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(54) Title: IMMUNOCONJUGATES TARGETING ADAM9 AND METHODS OF USE THEREOF

(57) Abstract: The present invention is directed to immunoconjugates comprising an antibody or fragment thereof capable of specifically binding to "Disintegrin and Metalloproteinase Domain-containing Protein 9" ("ADAM9") conjugated to at least one maytansinoid compound. The invention particularly concerns such immunoconjugates that are cross-reactive with human ADAM9 and the ADAM9 of a non-human primate (e.g., a cynomolgus monkey). The invention additionally pertains to all such immunoconjugates that comprise a Light Chain Variable (VL) Domain and/or a Heavy Chain Variable (VH) Domain that has been humanized and/or deimmunized so as to exhibit reduced immunogenicity upon administration of such immunoconjugate to a recipient subject. The invention is also directed to pharmaceutical compositions that contain any of such immunoconjugates, and to methods involving the use of any of such immunoconjugates in the treatment of cancer and other diseases and conditions.

Immunoconjugates Targeting ADAM9 and Methods of Use Thereof

RELATED APPLICATIONS

[0001.1] This application claims priority to U.S. Provisional Application No.: 62/690,052, filed June 26, 2018, and to U.S. Provisional Application No.: 62/691,342, filed June 28, 2018, and to U.S. Provisional Application No.: 62/810,703, filed February 26, 2019. The entirety of these applications are incorporated herein by reference.

SEQUENCE LISTING

[0001.2] The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on May 16, 2019, is named 121162-04820_SL.txt and is 163,070 bytes in size.

FIELD OF THE INVENTION

[0001] The present invention is directed to immunoconjugates comprising an antibody or fragment thereof capable of specifically binding to "Disintegrin and Metalloproteinase Domain-containing Protein 9" ("**ADAM9**") conjugated to at least one pharmacological agent. The invention particularly concerns such immunoconjugates that are cross-reactive with human ADAM9 and the ADAM9 of a non-human primate (*e.g.*, a cynomolgus monkey). The invention additionally pertains to all such immunoconjugates that comprise a Light Chain Variable (VL) Domain and/or a Heavy Chain Variable (VH) Domain that has been humanized and/or deimmunized so as to exhibit reduced immunogenicity upon administration of such immunoconjugates to a recipient subject. The invention is also directed to pharmaceutical compositions that contain any of such immunoconjugates, and to methods involving the use of any of such immunoconjugates in the treatment of cancer and other diseases and conditions.

BACKGROUND OF THE INVENTION

[0002] ADAM is a family of proteins involved in various physiologic and pathologic processes (Amendola, R.S. *et al.* (2015) "*ADAM9 Disintegrin Domain Activates Human Neutrophils Through An Autocrine Circuit Involving Integrins And CXCR2*," J. Leukocyte

Biol. 97(5):951-962; Edwars, D.R. *et al.* (2008) "*The ADAM Metalloproteases*," Molec. Aspects Med. 29:258-289). At least 40 gene members of the family have been identified, and at least 21 of such members are believed to be functional in humans (Li, J. *et al.* (2016) "*Overexpression of ADAM9 Promotes Colon Cancer Cells Invasion*," J. Invest. Surg. 26(3):127-133; Duffy, M.J. *et al.* (2011) "*The ADAMs Family Of Proteases: New Biomarkers And Therapeutic Targets For Cancer*?," Clin. Proteomics 8:9:1-13; see also US Patent Publication No. 2013/0045244).

[0003] ADAM family members have a well-conserved structure with 8 domains, among which are a metalloprotease domain and an integrin-binding (disintegrin) domain (Duffy, M.J. *et al.* (2009) "*The Role Of ADAMs In Disease Pathophysiology*," Clin. Chim. Acta 403:31-36). The ADAM metalloprotease domain acts as a sheddase and has been reported to modulate a series of biologic processes by cleaving transmembrane proteins, which then can act as soluble ligands and regulate cellular signaling (Amendola, R.S. *et al.* (2015) "*ADAM9 Disintegrin Domain Activates Human Neutrophils Through An Autocrine Circuit Involving Integrins And CXCR2*," J. Leukocyte Biol. 97(5):951-962; Ito, N. *et al.* (2004) "*ADAMs, A Disintegrin And Metalloproteinases, Mediate Shedding Of Oxytocinase*," Biochem. Biophys. Res. Commun. 314 (2004) 1008–1013).

[0004] ADAM9 is a member of the ADAM family of molecule. It is synthesized as an inactive form which is proteolytically cleaved to generate an active enzyme. Processing at the upstream site is particularly important for activation of the proenzyme. ADAM9 is expressed in fibroblasts (Zigrino, P. *et al.* (2011) "*The Disintegrin-Like And Cysteine-Rich Domains Of ADAM-9 Mediate Interactions Between Melanoma Cells And Fibroblasts*," J. Biol. Chem. 286:6801-6807), activated vascular smooth muscle cells (Sun, C. *et al.* (2010) "*ADAM15 Regulates Endothelial Permeability And Neutrophil Migration Via Src/ERK1/2 Signalling*," Cardiovasc. Res. 87:348-355), monocytes (Namba, K. *et al.* (2001) "*Involvement Of ADAM9 In Multinucleated Giant Cell Formation Of Blood Monocytes*," Cell. Immunol. 213:104-113), activated macrophages (Oksala, N. *et al.* (2009) "*ADAM-9, ADAM-15, And ADAM-17 Are Upregulated In Macrophages In Advanced Human Atherosclerotic Plaques In Aorta And Carotid And Femoral Arteries – Tampere Vascular Study*," Ann. Med. 41:279-290).

[0005] ADAM9's metalloprotease activity participates in the degradation of matrix components, to thereby allow migration of tumor cells (Amendola, R.S. *et al.* (2015) "*ADAM9 Disintegrin Domain Activates Human Neutrophils Through An Autocrine Circuit Involving Integrins And CXCR2*," J. Leukocyte Biol. 97(5):951-962). Its disintegrin domain, which is highly homologous to many snake-venom disintegrins, allows the interaction between ADAM9 and integrins, and enables ADAM9 to modulate, positively or negatively, cell adhesion events (Zigrino, P. *et al.* (2011) "*The Disintegrin-Like And Cysteine-Rich Domains Of ADAM-9 Mediate Interactions Between Melanoma Cells And Fibroblasts*," J. Biol. Chem. 286:6801-6807; Karadag, A. *et al.* (2006) "*ADAM-9 (MDC-9/Meltringamma), A Member Of The A Disintegrin And Metalloproteinase Family, Regulates Myeloma-Cell-Induced Interleukin-6 Production In Osteoblasts By Direct Interaction With The Alpha(v)Beta5 Integrin*," Blood 107:3271-3278; Cominetti, M.R. *et al.* (2009) "*Inhibition Of Platelets And Tumor Cell Adhesion By The Disintegrin Domain Of Human ADAM9 To Collagen I Under Dynamic Flow Conditions*," Biochimie, 91:1045-1052). The ADAM9 disintegrin domain has been shown to interact with the α6β1, α6β4, αvβ5 and α9β1 integrins.

[0006] The expression of ADAM9 has been found to be relevant to disease, especially cancer. ADAM9 has been found to cleave and release a number of molecules with important roles in tumorigenesis and angiogenesis, such as TEK, KDR, EPHB4, CD40, VCAM1 and CDH5. ADAM9 is expressed by many types of tumor cells, including tumor cells of breast cancers, colon cancers, gastric cancers, gliomas, liver cancers, non-small cell lung cancers, melanomas, myelomas, pancreatic cancers and prostate cancers (Yoshimasu, T. *et al.* (2004) "*Overexpression Of ADAM9 In Non-Small Cell Lung Cancer Correlates With Brain Metastasis*," Cancer Res. 64:4190-4196; Peduto, L. *et al.* (2005) "*Critical Function For ADAM9 In Mouse Prostate Cancer*," Cancer Res. 65:9312-9319; Zigrino, P. *et al.* (2005) "*ADAM-9 Expression And Regulation In Human Skin Melanoma And Melanoma Cell Lines*," Int. J. Cancer 116:853-859; Fritzsche, F.R. *et al.* (2008) "*ADAM9 Is Highly Expressed In Renal Cell Cancer And Is Associated With Tumour Progression*," BMC Cancer 8:179:1-9; Fry, J.L. *et al.* (2010) "*Secreted And Membrane-Bound Isoforms Of Protease ADAM9 Have Opposing Effects On Breast Cancer Cell Migration*," Cancer Res. 70, 8187-8198; Chang, L. *et al.* (2016) "*Combined Rnai Targeting Human Stat3 And ADAM9 As Gene Therapy For Non -Small Cell Lung Cancer*," Oncology Letters 11:1242-1250; Fan, X. *et al.* (2016) "*ADAM9 Expression Is Associate with Glioma Tumor Grade*

and Histological Type, and Acts as a Prognostic Factor in Lower-Grade Gliomas," Int. J. Mol. Sci. 17:1276:1-11).

[0007] Significantly, increased ADAM9 expression has been found to correlate positively with tumor malignancy and metastatic potential (Amendola, R.S. *et al.* (2015) "*ADAM9 Disintegrin Domain Activates Human Neutrophils Through An Autocrine Circuit Involving Integrins And CXCR2*," J. Leukocyte Biol. 97(5):951-962; Fan, X. *et al.* (2016) "*ADAM9 Expression Is Associate with Glioma Tumor Grade and Histological Type, and Acts as a Prognostic Factor in Lower-Grade Gliomas*," Int. J. Mol. Sci. 17:1276:1-11; Li, J. *et al.* (2016) "*Overexpression of ADAM9 Promotes Colon Cancer Cells Invasion*," J. Invest. Surg. 26(3):127-133). Additionally, ADAM9 and its secreted soluble isoform seem to be crucial for cancer cells to disseminate (Amendola, R.S. *et al.* (2015) "*ADAM9 Disintegrin Domain Activates Human Neutrophils Through An Autocrine Circuit Involving Integrins And CXCR2*," J. Leukocyte Biol. 97(5):951-962; Fry, J.L. *et al.* (2010) "*Secreted And Membrane-Bound Isoforms Of Protease ADAM9 Have Opposing Effects On Breast Cancer Cell Migration*," Cancer Res. 70, 8187–8198; Mazzocca, A. (2005) "*A Secreted Form Of ADAM9 Promotes Carcinoma Invasion Through Tumor-Stromal Interactions*," Cancer Res. 65:4728-4738; see also US Patent Nos. 9,150,656; 7,585,634; 7,829,277; 8,101,361; and 8,445,198 and US Patent Publication No. 2009/0023149).

[0008] A number of studies have thus identified ADAM9 as a potential target for anticancer therapy (Peduto, L. (2009) "*ADAM9 As A Potential Target Molecule In Cancer*," Curr. Pharm. Des. 15:2282-2287; Duffy, M.J. *et al.* (2009) "*Role Of ADAMs In Cancer Formation And Progression*," Clin. Cancer Res. 15:1140-1144; Duffy, M.J. *et al.* (2011) "*The ADAMs Family Of Proteases: New Biomarkers And Therapeutic Targets For Cancer?*," Clin. Proteomics 8:9:1-13; Josson, S. *et al.* (2011) "*Inhibition of ADAM9 Expression Induces Epithelial Phenotypic Alterations and Sensitizes Human Prostate Cancer Cells to Radiation and Chemotherapy*," Prostate 71(3):232-240; see also US Patent Publication Nos. 2016/0138113, 2016/0068909, 2016/0024582, 2015/0368352, 2015/0337356, 2015/0337048, 2015/0010575, 2014/0342946, 2012/0077694, 2011/0151536, 2011/0129450, 2010/0291063, 2010/0233079, 2010/0112713, 2009/0285840, 2009/0203051, 2004/0092466, 2003/0091568, and 2002/0068062, and PCT Publication Nos. WO 2016/077505, WO 2014/205293, WO 2014/186364, WO 2014/124326, WO 2014/108480, WO 2013/119960, WO 2013/098797,

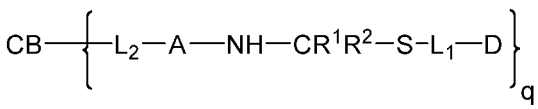
WO 2013/049704, and WO 2011/100362). Additionally, the expression of ADAM9 has also been found to be relevant to pulmonary disease and inflammation (see, *e.g.*, US Patent Publication Nos. 2016/0068909; 2012/0149595; 2009/0233300; 2006/0270618; and 2009/0142301). Antibodies that bind to ADAM9 are commercially available from Abcam, Thermofisher, Sigma-Aldrich, and other companies.

