 and each C_{3-12} carbocycle and 3- to 12-membered heterocycle in R^4 and R^8 is optionally substituted with one or more substituents independently selected from halogen, -OR^{10}, -SR^{10}, -C(O)N(R^{10})$_2$, -N(R^{10})C(O)R^{10}, -N(R^{10})C(O)N(R^{10})$_2$, -N(R^{10})$_2$, -C(O)R^{10}, -C(O)OR^{10}, -OC(O)R^{10}, -NO$_2$, =O, =S, =N(R^{10}), -CN, C_{1-6} alkyl, C_{2-6} alkenyl, and C_{2-6} alkynyl;

R^{10} is independently selected at each occurrence from L^3, hydrogen, -NH$_2$, -C(O)OCH$_2$C$_6$H$_5$; and C_{1-10} alkyl, C_{2-10} alkenyl, C_{2-10} alkynyl, C_{3-12} carbocycle, and 3- to 12-membered heterocycle, each of which is optionally substituted with one or more substituents independently selected from halogen, -CN, -NO$_2$, -NH$_2$, =O, =S, -C(O)OCH$_2$C$_6$H$_5$, -NHC(O)OCH$_2$C$_6$H$_5$, C_{1-10} alkyl, C_{2-10} alkenyl, C_{2-10} alkynyl, C_{3-12} carbocycle, 3- to 12-membered heterocycle, and haloalkyl;

L^3 is a linker moiety, wherein there is at least one occurrence of L^3;

R^{12} is independently selected at each occurrence from halogen, -OR^{10}, -SR^{10}, -N(R^{10})$_2$, -C(O)R^{10}, -C(O)N(R^{10})$_2$, -N(R^{10})C(O)R^{10}, -C(O)OR^{10}, -OC(O)R^{10}, -S(O)R^{10}, -S(O)$_2$$R^{10}$, -P(O)(O$R^{10}$)$_2$, -OP(O)(O$R^{10}$)$_2$, -NO$_2$, =O, =S, =N($R^{10}$), and -CN; C_{1-10} alkyl, C_{2-10} alkenyl, C_{2-10} alkynyl, each of which is optionally substituted with one or more substituents independently selected from halogen, -OR^{10}, -SR^{10}, -N(R^{10})$_2$, -C(O)R^{10}, -C(O)N(R^{10})$_2$, -N(R^{10})C(O)R^{10}, -C(O)OR^{10}, -OC(O)R^{10}, -S(O)R^{10}, -S(O)$_2$$R^{10}$, -P(O)(O$R^{10}$)$_2$, -OP(O)(O$R^{10}$)$_2$, -NO$_2$, =O, =S, =N($R^{10}$), -CN, C_{3-10} carbocycle and 3- to 10-membered heterocycle; and C_{3-10} carbocycle and 3- to 10-membered heterocycle, wherein each C_{3-10} carbocycle and 3- to 10-membered heterocycle in R^{12} is optionally substituted with one or more substituents

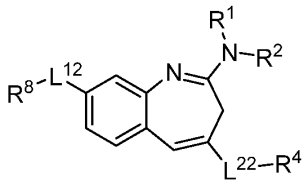
independently selected from halogen, -OR^{10}, -SR^{10}, -$N(R^{10})_2$, -$C(O)R^{10}$, -$C(O)N(R^{10})_2$, -$N(R^{10})C(O)R^{10}$, -$C(O)OR^{10}$, -$OC(O)R^{10}$, -$S(O)R^{10}$, -$S(O)_2R^{10}$, -$P(O)(OR^{10})_2$, -$OP(O)(OR^{10})_2$, -NO_2, =O, =S, =$N(R^{10})$, -CN, C_{1-6} alkyl, C_{2-6} alkenyl, C_{2-6} alkynyl; and

wherein any substitutable carbon on the benzazepine core is optionally substituted by a substituent independently selected from R^{12} or two substituents on a single carbon atom combine to form a 3- to 7- membered carbocycle.

R^{20}, R^{21}, R^{22}, and R^{23} are independently selected from hydrogen, halogen, -OR^{10}, -SR^{10}, -$N(R^{10})_2$, -$S(O)R^{10}$, -$S(O)_2R^{10}$, -$C(O)R^{10}$, -$C(O)OR^{10}$, -$OC(O)R^{10}$, -NO_2, =O, =S, =$N(R^{10})$, -CN, C_{1-10} alkyl, C_{2-10} alkenyl, and C_{2-10} alkynyl; and

R^{24} and R^{25} are independently selected from hydrogen, halogen, -OR^{10}, -SR^{10}, -$N(R^{10})_2$, -$S(O)R^{10}$, -$S(O)_2R^{10}$, -$C(O)R^{10}$, -$C(O)OR^{10}$, -$OC(O)R^{10}$, -NO_2, =O, =S, =$N(R^{10})$, -CN, C_{1-10} alkyl, C_{2-10} alkenyl, and C_{2-10} alkynyl; or R^{24} and R^{25} taken together form an optionally substituted saturated C_{3-7} carbocycle.

67. The aqueous formulation of any one of claims 1-63, wherein the conjugate comprises the compound linked to the polypeptide through a linker, wherein the compound and the linker together are a compound of Formula (IVC), or the aqueous formulation of any one of claims 64-66, wherein the compound and the linker together or L and Dx together are a compound of Formula (IVC):



(IVC)

wherein:

R^1 and R^2 are each hydrogen;

L^{22} is -C(O)-;

R^4 is -$N(R^{10})_2$;

R^{10} is independently selected at each occurrence from hydrogen, -NH_2, -$C(O)OCH_2C_6H_5$; and C_{1-10} alkyl, C_{2-10} alkenyl, C_{2-10} alkynyl, C_{3-12} carbocycle, and 3- to 12-membered heterocycle, each of which is optionally substituted with one or more substituents independently selected from halogen, -CN, -NO_2, -NH_2, =O, =S, -$C(O)OCH_2C_6H_5$, -$NHC(O)OCH_2C_6H_5$, C_{1-10} alkyl, C_{2-10} alkenyl, C_{2-10} alkynyl, C_{3-12} carbocycle, 3- to 12-membered heterocycle, and haloalkyl;

L^{12} is -C(O)N(R^{10})-*, wherein * represents where L^{12} is bound to R^8;

R^8 is an optionally substituted fused 5-5, fused 5-6, or fused 6-6 bicyclic heterocycle bound to linker moiety L^3 ,

and wherein optional substituents are independently selected at each occurrence from:

halogen, -OR^{10}, -SR^{10}, -C(O)N(R^{10})$_2$, -N(R^{10})C(O)R^{10}, -N(R^{10})C(O)N(R^{10})$_2$, -N(R^{10})$_2$, -C(O)R^{10}, -C(O)OR^{10}, -OC(O)R^{10}, -NO_2, =O, =S, =N(R^{10}), and -CN;

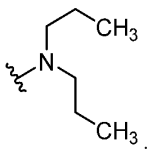
C_{1-10} alkyl, C_{2-10} alkenyl, C_{2-10} alkynyl, each of which is optionally substituted with one or more substituents independently selected from halogen, -OR^{10}, -SR^{10}, -C(O)N(R^{10})$_2$, -N(R^{10})C(O)R^{10}, -N(R^{10})C(O)N(R^{10})$_2$, -N(R^{10})$_2$, -C(O)R^{10}, -C(O)OR^{10}, -OC(O)R^{10}, -NO_2, =O, =S, =N(R^{10}), -CN, C_{3-12} carbocycle, and 3- to 12-membered heterocycle; and

C_{3-12} carbocycle and 3- to 12-membered heterocycle, each of which is optionally substituted with one or more substituents independently selected from halogen, -OR^{10}, -SR^{10}, -C(O)N(R^{10})$_2$, -N(R^{10})C(O)R^{10}, -N(R^{10})C(O)N(R^{10})$_2$, -N(R^{10})$_2$, -C(O)R^{10}, -C(O)OR^{10}, -OC(O)R^{10}, -NO_2, =O, =S, =N(R^{10}), -CN, C_{1-6} alkyl, C_{2-6} alkenyl, and C_{2-6} alkynyl.

68. The aqueous formulation of claim 66 or claim 67, wherein:

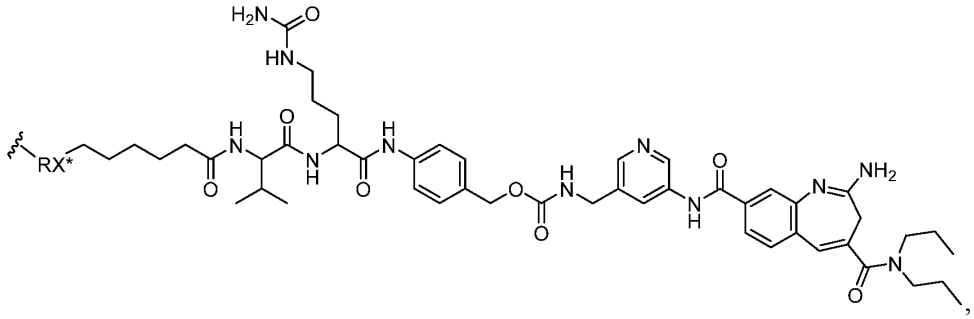
R^4 is -N(C_{1-4} alkyl)$_2$ and L^{12} is -C(O)N(H)-*.

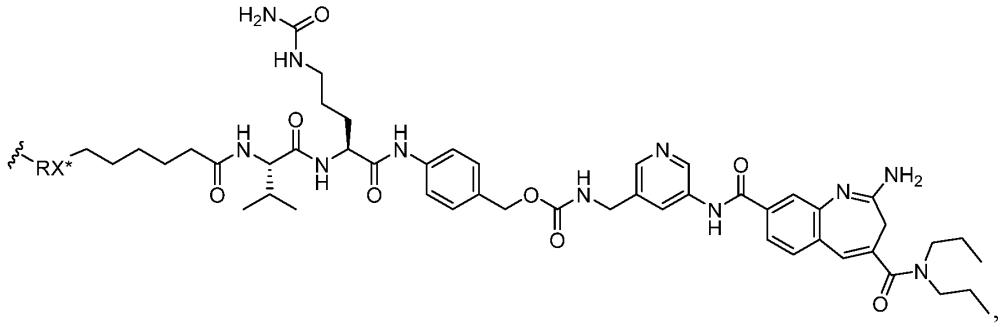
69. The aqueous formulation of claim 66 or claim 67, wherein:

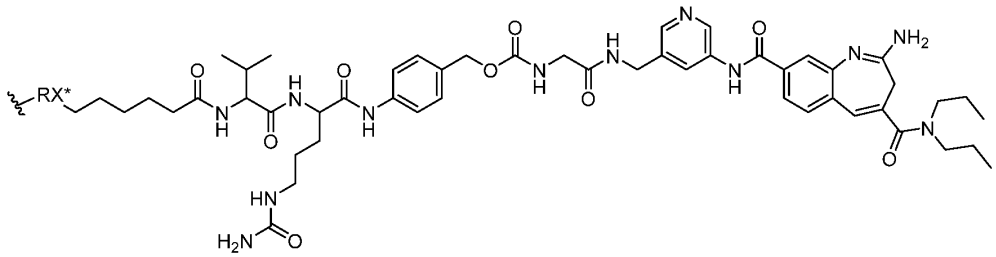
R^4 is 

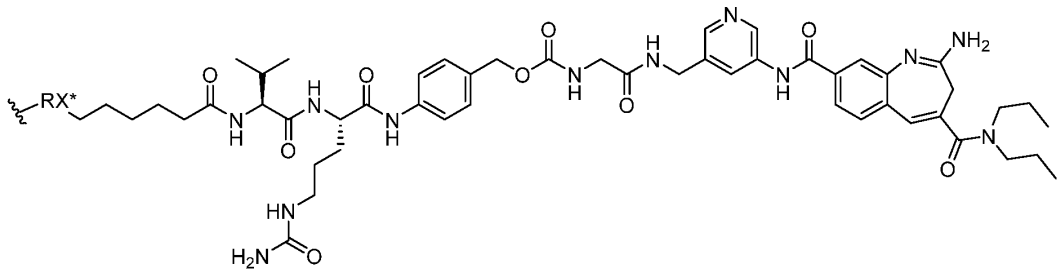
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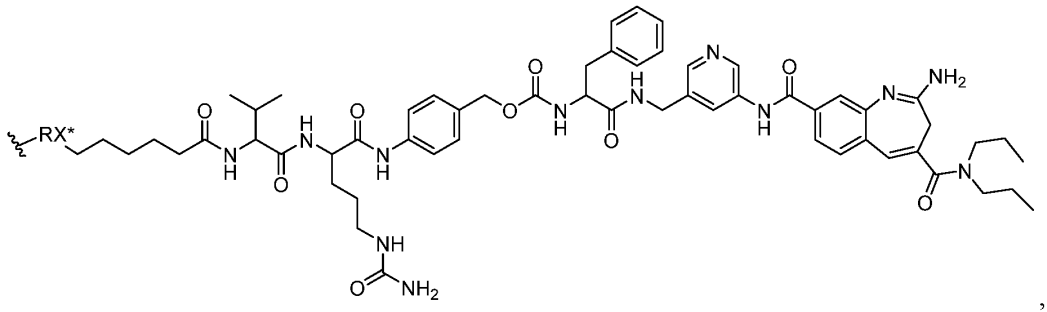
70. The aqueous formulation of any one of claims 64-69, wherein L and Dx together have a structure selected from:

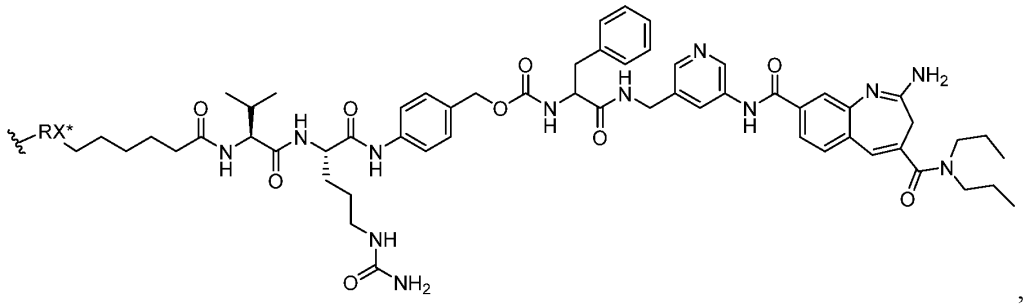




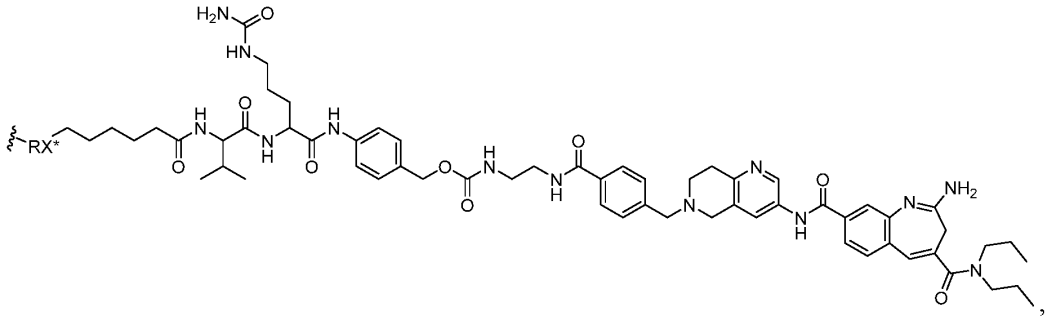




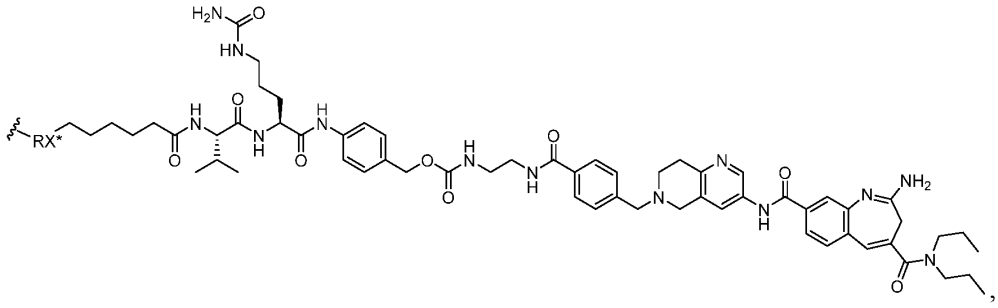




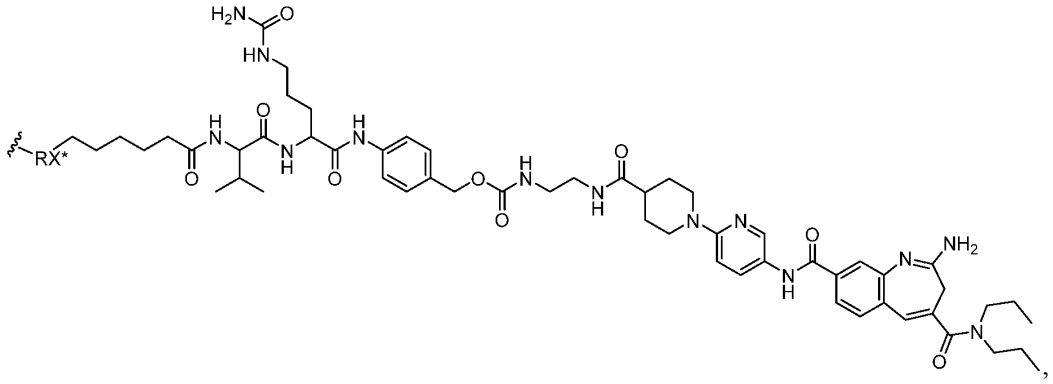
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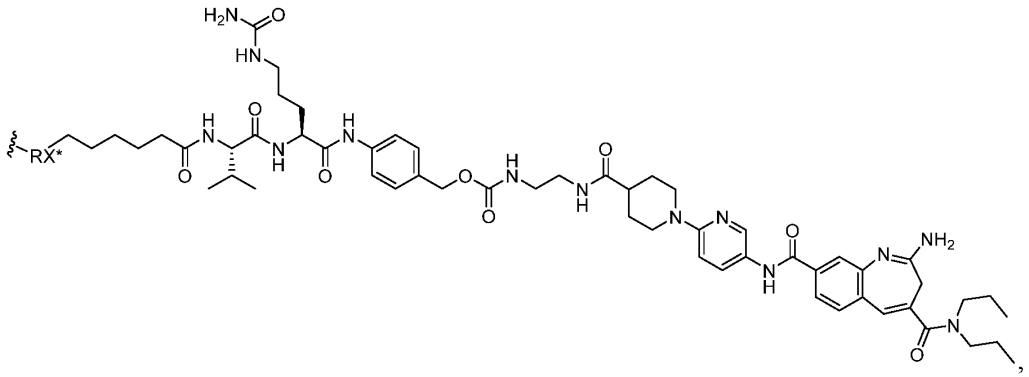
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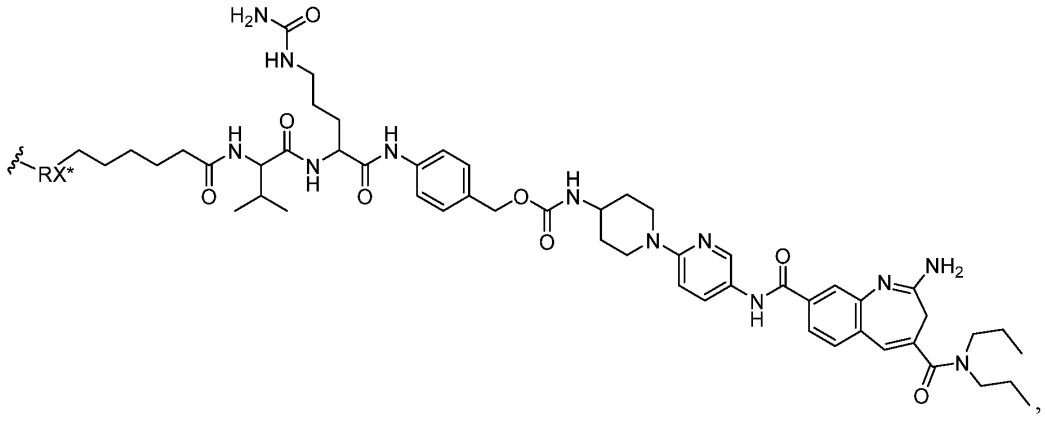


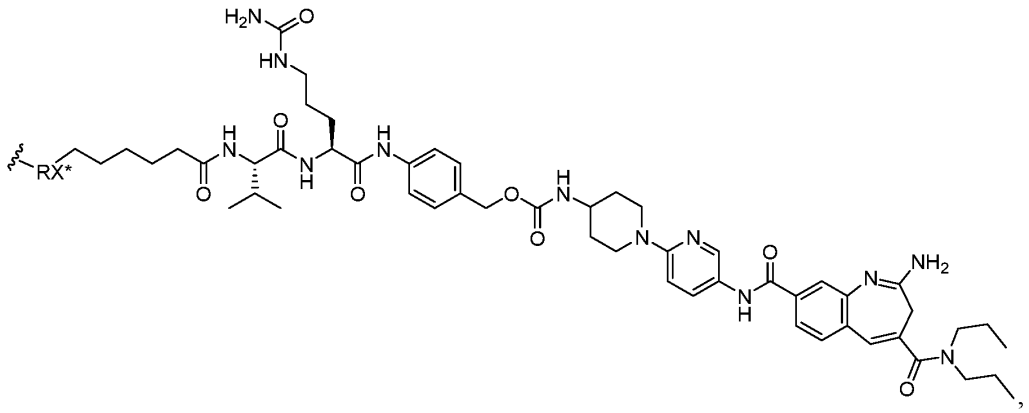
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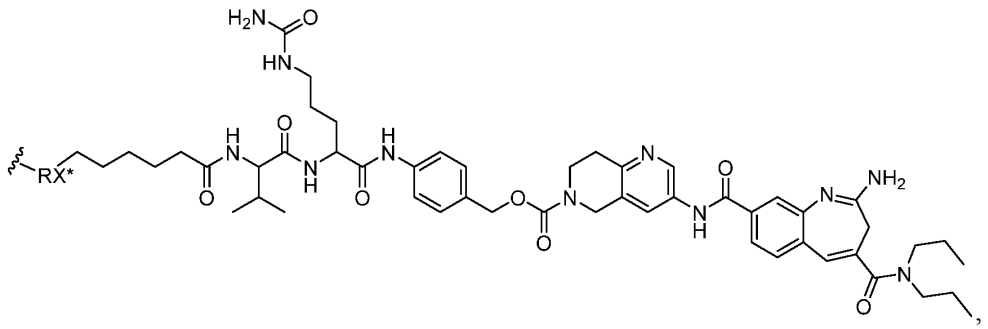


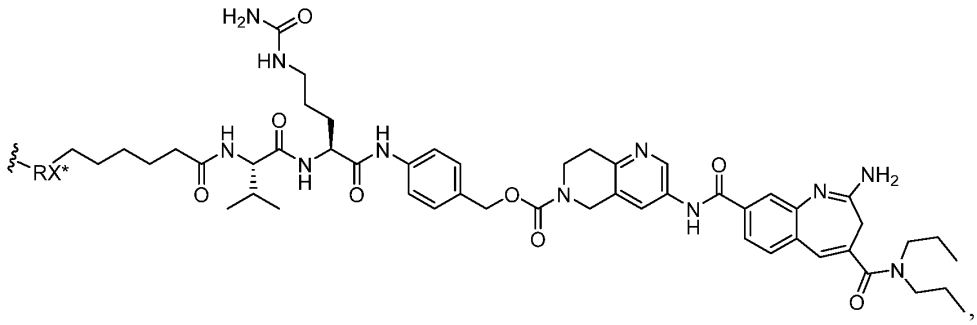
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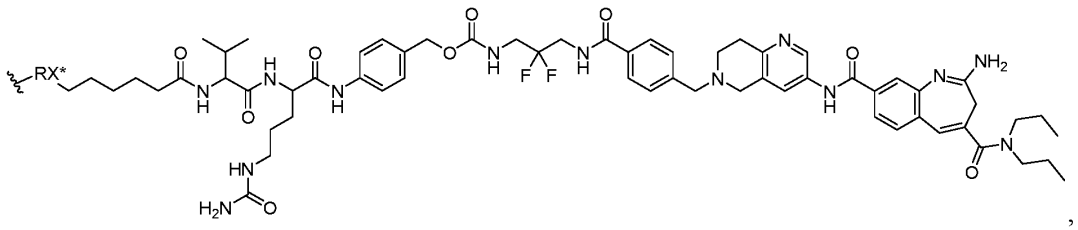




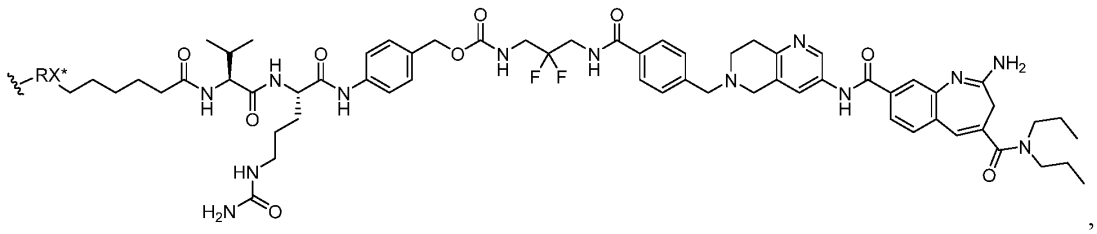








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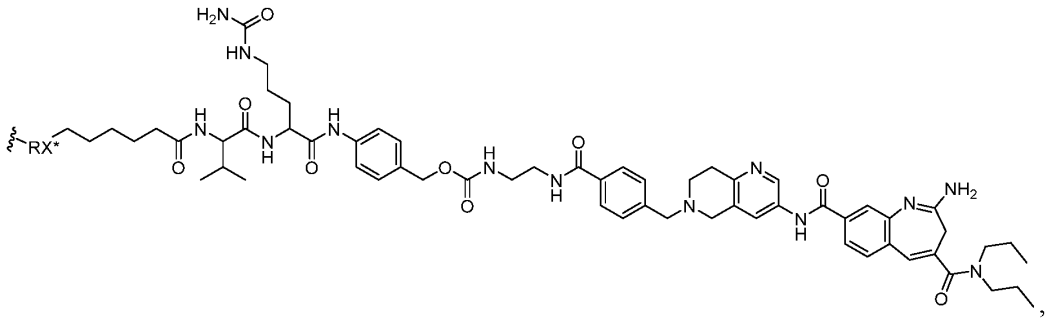


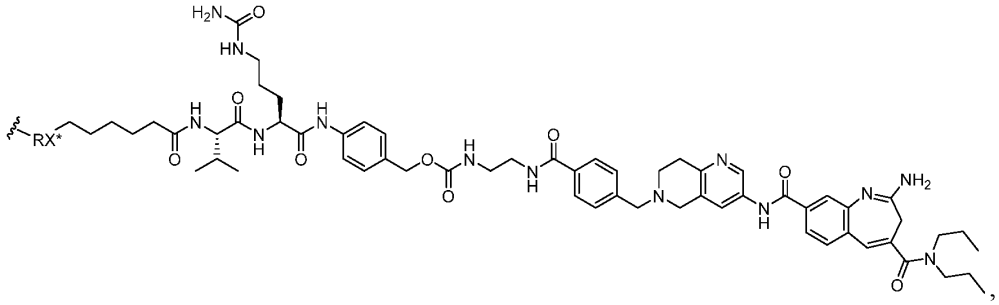
and salts thereof,

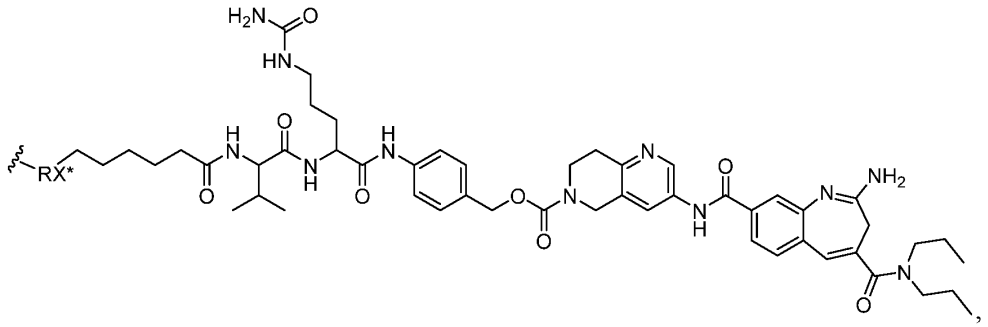
wherein the RX^* is a bond, a succinimide moiety, or a hydrolyzed succinimide moiety bound to a residue of a polypeptide,

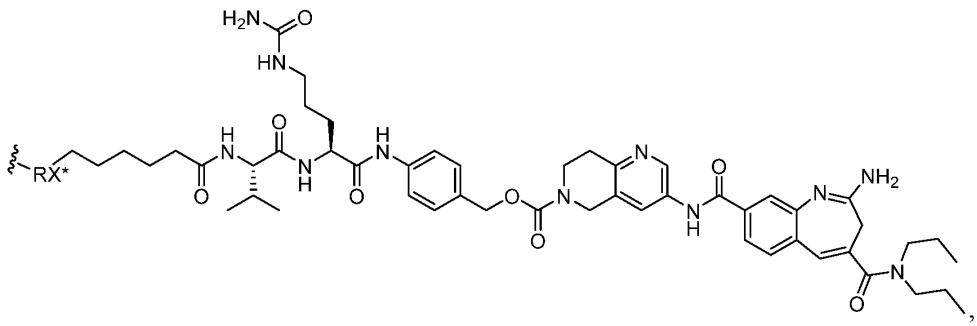
wherein  on RX* represents the point of attachment to the residue of the polypeptide.

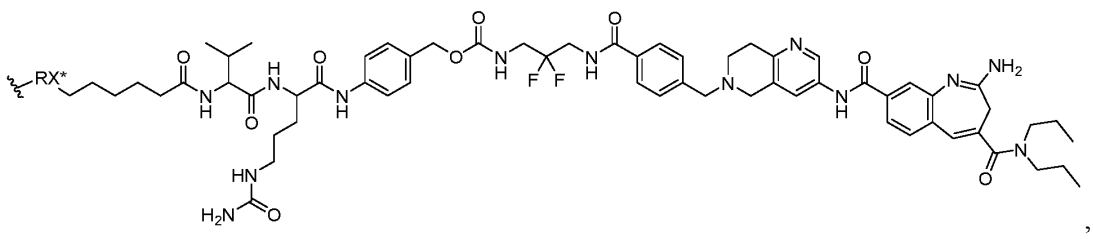
71. The aqueous formulation of claim 70, wherein L and Dx together have a structure selected from:



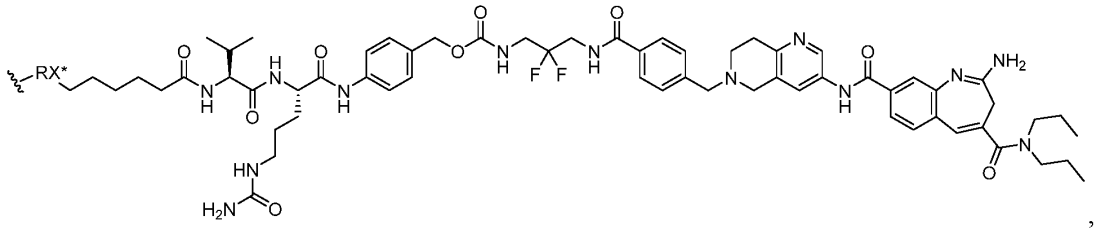








and



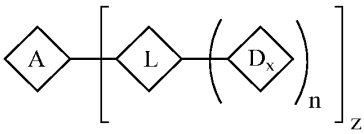
,

and salts thereof,

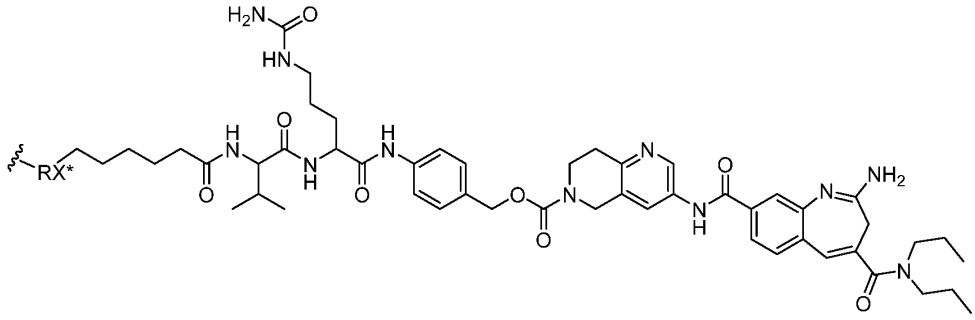
wherein the RX* is a bond, a succinimide moiety, or a hydrolyzed succinimide moiety bound to a residue of a polypeptide,

wherein  on RX* represents the point of attachment to the residue of the polypeptide.

72. The aqueous formulation of claim 64, comprising:

a) a conjugate at a total concentration ranging from about 50 mg/mL to about 100 mg/mL and represented by Formula (I):  (I),

wherein A is an antibody; n is 1; z ranges from 2 to 8; and L is a linker and D_x is a benzazepine compound, wherein L and Dx together have a structure of:



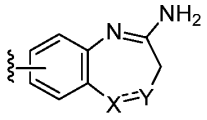
, wherein RX* comprises a hydrolyzed succinamide moiety and is bound to a cysteine residue of the antibody;

b) a buffer comprised of histidine and aspartate at a total concentration ranging from about 15mM to about 25mM;

c) a lyoprotectant comprised of sucrose at a total concentration ranging from about 7% to about 8%; and

d) a surfactant comprised of polysorbate 80 at a total concentration ranging from about 0.01% to about 0.03%.

73. A lyophilized composition comprising a conjugate comprising a compound linked to a polypeptide, wherein the compound comprises the structure:



wherein ≡ is a double bond or a single bond;

wherein when ≡ is a double bond, X and Y are each CH; and

when ≡ is a single bond, one of X and Y is CH_2 and the other is CH_2, O, or NH; and

the structure is optionally substituted at any position other than the $-NH_2$;

wherein upon reconstitution of the lyophilized composition in water to form an aqueous formulation, the pH of the aqueous formulation is from 4 to 5.2 or from 4.4 to 5.4.

74. The lyophilized composition of claim 53, wherein the pH of the aqueous formulation is from 4.4 to 5.4, 4.5 to 5.3, 4.6 to 5.2, 4.7 to 5.1, 4.8 to 5.1, 4.9 to 5.1, 4.4 to 5.0, 4.5 to 5.0, 4.6 to 5.0, 4.7 to 5.0, 4.8 to 5.0, or 4.9 to 5.0.

75. The lyophilized composition of claim 73, wherein the pH of the aqueous formulation is from 4.4 to 5.4.

76. The lyophilized composition of claim 73, wherein the pH of the aqueous formulation is from 4.4 to 5.3.

77. The lyophilized composition of claim 73, wherein the pH of the aqueous formulation is from 4.4 to 5.2.

78. The lyophilized composition of claim 73, wherein the pH of the aqueous formulation is from 4.4 to 5.1.

79. The lyophilized composition of claim 73, wherein the pH of the aqueous formulation is from 4.5 to 5.1.

80. The lyophilized composition of claim 73, wherein the pH of the aqueous formulation is from 4.6 to 5.0.

81. The lyophilized composition of claim 73, wherein the pH of the aqueous formulation is from 4.7 to 4.9.

82. The lyophilized composition of claim 73, wherein the pH of the aqueous formulation is 4.8.

83. The lyophilized composition of claim 73, wherein the pH of the aqueous formulation is 4.9.

84. The lyophilized composition of claim 73, wherein the pH of the aqueous formulation is 5.0.

85. The lyophilized composition of any one of claims 73-84, wherein the composition comprises at least one buffering agent.

86. The lyophilized composition of claim 85, wherein the at least one buffering agent is selected from histidine, citrate, aspartate, acetate, phosphate, lactate, tromethamine, gluconate, glutamate, tartrate, succinate, malic acid, fumarate, α-ketoglutarate, and combinations thereof.

87. The lyophilized composition of claim 86, wherein the at least one buffering agent is histidine and aspartate.

88. The lyophilized composition of any one of claims 73-87, wherein upon reconstitution of the lyophilized composition in water to form an aqueous formulation, the total concentration of buffering agents in the aqueous formulation is about 15mM to about 25mM.

89. The lyophilized composition of any one of claims 73-88, wherein the lyophilized composition comprises at least one lyoprotectant selected from sucrose, arginine, glycine, sorbitol, glycerol, trehalose, dextrose, alpha-cyclodextrin, hydroxypropyl beta-cyclodextrin, hydroxypropyl gamma-cyclodextrin, proline, methionine, albumin, mannitol, maltose, dextran, and combinations thereof.

90. The lyophilized composition of claim 89, wherein the at least one lyoprotectant is sucrose.

91. The lyophilized composition of claim 89 or claim 90, wherein upon reconstitution of the lyophilized composition in water to form an aqueous formulation, upon reconstitution of the lyophilized composition in water to form an aqueous formulation, the total concentration of the at least one lyoprotectant in the aqueous formulation about 7% to about 9%.

92. The lyophilized composition of any one of claims 73-91, wherein the lyophilized composition comprises at least one surfactant.

93. The lyophilized composition of claim 92, wherein the at least one surfactant is selected from polysorbate 80, polysorbate 20, poloxamer 88, and combinations thereof.

94. The lyophilized composition of claim 93, wherein the at least one surfactant is polysorbate 80.

95. The lyophilized composition of any one of claims 92-94, wherein upon reconstitution of the lyophilized composition in water to form an aqueous formulation, the total concentration of the at least one surfactant in the aqueous formulation is about 0.01% to about 0.05%.

96. The lyophilized composition of any one of claims 73-95, wherein upon reconstitution of the lyophilized composition in water to form an aqueous formulation, the concentration of the conjugate in the aqueous formulation is about 70 mg/mL to about 100 mg/mL.

97. The lyophilized composition of any one of claims 73-96, wherein the polypeptide is an antibody.

98. The lyophilized composition of claim 97, wherein the antibody comprises an antigen binding domain and an Fc domain.

99. The lyophilized composition of claim 98, wherein the Fc domain exhibits the same or substantially similar binding affinity to Fcgamma and/or FcRn receptors as compared to a wild-type Fc domain from an IgG1 antibody.

100. The lyophilized composition of any one of claims 97-99, wherein the antibody binds a tumor associated antigen.

101. The lyophilized composition of claim 100, wherein the tumor associated antigen is selected from HER2, Nectin-4, ASGR1, mesothelin, PSMA, rsPSMA, TROP2, LIV-1, MUC16, CEACAM1, CEACAM3, CEACAM4, CEACAM5, CEACAM6, CEACAM7, CEACAM8, CEACAM16, CEACAM18, CEACAM19, CEACAM20, CEACAM21, URLC10, NY-ESO-1, GAA, OFA, cyclin B1, WT-1, CEF, VEGRR1, VEGFR2, TTK, MUC1, HPV16E7, CEA, IMA910, KOC1, SL-701, MART-1, gp100, tyrosinase, GSK2302050A, survivin, MAGE-3.1, MAGE-10.A2, OVA BiP, gp209-2M, melan-A, NA17.A2, KOC1, CO16, DEPDC1, MPHOSPH1, MAGE12, ONT-10, GD2L, GD3L, GSK2302032A, URLC10, CDCA1, TF, rsPSMA, PSA, MUC-2, TERT, HPV16, HPV18, STF-II, G17DT, ICT-107, Dex2, hTERT, PAP, tyrosinase related peptide 2 (TRP2), and LRRC15.