[0009] However, despite all prior advances, a need remains for high affinity ADAM9 targeting immunoconjugates that exhibit minimal binding to normal tissues and are capable binding to human and non-human ADAM9 with similar high affinity. The present invention addresses this need and the need for improved therapeutics for cancer.

SUMMARY OF THE INVENTION

[0010] The present invention is directed to immunoconjugates comprising an antibody or fragment thereof capable of specifically binding to "Disintegrin and Metalloproteinase Domain-containing Protein 9" ("**ADAM9**") conjugated to at least one maytansinoid described herein. The invention particularly concerns such immunoconjugates that are cross-reactive with human ADAM9 and the ADAM9 of a non-human primate (*e.g.*, a cynomolgus monkey). The invention additionally pertains to all such immunoconjugates that comprise a Light Chain Variable (VL) Domain and/or a Heavy Chain Variable (VH) Domain that have been humanized and/or deimmunized so as to exhibit reduced immunogenicity upon administration of such immunoconjugates to a recipient subject. The invention is also directed to pharmaceutical compositions that contain any of such immunoconjugates, and to methods involving the use of any of such immunoconjugates in the treatment of cancer and other diseases and conditions.

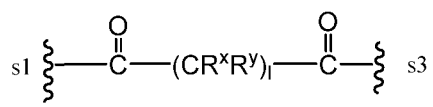
[0011] In detail, the present invention provides an immunoconjugate represented by the following formula:



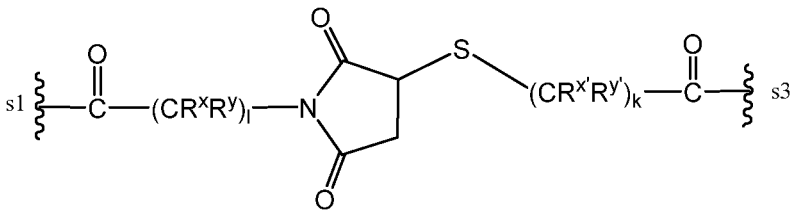
or a pharmaceutically acceptable salt thereof, wherein:

CB is an anti-ADAM9 antibody or ADAM9-binding fragment thereof;

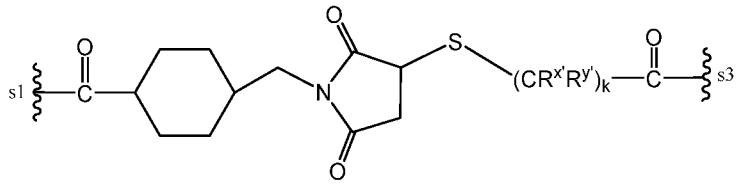
L_2 is represented by one of the following formula:



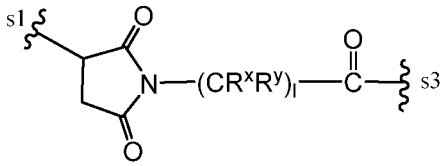
(L2a),



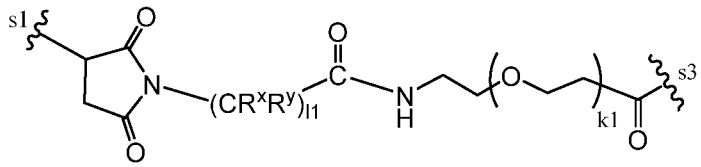
(L2b),



(L2c),



(L2d), or



(L2e);

wherein:

R^x, R^y, $R^{x'}$ and $R^{y'}$, for each occurrence, are independently H, -OH, halogen, -O-(C_{1-4} alkyl), -SO_3H, -$NR_{40}R_{41}R_{42}^+$, or a C_{1-4} alkyl optionally substituted with -OH, halogen, SO_3H or $NR_{40}R_{41}R_{42}^+$, wherein R_{40}, R_{41} and R_{42} are each independently H or a C_{1-4} alkyl;

l and k are each independently an integer from 1 to 10;

l1 is an integer from 2 to 5;

k1 is an integer from 1 to 5; and

s1 indicates the site connected to the cell-binding agent CB and s3 indicates the site connected to the A group;

A is an amino acid residue or a peptide comprising 2 to 20 amino acid residues;

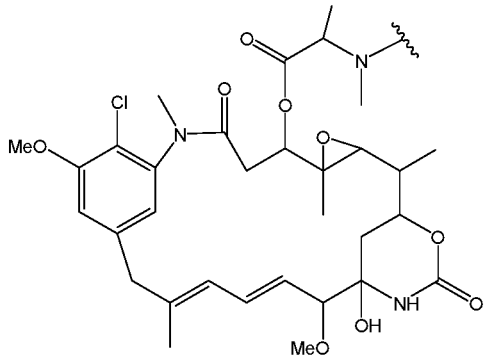
R^1 and R^2 are each independently H or a C_{1-3}alkyl;

L_1 is represented by the following formula:

$$–CR^3R^4\text{-}(CH_2)_{1-8}\text{-}C(=O)\text{-}$$

wherein R^3 and R^4 are each independently H or Me, and the –C(=O)- moiety in L_1 is connected to D;

D is represented by the following formula:



;

q is an integer from 1 to 20.

[0012] In certain embodiments, the anti-ADAM9 antibody or ADAM9-binding fragment thereof comprises a Light Chain Variable (VL) Domain and a Heavy Chain Variable (VH) Domain, wherein the Heavy Chain Variable Domain comprises a CDR_H1 Domain, a CDR_H2 Domain and a CDR_H3 Domain, and the Light Chain Variable Domain comprises a CDR_L1 Domain, a CDR_L2 Domain, and a CDR_L3 Domain, wherein:

(A) said CDR_H1 Domain, CDR_H2 Domain and CDR_H3 Domain have the amino acid sequence of the CDR_H1 Domain, CDR_H2 Domain and CDR_H3 Domain of a Heavy Chain Variable (VH) Domain of an optimized variant of MAB-A; and said CDR_L1 Domain, CDR_L2 Domain, and CDR_L3 Domain have the amino acid sequence of the CDR_L1 Domain, CDR_L2 Domain, and CDR_L3 Domain of the Light Chain Variable (VL) Domain of MAB-A; or

(B) said CDR_H1 Domain, CDR_H2 Domain and CDR_H3 Domain have the amino acid sequence of the CDR_H1 Domain, CDR_H2 Domain and CDR_H3 Domain of the Heavy Chain Variable (VH) Domain of MAB-A; and said CDR_L1 Domain, CDR_L2 Domain, and CDR_L3 Domain have the amino acid sequence of the CDR_L1 Domain, CDR_L2 Domain, and CDR_L3 Domain of a Light Chain Variable (VL) Domain of an optimized variant of MAB-A; or

(C) said CDR_H1 Domain, CDR_H2 Domain and CDR_H3 Domain have the amino acid sequence of the CDR_H1 Domain, CDR_H2 Domain and CDR_H3 Domain of a Heavy Chain Variable (VH) Domain of an optimized variant of MAB-A; and said CDR_L1 Domain, CDR_L2 Domain, and CDR_L3 Domain have the amino acid sequence of the CDR_L1 Domain, CDR_L2 Domain, and CDR_L3 Domain of a Light Chain Variable (VL) Domain of an optimized variant of MAB-A

[0013] In certain embodiments, the anti-ADAM9 antibody or ADAM9-binding fragment thereof comprises:

(A) (1) the CDR_H1 Domain, CDR_H2 Domain and CDR_H3 Domain of the Heavy Chain Variable (VH) Domain of MAB-A; and

(2) the FR1, FR2, FR3 and FR4 of a VH Domain of a humanized variant of MAB-A; or

(B) (1) the CDR_L1 Domain, CDR_L2 Domain and CDR_L3 Domain of the Light Chain Variable (VL) Domain MAB-A; and

(2) the FR1, FR2, FR3 and FR4 of a VL Domain of a humanized variant of MAB-A; or

(C) (1) the CDR_H1 Domain, CDR_H2 Domain and CDR_H3 Domain of a Heavy Chain Variable (VH) Domain of an optimized variant of MAB-A; and

(2) the FR1, FR2, FR3 and FR4 of the VH Domain of a humanized variant of MAB-A; or

(D) (1) the CDR_L1 Domain, CDR_L2 Domain and CDR_L3 Domain of a Light Chain Variable (VL) Domain of an optimized variant of MAB-A; and

(2) the FR1, FR2, FR3 and FR4 of the VL Domain of a humanized variant of MAB-A; or

(E) (1) the Heavy Chain Variable (VH) Domain of a humanized/optimized variant of MAB-A; and

(2) the VL Light Chain Variable (VL) Domain of a humanized/optimized variant of MAB-A.

[0014] In certain embodiments, the CDR_H1 Domain, CDR_H2 Domain and CDR_H3 Domain of the Heavy Chain Variable (VH) Domain of the optimized variant of MAB-A respectively have the amino acid sequences of:

(1) **SEQ ID NO:47** ($SYWX_1H$)

wherein: $\mathbf{X_1}$ is M or I;

(2) **SEQ ID NO:48** ($EIIPIX_2GHTNYNEX_3FX_4X_5$)

wherein: $\mathbf{X_2}$, $\mathbf{X_3}$, $\mathbf{X_4}$, and $\mathbf{X_5}$ are independently selected, and

wherein: $\mathbf{X_2}$ is N or F; $\mathbf{X_3}$ is K or R;

$\mathbf{X_4}$ is K or Q; and

$\mathbf{X_5}$ is S or G; and

(3) **SEQ ID NO:49** ($GGYYYYX_6X_7X_8X_9X_{10}X_{11}DY$)

wherein: X_6, is P, F, Y, W, I, L, V, T, G or D, and X_7, X_8, X_9, X_{10}, and X_{11} are selected such that:

(A) when X_6 is P:

X_7 is K or R; X_8 is F or M; X_9 is G;

X_{10} is W or F; and X_{11} is M, L or K;

(B) when X_6 is F, Y or W:

X_7 is N or H; X_8 is S or K; X_9 is G or A;

X_{10} is T or V; and X_{11} is M, L or K;

(C) when X_6 is I, L or V:

X_7 is G; X_8 is K; X_9 is G or A;

X_{10} is V; and X_{11} is M, L or K;

(D) when X_6 is T:

X_7 is G; X_8 is K, M or N; X_9 is G;

X_{10} is V or T; and X_{11} is L or M;

(E) when X_6 is G:

X_7 is G; X_8 is S; X_9 is G;

X_{10} is V; and X_{11} is L; and

(F) when X_6 is D:

X_7 is S; X_8 is N; X_9 is A;

X_{10} is V; and X_{11} is L.

[0015] In certain embodiments, the Heavy Chain Variable (VH) Domain of the optimized variant of MAB-A comprises the amino acid sequence of **SEQ ID NO:15**:

EVQLVESGGG LVKPGGSLRL SCAASGFTFS **SYWX$_1$H**WVRQA
PGKGLEWVG**E** **IIPIX$_2$GHTNY** **NEX$_3$FX$_4$X$_5$**RFTI SLDNSKNTLY
LQMGSLRAED TAVYYCAR**GG** **YYYYX$_6$X$_7$X$_8$X$_9$X$_{10}$X$_{11}$**
DYWGQGTTVT VSS

wherein: X_1, X_2, X_3, X_4, X_5, and X_6 are independently selected,

wherein: X_1 is M or I; X_2 is N or F;

X_3 is K or R; X_4 is K or Q;

X_5 is S or G, and X_6 is P, F, Y, W, I, L, V, T, G or D;

wherein: X_7, X_8, X_9, X_{10}, and X_{11} are selected such that:

when X_6 is P; X_7 is K or R; X_8 is F or M; X_9 is G; X_{10} is W or F; and X_{11} is M, L or K;

when $\mathbf{X_6}$ is F, Y or W; $\mathbf{X_7}$ is N or H; $\mathbf{X_8}$ is S or K; $\mathbf{X_9}$ is G or A; $\mathbf{X_{10}}$ is T or V; and $\mathbf{X_{11}}$ is M, L or K;

when $\mathbf{X_6}$ is I, L or V; $\mathbf{X_7}$ is G; $\mathbf{X_8}$ is K; $\mathbf{X_9}$ is G or A; $\mathbf{X_{10}}$ is V; and $\mathbf{X_{11}}$ is M, L or K;

when $\mathbf{X_6}$ is T; $\mathbf{X_7}$ is G; $\mathbf{X_8}$ is K, M or N; $\mathbf{X_9}$ is G; $\mathbf{X_{10}}$ is V or T; and $\mathbf{X_{11}}$ is L or M;

when $\mathbf{X_6}$ is G; $\mathbf{X_7}$ is G; $\mathbf{X_8}$ is S; $\mathbf{X_9}$ is G; $\mathbf{X_{10}}$ is V; and $\mathbf{X_{11}}$ is L;

when $\mathbf{X_6}$ is D; $\mathbf{X_7}$ is S; $\mathbf{X_8}$ is N; $\mathbf{X_9}$ is A; $\mathbf{X_{10}}$ is V; and $\mathbf{X_{11}}$ is L.

[0016] In certain embodiments, the Heavy Chain Variable (VH) Domain of the optimized variant of MAB-A is selected from the group consisting of:

(1) hMAB-A VH(1) (**SEQ ID NO:16**);

(2) hMAB-A VH(2) (**SEQ ID NO:17**);

(3) hMAB-A VH(3) (**SEQ ID NO:18**);

(4) hMAB-A VH(4) (**SEQ ID NO:19**);

(5) hMAB-A VH(2A) (**SEQ ID NO:20**);

(6) hMAB-A VH(2B) (**SEQ ID NO:21**);

(7) hMAB-A VH(2C) (**SEQ ID NO:22**);

(8) hMAB-A VH(2D) (**SEQ ID NO:23**);

(9) hMAB-A VH(2E) (**SEQ ID NO:24**);

(10) hMAB-A VH(2F) (**SEQ ID NO:25**);

(11) hMAB-A VH(2G) (**SEQ ID NO:26**);

(12) hMAB-A VH(2H) (**SEQ ID NO:27**);

(13) hMAB-A VH(2I) (**SEQ ID NO:28**); and

(14) hMAB-A VH(2J) (**SEQ ID NO:29**).

[0017] In certain embodiments, the CDR_L1 Domain, CDR_L2 Domain and CDR_L3 Domain of the Light Chain Variable (VL) Domain of the optimized variant of MAB-A respectively have the amino acid sequences of:

(1) **SEQ ID NO:66** (X_{12}ASQSVDYX_{13}GDSYX_{14}N)

wherein: $\mathbf{X_{12}}$, $\mathbf{X_{13}}$, $\mathbf{X_{14}}$, are independently selected, and

wherein: $\mathbf{X_{12}}$ is K or R; $\mathbf{X_{13}}$ is D or S; and $\mathbf{X_{14}}$ is M or L;

(2) **SEQ ID NO:13** (AASDLES); and

(3) **SEQ ID NO:67** (QQS$X_{15}X_{16}X_{17}$PFT)

wherein: $\mathbf{X_{15}}$, $\mathbf{X_{16}}$, and $\mathbf{X_{17}}$, are independently selected, and

wherein: $\mathbf{X_{15}}$ is H or Y; $\mathbf{X_{16}}$ is E or S; and $\mathbf{X_{17}}$ is D or T.

[0018] In certain embodiments, the Light Chain Variable (VL) Domain comprises the amino acid sequence of **SEQ ID NO:53**:

DIVMTQSPDS LAVSLGERAT ISC**X_{12}ASQSVD**
YX$_{13}$GDSYX$_{14}$NWY QQKPGQPPKL LIY**AASDLES**
GIPARFSGSG SGTDFTLTIS SLEPEDFATY
YC**QQSX$_{15}$X$_{16}$X$_{17}$PF** **T**FGQGTKLEI K

wherein: $\mathbf{X_{12}}$, $\mathbf{X_{13}}$, $\mathbf{X_{14}}$, $\mathbf{X_{15}}$, $\mathbf{X_{16}}$, and $\mathbf{X_{17}}$, are independently selected, and

wherein: $\mathbf{X_{12}}$ is K or R; $\mathbf{X_{13}}$ is D or S;

$\mathbf{X_{14}}$ is M or L; $\mathbf{X_{15}}$ is H or Y;

$\mathbf{X_{16}}$ is E or S; and $\mathbf{X_{17}}$ is D or T.

[0019] In certain embodiments, the Light Chain Variable (VL) Domain of the optimized variant of MAB-A is selected from the group consisting of:

(1) hMAB-A VL(1) (**SEQ ID NO:54**);

(2) hMAB-A VL(2) (**SEQ ID NO:55**);

(3) hMAB-A VL(3) (**SEQ ID NO:56**);

(4) hMAB-A VL(4) (**SEQ ID NO:57**);

(5) hMAB-A VL(2A) (**SEQ ID NO:20**).

[0020] In certain embodiments, the CDR_H1 Domain comprises the amino acid sequence SYWMH (**SEQ ID NO:8**), the CDR_H2 Domain comprises the amino acid sequence EIIPIFGHTNYNEKFKS (**SEQ ID NO:35**), and the CDR_H3 Domain comprises the amino acid sequence GGYYYYPRQGFLDY (**SEQ ID NO:45**)

[0021] In certain embodiments, the CDR_L1 Domain comprises the amino acid sequence KASQSVDYSGDSYMN (**SEQ ID NO:62**), the CDR_L2 Domain comprises the amino acid sequence AASDLES (**SEQ ID NO:13**), and the CDR_L3 Domain comprises the amino acid sequence QQSHEDPFT (**SEQ ID NO:14**).

[0022] In certain embodiments, the immunoconjugate comprises:

(A) the Heavy Chain Variable (VH) Domain of hMAB-A (**2I.2**) (**SEQ ID NO:28**); or

(B) the Light Chain Variable (VL) Domain of hMAB-A **(2I.2)** (**SEQ ID NO:55**); or

(C) the Heavy Chain Variable (VH) Domain of hMAB-A **(2I.2)** (**SEQ ID NO:28**) and the Light Chain Variable (VL) Domain of hMAB-A **(2I.2)** (**SEQ ID NO:55**)

[0023] In certain embodiments, the immunoconjugate comprises an Fc Region. In some embodiments, the Fc Region is a variant Fc Region that comprises: (a) one or more amino acid modification(s) that reduce(s) the affinity of the variant Fc Region for an FcγR; and/or (b) one or more amino acid modification(s) that introduces a cysteine residue. In some embodiments, the one or more amino acid modification(s) that reduce(s) the affinity of the variant Fc Region for an FcγR comprise: (A) L234A; (B) L235A; or (C) L234A and L235A; wherein said numbering is that of the EU index as in Kabat. In some embodiments, the one or more amino acid modification(s) that that introduces a cysteine residue comprises S442C, wherein said numbering is that of the EU index as in Kabat.

[0024] In certain embodiments, the immunoconjugate of the present invention comprises a humanized anti-ADAM9 antibody or ADAM9-binding fragment thereof that specifically binds to human ADAM9 and cyno ADAM9, wherein the humanized anti-ADAM9 antibody or ADAM9-binding fragment thereof is conjugated to the pharmacological agent.

[0025] In some embodiments, the humanized anti-ADAM9 antibody or ADAM9-binding fragment thereof comprises a CDR_H1 domain, a CDR_H2 domain, and a CDR_H3 domain and a CDR_L1 domain, a CDR_L2 domain, and a CDR_L3 domain having the sequences selected from the group consisting of:

(a) SEQ ID NOs: 8, 35, and 10 and SEQ ID NOs: 62, 13, 14, respectively;

(b) SEQ ID NOs: 8, 35, and 10 and SEQ ID NOs: 63, 13, 14, respectively;

(c) SEQ ID NOs: 8, 36, and 10 and SEQ ID NOs: 63, 13, 14, respectively; and

(d) SEQ ID NOs: 34, 36, and 10 and SEQ ID NO:64, 13, 65, respectively.

[0026] In some embodiments, the humanized anti-ADAM9 antibody or ADAM9-binding fragment thereof comprises a heavy chain variable domain (VH) and a light chain variable domain (VL) having sequences that are at least 90%, at least 95%, or at least 99% identical to sequences selected from the group consisting of:

(a) SEQ ID NO:17 and SEQ ID NO:55, respectively;

(b) SEQ ID NO:17 and SEQ ID NO:56, respectively;

(c) SEQ ID NO:18 and SEQ ID NO:56, respectively; and (d) SEQ ID NO:19 and SEQ ID NO:57, respectively.

[0027] In certain embodiments, the humanized anti-ADAM9 antibody or ADAM9-binding fragment thereof comprises a heavy chain variable domain (VH) and a light chain variable domain (VL) having the sequences selected from the group consisting of:

(a) SEQ ID NO:17 and SEQ ID NO:55, respectively;

(b) SEQ ID NO:17 and SEQ ID NO:56, respectively;

(c) SEQ ID NO:18 and SEQ ID NO:56, respectively; and

(d) SEQ ID NO:19 and SEQ ID NO:57, respectively.

[0028] In certain embodiments, the humanized anti-ADAM9 antibody or ADAM9-binding fragment thereof is optimized to have at least a 100-fold enhancement in binding affinity to cyno ADAM9 and retains high affinity binding to human ADAM9 as compared to the chimeric or murine parental antibody.

[0029] In certain embodiments, the anti-ADAM9 antibody or ADAM9-binding fragment thereof comprises a CDR_H1 domain, a CDR_H2 domain, and a CDR_H3 domain and a CDR_L1 domain, a CDR_L2 domain, and a CDR_L3 domain having the sequences selected from the group consisting of:

(a) SEQ ID NOs: 8, 35, and 37 and SEQ ID NOs: 62, 13, 14, respectively;

(b) SEQ ID NOs: 8, 35, and 38 and SEQ ID NOs: 62, 13, 14, respectively;

(c) SEQ ID NOs: 8, 35, and 39 and SEQ ID NOs: 62, 13, 14, respectively;

(d) SEQ ID NOs: 8, 35, and 40 and SEQ ID NOs: 62, 13, 14, respectively;

(e) SEQ ID NOs: 8, 35, and 41 and SEQ ID NOs: 62, 13, 14, respectively;

(f) SEQ ID NOs: 8, 35, and 42 and SEQ ID NOs: 62, 13, 14, respectively;

(g) SEQ ID NOs: 8, 35, and 43 and SEQ ID NOs: 62, 13, 14, respectively;

(h) SEQ ID NOs: 8, 35, and 44 and SEQ ID NOs: 62, 13, 14, respectively;

(i) SEQ ID NOs: 8, 35, and 45 and SEQ ID NOs: 62, 13, 14, respectively; and

(j) SEQ ID NOs: 8, 35, and 46 and SEQ ID NOs: 62, 13, 14, respectively.

[0030] In certain embodiments, the humanized anti-ADAM9 antibody or ADAM9-binding fragment thereof comprises a heavy chain variable domain (VH) and a light chain variable domain (VL) having sequences that are at least 90%, at least 95%, or at least 99% identical to sequences selected from the group consisting of:

(a) SEQ ID NO:20 and SEQ ID NO:55, respectively;

(b) SEQ ID NO:21 and SEQ ID NO:55, respectively;

(c) SEQ ID NO:22 and SEQ ID NO:55, respectively;

(d) SEQ ID NO:23 and SEQ ID NO:55, respectively;

(e) SEQ ID NO:24 and SEQ ID NO:55, respectively;

(f) SEQ ID NO:25 and SEQ ID NO:55, respectively;

(g) SEQ ID NO:26 and SEQ ID NO:55, respectively;

(h) SEQ ID NO:27 and SEQ ID NO:55, respectively;

(i) SEQ ID NO:28 and SEQ ID NO:55, respectively; and

(j) SEQ ID NO:29 and SEQ ID NO:55, respectively.

[0031] In certain embodiments, the humanized anti-ADAM9 antibody or ADAM9-binding fragment thereof comprises a heavy chain variable domain (VH) and a light chain variable domain (VL) having the sequences selected from the group consisting of:

(a) SEQ ID NO:20 and SEQ ID NO:55, respectively;

(b) SEQ ID NO:21 and SEQ ID NO:55, respectively;

(c) SEQ ID NO:22 and SEQ ID NO:55, respectively;

(d) SEQ ID NO:23 and SEQ ID NO:55, respectively;

(e) SEQ ID NO:24 and SEQ ID NO:55, respectively;

(f) SEQ ID NO:25 and SEQ ID NO:55, respectively;

(g) SEQ ID NO:26 and SEQ ID NO:55, respectively;

(h) SEQ ID NO:27 and SEQ ID NO:55, respectively;

(i) SEQ ID NO:28 and SEQ ID NO:55, respectively; and

(j) SEQ ID NO:29 and SEQ ID NO:55, respectively.