102. The lyophilized composition of claim 100, wherein the tumor associated antigen is selected from:

a) an antigen present on lung cancer, wherein the antigen is optionally selected from mesothelin, HER2, EGFR, PD-L1, MSLN, LY6K, CD56, PTK7, FOLR1, DLL3, SLC34A2, CECAM5, MUC16, LRRC15, ADAM12, EGFRvIII, LYPD3, EFNA4, and MUC1;
b) an antigen present on liver cancer, wherein the antigen is optionally selected from GPC3, EPCAM, and CECAM5;
c) an antigen present on kidney cancer, wherein the antigen is optionally selected from HAVCR1, ENPP3, CDH6, CD70, and cMET;
d) an antigen present on pancreatic cancer, wherein the antigen is optionally selected from PTK7, MUC16, MSLN, LRRC15, ADAM12, EFNA4, MUC5A, and MUC1;
e) an antigen present on colorectal cancer, wherein the antigen is optionally selected from EPHB2, TMEM238, CECAM5, LRRC15, ADAM12, EFNA4, and GPA33;
f) an antigen present on ovarian cancer, wherein the antigen is optionally selected from MUC16, MUC1, MSLN, FOLR1, sTN, VTCN1, HER2, PTK7, FAP, TMEM238, LRRC15, CLDN6, SLC34A2, and EFNA4;

g) an antigen present on head and neck cancer, wherein the antigen is optionally selected from LY6K, PTK7, LRRC15, ADAM12, LYPD3, EFNA4 and TNC;

h) an antigen present on bone cancer, wherein the antigen is optionally selected from EPHA2, LRRC15, ADAM12, GPNMB, TP-3, and CD248;

i) an antigen present on mesothelioma, wherein the antigen is optionally MSLN;

j) an antigen present on bladder cancer, wherein the antigen is optionally selected from LY6K, PTK7, UPK1B, UPK2, TNC, Nectin4, SLITRK6, LYPD3, EFNA4, and HER2;

k) an antigen present on stomach cancer, wherein the antigen is optionally selected from HER2, EPHB2, TMEM238, CECAM5, and EFNA4;

l) an antigen present on prostate cancer, wherein the antigen is optionally selected from PSMA, FOLH1, PTK7, STEAP, TMEFF2 (TENB2), OR51E2, SLC30A4, and EFNA4;

m) an antigen present on thyroid cancer, wherein the antigen is optionally PTK7;

n) an antigen present on uterine cancer, wherein the antigen is optionally selected from LY6K, PTK7, EPHB2, FOLR1, ALPPL2, MUC16, and EFNA4;

o) an antigen present on cervical/endometrial cancer, wherein the antigen is optionally selected from LY6K, PTK7, MUC16, LYPD3, EFNA4, and MUC1; and

p) an antigen present on breast cancer, wherein the antigen is optionally selected from HER2, TROP2, LIV-1, CDH3 (p-cadherin), MUC1, Sialo-epitope CA6, PTK7, GPNMB, LAMP-1, LRRC15, ADAM12, EPHA2, TNC, LYPD3, EFNA4, and CLDN6.

103. The lyophilized composition of any one of claims 97-102, wherein the antibody is an anti-HER2 antibody.

104. The lyophilized composition of claim 103, wherein the anti-HER2 antibody comprises heavy chain (HC)-CDR1, HC-CDR2, HC-CDR3, light chain (LC)-CDR1, LC-CDR2, and LC-CDR3 of SEQ ID NOS:1-6, respectively.

105. The lyophilized composition of claim 104, wherein the anti-HER2 antibody comprises a heavy chain variable region (V_H) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_H amino acid sequence of SEQ ID NO:7 and a light chain variable region (V_L) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at

least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_L amino acid sequence of SEQ ID NO:8.

106. The lyophilized composition of claim 103 or 104, wherein the anti-HER2 antibody comprises a V_H comprising or consisting of the amino acid sequence of SEQ ID NO:7 and a V_L comprising or consisting of the amino acid sequence of SEQ ID NO:8.

107. The lyophilized composition of any one of claims 104-106, wherein the anti-HER2 antibody comprises a heavy chain and light chain, wherein the heavy chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the heavy chain amino acid sequence of SEQ ID NO:9; and the light chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the light chain amino acid sequence of SEQ ID NO:10.

108. The lyophilized composition of claim 103 or claim 104, wherein the anti-HER2 antibody comprises a heavy chain comprising or consisting of the amino acid sequence of SEQ ID NO:9 and a light chain comprising or consisting of the amino acid sequence of SEQ ID NO:10.

109. The lyophilized composition of any one of claims 97-102, wherein the antibody is an anti-Nectin-4 antibody.

110. The lyophilized composition of claim 109, wherein the anti-Nectin-4 antibody comprises heavy chain (HC)-CDR1, HC-CDR2, HC-CDR3 of SEQ ID NOS: 11-13, respectively, and light chain (LC)-CDR1 of SEQ ID NO:14 or 15, LC-CDR2 of SEQ ID NO:16, and LC-CDR3 of SEQ ID NO:17.

111. The lyophilized composition of claim 110, wherein the anti-Nectin-4 antibody comprises a heavy chain variable region (V_H) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_H amino acid sequence of SEQ ID NO:18 and a light chain variable region (V_L) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_L amino acid sequence of SEQ ID NO:19 or 20.

112. The lyophilized composition of claim 109 or claim 110, wherein the anti-Nectin-4 antibody comprises a V_H comprising or consisting of the amino acid sequence of SEQ ID NO:18 and a V_L comprising or consisting of the amino acid sequence of SEQ ID NO:19 or 20.

113. The lyophilized composition of any one of claims 110-112, wherein the anti-Nectin-4 antibody comprises a heavy chain and light chain, wherein the heavy chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the heavy chain amino acid sequence of SEQ ID NO:21; and the light chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the light chain amino acid sequence of SEQ ID NO:22 or 23.

114. The lyophilized composition of claim 109 or claim 110, wherein the anti-Nectin-4 antibody comprises a heavy chain comprising or consisting of the amino acid sequence of SEQ ID NO:21 and a light chain comprising or consisting of the amino acid sequence of SEQ ID NO:22 or 23.

115. The lyophilized composition of any one of claims 97-102, wherein the antibody is an anti-ASGR1 antibody.

116. The lyophilized composition of claim 115, wherein the anti-ASGR1 antibody comprises heavy chain (HC)-CDR1 of SEQ ID NO: 24 or 25, HC-CDR2 of SEQ ID NO:26, 27, or 28, HC-CDR3 of SEQ ID NO:29 or 30, light chain (LC)-CDR1 of SEQ ID NO:31 or 32, LC-CDR2 of SEQ ID NO:33, 34, 35 or 36, and LC-CDR3 of SEQ ID NO:37 or 38.

117. The lyophilized composition of claim 116, wherein the anti-ASGR1 antibody comprises (a) heavy chain (HC)-CDR1 of SEQ ID NO: 24, HC-CDR2 of SEQ ID NO:26, HC-CDR3 of SEQ ID NO:29, light chain (LC)-CDR1 of SEQ ID NO:31, LC-CDR2 of SEQ ID NO:33 or 34, and LC-CDR3 of SEQ ID NO:37; or (b) heavy chain (HC)-CDR1 of SEQ ID NO: 25, HC-CDR2 of SEQ ID NO:27 or 28, HC-CDR3 of SEQ ID NO:30, light chain (LC)-CDR1 of SEQ ID NO:32, LC-CDR2 of SEQ ID NO:35 or 36, and LC-CDR3 of SEQ ID NO:38.

118. The lyophilized composition of claim 116 or claim 117, wherein the anti-ASGR1 antibody comprises a heavy chain variable region (V_H) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_H amino acid sequence of SEQ ID NO:39 and a light chain variable region (V_L) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_L amino acid sequence of SEQ ID NO:42 or 43.

119. The lyophilized composition of claim 116 or claim 117, wherein the anti-ASGR1 antibody comprises a heavy chain variable region (V_H) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at

least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_H amino acid sequence of SEQ ID NO:40 or 41 and a light chain variable region (V_L) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_L amino acid sequence of SEQ ID NO:44 or 45.

120. The lyophilized composition of any one of claims 115-117, wherein the anti-ASGR1 antibody comprises a V_H comprising or consisting of the amino acid sequence of SEQ ID NO:39 and a V_L comprising or consisting of the amino acid sequence of SEQ ID NO:42 or 43.

121. The lyophilized composition of any one of claims 115-117, wherein the anti-ASGR1 antibody comprises a V_H comprising or consisting of the amino acid sequence of SEQ ID NO:40 or 41 and a V_L comprising or consisting of the amino acid sequence of SEQ ID NO:44 or 45.

122. The lyophilized composition of any one of claims 116-118 and 120, wherein the anti-ASGR1 antibody comprises a heavy chain and light chain, wherein the heavy chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the heavy chain amino acid sequence of SEQ ID NO:46; and the light chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the light chain amino acid sequence of SEQ ID NO:49 or 50.

123. The lyophilized composition of any one of claims 115-117, wherein the anti-ASGR1 antibody comprises a heavy chain comprising or consisting of the amino acid sequence of SEQ ID NO:46 and a light chain comprising or consisting of the amino acid sequence of SEQ ID NO:49 or 50.

124. The lyophilized composition of any one of claims 116-117, 119, and 121, wherein the anti-ASGR1 antibody comprises a heavy chain and light chain, wherein the heavy chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the heavy chain amino acid sequence of SEQ ID NO:47 or 48; and the light chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the light chain amino acid sequence of SEQ ID NO:51 or 52.

125. The lyophilized composition of any one of claims 115-117, wherein the anti-ASGR1 antibody comprises a heavy chain comprising or consisting of the amino acid sequence of SEQ ID NO:47 or 48 and a light chain comprising or consisting of the amino acid sequence of SEQ ID NO:51 or 52.

126. The lyophilized composition of any one of claims 97-102, wherein the antibody is an anti-mesothelin antibody.

127. The lyophilized composition of claim 126, wherein the anti-mesothelin antibody comprises heavy chain (HC)-CDR1, HC-CDR2, HC-CDR3, light chain (LC)-CDR1, LC-CDR2, and LC-CDR3 of SEQ ID NOS:53-58, respectively.

128. The lyophilized composition of claim 127, wherein the anti-mesothelin antibody comprises a heavy chain variable region (V_H) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_H amino acid sequence of SEQ ID NO:59 and a light chain variable region (V_L) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_L amino acid sequence of SEQ ID NO:60.

129. The lyophilized composition of claim 126 or claim 127, wherein the anti-mesothelin antibody comprises a V_H comprising or consisting of the amino acid sequence of SEQ ID NO:59 and a V_L comprising or consisting of the amino acid sequence of SEQ ID NO:60.

130. The lyophilized composition of any one of claims 127-129, wherein the anti-mesothelin antibody comprises a heavy chain and light chain, wherein the heavy chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the heavy chain amino acid sequence of SEQ ID NO:70; and the light chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the light chain amino acid sequence of SEQ ID NO:71.

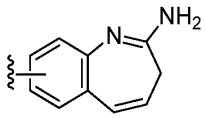
131. The lyophilized composition of claim 126 or claim 127, wherein the anti-mesothelin antibody comprises a heavy chain comprising or consisting of the amino acid sequence of SEQ ID NO:70 and a light chain comprising or consisting of the amino acid sequence of SEQ ID NO:71.

132. The lyophilized composition of claim 103, wherein the antibody is pertuzumab, trastuzumab, sacituzumab, or ladiratuzumab or comprises an antigen binding fragment of pertuzumab, trastuzumab, sacituzumab, or ladiratuzumab.

133. The lyophilized composition of any one of claims 73-132, wherein the compound is a myeloid agonist.

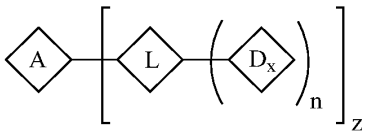
134. The lyophilized composition of any one of claims 73-133, wherein the compound is a TLR8 agonist.

135. The lyophilized composition of any one of claims 73-134, wherein the compound comprises the structure:



wherein the structure is optionally substituted at any position other than the -NH_2.

136. The lyophilized composition of any one of claims 73-135, wherein the conjugate is represented by Formula (I):



(I);

wherein:

A is the polypeptide,

L is a linker;

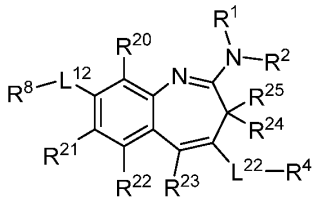
D_x is the compound;

n is selected from 1 to 20; and

z is selected from 1 to 20.

137. The lyophilized composition of claim 136, wherein n is 1 and z is from 1 to 8.

138. The lyophilized composition of of any one of claims 73 to 135, wherein the conjugate comprises the compound linked to the polypeptide through a linker, wherein the compound and the linker together are a compound of Formula (IVB), or the lyophilized composition of claim 136 or claim 137, wherein L and Dx together are a compound of Formula (IVB):



(IVB)

or a pharmaceutically acceptable salt thereof, wherein:

L^{12} is selected from $-X^3-$, $-X^3-C_{1-6}$ alkylene-X^3-, $-X^3-C_{2-6}$ alkenylene-X^3-, and $-X^3-C_{2-6}$ alkynylene-X^3-, each of which is optionally substituted on alkylene, alkenylene, or alkynylene with one or more substituents independently selected from R^{12};

L^{22} is independently selected from $-X^4-$, $-X^4-C_{1-6}$ alkylene-X^4-, $-X^4-C_{2-6}$ alkenylene-X^4-, and $-X^4-C_{2-6}$ alkynylene-X^4-, each of which is optionally substituted on alkylene, alkenylene, or alkynylene with one or more substituents independently selected from R^{10};

X^3 and X^4 are independently selected at each occurrence from a bond, -O-, -S-, $-N(R^{10})-$, -C(O)-, -C(O)O-, -OC(O)-, -OC(O)O-, $-C(O)N(R^{10})-$, $-C(O)N(R^{10})C(O)-$, $-C(O)N(R^{10})C(O)N(R^{10})-$, $-N(R^{10})C(O)-$, $-N(R^{10})C(O)N(R^{10})-$, $-N(R^{10})C(O)O-$, $-OC(O)N(R^{10})-$, $-C(NR^{10})-$, $-N(R^{10})C(NR^{10})-$, $-C(NR^{10})N(R^{10})-$, $-N(R^{10})C(NR^{10})N(R^{10})-$, $-S(O)_2-$, -OS(O)-, -S(O)O-, -S(O)-, $-OS(O)_2-$, $-S(O)_2O-$, $-N(R^{10})S(O)_2-$, $-S(O)_2N(R^{10})-$, $-N(R^{10})S(O)-$, $-S(O)N(R^{10})-$, $-N(R^{10})S(O)_2N(R^{10})-$, and $-N(R^{10})S(O)N(R^{10})-$;

R^1 and R^2 are each hydrogen;

R^4 and R^8 are independently selected from: $-OR^{10}$, $-N(R^{10})_2$, $-C(O)N(R^{10})_2$, $-C(O)R^{10}$, $-C(O)OR^{10}$, $-S(O)R^{10}$, and $-S(O)_2R^{10}$; C_{1-10} alkyl, C_{2-10} alkenyl, C_{2-10} alkynyl, each of which is optionally bound to L^3 and each of which is optionally substituted with one or more substituents independently selected from halogen, $-OR^{10}$, $-SR^{10}$, $-C(O)N(R^{10})_2$, $-N(R^{10})C(O)R^{10}$, $-N(R^{10})C(O)N(R^{10})_2$, $-N(R^{10})_2$, $-C(O)R^{10}$, $-C(O)OR^{10}$, $-OC(O)R^{10}$, $-NO_2$, =O, =S, $=N(R^{10})$, -CN, C_{3-12} carbocycle, and 3- to 12-membered heterocycle; and C_{3-12} carbocycle and 3- to 12-membered heterocycle, wherein each C_{3-12} carbocycle and 3- to 12-membered heterocycle in R^4 and R^8 is optionally bound to L^3 and each C_{3-12} carbocycle and 3- to 12-membered heterocycle in R^4 and R^8 is optionally substituted with one or more substituents independently selected from halogen, $-OR^{10}$, $-SR^{10}$, $-C(O)N(R^{10})_2$, $-N(R^{10})C(O)R^{10}$, $-N(R^{10})C(O)N(R^{10})_2$, $-N(R^{10})_2$, $-C(O)R^{10}$, $-C(O)OR^{10}$, $-OC(O)R^{10}$, $-NO_2$, =O, =S, $=N(R^{10})$, -CN, C_{1-6} alkyl, C_{2-6} alkenyl, and C_{2-6} alkynyl;

R^{10} is independently selected at each occurrence from L^3, hydrogen, $-NH_2$, $-C(O)OCH_2C_6H_5$; and C_{1-10} alkyl, C_{2-10} alkenyl, C_{2-10} alkynyl, C_{3-12} carbocycle, and 3- to 12-membered heterocycle, each of which is optionally substituted with one or more substituents independently selected from halogen, $-CN$, $-NO_2$, $-NH_2$, $=O$, $=S$, $-C(O)OCH_2C_6H_5$, $-NHC(O)OCH_2C_6H_5$, C_{1-10} alkyl, C_{2-10} alkenyl, C_{2-10} alkynyl, C_{3-12} carbocycle, 3- to 12-membered heterocycle, and haloalkyl;

L^3 is a linker moiety, wherein there is at least one occurrence of L^3;

R^{12} is independently selected at each occurrence from halogen, $-OR^{10}$, $-SR^{10}$, $-N(R^{10})_2$, $-C(O)R^{10}$, $-C(O)N(R^{10})_2$, $-N(R^{10})C(O)R^{10}$, $-C(O)OR^{10}$, $-OC(O)R^{10}$, $-S(O)R^{10}$, $-S(O)_2R^{10}$, $-P(O)(OR^{10})_2$, $-OP(O)(OR^{10})_2$, $-NO_2$, $=O$, $=S$, $=N(R^{10})$, and $-CN$; C_{1-10} alkyl, C_{2-10} alkenyl, C_{2-10} alkynyl, each of which is optionally substituted with one or more substituents independently selected from halogen, $-OR^{10}$, $-SR^{10}$, $-N(R^{10})_2$, $-C(O)R^{10}$, $-C(O)N(R^{10})_2$, $-N(R^{10})C(O)R^{10}$, $-C(O)OR^{10}$, $-OC(O)R^{10}$, $-S(O)R^{10}$, $-S(O)_2R^{10}$, $-P(O)(OR^{10})_2$, $-OP(O)(OR^{10})_2$, $-NO_2$, $=O$, $=S$, $=N(R^{10})$, $-CN$, C_{3-10} carbocycle and 3- to 10-membered heterocycle; and C_{3-10} carbocycle and 3- to 10-membered heterocycle, wherein each C_{3-10} carbocycle and 3- to 10-membered heterocycle in R^{12} is optionally substituted with one or more substituents independently selected from halogen, $-OR^{10}$, $-SR^{10}$, $-N(R^{10})_2$, $-C(O)R^{10}$, $-C(O)N(R^{10})_2$, $-N(R^{10})C(O)R^{10}$, $-C(O)OR^{10}$, $-OC(O)R^{10}$, $-S(O)R^{10}$, $-S(O)_2R^{10}$, $-P(O)(OR^{10})_2$, $-OP(O)(OR^{10})_2$, $-NO_2$, $=O$, $=S$, $=N(R^{10})$, $-CN$, C_{1-6} alkyl, C_{2-6} alkenyl, C_{2-6} alkynyl; and

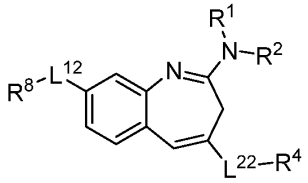
wherein any substitutable carbon on the benzazepine core is optionally substituted by a substituent independently selected from R^{12} or two substituents on a single carbon atom combine to form a 3- to 7- membered carbocycle.