[0032] In certain embodiments, the humanized anti-ADAM9 antibody is a full length antibody comprising an Fc region. In some embodiments, the Fc region is a variant Fc region that comprises:

(a) one or more amino acid modification(s) that reduces(s) the affinity of the variant Fc region for an FcγR selected from the group consisting of: L234A, L235A, and L234A and L235A; and/or

(b) an amino acid modification that introduces a cysteine residue at S442, wherein said numbering is that of the EU index as in Kabat; and/or

(c) one or more amino acid substitution(s) that extend(s) the half-life of the variant Fc region for FcRn selected from the group consisting of: M252Y, S254T, and T256E

[0033] In some embodiments, the humanized anti-ADAM9 antibody comprises a heavy chain and a light chain having the sequences selected from the group consisting of:

(a) SEQ ID NO:50 and SEQ ID NO:68, respectively;

(b) SEQ ID NO:51 and SEQ ID NO:68, respectively; and

(c) SEQ ID NO:52 and SEQ ID NO:68, respectively.

[0034] In certain embodiments, the humanized anti-ADAM9 antibody comprises a heavy chain and a light chain having the sequences selected from the group consisting of:

(a) SEQ ID NO:141 and SEQ ID NO:68, respectively;

(b) SEQ ID NO:142 and SEQ ID NO:68, respectively;

(c) SEQ ID NO:143 and SEQ ID NO:68, respectively;

(d) SEQ ID NO:151 and SEQ ID NO:68, respectively;

(e) SEQ ID NO:152 and SEQ ID NO:68, respectively;

(f) SEQ ID NO:153 and SEQ ID NO:68, respectively; and

(g) SEQ ID NO:154 and SEQ ID NO:68, respectively.

[0035] In certain embodiments, X in SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153 or SEQ ID NO:154 is lysine.

[0036] In certain embodiments, X in SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153 or SEQ ID NO:154 is absent.

[0037] In certain embodiments, the humanized anti-ADAM9 antibody comprises a heavy chain and a light chain having the sequences of SEQ ID NO:156 and SEQ ID NO:68, respectively. In certain embodiments, the humanized anti-ADAM9 antibody comprises a heavy chain and a light chain having the sequences of SEQ ID NO:155 and SEQ ID NO:68, respectively.

[0038] In certain embodiments, the humanized anti-ADAM9 antibody comprises a light chain encoded by SEQ ID NO:157 and a heavy chain encoded by (i) SEQ ID NO:159, (ii) SEQ ID NO:160, (iii) SEQ ID NO:161, or (iv) SEQ ID NO:162.

[0039] In certain embodiments, the humanized anti-ADAM9 antibody comprises a light chain encoded by SEQ ID NO:158 and a heavy chain encoded by (i) SEQ ID NO:159, (ii) SEQ ID NO:160, (iii) SEQ ID NO:161, or (iv) SEQ ID NO:162.

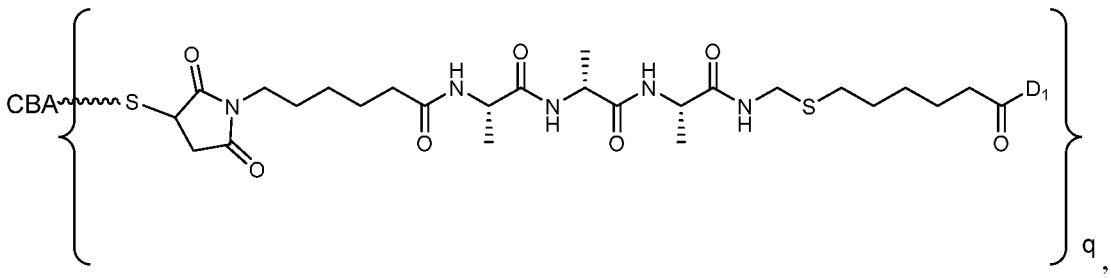
[0040] In certain embodiments, the humanized anti-ADAM9 antibody comprises a light chain encoded by SEQ ID NO:157 and a heavy chain encoded by SEQ ID NO:161.

[0041] In certain embodiments, the humanized anti-ADAM9 antibody comprises a light chain encoded by SEQ ID NO:157 and a heavy chain encoded by SEQ ID NO:162.

[0042] In certain embodiments, the humanized anti-ADAM9 antibody comprises a light chain encoded by SEQ ID NO:158 and a heavy chain encoded by SEQ ID NO:161.

[0043] In certain embodiments, the humanized anti-ADAM9 antibody comprises a light chain encoded by SEQ ID NO:158 and a heavy chain encoded by SEQ ID NO:162.

[0044] In certain embodiments, the immunoconjugate of the present invention is represented by the following formula:

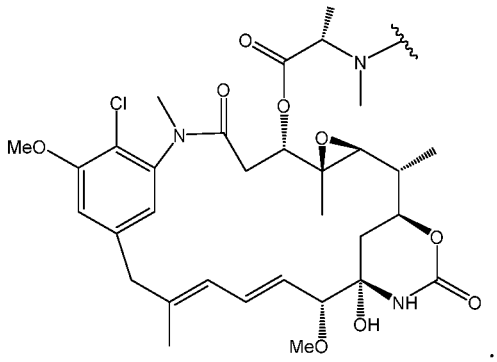


wherein:

CBA is an humanized anti-ADAM9 antibody or ADAM9-binding fragment thereof comprising a CDR_H1 domain, a CDR_H2 domain, and a CDR_H3 domain and a CDR_L1 domain, a CDR_L2 domain, and a CDR_L3 domain having the sequences of SEQ ID NOs: 8, 35, and 45 and SEQ ID NOs: 62, 13, 14, respectively;

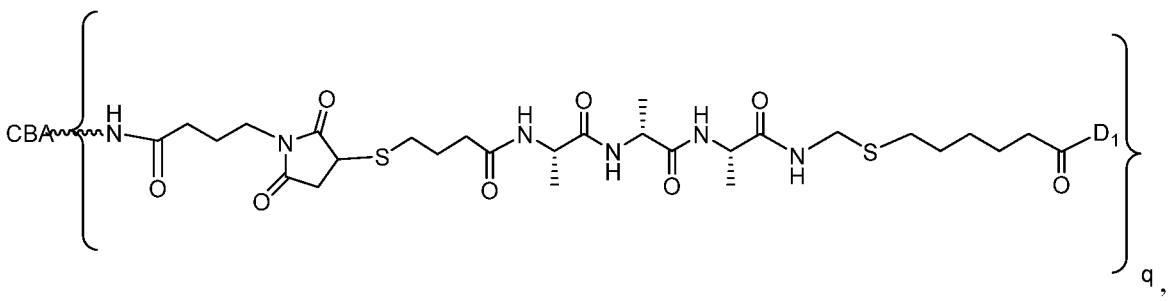
q is 1 or 2;

D_1 is represented by the following formula:



[0045] In certain embodiments, the humanized anti-ADAM9 antibody or ADAM9-binding fragment thereof comprises a heavy chain variable domain (VH) and a light chain variable domain (VL) having sequences of SEQ ID NO:28 and SEQ ID NO:55, respectively. In some embodiments, the humanized anti-ADAM9 antibody comprises a heavy chain and a light chain having the sequences of SEQ ID NO:142 and SEQ ID NO:68, respectively. In some embodiments, the humanized anti-ADAM9 antibody comprises a heavy chain and a light chain having the sequences of SEQ ID NO:152 and SEQ ID NO:68, respectively. In some embodiments, In some embodiments, X in SEQ ID NO:142 or SEQ ID NO:152 is lysine. In some embodiments, In some embodiments, X in SEQ ID NO:142 or SEQ ID NO:152 is absent. In some embodiments, the humanized anti-ADAM9 antibody comprises a heavy chain and a light chain having the sequences of SEQ ID NO:156 and SEQ ID NO:68, respectively. In some embodiments, the DAR value for a composition (*e.g.*, pharmaceutical compositions) comprising the immunoconjugate is in the range of 1.0 to 2.5, 1.5 to 2.5, 1.8 to 2.2, or 1.9 to 2.1. In some embodiments, the DAR is 1.8, 1.9, 2.0 or 2.1.

[0046] In certain embodiments, the immunoconjugate of the present invention is represented by the following formula:



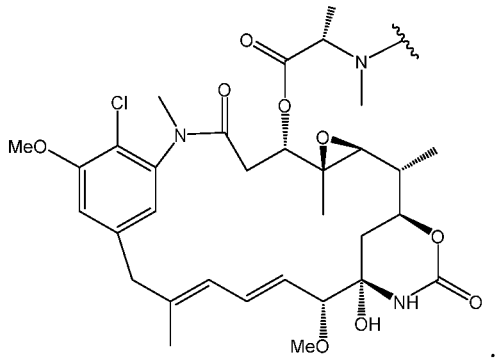
wherein:

CBA is an humanized anti-ADAM9 antibody or ADAM9-binding fragment thereof comprising a CDR_H1 domain, a CDR_H2 domain, and a CDR_H3 domain and a CDR_L1 domain, a CDR_L2 domain, and a CDR_L3 domain having the sequences of SEQ ID NOs: 8,

35, and 45 and SEQ ID NOs: 62, 13, 14, respectively;

q is an integer from 1 or 10;

D_1 is represented by the following formula:



[0047] In certain embodiments, the humanized anti-ADAM9 antibody or ADAM9-binding fragment thereof comprises a heavy chain variable domain (VH) and a light chain variable domain (VL) having sequences of SEQ ID NO:28 and SEQ ID NO:55, respectively. In some embodiments, the humanized anti-ADAM9 antibody comprises a heavy chain and a light chain having the sequences of SEQ ID NO:52 and SEQ ID NO:68, respectively. In some embodiments, the humanized anti-ADAM9 antibody comprises a heavy chain and a light chain having the sequences of SEQ ID NO:151 and SEQ ID NO:68, respectively. In some embodiments, X in SEQ ID NO:52 and SEQ ID NO:151 is lysine. In some embodiments, X in SEQ ID NO:52 and SEQ ID NO:151 is absent. In some embodiments, the humanized anti-ADAM9 antibody comprises a heavy chain and a light chain having the sequences of SEQ ID NO:155 and SEQ ID NO:68, respectively. In some embodiments, the DAR value for a composition (*e.g.*, pharmaceutical compositions) comprising the immunoconjugate is in the range of 1.0 to 5.0, 1.0 to 4.0, 1.5 to 4.0, 2.0 to 4.0, 2.5 to 4.0, 2.9 to 3.3, 3.3 to 3.8, 1.5 to 2.5, or 1.8 to 2.2. In some embodiments, the DAR is less than 4.0, less than 3.8, less than 3.6, less than 3.5, less than 3.0 or less than 2.5. In some embodiments, the DAR is in the range of 3.0 to 3.2. In some embodiments, the DAR is in the range of 3.5 to 3.7. In some embodiments, the DAR is 3.1, 3.2, 3.3, 3.4, 3.5, 3.6 or 3.7. In some embodiments, the DAR is in the range of 1.9 to 2.1. In some embodiments, the DAR is 1.9, 2.0 or 2.1.

[0048] Another aspect of the present invention provides a pharmaceutical composition comprising an effective amount of the immunoconjugate of the present invention described herein and a pharmaceutically acceptable carrier, excipient or diluent.

[0049] In another aspect, the present invention provides a method for treating a disease or condition associated with, or characterized by, the expression of ADAM9 in a subject comprising administering to said subject an effective amount of the immunoconjugate or the pharmaceutical composition of the present invention described herein. Also provided in the present invention is the use of the immunoconjugate or the pharmaceutical composition of the present invention described herein in the treatment of a disease or condition associated with, or characterized by, the expression of ADAM9 in a subject. The present invention also provides the use of the immunoconjugate or the pharmaceutical composition of the present invention described herein for the manufacture of a medicament for treating a disease or condition associated with, or characterized by, the expression of ADAM9 in a subject.

[0050] In certain embodiments, the disease or condition associated with, or characterized by, the expression of ADAM9 is cancer. In some embodiments, the cancer is selected from the group consisting of non-small-cell lung cancer, colorectal cancer, gastric cancer, pancreatic cancer, renal cell carcinoma, prostate cancer, esophageal cancer, breast cancer, head and neck cancer, ovarian cancer, liver cancer, cervical cancer, thyroid cancer, testicular cancer, myeloid cancer, melanoma, and lymphoid cancer. In certain embodiments, the cancer is non-small-cell lung cancer, gastric cancer, pancreatic cancer or colorectal cancer. In certain embodiments, the non-small-cell lung cancer is squamous cell carcinoma, adenocarcinoma, or large-cell undifferentiated carcinoma. In certain embodiments, the colorectal cancer is adenocarcinoma, gastrointestinal carcinoid tumors, gastrointestinal stromal tumors, primary colorectal lymphoma, leiomyosarcoma, or squamous cell carcinoma.

BRIEF DESCRIPTION OF THE DRAWINGS

[0051] **FIGs. 1A-1C** present the results of an immunohistochemistry (IHC) studies and show the ability of MAB-A to specifically label a variety of non-small cell lung cancer types (**FIG. 1A**), breast cancer cells, prostate cancer cells, gastric cancer cells (**FIG. 1B**), and colon cancer cells (**FIG. 1C**) while the isotype control failed to specifically label any of these cancer cell types (**FIGs. 1A-1C**).

[0052] **FIG. 2** presents the results of cell staining studies and show that MAB-A binds to human ADAM9, and to a lesser extent, cynomolgus monkey ADAM9, transiently expressed on the surface of 293-FT and CHO-K cells (top and bottom panels respectively).

[0053] **FIGs. 3A-3B** depict the amino acid sequences of the murine anti-ADAM9-VH Domain aligned with several humanized/optimized variants of MAB-A (**FIG. 3A, SEQ ID NOs:7, 16, 17, 18, 19, 21, 22, 23** and **28**) and the murine anti-ADAM9-VL Domain aligned with several humanized/optimized variants of MAB-A (**FIG. 3B, SEQ ID NOs:11, 54, 55, 56** and **57**). Positions substituted within the CDRs during the initial optimization are underlined as follows: potential deamidation and isomeration sites are indicated with a single underline, lysine residues are indicated with double underline, additional labile residues are indicated with a dashed underline.

[0054] **FIGs. 4A-4B** present the ELISA binding curves of the ten selected optimized hMAB-A clones comprising CDR_H3 variants, the parental hMAB-A (2.2), and an isotype control antibody. **FIG. 4A** presents the binding curves for cynoADAM9 and **FIG. 4B** presents the binding curves for huADAM9.

[0055] **FIGs. 5A-5B** present the ELISA binding curves of the Fc variants. **FIG. 5A** presents the binding curves for huADAM9 and **FIG. 5B** presents the binding curves for cynoADAM9.

[0056] **FIGs. 6A-6B** show ADAM9 IHC membrane staining in a 20 carcinoma tissue microarray and ADAM IHC membrane and cytoplasmic staining in eight selected indications, respectively.

[0057] **FIGs. 7A-7B** show pulse internalization and continuous internalization of various anti-ADAM9 antibody conjugates.

[0058] **FIG. 8A** shows the binding of 250nM & 1000nM huFcRn to captured anti-ADAM9 antibodies with and without the YTE mutation at pH 6.0.

[0059] **FIG. 8B** shows the binding of 25nM & 100nM anti-ADAM9 antibodies with and without the YTE mutation to immobilized FcRn at pH 6.0.

[0060] **FIGs. 9A, 9B** and **9C** show synthetic schemes for preparing exemplary maytansinoid compounds and immunoconjugates of the present invention.

[0061] **FIG. 10** shows FACS binding curves of hMAB-A(2I.2), hMAB-A(2I.2)-sSPDB-DM4, hMAB-A(2I.2)(YTE/-K)-LDL-DM and hMAB-A(2I.2)(YTE/C/-K)-LDL-DM.

[0062] **FIGs. 11A** and **11B** show *in vitro* cytotoxicity of various anti-ADAM9 immunoconjugates against various non-small cell lung cancer cell lines. The non-targeting IgG1 based conjugates are included as negative controls.

[0063] **FIG. 12** shows the anti-tumor activity of hMAB-A(2I.2)-sSPDB-DM4 (3.6 DAR), hMAB-A(2I.2)-sGMBS-LDL-DM (3.3 DAR), hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR), hMAB-A(2I.2)-sGMBS-LDL-DM (1.9 DAR), hMAB-A(2I.2)-S442C-Mal-SPBD-DM4 (1.8 DAR), and hMAB-A(2I.2)-S442C-Mal-LDL-DM (1.8 DAR) in the Calu-3 human non-small cell lung adenocarcinoma xenograft model.

[0064] **FIG. 13** shows the anti-tumor activity of hMAB-A(2I.2)-sSPDB-DM4 (3.6 DAR), hMAB-A(2I.2)-sGMBS-LDL-DM (3.3 DAR), hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR), hMAB-A(2I.2)-sGMBS-LDL-DM (1.9 DAR), hMAB-A(2I.2)-S442C-Mal-SPBD-DM4 (1.8 DAR), and hMAB-A(2I.2)-S442C-Mal-LDL-DM (1.8 DAR) in the H1703 human non-small cell lung squamous cell carcinoma xenografts.

[0065] **FIG. 14** shows the anti-tumor activity of hMAB-A(2I.2)-sSPDB-DM4 (3.6 DAR), hMAB-A(2I.2)-sGMBS-LDL-DM (3.3 DAR), hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR), hMAB-A(2I.2)-sGMBS-LDL-DM (1.9 DAR), hMAB-A(2I.2)-S442C-Mal-SPBD-DM4 (1.8 DAR), and hMAB-A(2I.2)-S442C-Mal-LDL-DM (1.8 DAR) in the SNU-5 human gastric carcinoma xenografts.

[0066] **FIG. 15** shows the anti-tumor activity of 25, 50, and 100 μg/kg of DM payload of hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR) and hMAB-A(2I.2)-S442C-Mal-LDL-DM (2.1 DAR) conjugates in SCID mice bearing EBC-1 human non-small cell lung squamous cell carcinoma xenografts.

[0067] **FIG. 16** shows the anti-tumor activity of 25, 50, and 100 μg/kg of DM payload of hMAB-A(2I.2)(YTE/C/-K)-Mal-LDL-DM conjugate and 100 μg/kg of DM payload for the nonbinding control huKTI-Mal-LDL-DM (2.0 DAR) conjugate in CD1 nude mice bearing SW48 human colorectal adenocarcinoma xenografts.

[0068] **FIG. 17** shows the anti-tumor activity of 25, 50, and 100 μg/kg of DM payload of hMAB-A(2I.2)(YTE/C/-K)-Mal-LDL-DM conjugate and 100 μg/kg of DM payload for the nonbinding control huKTI-Mal-LDL-DM (2.0 DAR) conjugate in CD1 nude mice bearing HPAF-II human pancreatic adenocarcinoma xenografts.

[0069] **FIG. 18** shows the anti-tumor activity of 25, 50, and 100 μg/kg of DM payload of hMAB-A(2I.2)-sSPDB-DM4(2.1 DAR) conjugate and 25, 50, and 100 μg/kg of DM payload of hMAB-A(2I.2)-S442C-Mal-LDL-DM (2.1 DAR) conjugate in CD1 nude mice bearing H1975 human non-small cell lung adenocarcinoma xenografts.

[0070] **FIG. 19** shows the anti-tumor activity of 25, 50, and 100 μg/kg of DM payload of hMAB-A(2I.2)-sSPDB-DM4(2.1 DAR) conjugate and 25, 50, and 100 μg/kg of DM payload of hMAB-A(2I.2)-S442C-Mal-LDL-DM (2.1 DAR) conjugate in CD1 nude mice bearing Hs 746T human gastric carcinoma xenografts.

DETAILED DESCRIPTION OF THE INVENTION

[0071] The present invention is directed to immunoconjugates comprising an antibody or fragment thereof capable of specifically binding to "Disintegrin and Metalloproteinase Domain-containing Protein 9" ("**ADAM9**") conjugated to at least one maytansinoid compound described herein. The invention particularly concerns such immunoconjugates that are cross-reactive with human ADAM9 and the ADAM9 of a non-human primate (*e.g.*, a cynomolgus monkey). The invention additionally pertains to all such immunoconjugates that comprise a Light Chain Variable (VL) Domain and/or a Heavy Chain Variable (VH) Domain that has been humanized and/or deimmunized so as to exhibit reduced immunogenicity upon administration of such immunoconjugates to a recipient subject. The invention is also directed to pharmaceutical compositions that contain any of such immunoconjugates, and to methods involving the use of any of such immunoconjugates in the treatment of cancer and other diseases and conditions.

I. Antibodies and Their Binding Domains

[0072] The immunoconjugates of the present invention comprise an antibody that binds to ADAM9 or an ADAM9-binding fragment thereof. "**Antibodies**" are immunoglobulin molecules capable of specific binding to a target, such as a carbohydrate, polynucleotide, lipid, polypeptide, *etc.*, through at least one antigen recognition site, located

in the **Variable Domain** of the immunoglobulin molecule. As used herein, the terms "**antibody**" and "**antibodies**" refer to monoclonal antibodies, multispecific antibodies, human antibodies, humanized antibodies, synthetic antibodies, chimeric antibodies, polyclonal antibodies, camelized antibodies, single-chain Fvs (scFv), single-chain antibodies, Fab fragments, F(ab') fragments, intrabodies, and epitope-binding fragments of any of the above. In particular, the term "antibody" includes immunoglobulin molecules and immunologically active fragments of immunoglobulin molecules, *i.e.*, molecules that contain an epitope-binding site. Immunoglobulin molecules can be of any type (*e.g.*, IgG, IgE, IgM, IgD, IgA and IgY), class (*e.g.*, IgG_1, IgG_2, IgG_3, IgG_4, IgA_1 and IgA_2) or subclass. The last few decades have seen a revival of interest in the therapeutic potential of antibodies, and antibodies have become one of the leading classes of biotechnology-derived drugs (Chan, C.E. *et al.* (2009) "*The Use Of Antibodies In The Treatment Of Infectious Diseases*," Singapore Med. J. 50(7):663-666). In addition to their use in diagnostics, antibodies have been shown to be useful as therapeutic agents. Over 200 antibody-based drugs have been approved for use or are under development.

[0073] Antibodies are capable of "**immunospecifically binding**" to a polypeptide or protein or a non-protein molecule due to the presence on such molecule of a particular domain or moiety or conformation (an "**epitope**"). An epitope-containing molecule may have immunogenic activity, such that it elicits an antibody production response in an animal; such molecules are termed "**antigens**." As used herein, an antibody is said to "**immunospecifically**" bind a region of another molecule (*i.e.*, an epitope) if it reacts or associates more frequently, more rapidly, with greater duration and/or with greater affinity with that epitope relative to alternative epitopes. For example, an antibody that immunospecifically binds to a viral epitope is an antibody that binds that viral epitope with greater affinity, avidity, more readily, and/or with greater duration than it immunospecifically binds to other viral epitopes or to non-viral epitopes. It is also understood by reading this definition that, for example, an antibody (or moiety or epitope) that immunospecifically binds to a first target may or may not specifically or preferentially bind to a second target. As such, "immunospecific binding" to a particular epitope does not necessarily require (although it can include) exclusive binding to that epitope. Generally, but not necessarily, reference to binding means "immunospecific" binding. Two molecules are said to be capable of binding to one another in a "**physiospecific**" manner, if such binding exhibits the specificity with which receptors bind to their respective ligands.

[0074] The term "**monoclonal antibody**" refers to a homogeneous antibody population wherein the monoclonal antibody is comprised of amino acids (naturally occurring or non-naturally occurring) that are involved in the selective binding of an antigen. Monoclonal antibodies are highly specific, being directed against a single epitope (or antigenic site). The term "monoclonal antibody" encompasses not only intact monoclonal antibodies and full-length monoclonal antibodies, but also fragments thereof (such as Fab, Fab', $F(ab')_2$ Fv), single-chain (scFv), mutants thereof, fusion proteins comprising an antibody portion, humanized monoclonal antibodies, chimeric monoclonal antibodies, and any other modified configuration of the immunoglobulin molecule that comprises an antigen recognition site of the required specificity and the ability to bind to an antigen. The term is not intended to be limited as regards to the source of the antibody or the manner in which it is made (*e.g.*, by hybridoma, phage selection, recombinant expression, transgenic animals, *etc.*). The term includes whole immunoglobulins as well as the fragments *etc.* described above under the definition of "antibody." Methods of making monoclonal antibodies are known in the art. One method which may be employed is the method of Kohler, G. *et al.* (1975) "*Continuous Cultures Of Fused Cells Secreting Antibody Of Predefined Specificity*," Nature 256:495-497, or a modification thereof. Typically, monoclonal antibodies are developed in mice, rats or rabbits. The antibodies are produced by immunizing an animal with an immunogenic amount of cells, cell extracts, or protein preparations that contain the desired epitope. The immunogen can be, but is not limited to, primary cells, cultured cell lines, cancerous cells, proteins, peptides, nucleic acids, or tissue. Cells used for immunization may be cultured for a period of time (*e.g.*, at least 24 hours) prior to their use as an immunogen. Cells may be used as immunogens by themselves or in combination with a non-denaturing adjuvant, such as Ribi (see, *e.g.*, Jennings, V.M. (1995) "*Review of Selected Adjuvants Used in Antibody Production*," ILAR J. 37(3):119-125). In general, cells should be kept intact and preferably viable when used as immunogens. Intact cells may allow antigens to be better detected than ruptured cells by the immunized animal. Use of denaturing or harsh adjuvants, *e.g.*, Freund's adjuvant, may rupture cells and therefore is discouraged. The immunogen may be administered multiple times at periodic intervals such as, bi weekly, or weekly, or may be administered in such a way as to maintain viability in the animal (*e.g.*, in a tissue recombinant). Alternatively, existing monoclonal antibodies and any other equivalent antibodies that are immunospecific for a desired pathogenic epitope can be sequenced and produced recombinantly by any means known in the art. In one embodiment, such an antibody is sequenced and the polynucleotide sequence

is then cloned into a vector for expression or propagation. The sequence encoding the antibody of interest may be maintained in a vector in a host cell and the host cell can then be expanded and frozen for future use. The polynucleotide sequence of such antibodies may be used for genetic manipulation to generate an affinity optimized, a chimeric antibody, a humanized antibody, and/or a caninized antibody, to improve the affinity, or other characteristics of the antibody, as well as the immunoconjugates of the invention. The general principle in humanizing an antibody involves retaining the basic sequence of the antigen-binding portion of the antibody, while swapping the non-human remainder of the antibody with human antibody sequences.