R^{20}, R^{21}, R^{22}, and R^{23} are independently selected from hydrogen, halogen, $-OR^{10}$, $-SR^{10}$, $-N(R^{10})_2$, $-S(O)R^{10}$, $-S(O)_2R^{10}$, $-C(O)R^{10}$, $-C(O)OR^{10}$, $-OC(O)R^{10}$, $-NO_2$, $=O$, $=S$, $=N(R^{10})$, $-CN$, C_{1-10} alkyl, C_{2-10} alkenyl, and C_{2-10} alkynyl; and

R^{24} and R^{25} are independently selected from hydrogen, halogen, $-OR^{10}$, $-SR^{10}$, $-N(R^{10})_2$, $-S(O)R^{10}$, $-S(O)_2R^{10}$, $-C(O)R^{10}$, $-C(O)OR^{10}$, $-OC(O)R^{10}$, $-NO_2$, $=O$, $=S$, $=N(R^{10})$, $-CN$, C_{1-10} alkyl, C_{2-10} alkenyl, and C_{2-10} alkynyl; or R^{24} and R^{25} taken together form an optionally substituted saturated C_{3-7} carbocycle.

139. The lyophilized composition of of any one of claims 73-135, wherein the conjugate comprises the compound linked to the polypeptide through a linker, wherein the compound and the linker together are a compound of Formula (IVB), or the lyophilized

composition of any one of claims 136-138, wherein L and Dx together are a compound of Formula (IVC):



(IVC)

wherein:

R^1 and R^2 are each hydrogen;

L^{22} is -C(O)-;

R^4 is $-N(R^{10})_2$;

R^{10} is independently selected at each occurrence from hydrogen, $-NH_2$, $-C(O)OCH_2C_6H_5$; and C_{1-10} alkyl, C_{2-10} alkenyl, C_{2-10} alkynyl, C_{3-12} carbocycle, and 3- to 12-membered heterocycle, each of which is optionally substituted with one or more substituents independently selected from halogen, -CN, $-NO_2$, $-NH_2$, =O, =S, $-C(O)OCH_2C_6H_5$, $-NHC(O)OCH_2C_6H_5$, C_{1-10} alkyl, C_{2-10} alkenyl, C_{2-10} alkynyl, C_{3-12} carbocycle, 3- to 12-membered heterocycle, and haloalkyl;

L^{12} is $-C(O)N(R^{10})-*$, wherein * represents where L^{12} is bound to R^8;

R^8 is an optionally substituted fused 5-5, fused 5-6, or fused 6-6 bicyclic heterocycle bound to linker moiety L^3 ,

and wherein optional substituents are independently selected at each occurrence from:

halogen, $-OR^{10}$, $-SR^{10}$, $-C(O)N(R^{10})_2$, $-N(R^{10})C(O)R^{10}$, $-N(R^{10})C(O)N(R^{10})_2$, $-N(R^{10})_2$, $-C(O)R^{10}$, $-C(O)OR^{10}$, $-OC(O)R^{10}$, $-NO_2$, =O, =S, $=N(R^{10})$, and -CN;

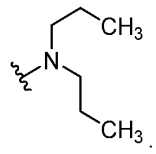
C_{1-10} alkyl, C_{2-10} alkenyl, C_{2-10} alkynyl, each of which is optionally substituted with one or more substituents independently selected from halogen, $-OR^{10}$, $-SR^{10}$, $-C(O)N(R^{10})_2$, $-N(R^{10})C(O)R^{10}$, $-N(R^{10})C(O)N(R^{10})_2$, $-N(R^{10})_2$, $-C(O)R^{10}$, $-C(O)OR^{10}$, $-OC(O)R^{10}$, $-NO_2$, =O, =S, $=N(R^{10})$, -CN, C_{3-12} carbocycle, and 3- to 12-membered heterocycle; and

C_{3-12} carbocycle and 3- to 12-membered heterocycle, each of which is optionally substituted with one or more substituents independently selected from halogen, $-OR^{10}$, $-SR^{10}$, $-C(O)N(R^{10})_2$, $-N(R^{10})C(O)R^{10}$, $-N(R^{10})C(O)N(R^{10})_2$, $-N(R^{10})_2$, $-C(O)R^{10}$, -

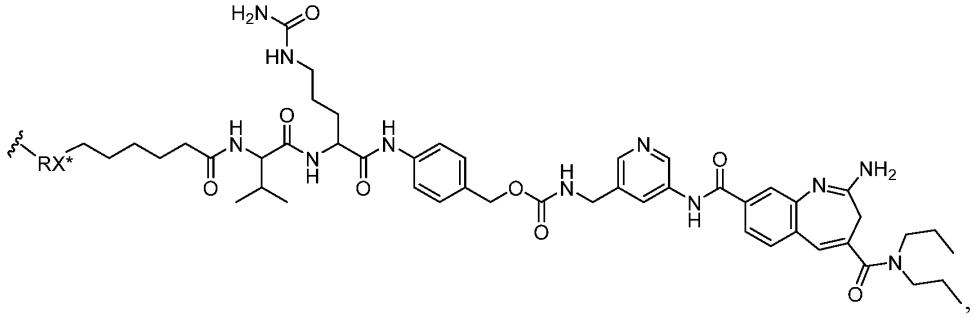
$C(O)OR^{10}$, $-OC(O)R^{10}$, $-NO_2$, =O, =S, $=N(R^{10})$, -CN, C_{1-6} alkyl, C_{2-6} alkenyl, and C_{2-6} alkynyl.

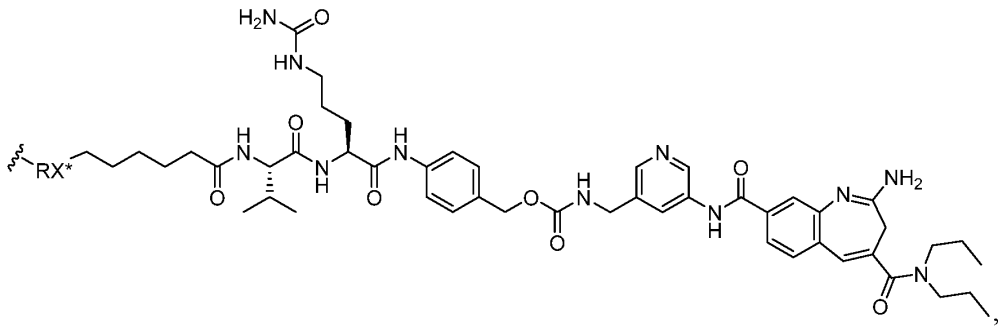
140. The lyophilized composition of claim 138 or claim 139, wherein: R^4 is $-N(C_{1-4}\text{ alkyl})_2$ and L^{12} is -C(O)N(H)-*,

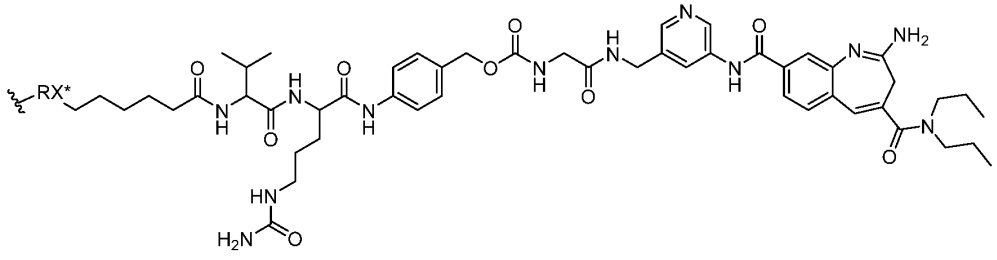
141. The lyophilized composition of claim 138 or claim 139, wherein:

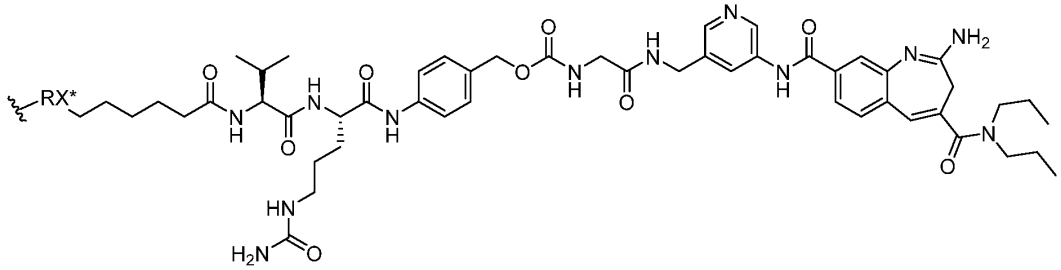
R^4 is .

142. The lyophilized composition of any one of claims 136-141, wherein L and Dx together have a structure selected from:

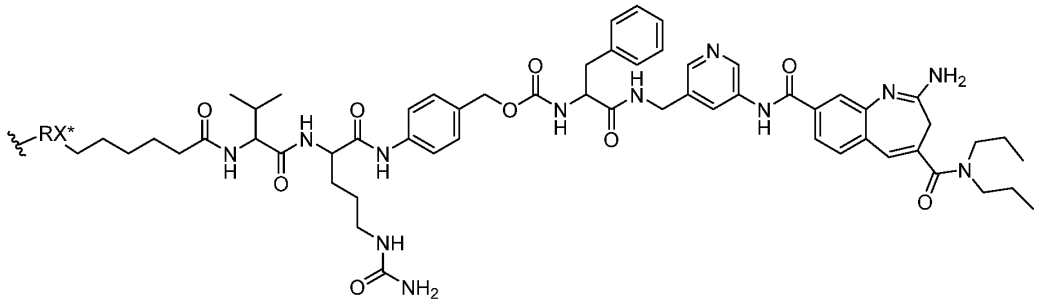
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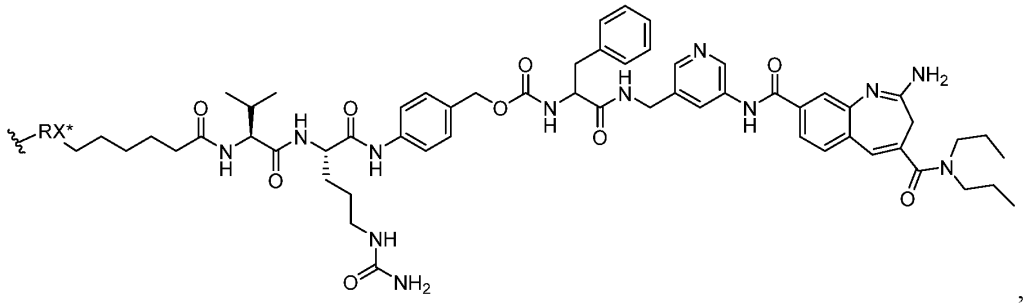
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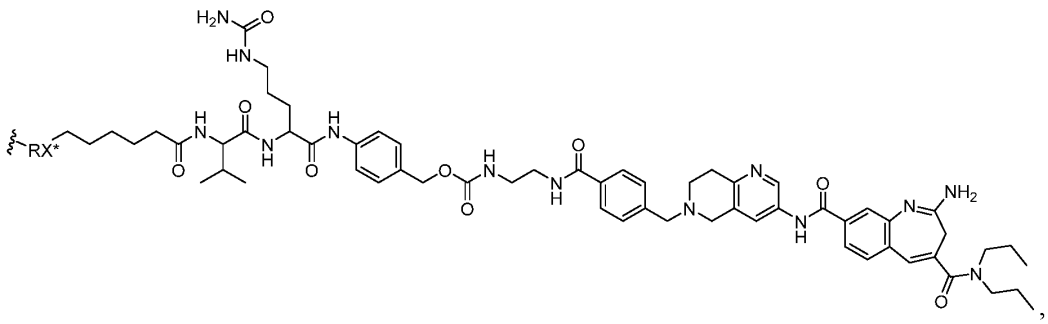
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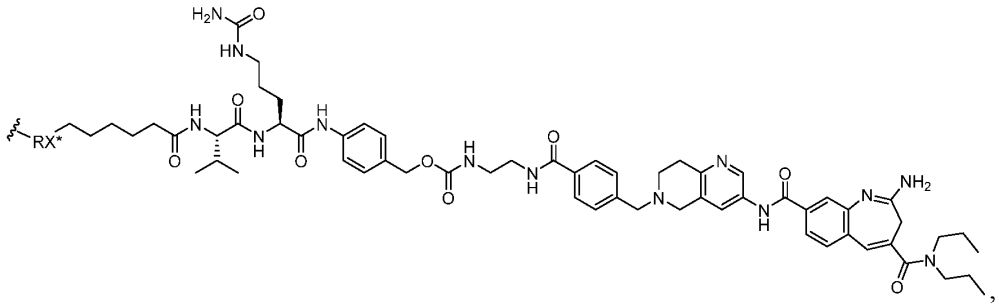
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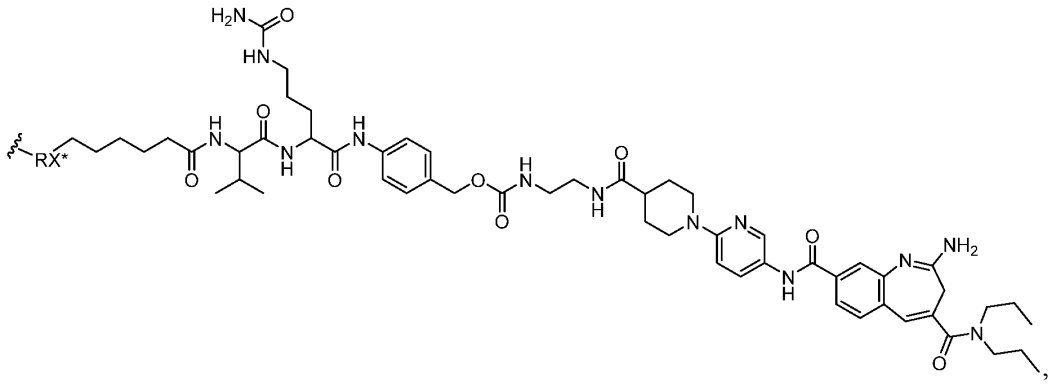
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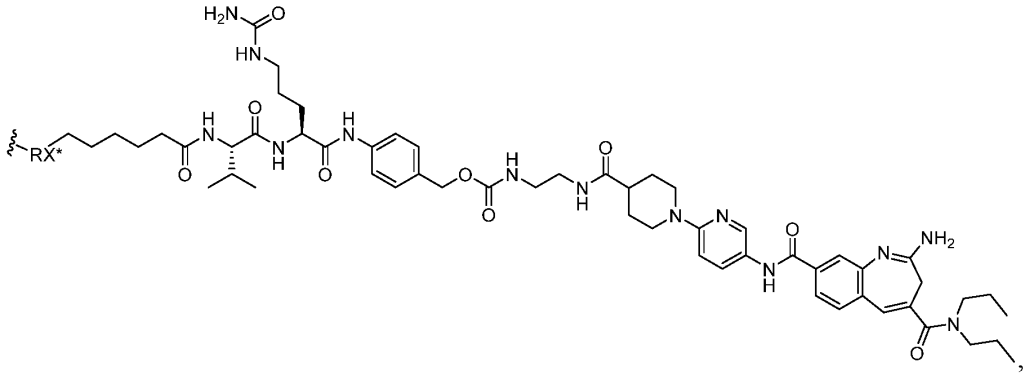


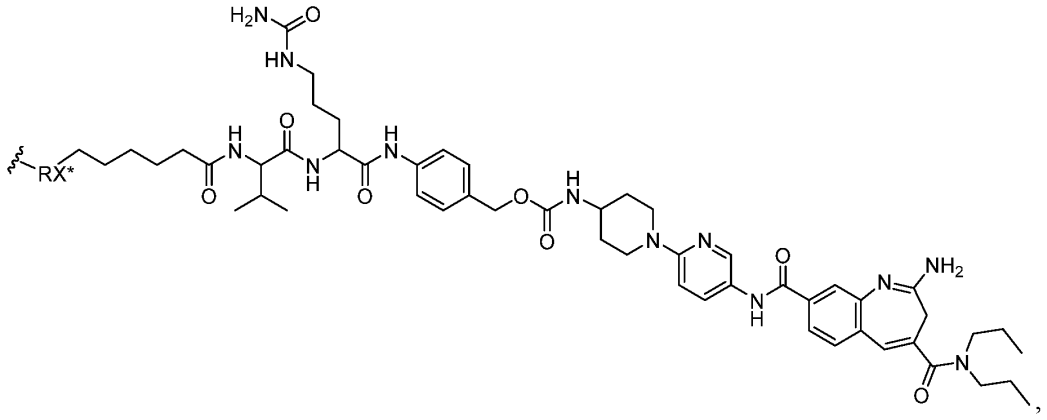
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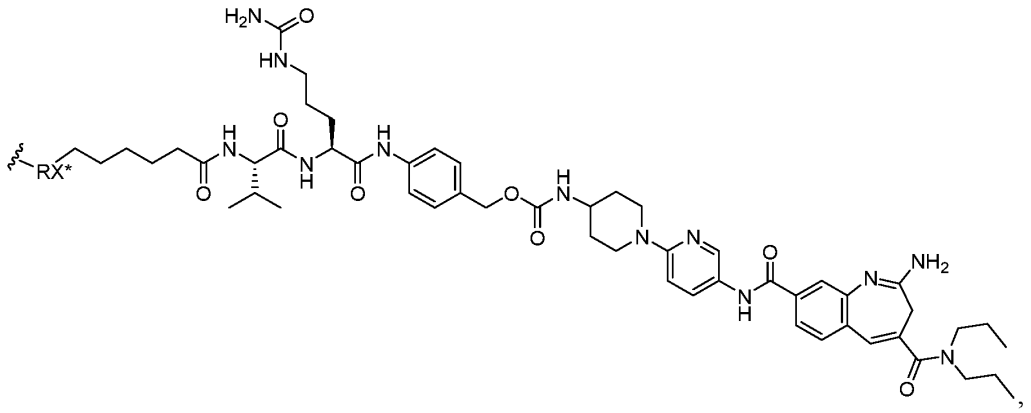


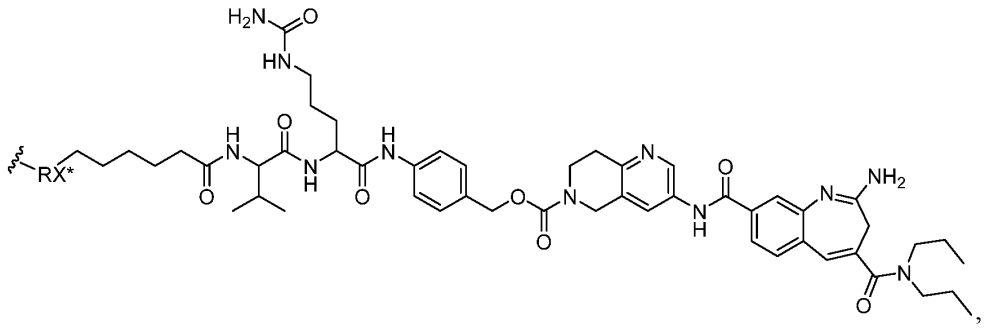
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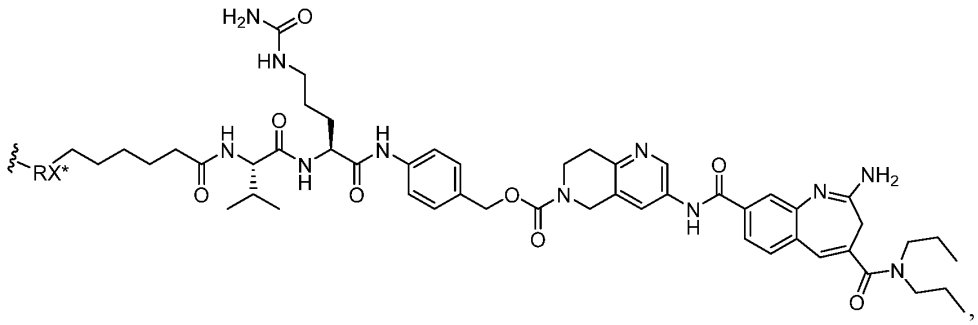