[0075] Natural antibodies (such as natural IgG antibodies) are composed of two "**Light Chains**" complexed with two "**Heavy Chains**." Each Light Chain contains a Variable Domain ("**VL**") and a Constant Domain ("**CL**"). Each Heavy Chain contains a Variable Domain ("**VH**"), three Constant Domains ("**CH1**," "**CH2**" and "**CH3**"), and a "**Hinge**" Region ("**H**") located between the **CH1** and **CH2** Domains. In contrast, scFvs are single chain molecules made by linking Light and Heavy Chain Variable Domains together via a short linking peptide.

[0076] The basic structural unit of naturally occurring immunoglobulins (*e.g.*, IgG) is thus a tetramer having two light chains and two heavy chains, usually expressed as a glycoprotein of about 150,000 Da. The amino-terminal ("**N-terminal**") portion of each chain includes a Variable Domain of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The carboxy-terminal ("**C-terminal**") portion of each chain defines a constant region, with light chains having a single Constant Domain and heavy chains usually having three Constant Domains and a Hinge Region. Thus, the structure of the light chains of an IgG molecule is n-VL-CL-c and the structure of the IgG heavy chains is **n-VH-CH1-H-CH2-CH3-c** (where n and c represent, respectively, the N-terminus and the C-terminus of the polypeptide).

A. Characteristics of Antibody Variable Domains

[0077] The Variable Domains of an IgG molecule consist of 1, 2, and most commonly 3, complementarity determining regions ("**CDR**", *i.e.*, **CDR1**, **CDR2** and **CDR3**, respectively), which contain the residues in contact with epitope, and non-CDR segments, referred to as **framework regions** ("**FR**"), which in general maintain the structure and

determine the positioning of the CDR regions so as to permit such contacting (although certain framework residues may also contact the epitope). Thus, the VL and VH Domains typically have the structure: **n-FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4-c** (where "n" denotes the N-terminus and "c" denotes the C-terminus). Polypeptides that are (or may serve as) the first, second, third, and fourth FR of the Light Chain of an antibody are herein respectively designated as: **FR_L1 Domain**, **FR_L2 Domain**, **FR_L3 Domain**, and **FR_L4 Domain**. Similarly, polypeptides that are (or may serve as) the first, second, third and fourth FR of the Heavy Chain of an antibody are herein respectively designated as: **FR_H1 Domain**, **FR_H2 Domain**, **FR_H3 Domain** and **FR_H4 Domain**. Polypeptides that are (or may serve as) the first, second and third CDR of the Light Chain of an antibody are herein respectively designated as: **CDR_L1 Domain**, **CDR_L2 Domain**, and **CDR_L3 Domain**. Similarly, polypeptides that are (or may serve as) the first, second and third CDR of the Heavy Chain of an antibody are herein respectively designated as: **CDR_H1 Domain**, **CDR_H2 Domain**, and **CDR_H3 Domain**. Thus, the terms CDR_L1 Domain, CDR_L2 Domain, CDR_L3 Domain, CDR_H1 Domain, CDR_H2 Domain, and CDR_H3 Domain are directed to polypeptides that when incorporated into an antibody causes the antibody to be able to bind to a specific epitope.

[0078] Throughout the present specification, the numbering of the residues in the Variable Domains of the mature heavy and light chains of immunoglobulins are designated by the position of an amino acid in the chain. Kabat described numerous amino acid sequences for antibodies, identified an amino acid consensus sequence for each subgroup, and assigned a residue number to each amino acid, and the CDRs are identified as defined by Kabat (it will be understood that CDR_H1 as defined by Chothia, C. & Lesk, A. M. ((1987) "*Canonical structures for the hypervariable regions of immunoglobulins*," J. Mol. Biol. 196:901-917) begins five residues earlier). Kabat's numbering scheme is extendible to antibodies not included in his compendium by aligning the antibody in question with one of the consensus sequences in Kabat by reference to conserved amino acids. This method for assigning residue numbers has become standard in the field and readily identifies amino acids at equivalent positions in different antibodies, including chimeric or humanized variants. For example, an amino acid at position 50 of a human antibody light chain occupies the equivalent position to an amino acid at position 50 of a mouse antibody light chain.

[0079] The ability of an antibody to bind an epitope of an antigen depends upon the presence and amino acid sequence of the antibody's VL and VH Domains. Interaction of an antibody's Light Chain and Heavy Chain and, in particular, interaction of its VL and VH Domains forms one of the two epitope-binding sites of a natural antibody, such as an IgG. Natural antibodies are capable of binding to only one epitope species (*i.e.*, they are monospecific), although they can bind multiple copies of that epitope species (*i.e.*, exhibiting bivalency or multivalency).

[0080] Accordingly, as used herein, the term "**epitope-binding fragment**" means a fragment of an antibody capable of immunospecifically binding to an epitope, and the term "**epitope-binding site**" refers to a portion of a molecule comprising an epitope-binding fragment. An epitope-binding fragment may contain any 1, 2, 3, 4, or 5 the CDR Domains of an antibody, or may contain all 6 of the CDR Domains of an antibody and, although capable of immunospecifically binding to such epitope, may exhibit an immunospecificity, affinity or selectivity toward such epitope that differs from that of such antibody. Preferably, however, an epitope-binding fragment will contain all 6 of the CDR Domains of such antibody. An epitope-binding fragment of an antibody may be a single polypeptide chain (*e.g.*, an scFv), or may comprise two or more polypeptide chains, each having an amino terminus and a carboxy terminus (*e.g.*, a Fab fragment, an Fab_2 fragment, *etc.*). Unless specifically noted, the order of domains of the protein molecules described herein is in the "**N-terminal to C-terminal**" direction.

[0081] The invention also encompasses immunoconjugates comprising single-chain Variable Domain fragments ("**scFv**") comprising an anti-ADAM9-VL and/or VH Domain of the invention. Single-chain Variable Domain fragments comprise VL and VH Domains that are linked together using a short "Linker" peptide. Such Linkers can be modified to provide additional functions, such as to permit the attachment of a drug or to permit attachment to a solid support. The single-chain variants can be produced either recombinantly or synthetically. For synthetic production of scFv, an automated synthesizer can be used. For recombinant production of scFv, a suitable plasmid containing polynucleotide that encodes the scFv can be introduced into a suitable host cell, either eukaryotic, such as yeast, plant, insect or mammalian cells, or prokaryotic, such as E. coli. Polynucleotides encoding the scFv of interest can be made by routine manipulations such as

ligation of polynucleotides. The resultant scFv can be isolated using standard protein purification techniques known in the art.

[0082] The invention also particularly encompasses immunoconjugates comprising the CDR_H1, CDR_H2, CDR_H3, CDR_L1, CDR_L2, and CDR_L3 Domains of humanized/optimized variants of the anti-ADAM9 antibodies of the invention, as well as VL Domains that contain any 1, 2, or 3 of such CDR_Ls and VH Domains that contain any 1, 2, or 3 of such CDR_Hs, as well as multispecific-binding molecules comprising the same. The term "**humanized**" antibody refers to a chimeric molecule having an epitope-binding site of an immunoglobulin from a non-human species and a remaining immunoglobulin structure that is based upon the structure and /or sequence of a human immunoglobulin. Humanized antibodies are generally prepared using recombinant techniques. The immunoconjugates of the present invention may comprise humanized, chimeric or caninized variants of an antibody that is designated herein as "**MAB-A**." The polynucleotide sequences that encode the Variable Domains of MAB-A may be used for genetic manipulation to generate MAB-A derivatives possessing improved or altered characteristics (*e.g.*, affinity, cross-reactivity, specificity, *etc.*). The general principle in humanizing an antibody involves retaining the basic sequence of the epitope-binding portion of the antibody, while swapping the non-human remainder of the antibody with human antibody sequences. There are four general steps to humanize a monoclonal antibody. These are: (1) determining the nucleotide and predicted amino acid sequence of the starting antibody light and heavy variable domains; (2) designing the humanized antibody or caninized antibody, *i.e.*, deciding which antibody framework region to use during the humanizing or canonizing process; (3) employing the actual humanizing or caninizing methodologies/techniques; and (4) transfecting and expressing the humanized antibody. See, for example, U.S. Patent Nos. 4,816,567; 5,807,715; 5,866,692; and 6,331,415. The term "**optimized**" antibody refers to an antibody having at least one amino acid which is different from the parent antibody in at least one complementarity determining region (CDR) in the light or heavy chain variable region, which confers a higher binding affinity, (e.g., a 2-fold or more fold) higher binding affinity, to human ADAM9 and/or cynomolgus monkey ADAM9 as compared to the parental antibody. It will be understood from the teaching provided herein that the antibodies of the invention may be humanized, optimized, or both humanized and optimized.

[0083] The epitope-binding site may comprise either a complete Variable Domain fused to one or more Constant Domains or only the CDRs of such Variable Domain grafted to appropriate framework regions. Epitope-binding sites may be wild-type or may be modified by one or more amino acid substitutions, insertions or deletions. Such action partially or completely eliminates the ability of the Constant Region to serve as an immunogen in recipients (*e.g.*, human individuals), however, the possibility of an immune response to the foreign Variable Domain remains (LoBuglio, A.F. *et al.* (1989) "*Mouse/Human Chimeric Monoclonal Antibody In Man: Kinetics And Immune Response*," Proc. Natl. Acad. Sci. (U.S.A.) 86:4220-4224). Another approach focuses not only on providing human-derived constant regions, but on modifying the Variable Domains as well so as to reshape them as closely as possible to a form found in human immunoglobulins. It is known that the Variable Domains of both the Heavy and Light Chains of antibodies contain three CDRs which vary in response to the antigens in question and determine binding capability, flanked by the four framework regions, which are relatively conserved in a given species and which putatively provide a scaffolding for the CDRs. When non-human antibodies are prepared with respect to a particular antigen, the variable domains can be "reshaped" or "humanized" by grafting CDRs derived from non-human antibody on the FRs present in the human antibody to be modified. Application of this approach to various antibodies has been reported by Sato, K. *et al.* (1993) Cancer Res 53:851-856. Riechmann, L. *et al.* (1988) "*Reshaping Human Antibodies for Therapy*," Nature 332:323-327; Verhoeyen, M. *et al.* (1988) "*Reshaping Human Antibodies: Grafting An Antilysozyme Activity*," Science 239:1534-1536; Kettleborough, C. A. *et al.* (1991) "*Humanization Of A Mouse Monoclonal Antibody By CDR-Grafting: The Importance Of Framework Residues On Loop Conformation*," Protein Engineering 4:773-3783; Maeda, H. *et al.* (1991) "*Construction Of Reshaped Human Antibodies With HIV-Neutralizing Activity*," Human Antibodies Hybridoma 2:124-134; Gorman, S. D. *et al.* (1991) "*Reshaping A Therapeutic CD4 Antibody*," Proc. Natl. Acad. Sci. (U.S.A.) 88:4181-4185; Tempest, P.R. *et al.* (1991) "*Reshaping A Human Monoclonal Antibody To Inhibit Human Respiratory Syncytial Virus Infection in vivo*," Bio/Technology 9:266-271; Co, M. S. *et al.* (1991) "*Humanized Antibodies For Antiviral Therapy*," Proc. Natl. Acad. Sci. (U.S.A.) 88:2869-2873; Carter, P. *et al.* (1992) "*Humanization Of An Anti-p185her2 Antibody For Human Cancer Therapy*," Proc. Natl. Acad. Sci. (U.S.A.) 89:4285-4289; and Co, M.S. *et al.* (1992) "*Chimeric And Humanized Antibodies With Specificity For The CD33 Antigen*," J. Immunol. 148:1149-1154. In some embodiments, humanized antibodies preserve all CDR sequences (for

example, a humanized murine antibody which contains all six of the CDRs present in the murine antibody). In other embodiments, humanized antibodies have one or more CDRs (one, two, three, four, five, or six) that differ in sequence relative to the CDRs of the original antibody.