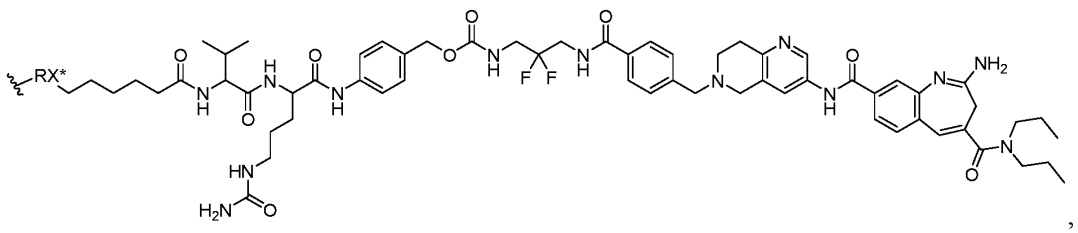




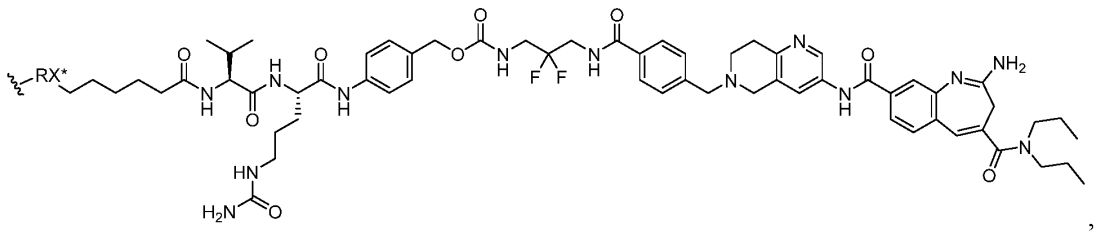








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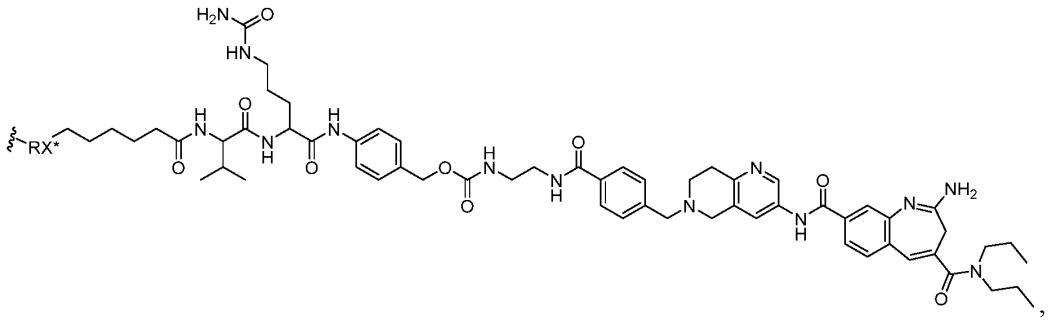


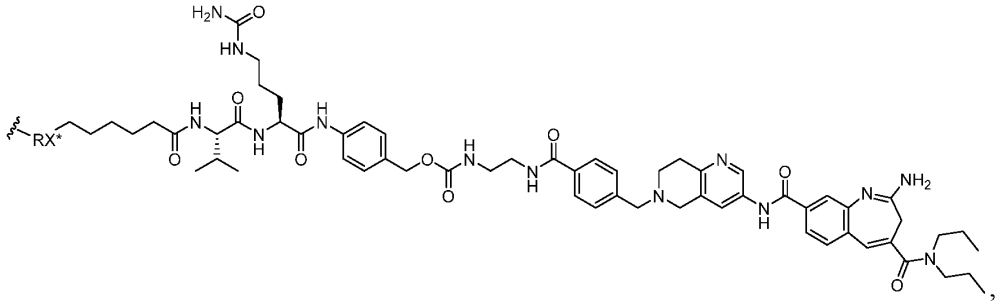
and salts thereof,

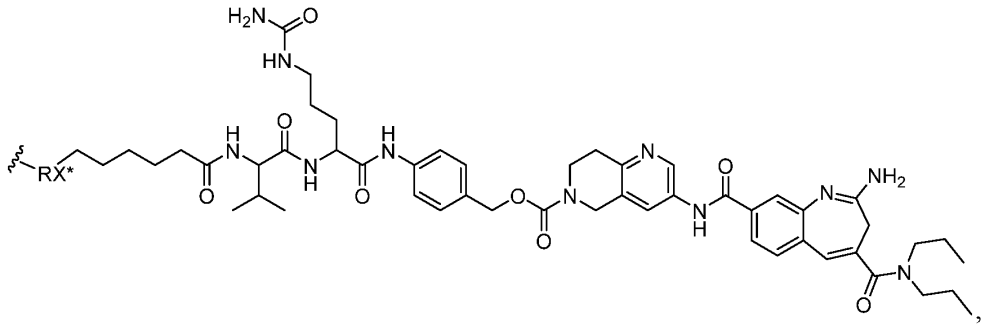
wherein the RX* is a bond, a succinimide moiety, or a hydrolyzed succinimide moiety bound to a residue of a polypeptide,

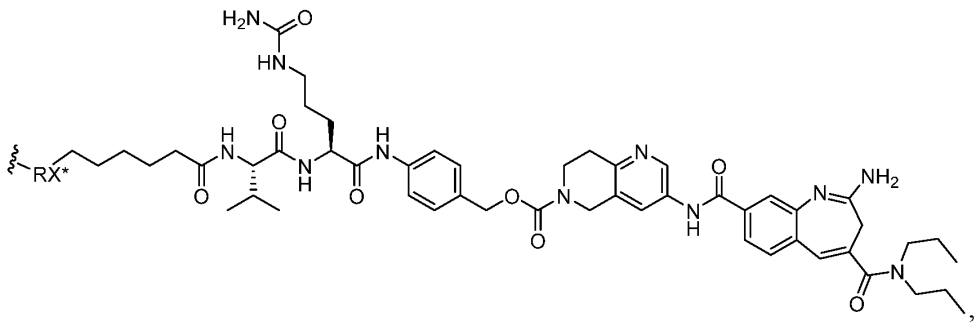
wherein on RX* represents the point of attachment to the residue of the polypeptide.

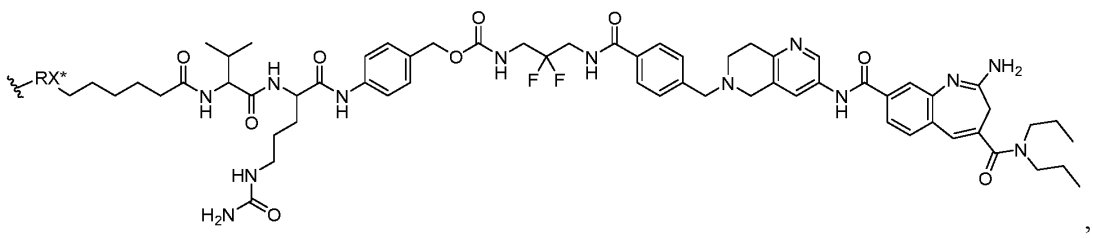
143. The lyophilized composition of claim 142, wherein L and Dx together have a structure selected from:



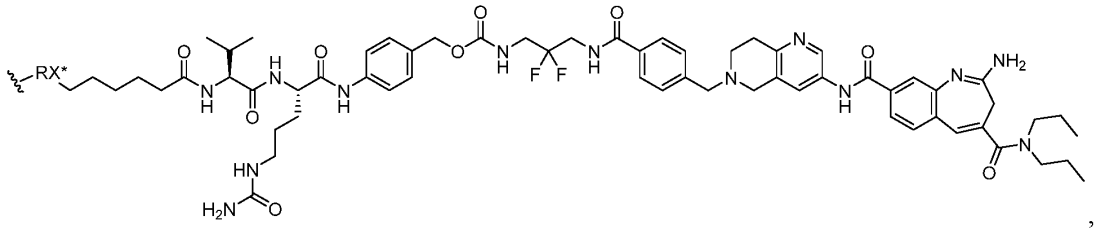








and



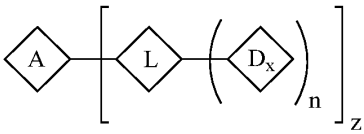
,

and salts thereof,

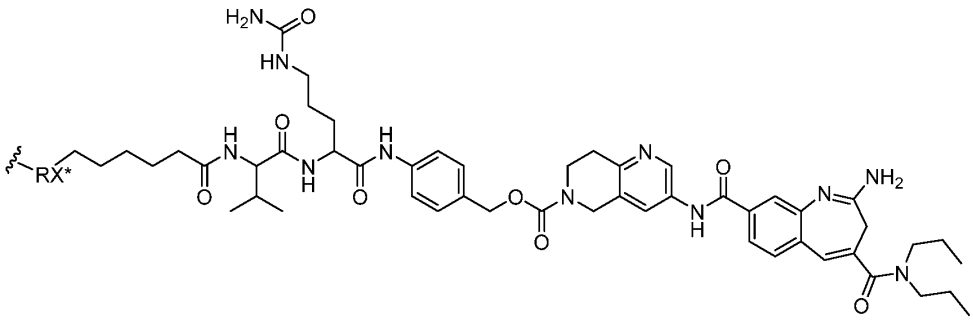
wherein the RX* is a bond, a succinimide moiety, or a hydrolyzed succinimide moiety bound to a residue of a polypeptide,

wherein  on RX* represents the point of attachment to the residue of the polypeptide.

144. The lyophilized composition of claim 136, wherein upon reconstitution of the lyophilized composition in water to form an aqueous formulation, the aqueous formulation comprises:

a) a conjugate at a total concentration ranging from about 50 mg/mL to about 100 mg/mL and represented by Formula (I):  (I),

wherein A is an antibody; n is 1; z ranges from 2 to 8; and L is a linker and D_x is a benzazepine compound, wherein L and Dx together have a structure of:



, wherein RX* comprises a hydrolyzed succinamide moiety and is bound to a cysteine residue of the antibody;

b) a buffer comprised of histidine and aspartate at a total concentration ranging from about 15mM to about 25mM;

c) a lyoprotectant comprised of sucrose at a total concentration ranging from about 7% to about 8%; and

d) a surfactant comprised of polysorbate 80 at a total concentration ranging from about 0.01% to about 0.03%.

145. A lyophilized composition formed by lyophilizing the aqueous formulation of any one of claims 1-72.

146. An aqueous formulation formed by reconstituting the lyophilized composition of any one of claims 73-144.

147. The aqueous formulation of claim 146, wherein the lyophilized composition has been reconstituted in water.

148. A method of treating a disease or disorder in a subject, comprising administering to a subject in need thereof a therapeutically effective amount of the aqueous formulation of any one of claims 1-72, 146, and 147.

149. A method of treating a cancer in a subject, comprising administering to a subject in need thereof a therapeutically effective amount of the aqueous formulation of any one of claims 1-72, 146, and 147.

150. The method of claim 149, wherein the cancer is selected from lung cancer, liver cancer, kidney cancer, pancreatic cancer, colorectal cancer, ovarian cancer, head and neck cancer, bone cancer, mesothelioma, bladder cancer, stomach cancer, prostate cancer, thyroid cancer, uterine cancer, cervical/endometrial cancer, and breast cancer.

151. The method of claim 149 or claim 150, wherein the polypeptide is an antibody.

152. The method of claim 151, wherein the antibody comprises an antigen binding domain and an Fc domain.

153. The method of claim 152, wherein the Fc domain exhibits the same or substantially similar binding affinity to Fcgamma and/or FcRn receptors as compared to a wild-type Fc domain from an IgG1 antibody.

154. The method of any one of claims 151-153, wherein the antibody binds a tumor associated antigen.

155. The method of claim 154, wherein the tumor associated antigen is selected from HER2, Nectin-4, ASGR1, mesothelin, PSMA, rsPSMA, TROP2, LIV-1, MUC16, CEACAM1, CEACAM3, CEACAM4, CEACAM5, CEACAM6, CEACAM7, CEACAM8, CEACAM16, CEACAM18, CEACAM19, CEACAM20, CEACAM21, URLC10, NY-ESO-1, GAA, OFA, cyclin B1, WT-1, CEF, VEGRR1, VEGFR2, TTK, MUC1, HPV16E7, CEA, IMA910, KOC1, SL-701, MART-1, gp100, tyrosinase, GSK2302050A, survivin, MAGE-3.1, MAGE-10.A2, OVA BiP, gp209-2M, melan-A, NA17.A2, KOC1, CO16, DEPDC1, MPHOSPH1, MAGE12, ONT-10, GD2L, GD3L, GSK2302032A, URLC10, CDCA1, TF, rsPSMA, PSA, MUC-2, TERT, HPV16, HPV18, STF-II, G17DT, ICT-107, Dex2, hTERT, PAP, tyrosinase related peptide 2 (TRP2), and LRRC15.

156. The method of claim 154, wherein the tumor associated antigen is selected from:

a) an antigen present on lung cancer, wherein the antigen is optionally selected from mesothelin, HER2, EGFR, PD-L1, MSLN, LY6K, CD56, PTK7, FOLR1, DLL3, SLC34A2, CECAM5, MUC16, LRRC15, ADAM12, EGFRvIII, LYPD3, EFNA4, and MUC1;

b) an antigen present on liver cancer, wherein the antigen is optionally selected from GPC3, EPCAM, and CECAM5;

c) an antigen present on kidney cancer, wherein the antigen is optionally selected from HAVCR1, ENPP3, CDH6, CD70, and cMET;

d) an antigen present on pancreatic cancer, wherein the antigen is optionally selected from PTK7, MUC16, MSLN, LRRC15, ADAM12, EFNA4, MUC5A, and MUC1;

e) an antigen present on colorectal cancer, wherein the antigen is optionally selected from EPHB2, TMEM238, CECAM5, LRRC15, ADAM12, EFNA4, and GPA33;

f) an antigen present on ovarian cancer, wherein the antigen is optionally selected from MUC16, MUC1, MSLN, FOLR1, sTN, VTCN1, HER2, PTK7, FAP, TMEM238, LRRC15, CLDN6, SLC34A2, and EFNA4;

g) an antigen present on head and neck cancer, wherein the antigen is optionally selected from LY6K, PTK7, LRRC15, ADAM12, LYPD3, EFNA4 and TNC;

h) an antigen present on bone cancer, wherein the antigen is optionally selected from EPHA2, LRRC15, ADAM12, GPNMB, TP-3, and CD248;

i) an antigen present on mesothelioma, wherein the antigen is optionally MSLN;

j) an antigen present on bladder cancer, wherein the antigen is optionally selected from LY6K, PTK7, UPK1B, UPK2, TNC, Nectin4, SLITRK6, LYPD3, EFNA4, and HER2;

k) an antigen present on stomach cancer, wherein the antigen is optionally selected from HER2, EPHB2, TMEM238, CECAM5, and EFNA4;

l) an antigen present on prostate cancer, wherein the antigen is optionally selected from PSMA, FOLH1, PTK7, STEAP, TMEFF2 (TENB2), OR51E2, SLC30A4, and EFNA4;

m) an antigen present on thyroid cancer, wherein the antigen is optionally PTK7;

n) an antigen present on uterine cancer, wherein the antigen is optionally selected from LY6K, PTK7, EPHB2, FOLR1, ALPPL2, MUC16, and EFNA4;

o) an antigen present on cervical/endometrial cancer, wherein the antigen is optionally selected from LY6K, PTK7, MUC16, LYPD3, EFNA4, and MUC1; and

p) an antigen present on breast cancer, wherein the antigen is optionally selected from HER2, TROP2, LIV-1, CDH3 (p-cadherin), MUC1, Sialo-epitope CA6, PTK7, GPNMB, LAMP-1, LRRC15, ADAM12, EPHA2, TNC, LYPD3, EFNA4, and CLDN6.

157. The method of any one of claims 151-154, wherein the method is for treating a HER2 expressing cancer, and the antibody is an anti-HER2 antibody.

158. The method of claim 157, wherein the HER2 expressing cancer expresses HER2 at a level of 2+ or 3+ as determined by immunohistochemistry.

159. The method of claim 157 or claim 158, wherein the HER2 expressing cancer is breast cancer, lung cancer, stomach cancer, bladder cancer, or ovarian cancer.

160. The method of claim 159, wherein the HER2 expressing cancer is breast cancer.

161. The method of any one of claims 157-160, wherein the anti-HER2 antibody comprises heavy chain (HC)-CDR1, HC-CDR2, HC-CDR3, light chain (LC)-CDR1, LC-CDR2, and LC-CDR3 of SEQ ID NOS:1-6, respectively.

162. The method of claim 161, wherein the anti-HER2 antibody comprises a heavy chain variable region (V_H) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_H amino acid sequence of SEQ ID NO:7 and a light chain variable region (V_L) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_L amino acid sequence of SEQ ID NO:8.

163. The method of any one of claims 157-162, wherein the anti-HER2 antibody comprises a V_H comprising or consisting of the amino acid sequence of SEQ ID NO:7 and a V_L comprising or consisting of the amino acid sequence of SEQ ID NO:8.

164. The method of any one of claims 161-163, wherein the anti-HER2 antibody comprises a heavy chain and light chain, wherein the heavy chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the heavy chain amino acid sequence of SEQ ID NO:9; and the light chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the light chain amino acid sequence of SEQ ID NO:10.

165. The method of any one of claims 157-162, wherein the anti-HER2 antibody comprises a heavy chain comprising or consisting of the amino acid sequence of SEQ ID NO:9 and a light chain comprising or consisting of the amino acid sequence of SEQ ID NO:10.

166. The method of any one of claims 151-154, wherein the method is for treating a Nectin-4 expressing cancer, and wherein the antibody is an anti-Nectin-4 antibody.

167. The method of claim 166, wherein the anti-Nectin-4 antibody comprises heavy chain (HC)-CDR1, HC-CDR2, HC-CDR3 of SEQ ID NOS: 11-13, respectively, and light chain (LC)-CDR1 of SEQ ID NO:14 or 15, LC-CDR2 of SEQ ID NO:16, and LC-CDR3 of SEQ ID NO:17.

168. The method of claim 167, wherein the anti-Nectin-4 antibody comprises a heavy chain variable region (V_H) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_H amino acid sequence of SEQ ID NO:18 and a light chain variable region (V_L) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_L amino acid sequence of SEQ ID NO:19 or 20.

169. The method of claim 166 or claim 167, wherein the anti-Nectin-4 antibody comprises a V_H comprising or consisting of the amino acid sequence of SEQ ID NO:18 and a V_L comprising or consisting of the amino acid sequence of SEQ ID NO:19 or 20.

170. The method of any one of claims 167-169, wherein the anti-Nectin-4 antibody comprises a heavy chain and light chain, wherein the heavy chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the heavy chain amino acid sequence of SEQ ID NO:21; and the light chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the light chain amino acid sequence of SEQ ID NO:22 or 23.

171. The aqueous formulation of claim 166 or claim 167, wherein the anti-Nectin-4 antibody comprises a heavy chain comprising or consisting of the amino acid sequence of SEQ ID NO:21 and a light chain comprising or consisting of the amino acid sequence of SEQ ID NO:22 or 23.

172. The method of any one of claims 151-154, wherein the method is for treating an ASGR1 expressing cancer, and wherein the antibody is an anti-ASGR1 antibody.

173. The method of claim 172, wherein the anti-ASGR1 antibody comprises heavy chain (HC)-CDR1 of SEQ ID NO: 24 or 25, HC-CDR2 of SEQ ID NO:26, 27, or 28, HC-CDR3 of SEQ ID NO:29 or 30, light chain (LC)-CDR1 of SEQ ID NO:31 or 32, LC-CDR2 of SEQ ID NO:33, 34, 35 or 36, and LC-CDR3 of SEQ ID NO:37 or 38.

174. The method of claim 172, wherein the anti-ASGR1 antibody comprises (a) heavy chain (HC)-CDR1 of SEQ ID NO: 24, HC-CDR2 of SEQ ID NO:26, HC-CDR3 of SEQ ID NO:29, light chain (LC)-CDR1 of SEQ ID NO:31, LC-CDR2 of SEQ ID NO:33 or 34, and LC-CDR3 of SEQ ID NO:37; or (b) heavy chain (HC)-CDR1 of SEQ ID NO: 25, HC-CDR2 of SEQ ID NO:27 or 28, HC-CDR3 of SEQ ID NO:30, light chain (LC)-CDR1 of SEQ ID NO:32, LC-CDR2 of SEQ ID NO:35 or 36, and LC-CDR3 of SEQ ID NO:38.

175. The method of claim 173 or claim 174, wherein the anti-ASGR1 antibody comprises a heavy chain variable region (V_H) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_H amino acid sequence of SEQ ID NO:39 and a light chain variable region (V_L) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_L amino acid sequence of SEQ ID NO:42 or 43.

176. The method of claim 173 or claim 174, wherein the anti-ASGR1 antibody comprises a heavy chain variable region (V_H) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_H amino acid sequence of SEQ ID NO:40 or 41 and a light chain variable region (V_L) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_L amino acid sequence of SEQ ID NO:44 or 45.

177. The method of any one of claims 172-174, wherein the anti-ASGR1 antibody comprises a V_H comprising or consisting of the amino acid sequence of SEQ ID NO:39 and a V_L comprising or consisting of the amino acid sequence of SEQ ID NO:42 or 43.

178. The method of any one of claims 172-174, wherein the anti-ASGR1 antibody comprises a V_H comprising or consisting of the amino acid sequence of SEQ ID NO:40 or 41 and a V_L comprising or consisting of the amino acid sequence of SEQ ID NO:44 or 45.

179. The method of any one of claims 173-175 and 177, wherein the anti-ASGR1 antibody comprises a heavy chain and light chain, wherein the heavy chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at

least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the heavy chain amino acid sequence of SEQ ID NO:46; and the light chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the light chain amino acid sequence of SEQ ID NO:49 or 50.

180. The method of any one of claims 172-174, wherein the anti-ASGR1 antibody comprises a heavy chain comprising or consisting of the amino acid sequence of SEQ ID NO:46 and a light chain comprising or consisting of the amino acid sequence of SEQ ID NO:49 or 50.

181. The method of any one of claims 173-174, 176, and 178, wherein the anti-ASGR1 antibody comprises a heavy chain and light chain, wherein the heavy chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the heavy chain amino acid sequence of SEQ ID NO:47 or 48; and the light chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the light chain amino acid sequence of SEQ ID NO:51 or 52.

182. The method of any one of claims 172-174, wherein the anti-ASGR1 antibody comprises a heavy chain comprising or consisting of the amino acid sequence of SEQ ID NO:47 or 48 and a light chain comprising or consisting of the amino acid sequence of SEQ ID NO:51 or 52.

183. The method of any one of claims 151-154, wherein the method is for treating a mesothelin expressing cancer, and wherein the antibody is an anti-mesothelin antibody.

184. The method of claim 184, wherein the anti-mesothelin antibody comprises heavy chain (HC)-CDR1, HC-CDR2, HC-CDR3, light chain (LC)-CDR1, LC-CDR2, and LC-CDR3 of SEQ ID NOS:53-58, respectively.

185. The method of claim 185, wherein the anti-mesothelin antibody comprises a heavy chain variable region (V_H) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_H amino acid sequence of SEQ ID NO:59 and a light chain variable region (V_L) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_L amino acid sequence of SEQ ID NO:60.

186. The method of claim 183 or claim 184, wherein the anti-mesothelin antibody comprises a V_H comprising or consisting of the amino acid sequence of SEQ ID NO:59 and a V_L comprising or consisting of the amino acid sequence of SEQ ID NO:60.

187. The method of any one of claims 184-186, wherein the anti-mesothelin antibody comprises a heavy chain and light chain, wherein the heavy chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the heavy chain amino acid sequence of SEQ ID NO:70; and the light chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the light chain amino acid sequence of SEQ ID NO:71.

188. The method of claim 183 or claim 184, wherein the anti-mesothelin antibody comprises a heavy chain comprising or consisting of the amino acid sequence of SEQ ID NO:70 and a light chain comprising or consisting of the amino acid sequence of SEQ ID NO:71.

189. The method of any one of claims 157-159, wherein the antibody is pertuzumab, trastuzumab, sacituzumab, or ladiratuzumab or comprises an antigen binding fragment of pertuzumab, trastuzumab, sacituzumab, or ladiratuzumab.

190. The method of any one of claims 148-189, wherein the method comprises administering an effective regimen of the aqueous formulation, wherein the effective regimen results in a Tmax of the conjugate in the subject of greater than 4 hours following each administration of the aqueous formulation.

191. The method of any one of claims 148-190, wherein the method comprises administering an effective regimen of the aqueous formulation, wherein the effective regimen comprises at least two cycles of administration of the conjugate to the subject and a total dose of greater than 0.4 mg/kg of the conjugate per cycle.

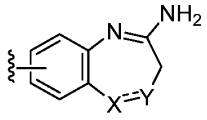
192. The method of any one of claims 148-191, wherein the aqueous formulation is administered subcutaneously.

193. The method of any one of claims 148-191, wherein the aqueous formulation is administered intravenously by a slow infusion.

194. The method of any one of claims 148-193, further comprising administering a B-cell depleting agent.

195. The method of claim 194, wherein the B-cell depleting agent is an anti-CD19 or anti-CD20 antibody.

196. A method of controlling hydrolysis of a compound conjugated to a polypeptide in an aqueous formulation, wherein the compound comprises the structure:



wherein ≡ is a double bond or a single bond;

wherein when ≡ is a double bond, X and Y are each CH; and

when ≡ is a single bond, one of X and Y is CH_2 and the other is CH_2, O, or NH; and the structure is optionally substituted at any position other than the $-NH_2$;

comprising formulating the conjugate to form an aqueous formulation, wherein the pH of the aqueous formulation is from 4 to 5.2 or from 4.4 to 5.4.

197. The method of claim 196, wherein the pH of the aqueous formulation is from 4.4 to 5.4, 4.5 to 5.3, 4.6 to 5.2, 4.7 to 5.1, 4.8 to 5.1, 4.9 to 5.1, 4.4 to 5.0, 4.5 to 5.0, 4.6 to 5.0, 4.7 to 5.0, 4.8 to 5.0, or 4.9 to 5.0.

198. The method of claim 196, wherein the pH of the aqueous formulation is from 4.4 to 5.4.

199. The method of claim 196, wherein the pH of the aqueous formulation is from 4.4-5.3.

200. The method of claim 196, wherein the pH of the aqueous formulation is from 4.4 to 5.2.

201. The method of claim 196, wherein the pH of the aqueous formulation is from 4.4 to 5.1.

202. The method of claim 196, wherein the pH of the aqueous formulation is from 4.5 to 5.1.

203. The method of claim 196, wherein the pH of the aqueous formulation is from 4.6 to 5.0.

204. The method of claim 196, wherein the pH of the aqueous formulation is from 4.7 to 4.9.

205. The method of claim 196, wherein the pH of the aqueous formulation is 4.8.

206. The method of claim 196, wherein the pH of the aqueous formulation is 4.9.

207. The method of claim 196, wherein the pH of the aqueous formulation is 5.0.

208. The method of any one of claims 196-207, wherein the aqueous formulation comprises at least one buffering agent.

209. The method of claim 208, wherein the at least one buffering agent is selected from histidine, citrate, aspartate, acetate, phosphate, lactate, tromethamine, gluconate, glutamate, tartrate, succinate, malic acid, fumarate, α-ketoglutarate, and combinations thereof.

210. The method of claim 209, wherein the at least one buffering agent is histidine and aspartate.

211. The method of any one of claims 196-210, wherein the total concentration of buffering agents in the aqueous formulation is about 15mM to about 25mM.

212. The method of any one of claims 196-211, wherein the aqueous formulation comprises at least one lyoprotectant selected from sucrose, arginine, glycine, sorbitol, glycerol, trehalose, dextrose, alpha-cyclodextrin, hydroxypropyl beta-cyclodextrin, hydroxypropyl gamma-cyclodextrin, proline, methionine, albumin, mannitol, maltose, dextran, and combinations thereof.

213. The method of claim 212, wherein the at least one lyoprotectant is sucrose.

214. The method of claim 212 or claim 213, wherein the total concentration of the at least one lyoprotectant in the aqueous formulation is about 7% to about 9%.

215. The method of any one of claims 196-214, wherein the aqueous formulation comprises at least one surfactant.

216. The method of claim 215, wherein the at least one surfactant is selected from polysorbate 80, polysorbate 20, poloxamer 88, and combinations thereof.

217. The method of claim 216, wherein the at least one surfactant is polysorbate 80.

218. The method of any one of claims 215-217, wherein the total concentration of the at least one surfactant in the aqueous formulation is about 0.01% to about 0.05%.

219. The method of any one of claims 196-218, wherein the concentration of the conjugate in the aqueous formulation is about 70 mg/mL to about 100 mg/mL.

220. The method of any one of claims 196-221, wherein the polypeptide is an antibody.

221. The method of claim 220, wherein the antibody comprises an antigen binding domain and an Fc domain.

222. The method of claim 221, wherein the Fc domain exhibits the same or substantially similar binding affinity to Fcgamma and/or FcRn receptors as compared to a wild-type Fc domain from an IgG1 antibody.

223. The method of any one of claims 220-222, wherein the antibody binds a tumor associated antigen.

224. The method of claim 223, wherein the tumor associated antigen is selected from HER2, Nectin-4, ASGR1, mesothelin, PSMA, rsPSMA, TROP2, LIV-1, MUC16, CEACAM1, CEACAM3, CEACAM4, CEACAM5, CEACAM6, CEACAM7, CEACAM8, CEACAM16, CEACAM18, CEACAM19, CEACAM20, CEACAM21, URLC10, NY-ESO-1, GAA, OFA, cyclin B1, WT-1, CEF, VEGRR1, VEGFR2, TTK, MUC1, HPV16E7, CEA, IMA910, KOC1,

SL-701, MART-1, gp100, tyrosinase, GSK2302050A, survivin, MAGE-3.1, MAGE-10.A2, OVA BiP, gp209-2M, melan-A, NA17.A2, KOC1, CO16, DEPDC1, MPHOSPH1, MAGE12, ONT-10, GD2L, GD3L, GSK2302032A, URLC10, CDCA1, TF, rsPSMA, PSA, MUC-2, TERT, HPV16, HPV18, STF-II, G17DT, ICT-107, Dex2, hTERT, PAP, tyrosinase related peptide 2 (TRP2), and LRRC15.

225. The method of claim 223, wherein the tumor associated antigen is selected from:

a) an antigen present on lung cancer, wherein the antigen is optionally selected from mesothelin, HER2, EGFR, PD-L1, MSLN, LY6K, CD56, PTK7, FOLR1, DLL3, SLC34A2, CECAM5, MUC16, LRRC15, ADAM12, EGFRvIII, LYPD3, EFNA4, and MUC1;

b) an antigen present on liver cancer, wherein the antigen is optionally selected from GPC3, EPCAM, and CECAM5;

c) an antigen present on kidney cancer, wherein the antigen is optionally selected from HAVCR1, ENPP3, CDH6, CD70, and cMET;

d) an antigen present on pancreatic cancer, wherein the antigen is optionally selected from PTK7, MUC16, MSLN, LRRC15, ADAM12, EFNA4, MUC5A, and MUC1;

e) an antigen present on colorectal cancer, wherein the antigen is optionally selected from EPHB2, TMEM238, CECAM5, LRRC15, ADAM12, EFNA4, and GPA33;

f) an antigen present on ovarian cancer, wherein the antigen is optionally selected from MUC16, MUC1, MSLN, FOLR1, sTN, VTCN1, HER2, PTK7, FAP, TMEM238, LRRC15, CLDN6, SLC34A2, and EFNA4;

g) an antigen present on head and neck cancer, wherein the antigen is optionally selected from LY6K, PTK7, LRRC15, ADAM12, LYPD3, EFNA4 and TNC;

h) an antigen present on bone cancer, wherein the antigen is optionally selected from EPHA2, LRRC15, ADAM12, GPNMB, TP-3, and CD248;

i) an antigen present on mesothelioma, wherein the antigen is optionally MSLN;

j) an antigen present on bladder cancer, wherein the antigen is optionally selected from LY6K, PTK7, UPK1B, UPK2, TNC, Nectin4, SLITRK6, LYPD3, EFNA4, and HER2;

k) an antigen present on stomach cancer, wherein the antigen is optionally selected from HER2, EPHB2, TMEM238, CECAM5, and EFNA4;

l) an antigen present on prostate cancer, wherein the antigen is optionally selected from PSMA, FOLH1, PTK7, STEAP, TMEFF2 (TENB2), OR51E2, SLC30A4, and EFNA4;

m) an antigen present on thyroid cancer, wherein the antigen is optionally PTK7;

n) an antigen present on uterine cancer, wherein the antigen is optionally selected from LY6K, PTK7, EPHB2, FOLR1, ALPPL2, MUC16, and EFNA4;

o) an antigen present on cervical/endometrial cancer, wherein the antigen is optionally selected from LY6K, PTK7, MUC16, LYPD3, EFNA4, and MUC1; and

p) an antigen present on breast cancer, wherein the antigen is optionally selected from HER2, TROP2, LIV-1, CDH3 (p-cadherin), MUC1, Sialo-epitope CA6, PTK7, GPNMB, LAMP-1, LRRC15, ADAM12, EPHA2, TNC, LYPD3, EFNA4, and CLDN6.

226. The method of any one of claims 220-225, wherein the antibody is an anti-HER2 antibody.

227. The method of claim 226, wherein the anti-HER2 antibody comprises heavy chain (HC)-CDR1, HC-CDR2, HC-CDR3, light chain (LC)-CDR1, LC-CDR2, and LC-CDR3 of SEQ ID NOS:1-6, respectively.

228. The method of claim 227, wherein the anti-HER2 antibody comprises a heavy chain variable region (V_H) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_H amino acid sequence of SEQ ID NO:7 and a light chain variable region (V_L) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_L amino acid sequence of SEQ ID NO:8.

229. The method of claim 226 or claim 227, wherein the anti-HER2 antibody comprises a V_H comprising or consisting of the amino acid sequence of SEQ ID NO:7 and a V_L comprising or consisting of the amino acid sequence of SEQ ID NO:8.

230. The method of any one of claims 227-229, wherein the anti-HER2 antibody comprises a heavy chain and light chain, wherein the heavy chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the heavy chain amino acid sequence of SEQ ID NO:9; and the light chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the light chain amino acid sequence of SEQ ID NO:10.

231. The method of claim 226 or claim 227, wherein the anti-HER2 antibody comprises a heavy chain comprising or consisting of the amino acid sequence of SEQ ID NO:9 and a light chain comprising or consisting of the amino acid sequence of SEQ ID NO:10.

232. The method of any one of claims 220-225, wherein the antibody is an anti-Nectin-4 antibody.

233. The method of claim 232, wherein the anti-Nectin-4 antibody comprises heavy chain (HC)-CDR1, HC-CDR2, HC-CDR3 of SEQ ID NOS: 11-13, respectively, and light chain (LC)-CDR1 of SEQ ID NO:14 or 15, LC-CDR2 of SEQ ID NO:16, and LC-CDR3 of SEQ ID NO:17.

234. The method of claim 233, wherein the anti-Nectin-4 antibody comprises a heavy chain variable region (V_H) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_H amino acid sequence of SEQ ID NO:18 and a light chain variable region (V_L) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_L amino acid sequence of SEQ ID NO:19 or 20.

235. The method of claim 232 or claim 233, wherein the anti-Nectin-4 antibody comprises a V_H comprising or consisting of the amino acid sequence of SEQ ID NO:18 and a V_L comprising or consisting of the amino acid sequence of SEQ ID NO:19 or 20.

236. The method of any one of claims 233-235, wherein the anti-Nectin-4 antibody comprises a heavy chain and light chain, wherein the heavy chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the heavy chain amino acid sequence of SEQ ID NO:21; and the light chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the light chain amino acid sequence of SEQ ID NO:22 or 23.

237. The method of claim 232 or claim 233, wherein the anti-Nectin-4 antibody comprises a heavy chain comprising or consisting of the amino acid sequence of SEQ ID NO:21 and a light chain comprising or consisting of the amino acid sequence of SEQ ID NO:22 or 23.

238. The method of any one of claims 220-225, wherein the antibody is an anti-ASGR1 antibody.

239. The method of claim 238, wherein the anti-ASGR1 antibody comprises heavy chain (HC)-CDR1 of SEQ ID NO: 24 or 25, HC-CDR2 of SEQ ID NO:26, 27, or 28, HC-CDR3

of SEQ ID NO:29 or 30, light chain (LC)-CDR1 of SEQ ID NO:31 or 32, LC-CDR2 of SEQ ID NO:33, 34, 35 or 36, and LC-CDR3 of SEQ ID NO:37 or 38.

240. The method of claim 239, wherein the anti-ASGR1 antibody comprises (a) heavy chain (HC)-CDR1 of SEQ ID NO: 24, HC-CDR2 of SEQ ID NO:26, HC-CDR3 of SEQ ID NO:29, light chain (LC)-CDR1 of SEQ ID NO:31, LC-CDR2 of SEQ ID NO:33 or 34, and LC-CDR3 of SEQ ID NO:37; or (b) heavy chain (HC)-CDR1 of SEQ ID NO: 25, HC-CDR2 of SEQ ID NO:27 or 28, HC-CDR3 of SEQ ID NO:30, light chain (LC)-CDR1 of SEQ ID NO:32, LC-CDR2 of SEQ ID NO:35 or 36, and LC-CDR3 of SEQ ID NO:38.

241. The method of claim 239 or claim 240, wherein the anti-ASGR1 antibody comprises a heavy chain variable region (V_H) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_H amino acid sequence of SEQ ID NO:39 and a light chain variable region (V_L) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_L amino acid sequence of SEQ ID NO:42 or 43.

242. The method of claim 239 or claim 240, wherein the anti-ASGR1 antibody comprises a heavy chain variable region (V_H) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_H amino acid sequence of SEQ ID NO:40 or 41 and a light chain variable region (V_L) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_L amino acid sequence of SEQ ID NO:44 or 45.

243. The method of any one of claims 238-240, wherein the anti-ASGR1 antibody comprises a V_H comprising or consisting of the amino acid sequence of SEQ ID NO:39 and a V_L comprising or consisting of the amino acid sequence of SEQ ID NO:42 or 43.

244. The method of any one of claims 238-240, wherein the anti-ASGR1 antibody comprises a V_H comprising or consisting of the amino acid sequence of SEQ ID NO:40 or 41 and a V_L comprising or consisting of the amino acid sequence of SEQ ID NO:44 or 45.

245. The method of any one of claims 239-241 and 243, wherein the anti-ASGR1 antibody comprises a heavy chain and light chain, wherein the heavy chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the heavy chain amino acid sequence of SEQ ID NO:46; and the light chain

comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the light chain amino acid sequence of SEQ ID NO:49 or 50.

246. The method of any one of claims, 238-240, wherein the anti-ASGR1 antibody comprises a heavy chain comprising or consisting of the amino acid sequence of SEQ ID NO:46 and a light chain comprising or consisting of the amino acid sequence of SEQ ID NO:49 or 50.

247. The method of any one of claims 239-240, 242, and 244, wherein the anti-ASGR1 antibody comprises a heavy chain and light chain, wherein the heavy chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the heavy chain amino acid sequence of SEQ ID NO:47 or 48; and the light chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the light chain amino acid sequence of SEQ ID NO:51 or 52.

248. The method of any one of claims 240-242, wherein the anti-ASGR1 antibody comprises a heavy chain comprising or consisting of the amino acid sequence of SEQ ID NO:47 or 48 and a light chain comprising or consisting of the amino acid sequence of SEQ ID NO:51 or 52.

249. The method of any one of claims 220-225, wherein the antibody is an anti-mesothelin antibody.

250. The method of claim 249, wherein the anti-mesothelin antibody comprises heavy chain (HC)-CDR1, HC-CDR2, HC-CDR3, light chain (LC)-CDR1, LC-CDR2, and LC-CDR3 of SEQ ID NOS:53-58, respectively.

251. The method of claim 250, wherein the anti-mesothelin antibody comprises a heavy chain variable region (V_H) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_H amino acid sequence of SEQ ID NO:59 and a light chain variable region (V_L) having an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the V_L amino acid sequence of SEQ ID NO:60.

252. The method of claim 249 or claim 250, wherein the anti-mesothelin antibody comprises a V_H comprising or consisting of the amino acid sequence of SEQ ID NO:59 and a V_L comprising or consisting of the amino acid sequence of SEQ ID NO:60.

253. The method of any one of claims 250-252, wherein the anti-mesothelin antibody comprises a heavy chain and light chain, wherein the heavy chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the heavy chain amino acid sequence of SEQ ID NO:70; and the light chain comprises an amino acid sequence that has at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or 100% identity to the light chain amino acid sequence of SEQ ID NO:71.

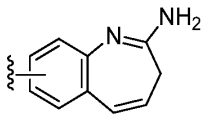
254. The method of claim 249 or claim 250, wherein the anti-mesothelin antibody comprises a heavy chain comprising or consisting of the amino acid sequence of SEQ ID NO:70 and a light chain comprising or consisting of the amino acid sequence of SEQ ID NO:71.

255. The method of claim 226, wherein the antibody is pertuzumab, trastuzumab, sacituzumab, or ladiratuzumab or comprises an antigen binding fragment of pertuzumab, trastuzumab, sacituzumab, or ladiratuzumab.

256. The method of any one of claims 196-255, wherein the compound is a myeloid agonist.

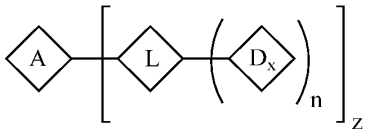
257. The method of any one of claims 196-256, wherein the compound is a TLR8 agonist.

258. The method of any one of claims 196-257, wherein the compound comprises the structure:



wherein the structure is optionally substituted at any position other than the -NH_2.

259. The method of any one of claims 196-258, wherein the conjugate is represented by Formula (I):



(I);

wherein:

A is the polypeptide,

L is a linker;

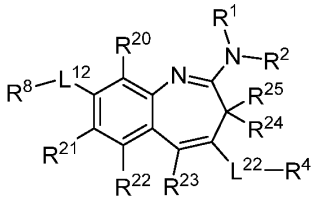
D_x is the compound;

n is selected from 1 to 20; and

z is selected from 1 to 20.

260. The method of claim 259, wherein n is 1 and z is from 1 to 8.

261. The method of any one of claims 196-258, wherein the conjugate comprises the compound linked to the polypeptide through a linker, wherein the compound and the linker together are a compound of Formula (IVB), or the method of claim 259 or claim 260, wherein L and Dx together are a compound of Formula (IVB):



(IVB)

wherein:

L^{12} is selected from -X^3-, -X^3-C_{1-6} alkylene-X^3-, -X^3-C_{2-6} alkenylene-X^3-, and -X^3-C_{2-6} alkynylene-X^3-, each of which is optionally substituted on alkylene, alkenylene, or alkynylene with one or more substituents independently selected from R^{12};

L^{22} is independently selected from -X^4-, -X^4-C_{1-6} alkylene-X^4-, -X^4-C_{2-6} alkenylene-X^4-, and -X^4-C_{2-6} alkynylene-X^4-, each of which is optionally substituted on alkylene, alkenylene, or alkynylene with one or more substituents independently selected from R^{10};

X^3 and X^4 are independently selected at each occurrence from a bond, -O-, -S-, -N(R^{10})-, -C(O)-, -C(O)O-, -OC(O)-, -OC(O)O-, -C(O)N(R^{10})-, -C(O)N(R^{10})C(O)-, -C(O)N(R^{10})C(O)N(R^{10})-, -N(R^{10})C(O)-, -N(R^{10})C(O)N(R^{10})-, -N(R^{10})C(O)O-, -OC(O)N(R^{10})-, -C(NR^{10})-, -N(R^{10})C(NR^{10})-, -C(NR^{10})N(R^{10})-, -N(R^{10})C(NR^{10})N(R^{10})-, -$S(O)_2$-, -OS(O)-, -S(O)O-, -S(O)-, -$OS(O)_2$-, -$S(O)_2$O-, -N(R^{10})$S(O)_2$-, -$S(O)_2$N(R^{10})-, -N(R^{10})S(O)-, -S(O)N(R^{10})-, -N(R^{10})$S(O)_2$N(R^{10})-, and -N(R^{10})S(O)N(R^{10})-;

R^1 and R^2 are each hydrogen;

R^4 and R^8 are independently selected from: -OR^{10}, -N(R^{10})$_2$, -C(O)N(R^{10})$_2$, -C(O)R^{10}, -C(O)OR^{10}, -S(O)R^{10}, and -$S(O)_2R^{10}$; C_{1-10} alkyl, C_{2-10} alkenyl, C_{2-10} alkynyl, each of which is optionally bound to L^3 and each of which is optionally substituted with one or more substituents independently selected from halogen, -OR^{10}, -SR^{10}, -C(O)N(R^{10})$_2$, -N(R^{10})C(O)R^{10}, -N(R^{10})C(O)N(R^{10})$_2$, -N(R^{10})$_2$, -C(O)R^{10}, -C(O)OR^{10}, -OC(O)R^{10}, -NO_2, =O, =S, =N(R^{10}), -CN, C_{3-12} carbocycle, and 3- to 12-membered heterocycle; and C_{3-12} carbocycle and 3- to 12-membered heterocycle, wherein each C_{3-12} carbocycle and 3- to 12-membered heterocycle in R^4 and R^8 is optionally bound to L^3 and each C_{3-12} carbocycle and

3- to 12-membered heterocycle in R^4 and R^8 is optionally substituted with one or more substituents independently selected from halogen, $-OR^{10}$, $-SR^{10}$, $-C(O)N(R^{10})_2$, $-N(R^{10})C(O)R^{10}$, $-N(R^{10})C(O)N(R^{10})_2$, $-N(R^{10})_2$, $-C(O)R^{10}$, $-C(O)OR^{10}$, $-OC(O)R^{10}$, $-NO_2$, =O, =S, $=N(R^{10})$, -CN, C_{1-6} alkyl, C_{2-6} alkenyl, and C_{2-6} alkynyl;

R^{10} is independently selected at each occurrence from L^3, hydrogen, $-NH_2$, $-C(O)OCH_2C_6H_5$; and C_{1-10} alkyl, C_{2-10} alkenyl, C_{2-10} alkynyl, C_{3-12} carbocycle, and 3- to 12-membered heterocycle, each of which is optionally substituted with one or more substituents independently selected from halogen, -CN, $-NO_2$, $-NH_2$, =O, =S, $-C(O)OCH_2C_6H_5$, $-NHC(O)OCH_2C_6H_5$, C_{1-10} alkyl, C_{2-10} alkenyl, C_{2-10} alkynyl, C_{3-12} carbocycle, 3- to 12-membered heterocycle, and haloalkyl;

L^3 is a linker moiety, wherein there is at least one occurrence of L^3;

R^{12} is independently selected at each occurrence from halogen, $-OR^{10}$, $-SR^{10}$, $-N(R^{10})_2$, $-C(O)R^{10}$, $-C(O)N(R^{10})_2$, $-N(R^{10})C(O)R^{10}$, $-C(O)OR^{10}$, $-OC(O)R^{10}$, $-S(O)R^{10}$, $-S(O)_2R^{10}$, $-P(O)(OR^{10})_2$, $-OP(O)(OR^{10})_2$, $-NO_2$, =O, =S, $=N(R^{10})$, and -CN; C_{1-10} alkyl, C_{2-10} alkenyl, C_{2-10} alkynyl, each of which is optionally substituted with one or more substituents independently selected from halogen, $-OR^{10}$, $-SR^{10}$, $-N(R^{10})_2$, $-C(O)R^{10}$, $-C(O)N(R^{10})_2$, $-N(R^{10})C(O)R^{10}$, $-C(O)OR^{10}$, $-OC(O)R^{10}$, $-S(O)R^{10}$, $-S(O)_2R^{10}$, $-P(O)(OR^{10})_2$, $-OP(O)(OR^{10})_2$, $-NO_2$, =O, =S, $=N(R^{10})$, -CN, C_{3-10} carbocycle and 3- to 10-membered heterocycle; and C_{3-10} carbocycle and 3- to 10-membered heterocycle, wherein each C_{3-10} carbocycle and 3- to 10-membered heterocycle in R^{12} is optionally substituted with one or more substituents independently selected from halogen, $-OR^{10}$, $-SR^{10}$, $-N(R^{10})_2$, $-C(O)R^{10}$, $-C(O)N(R^{10})_2$, $-N(R^{10})C(O)R^{10}$, $-C(O)OR^{10}$, $-OC(O)R^{10}$, $-S(O)R^{10}$, $-S(O)_2R^{10}$, $-P(O)(OR^{10})_2$, $-OP(O)(OR^{10})_2$, $-NO_2$, =O, =S, $=N(R^{10})$, -CN, C_{1-6} alkyl, C_{2-6} alkenyl, C_{2-6} alkynyl; and

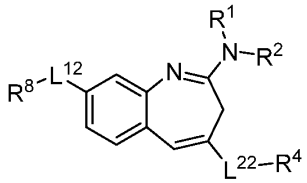
wherein any substitutable carbon on the benzazepine core is optionally substituted by a substituent independently selected from R^{12} or two substituents on a single carbon atom combine to form a 3- to 7- membered carbocycle.

R^{20}, R^{21}, R^{22}, and R^{23} are independently selected from hydrogen, halogen, $-OR^{10}$, $-SR^{10}$, $-N(R^{10})_2$, $-S(O)R^{10}$, $-S(O)_2R^{10}$, $-C(O)R^{10}$, $-C(O)OR^{10}$, $-OC(O)R^{10}$, $-NO_2$, =O, =S, $=N(R^{10})$, -CN, C_{1-10} alkyl, C_{2-10} alkenyl, and C_{2-10} alkynyl; and

R^{24} and R^{25} are independently selected from hydrogen, halogen, $-OR^{10}$, $-SR^{10}$, $-N(R^{10})_2$, $-S(O)R^{10}$, $-S(O)_2R^{10}$, $-C(O)R^{10}$, $-C(O)OR^{10}$, $-OC(O)R^{10}$, $-NO_2$, =O, =S, $=N(R^{10})$, -CN, C_{1-10}

alkyl, C_{2-10} alkenyl, and C_{2-10} alkynyl; or R^{24} and R^{25} taken together form an optionally substituted saturated C_{3-7} carbocycle.

262. The method of any one of claims 196-258, wherein the conjugate comprises the compound linked to the polypeptide through a linker, wherein the compound and the linker together are a compound of Formula (IVC), or the method of any one of claims 259-261, wherein the compound and the linker together or L and Dx together are a compound of Formula (IVC):



(IVC)

wherein:

R^1 and R^2 are each hydrogen;

L^{22} is -C(O)-;

R^4 is $-N(R^{10})_2$;

R^{10} is independently selected at each occurrence from hydrogen, $-NH_2$, $-C(O)OCH_2C_6H_5$; and C_{1-10} alkyl, C_{2-10} alkenyl, C_{2-10} alkynyl, C_{3-12} carbocycle, and 3- to 12-membered heterocycle, each of which is optionally substituted with one or more substituents independently selected from halogen, -CN, $-NO_2$, $-NH_2$, =O, =S, $-C(O)OCH_2C_6H_5$, $-NHC(O)OCH_2C_6H_5$, C_{1-10} alkyl, C_{2-10} alkenyl, C_{2-10} alkynyl, C_{3-12} carbocycle, 3- to 12-membered heterocycle, and haloalkyl;

L^{12} is $-C(O)N(R^{10})$-*, wherein * represents where L^{12} is bound to R^8;

R^8 is an optionally substituted fused 5-5, fused 5-6, or fused 6-6 bicyclic heterocycle bound to linker moiety L^3 ,

and wherein optional substituents are independently selected at each occurrence from:

halogen, $-OR^{10}$, $-SR^{10}$, $-C(O)N(R^{10})_2$, $-N(R^{10})C(O)R^{10}$, $-N(R^{10})C(O)N(R^{10})_2$, $-N(R^{10})_2$, $-C(O)R^{10}$, $-C(O)OR^{10}$, $-OC(O)R^{10}$, $-NO_2$, =O, =S, $=N(R^{10})$, and -CN;

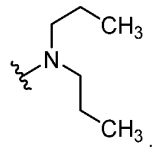
C_{1-10} alkyl, C_{2-10} alkenyl, C_{2-10} alkynyl, each of which is optionally substituted with one or more substituents independently selected from halogen, $-OR^{10}$, $-SR^{10}$, $-C(O)N(R^{10})_2$, $-N(R^{10})C(O)R^{10}$, $-N(R^{10})C(O)N(R^{10})_2$, $-N(R^{10})_2$, $-C(O)R^{10}$, $-C(O)OR^{10}$, $-OC(O)R^{10}$, $-NO_2$, =O, =S, $=N(R^{10})$, -CN, C_{3-12} carbocycle, and 3- to 12-membered heterocycle; and

C_{3-12} carbocycle and 3- to 12-membered heterocycle, each of which is optionally substituted with one or more substituents independently selected from halogen, $-OR^{10}$, $-SR^{10}$, $-C(O)N(R^{10})_2$, $-N(R^{10})C(O)R^{10}$, $-N(R^{10})C(O)N(R^{10})_2$, $-N(R^{10})_2$, $-C(O)R^{10}$, $-C(O)OR^{10}$, $-OC(O)R^{10}$, $-NO_2$, =O, =S, $=N(R^{10})$, -CN, C_{1-6} alkyl, C_{2-6} alkenyl, and C_{2-6} alkynyl.

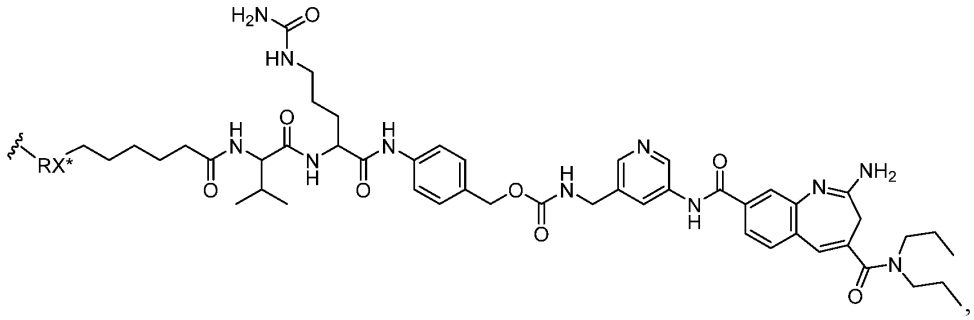
263. The method of claim 261 or claim 262, wherein:

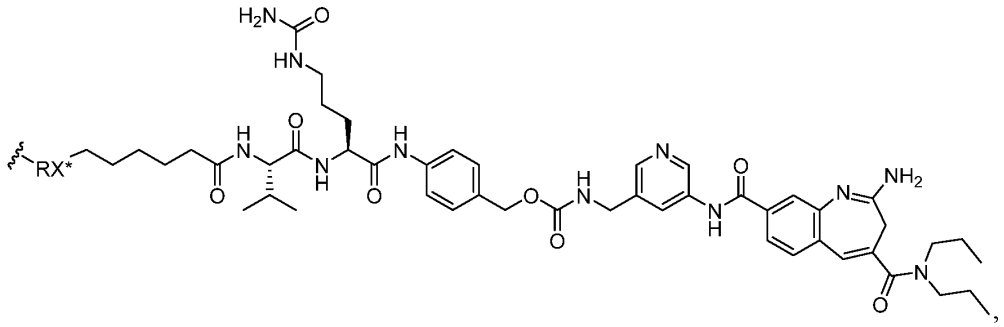
R^4 is $-N(C_{1-4}\text{ alkyl})_2$ and L^{12} is -C(O)N(H)-*.

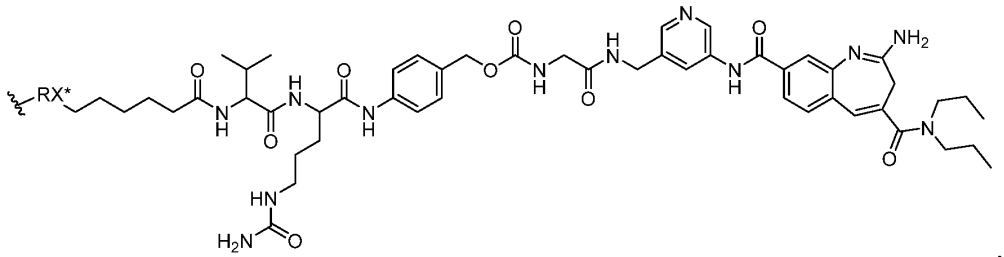
264. The method of claim 261 or claim 262, wherein:

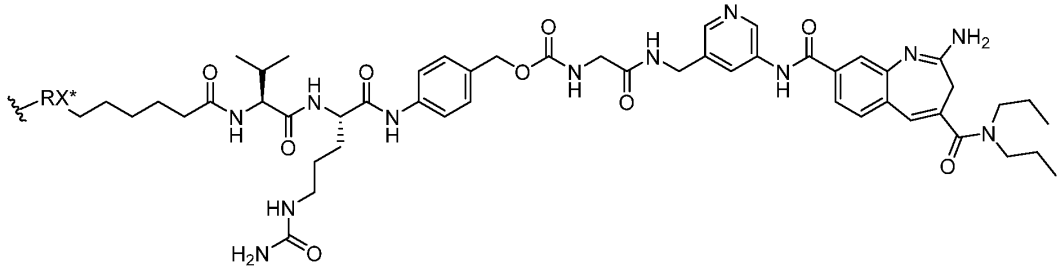
R^4 is .

265. The method of any one of claims 259-264, wherein L and Dx together have a structure selected from:

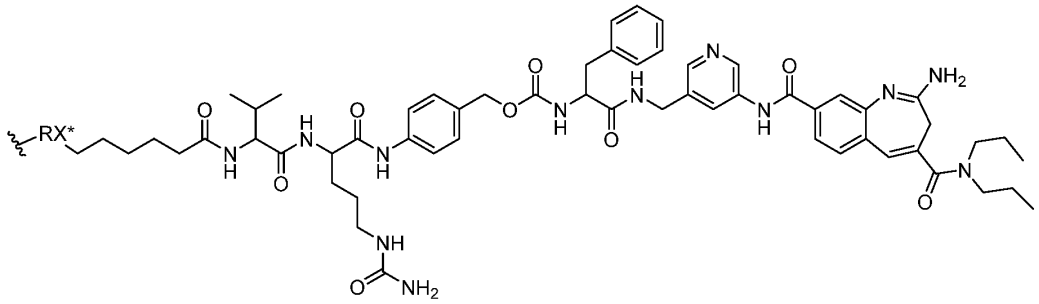
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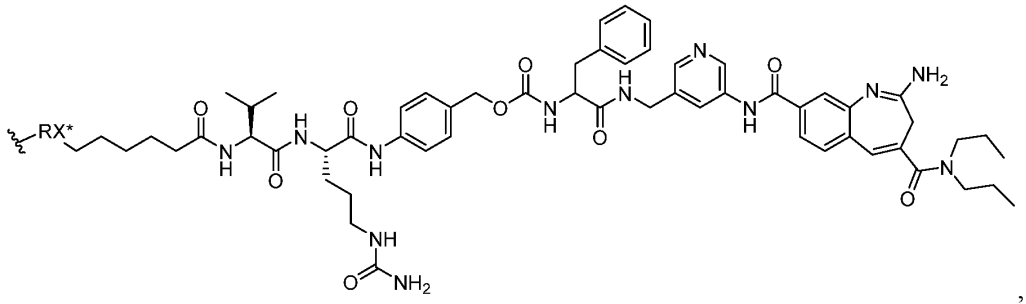
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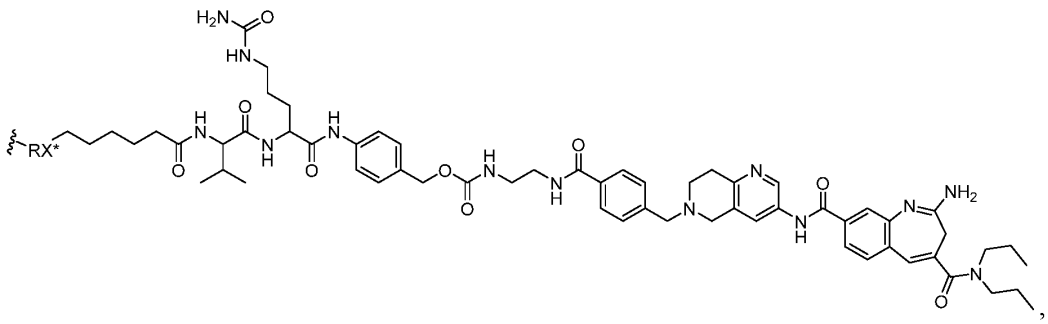
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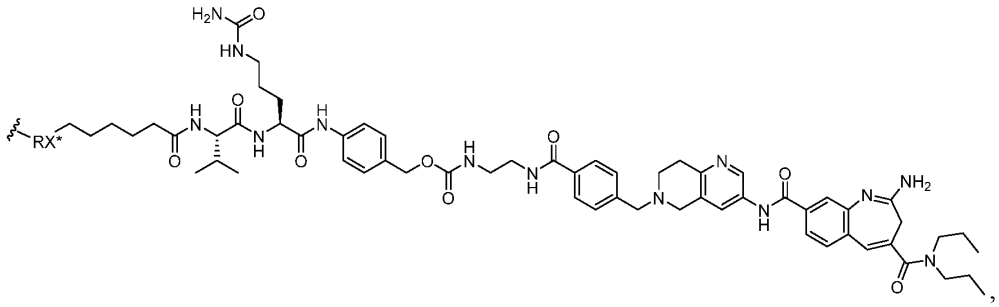
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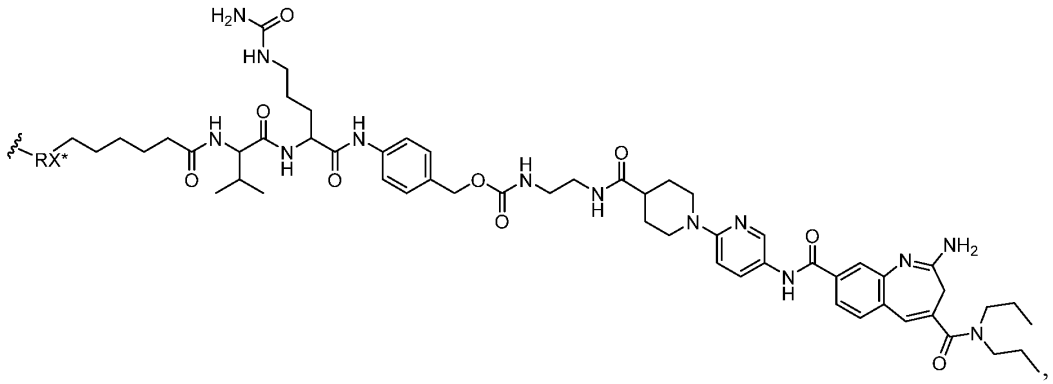
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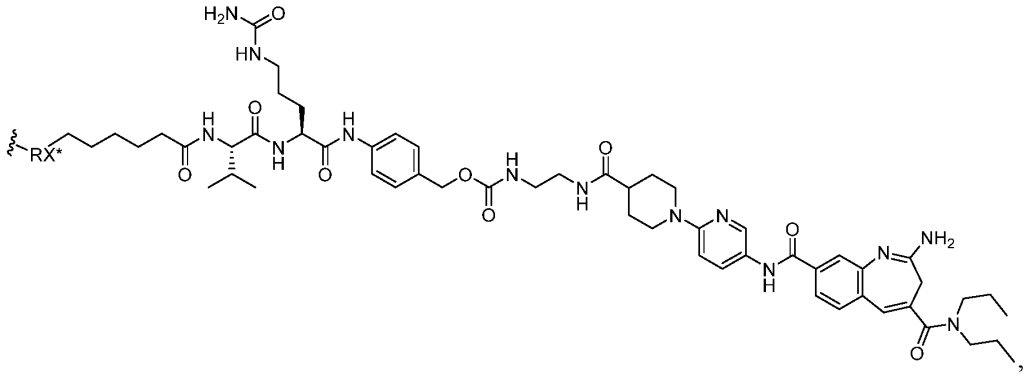


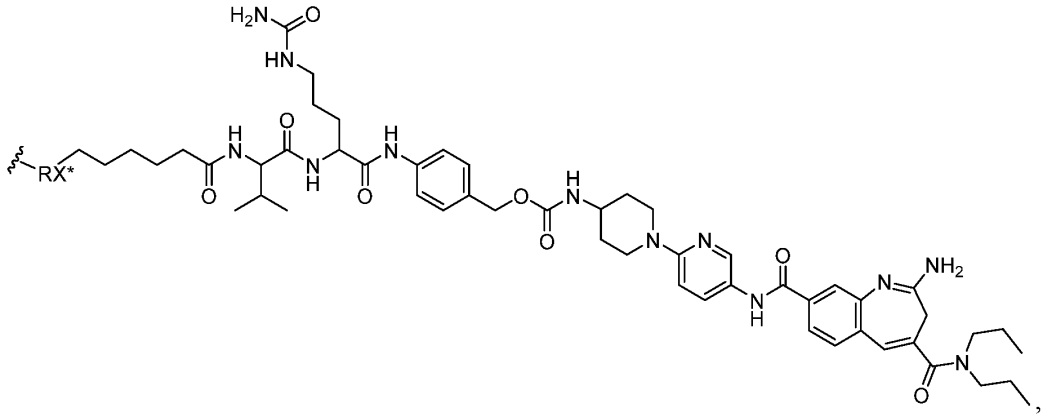
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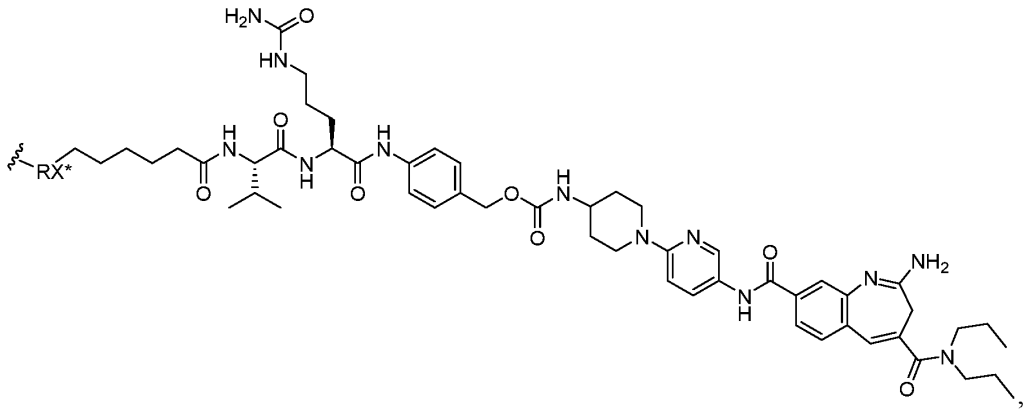


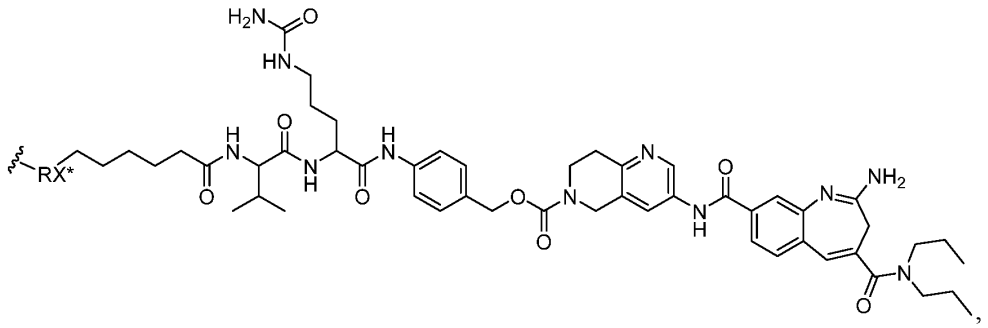
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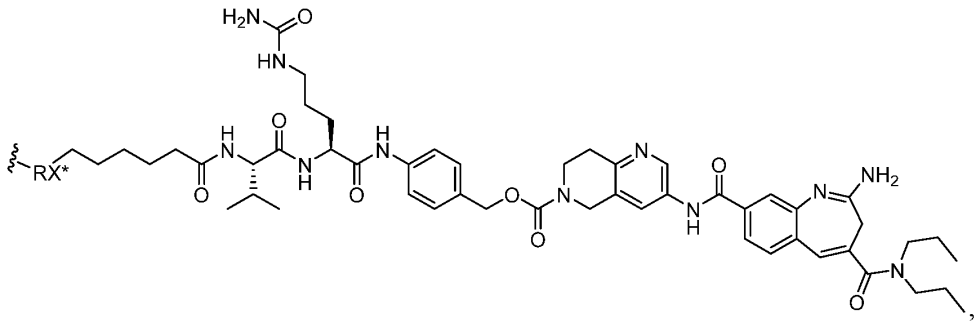


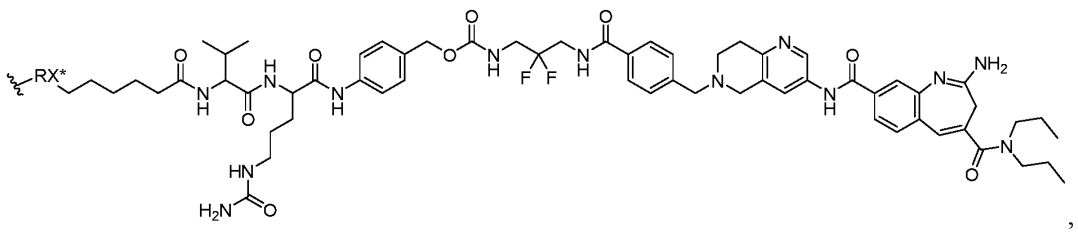




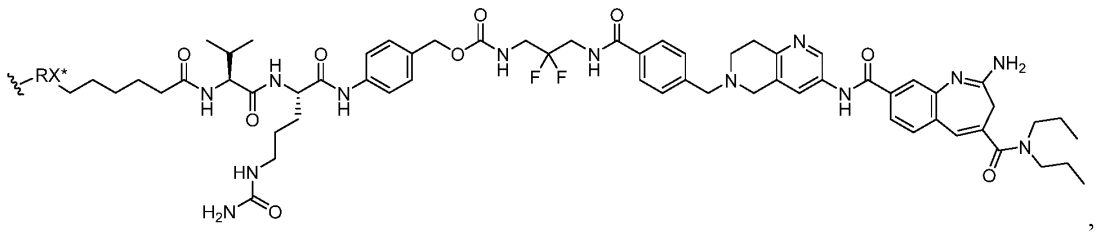








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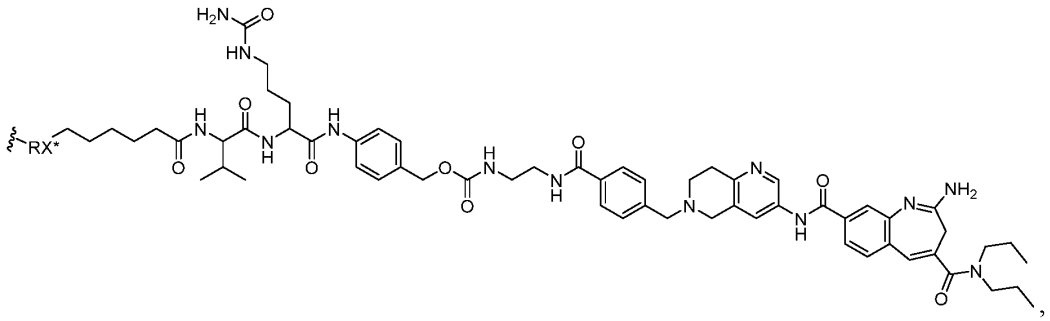


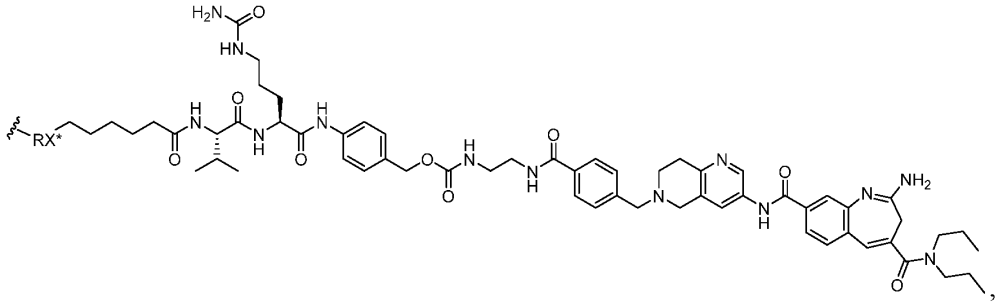
and salts thereof,

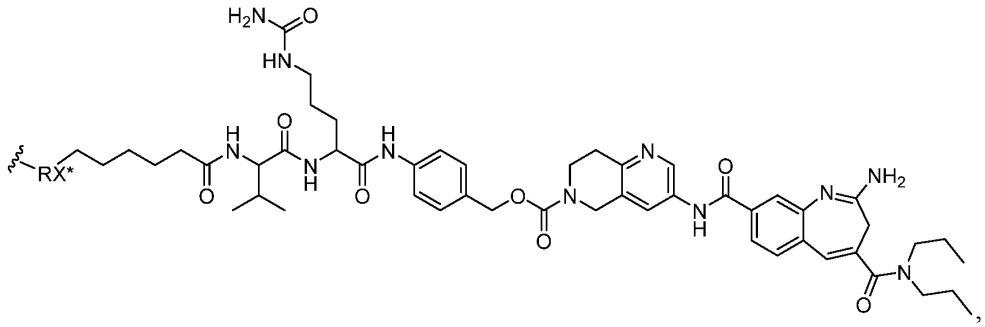
wherein the RX* is a bond, a succinimide moiety, or a hydrolyzed succinimide moiety bound to a residue of a polypeptide,

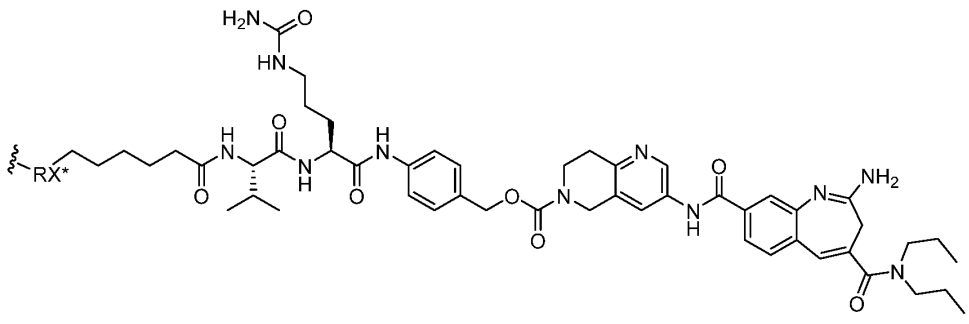
wherein  on RX* represents the point of attachment to the residue of the polypeptide.

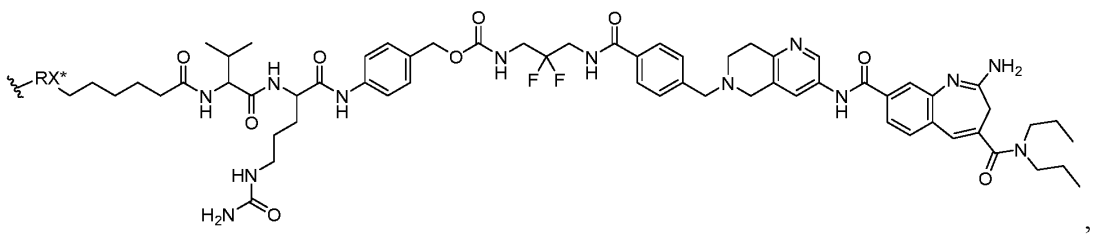
266. The method of claim 265, wherein L and Dx together have a structure selected from:



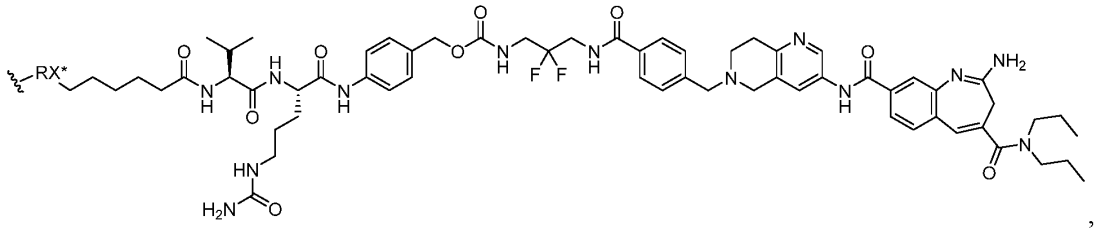








and



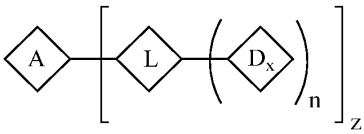
,

and salts thereof,

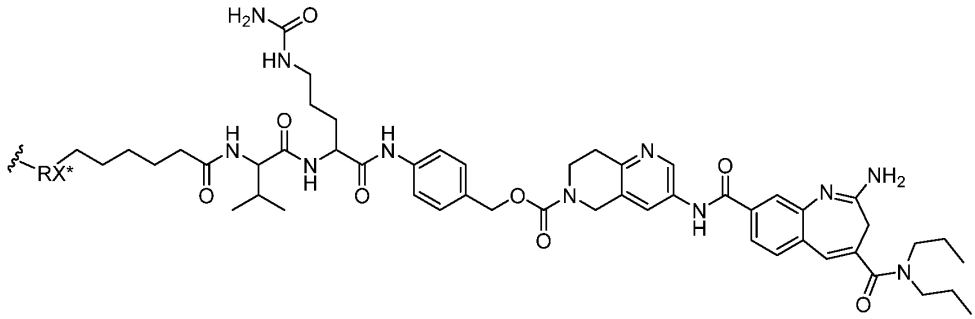
wherein the RX^* is a bond, a succinimide moiety, or a hydrolyzed succinimide moiety bound to a residue of a polypeptide,

wherein  on RX* represents the point of attachment to the residue of the polypeptide.

267. The method of claim 259, wherein the conjugate is formulated to form an aqueous formulation comprising:

a) a conjugate at a total concentration ranging from about 50 mg/mL to about 100 mg/mL and represented by Formula (I):  (I),

wherein A is an antibody; n is 1; z ranges from 2 to 8; and L is a linker and D_x is a benzazepine compound, wherein L and Dx together have a structure of:



, wherein RX^* comprises a hydrolyzed succinamide moiety and is bound to a cysteine residue of the antibody;

b) a buffer comprised of histidine and aspartate at a total concentration ranging from about 15mM to about 25mM;

c) a lyoprotectant comprised of sucrose at a total concentration ranging from about 7% to about 8%; and

d) a surfactant comprised of polysorbate 80 at a total concentration ranging from about 0.01% to about 0.03%.