[0084] A number of humanized antibody molecules comprising an epitope-binding site derived from a non-human immunoglobulin have been described, including chimeric antibodies having rodent or modified rodent Variable Domain and their associated complementarity determining regions (CDRs) fused to human constant domains (see, for example, Winter *et al.* (1991) "*Man-made Antibodies*," Nature 349:293-299; Lobuglio *et al.* (1989) "*Mouse/Human Chimeric Monoclonal Antibody In Man: Kinetics And Immune Response*," Proc. Natl. Acad. Sci. (U.S.A.) 86:4220-4224; Shaw *et al.* (1987) "*Characterization Of A Mouse/Human Chimeric Monoclonal Antibody (17-1A) To A Colon Cancer Tumor-Associated Antigen*," J. Immunol. 138:4534-4538; and Brown *et al.* (1987) "*Tumor-Specific Genetically Engineered Murine/Human Chimeric Monoclonal Antibody*," Cancer Res. 47:3577-3583). Other references describe rodent CDRs grafted into a human supporting framework region (FR) prior to fusion with an appropriate human antibody Constant Domain (see, for example, Riechmann, L. *et al.* (1988) "*Reshaping Human Antibodies for Therapy*," Nature 332:323-327; Verhoeyen, M. *et al.* (1988) "*Reshaping Human Antibodies: Grafting An Antilysozyme Activity*," Science 239:1534-1536; and Jones *et al.* (1986) "*Replacing The Complementarity-Determining Regions In A Human Antibody With Those From A Mouse*," Nature 321:522-525). Another reference describes rodent CDRs supported by recombinantly veneered rodent framework regions (see, for example, European Patent Publication No. 519,596). These "humanized" molecules are designed to minimize unwanted immunological response towards rodent anti-human antibody molecules, which limits the duration and effectiveness of therapeutic applications of those moieties in human recipients. Other methods of humanizing antibodies that may also be utilized are disclosed by Daugherty *et al.* (1991) "*Polymerase Chain Reaction Facilitates The Cloning, CDR-Grafting, And Rapid Expression Of A Murine Monoclonal Antibody Directed Against The CD18 Component Of Leukocyte Integrins*," Nucl. Acids Res. 19:2471-2476 and in U.S. Patent Nos. 6,180,377; 6,054,297; 5,997,867; and 5,866,692.

B. Characteristics of Antibody Constant Domains

[0085] Throughout the present specification, the numbering of the residues in the constant region of an IgG heavy chain is that of the EU index as in Kabat *et al.*, SEQUENCES OF PROTEINS OF IMMUNOLOGICAL INTEREST, 5th Ed. Public Health Service, NH1, MD (1991) ("**Kabat**"), expressly incorporated herein by reference. The term "**the EU index as set forth in Kabat**" refers to the numbering of the Constant Domains of human IgG1 EU antibody provided in Kabat. This method for assigning residue numbers has become standard in the field and readily identifies amino acids at equivalent positions in the constant regions of different antibody isotypes.

1. Constant Regions of the Light Chain

[0086] As indicated above, each Light Chain of an antibody contains a Variable Domain ("**VL**") and a Constant Domain ("**CL**").

[0087] A preferred CL Domain is a human IgG CL Kappa Domain. The amino acid sequence of an exemplary human CL Kappa Domain is (**SEQ ID NO:69**):

RTVAAPSVFI FPPSDEQLKS GTASVVCLLN NFYPREAKVQ WKVDNALQSG
NSQESVTEQD SKDSTYSLSS TLTLSKADYE KHKVYACEVT HQGLSSPVTK
SFNRGEC

[0088] Alternatively, an exemplary CL Domain is a human IgG CL Lambda Domain. The amino acid sequence of an exemplary human CL Lambda Domain is (**SEQ ID NO:70**):

QPKAAPSVTL FPPSSEELQA NKATLVCLIS DFYPGAVTVA WKADSSPVKA
GVETTPSKQS NNKYAASSYL SLTPEQWKSH RSYSCQVTHE GSTVEKTVAP
TECS

2. Constant Regions of the Heavy Chain

a. Naturally-Occurring Fc Regions

[0089] As provided herein, the immunoconjugates of the invention may comprise an Fc Region. The Fc Region of such immunoconjugates the invention may be of any isotype (*e.g.*, IgG1, IgG2, IgG3, or IgG4). The immunoconjugates of the invention may further comprise a CH1 Domain and/or a Hinge Region. When present, the CH1 Domain and/or Hinge Region may be of any isotype (*e.g.*, IgG1, IgG2, IgG3, or IgG4), and is preferably of the same isotype as the desired Fc Region.

[0090] The Fc Region of the Fc Region-containing immunoconjugates of the present invention may be either a complete Fc Region (*e.g.*, a complete IgG Fc Region) or only a fragment of an Fc Region. Optionally, the Fc Region of the Fc Region-containing immunoconjugates of the present invention lacks the C-terminal lysine amino acid residue.

[0091] The CH1 Domains of the two heavy chains of an antibody complex with the antibody's Light Chain's "CL" constant region, and are attached to the heavy chains CH2 Domains via an intervening Hinge Domain.

[0092] An exemplary CH1 Domain is a human IgG1 CH1 Domain. The amino acid sequence of an exemplary human IgG1 CH1 Domain is (**SEQ ID NO:71**):

ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV
HTFPAVLQSS GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKRV

[0093] An exemplary CH1 Domain is a human IgG2 CH1 Domain. The amino acid sequence of an exemplary human IgG2 CH1 Domain is (**SEQ ID NO:72**):

ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEPVTVS WNSGALTSGV
HTFPAVLQSS GLYSLSSVVT VPSSNFGTQT YTCNVDHKPS NTKVDKTV

[0094] An exemplary CH1 Domain is a human IgG4 CH1 Domain. The amino acid sequence of an exemplary human IgG4 CH1 Domain is (**SEQ ID NO:73**):

ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEPVTVS WNSGALTSGV
HTFPAVLQSS GLYSLSSVVT VPSSSLGTKT YTCNVDHKPS NTKVDKRV

[0095] One exemplary Hinge Region is a human IgG1 Hinge Region. The amino acid sequence of an exemplary human IgG1 Hinge Region is (**SEQ ID NO:74**): EPKSCDKTHTCPPCP.

[0096] Another exemplary Hinge Region is a human IgG2 Hinge Region. The amino acid sequence of an exemplary human IgG2 Hinge Region is (**SEQ ID NO:75**): ERKCCVECPPCP.

[0097] Another exemplary Hinge Region is a human IgG4 Hinge Region. The amino acid sequence of an exemplary human IgG4 Hinge Region is (**SEQ ID NO:76**): ESKYGPPCPSCP. As described above, an IgG4 Hinge Region may comprise a stabilizing mutation, such as the S228P substitution. The amino acid sequence of an exemplary stabilized IgG4 Hinge Region is (**SEQ ID NO:77**): ESKYGPPCPPCP.

[0098] The CH2 and CH3 Domains of the two Heavy Chains of an antibody interact to form an "**Fc Region**," which is a domain that is recognized by cellular "**Fc Receptors**," including but not limited to Fc gamma Receptors ("**FcγRs**"). As used herein, the term "Fc Region" is used to define the C-terminal region of an IgG Heavy Chain that comprises the CH2 and CH3 Domains of that chain. An Fc Region is said to be of a particular IgG isotype, class or subclass if its amino acid sequence is most homologous to that isotype, relative to other IgG isotypes.

[0099] The amino acid sequence of the CH2-CH3 Domain of an exemplary human IgG1 is (**SEQ ID NO:1**):

```
231       240         250         260         270         280
APELLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD

          290         300         310         320         330
GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKALPA

          340         350         360         370         380
PIEKTISKAK GQPREPQVYT LPPSREEMTK NQVSLTCLVK GFYPSDIAVE

          390         400         410         420         430
WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE

          440     447
ALHNHYTQKS LSLSPGX
```

as numbered by the EU index as set forth in Kabat, wherein **X** is a lysine (K) or is absent.

[00100] The amino acid sequence of the CH2-CH3 Domain of an exemplary human IgG2 is (**SEQ ID NO:2**):

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231       240         250         260         270         280
APPVA-GPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVQFNWYVD

          290         300         310         320         330
GVEVHNAKTK PREEQFNSTF RVVSVLTVVH QDWLNGKEYK CKVSNKGLPA

          340         350         360         370         380
PIEKTISKTK GQPREPQVYT LPPSREEMTK NQVSLTCLVK GFYPSDISVE

          390         400         410         420         430
WESNGQPENN YKTTPPMLDS DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE

          440     447
```

ALHNHYTQKS LSLSPG**X**

as numbered by the EU index as set forth in Kabat, wherein **X** is a lysine (K) or is absent.

[00101] The amino acid sequence of the CH2-CH3 Domain of an exemplary human IgG3 is (**SEQ ID NO:3**):

```
231       240         250         260         270         280
APELLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVQFKWYVD

          290         300         310         320         330
GVEVHNAKTK PREEQYNSTF RVVSVLTVLH QDWLNGKEYK CKVSNKALPA

          340         350         360         370         380
PIEKTISKTK GQPREPQVYT LPPSREEMTK NQVSLTCLVK GFYPSDIAVE

          390         400         410         420         430
WESSGQPENN YNTTPPMLDS DGSFFLYSKL TVDKSRWQQG NIFSCSVMHE

          440     447
ALHNRFTQKS LSLSPGX
```

as numbered by the EU index as set forth in Kabat, wherein **X** is a lysine (K) or is absent.

[00102] The amino acid sequence of the CH2-CH3 Domain of an exemplary human IgG4 is (**SEQ ID NO:4**):

```
231       240         250         260         270         280
APEFLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSQED PEVQFNWYVD

          290         300         310         320         330
GVEVHNAKTK PREEQFNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKGLPS

          340         350         360         370         380
SIEKTISKAK GQPREPQVYT LPPSQEEMTK NQVSLTCLVK GFYPSDIAVE

          390         400         410         420         430
WESNGQPENN YKTTPPVLDS DGSFFLYSRL TVDKSRWQEG NVFSCSVMHE

          440     447
ALHNHYTQKS LSLSLGX
```

as numbered by the EU index as set forth in Kabat, wherein **X** is a lysine (K) or is absent.

[00103] Polymorphisms have been observed at a number of different positions within antibody constant regions (*e.g.*, Fc positions, including but not limited to positions 270, 272, 312, 315, 356, and 358 as numbered by the EU index as set forth in Kabat), and thus slight differences between the presented sequence and sequences in the prior art can exist. Polymorphic forms of human immunoglobulins have been well-characterized. At present, 18 Gm allotypes are known: G1m (1, 2, 3, 17) or G1m (a, x, f, z), G2m (23) or G2m (n), G3m (5, 6, 10, 11, 13, 14, 15, 16, 21, 24, 26, 27, 28) or G3m (b1, c3, b3, b0, b3, b4, s, t, g1, c5, u, v, g5) (Lefranc, *et al.*, "*The Human IgG Subclasses: Molecular Analysis of Structure, Function And Regulation.*" Pergamon, Oxford, pp. 43-78 (1990); Lefranc, G. *et al.*, 1979, Hum. Genet.: 50, 199-211). It is specifically contemplated that the antibodies of the present invention may incorporate any allotype, isoallotype, or haplotype of any immunoglobulin gene, and are not limited to the allotype, isoallotype or haplotype of the sequences provided herein. Furthermore, in some expression systems the C-terminal amino acid residue (bolded above) of the CH3 Domain may be post-translationally removed. Accordingly, the C-terminal residue of the CH3 Domain is an optional amino acid residue in the immunoconjugates of the invention. Specifically encompassed by the instant invention are immunoconjugates lacking the C-terminal residue of the CH3 Domain. Also specifically encompassed by the instant invention are such constructs comprising the C-terminal lysine residue of the CH3 Domain.

b. Fcγ Receptors (FcγRs)

[00104] In traditional immune function, the interaction of antibody-antigen complexes with cells of the immune system results in a wide array of responses, ranging from effector functions such as antibody dependent cytotoxicity, mast cell degranulation, and phagocytosis to immunomodulatory signals such as regulating lymphocyte proliferation and antibody secretion. All of these interactions are initiated through the binding of the Fc Region of antibodies or immune complexes to specialized cell surface receptors on hematopoietic cells, and particularly to receptors (singularly referred to as an "**Fc gamma receptor**" "**FcγR**," and collectively as "**FcγRs**") found on the surfaces of multiple types of immune system cells (*e.g.*, B lymphocytes, follicular dendritic cells, natural killer cells, macrophages, neutrophils, eosinophils, basophils and mast cells).

[00105] The diversity of cellular responses triggered by antibodies and immune complexes results from the structural heterogeneity of the three Fc receptors: FcγRI (CD64), FcγRII (CD32), and FcγRIII (CD16). FcγRI (CD64), FcγRIIA (CD32A) and FcγRIII (CD16) are activating (*i.e.*, immune system enhancing) receptors; FcγRIIB (CD32B) is an inhibiting (*i.e.*, immune system dampening) receptor. In addition, interaction with the neonatal Fc Receptor (FcRn) mediates the recycling of IgG molecules from the endosome to the cell surface and release into the blood. The amino acid sequence of exemplary wild-type IgG1 (**SEQ ID NO:1**), IgG2 (**SEQ ID NO:2**), IgG3 (**SEQ ID NO:3**), and IgG4 (**SEQ ID NO:4**) are presented above.

[00106] The ability of the different FcγRs to mediate diametrically opposing functions reflects structural differences among the different FcγRs, and in particular reflects whether the bound FcγR possesses an Immunoreceptor Tyrosine-Based Activation Motif ("**ITAM**") or an Immunoreceptor Tyrosine-Based Inhibitory Motif ("**ITIM**"). The recruitment of different cytoplasmic enzymes to these structures dictates the outcome of the FcγR-mediated cellular responses. ITAM-containing FcγRs include FcγRI, FcγRIIA, FcγRIIIA, and activate the immune system when bound to Fc Regions (*e.g.*, aggregated Fc Regions present in an immune complex). FcγRIIB is the only currently known natural ITIM-containing FcγR; it acts to dampen or inhibit the immune system when bound to aggregated Fc Regions. Human neutrophils express the FcγRIIA gene. FcγRIIA clustering via immune complexes or specific antibody cross-linking serves to aggregate ITAMs with receptor-associated kinases which facilitate ITAM phosphorylation. ITAM phosphorylation serves as a docking site for Syk kinase, the activation of which results in the activation of downstream substrates (*e.g.*, PI_3K). Cellular activation leads to release of pro-inflammatory mediators. The FcγRIIB gene is expressed on B lymphocytes; its extracellular domain is 96% identical to FcγRIIA and binds IgG complexes in an indistinguishable manner. The presence of an ITIM in the cytoplasmic domain of FcγRIIB defines this inhibitory subclass of FcγR. Recently the molecular basis of this inhibition was established. When co-ligated along with an activating FcγR, the ITIM in FcγRIIB becomes phosphorylated and attracts the SH2 domain of the inositol polyphosphate 5'-phosphatase (SHIP), which hydrolyzes phosphoinositol messengers released as a consequence of ITAM-containing FcγR- mediated tyrosine kinase activation, consequently preventing the influx of intracellular Ca^{++}. Thus cross-linking of FcγRIIB dampens the activating response to FcγR ligation and inhibits

cellular responsiveness. B-cell activation, B-cell proliferation and antibody secretion is thus aborted.

c. Variant Fc Regions

[00107] Modification of the Fc Region may lead to an altered phenotype, for example altered serum half-life, altered stability, altered susceptibility to cellular enzymes or altered effector function. It may therefore be desirable to modify an Fc Region-containing molecule of the present invention with respect to effector function, for example, so as to enhance the effectiveness of such molecule in treating cancer. Reduction or elimination of effector function is desirable in certain cases, for example in the case of antibodies whose mechanism of action involves blocking or antagonism, but not killing of the cells bearing a target antigen. Increased effector function is generally desirable when directed to undesirable cells, such as tumor and foreign cells, where the FcγRs are expressed at low levels, for example, tumor-specific B cells with low levels of FcγRIIB (*e.g.*, non-Hodgkin's lymphoma, CLL, and Burkitt's lymphoma). Immunoconjugates of the invention possessing such conferred or altered effector function activity are useful for the treatment and/or prevention of a disease, disorder or infection in which an enhanced efficacy of effector function activity is desired.

[00108] Accordingly, in certain embodiments, the Fc Region of the Fc Region-containing immunoconjugates of the present invention may be an engineered variant Fc Region. Although the Fc Region of immunoconjugates of the present invention may possess the ability to bind to one or more Fc receptors (*e.g.*, FcγR(s)), more preferably such variant Fc Region have altered binding to FcγRIA (CD64), FcγRIIA (CD32A), FcγRIIB (CD32B), FcγRIIIA (CD16a) or FcγRIIIB (CD16b) (relative to the binding exhibited by a wild-type Fc Region), *e.g.*, will have enhanced binding to an activating receptor and/or will have substantially reduced or no ability to bind to inhibitory receptor(s). Thus, the Fc Region of the immunoconjugates of the present invention may include some or all of the CH2 Domain and/or some or all of the CH3 Domain of a complete Fc Region, or may comprise a variant CH2 and/or a variant CH3 sequence (that may include, for example, one or more insertions and/or one or more deletions with respect to the CH2 or CH3 domains of a complete Fc Region). Such Fc Regions may comprise non-Fc polypeptide portions, or may comprise portions of non-naturally complete Fc Regions, or may comprise non-naturally occurring orientations of CH2 and/or CH3 Domains (such as, for example, two

CH2 domains or two CH3 domains, or in the N-terminal to C-terminal direction, a CH3 Domain linked to a CH2 Domain, *etc.*).

[00109] Fc Region modifications identified as altering effector function are known in the art, including modifications that increase binding to activating receptors (*e.g.*, FcγRIIA (CD16A) and reduce binding to inhibitory receptors (*e.g.*, FcγRIIB (CD32B) (see, *e.g.*, Stavenhagen, J.B. *et al.* (2007) "*Fc Optimization Of Therapeutic Antibodies Enhances Their Ability To Kill Tumor Cells In Vitro And Controls Tumor Expansion In Vivo Via Low-Affinity Activating Fcgamma Receptors*," Cancer Res. 57(18):8882-8890). **Table 1** lists exemplary single, double, triple, quadruple and quintuple substitutions (numbering is that of the EU index as in Kabat, and substitutions are relative to the amino acid sequence of **SEQ ID NO:1**) of exemplary modification that increase binding to activating receptors and/or reduce binding to inhibitory receptors.

Table 1
Variations of Preferred Activating Fc Regions

Single-Site Variations			
F243L	R292G	D270E	R292P
Y300L	P396L		
Double-Site Variations			
F243L and R292P	F243L and Y300L	F243L and P396L	R292P and Y300L
D270E and P396L	R292P and V305I	P396L and Q419H	P247L and N421K
R292P and P396L	Y300L and P396L	R255L and P396L	R292P and P305I
K392T and P396L			
Triple-Site Variations			
F243L, P247L and N421K		P247L, D270E and N421K	
F243L, R292P and Y300L		R255L, D270E and P396L	
F243L, R292P and V305I		D270E, G316D and R416G	
F243L, R292P and P396L		D270E, K392T and P396L	
F243L, Y300L and P396L		D270E, P396L and Q419H	
V284M, R292L and K370N		R292P, Y300L and P396L	
Quadruple-Site Variations			
L234F, F243L, R292P and Y300L		F243L, P247L, D270E and N421K	
L234F, F243L, R292P and Y300L		F243L, R255L, D270E and P396L	
L235I, F243L, R292P and Y300L		F243L, D270E, G316D and R416G	
L235Q, F243L, R292P and Y300L		F243L, D270E, K392T and P396L	
P247L, D270E, Y300L and N421K		F243L, R292P, Y300L, and P396L	
R255L, D270E, R292G and P396L		F243L, R292P, V305I and P396L	
R255L, D270E, Y300L and P396L		F243L, D270E, P396L and Q419H	
D270E, G316D, P396L and R416G			
Quintuple-Site Variations			
L235V, F243L, R292P, Y300L and P396L		F243L, R292P, V305I, Y300L and P396L	
L235P, F243L, R292P, Y300L and P396L			

[00110] Exemplary variants of human IgG1 Fc Regions with reduced binding to CD32B and/or increased binding to CD16A contain F243L, R292P, Y300L, V305I or P396L substitutions, wherein the numbering is that of the EU index as in Kabat. These amino acid substitutions may be present in a human IgG1 Fc Region in any combination. In one embodiment, the variant human IgG1 Fc Region contains a F243L, R292P and Y300L substitution. In another embodiment, the variant human IgG1 Fc Region contains a F243L, R292P, Y300L, V305I and P396L substitution.

[00111] In certain embodiments, it is preferred for the Fc Regions of the immunoconjugates of the present invention to exhibit decreased (or substantially no) binding to FcγRIA (CD64), FcγRIIA (CD32A), FcγRIIB (CD32B), FcγRIIIA (CD16a) or FcγRIIIB (CD16b) (relative to the binding exhibited by the wild-type IgG1 Fc Region (**SEQ ID NO:1**). In a specific embodiment, the immunoconjugates of the present invention comprise an IgG Fc Region that exhibits reduced ADCC effector function. In a preferred embodiment the CH2-CH3 Domains of immunoconjugates include any 1, 2, 3, or 4 of the substitutions: L234A, L235A, D265A, N297Q, and N297G, wherein the numbering is that of the EU index as in Kabat. In another embodiment, the CH2-CH3 Domains contain an N297Q substitution, an N297G substitution, L234A and L235A substitutions or a D265A substitution, as these mutations abolish FcR binding. Alternatively, a CH2-CH3 Domain of a naturally occurring Fc region that inherently exhibits decreased (or substantially no) binding to FcγRIIIA (CD16a) and/or reduced effector function (relative to the binding and effector function exhibited by the wild-type IgG1 Fc Region (**SEQ ID NO:1**)) is utilized. In a specific embodiment, the immunoconjugates of the present invention comprise an IgG2 Fc Region (**SEQ ID NO:2**) or an IgG4 Fc Region (**SEQ ID:NO:4**). When an IgG4 Fc Region is utilized, the instant invention also encompasses the introduction of a stabilizing mutation, such as the Hinge Region S228P substitution described above (see, *e.g.*, **SEQ ID NO:77**). Since the N297G, N297Q, L234A, L235A and D265A substitutions abolish effector function, in circumstances in which effector function is desired, these substitutions would preferably not be employed.

[00112] A preferred IgG1 sequence for the CH2 and CH3 Domains of the Fc Region-containing immunoconjugates of the present invention having reduced or abolished effector function will comprise the substitutions L234A/L235A (shown underlined) (**SEQ ID NO:78**):

APE**AA**GGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD
GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKALPA
PIEKTISKAK GQPREPQVYT LPPSREEMTK NQVSLTCLVK GFYPSDIAVE
WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE
ALHNHYTQKS LSLSPG**X**

wherein, **X** is a lysine (K) or is absent.

[00113] A second preferred IgG1 sequence for the CH2 and CH3 Domains of the Fc Region-containing immunoconjugates of the present invention comprises an S442C substitution (shown underlined), that permits two CH3 domains to be covalently bonded to one another via a disulfide bond or conjugation of a pharmaceutical agent. The amino acid sequence of such molecule is (**SEQ ID NO:79**):

APELLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD
GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKALPA
PIEKTISKAK GQPREPQVYT LPPSREEMTK NQVSLTCLVK GFYPSDIAVE
WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE
ALHNHYTQKS L**C**LSPG**X**

wherein, **X** is a lysine (K) or is absent.

[00114] A third preferred IgG1 sequence for the CH2 and CH3 Domains of the Fc Region-containing immunoconjugates of the present invention comprises the L234A/L235A substitutions (shown underlined) that reduce or abolish effector function and the S442C substitution (shown underlined) that permits two CH3 domains to be covalently bonded to one another via a disulfide bond or conjugation of a pharmaceutical agent. The amino acid sequence of such molecule is (**SEQ ID NO:80**):

APE**AA**GGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED PEVKFNWYVD
GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKALPA
PIEKTISKAK GQPREPQVYT LPPSREEMTK NQVSLTCLVK GFYPSDIAVE
WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE
ALHNHYTQKS L**C**LSPG**X**

wherein, **X** is a lysine (K) or is absent.

[00115] The serum half-life of proteins comprising Fc Regions may be increased by increasing the binding affinity of the Fc Region for FcRn. The term "half-life" as used herein means a pharmacokinetic property of a molecule that is a measure of the mean survival time of the molecules following their administration. Half-life can be expressed as the time required to eliminate fifty percent (50%) of a known quantity of the molecule from a subject's (*e.g.*, a human patient or other mammal) body or a specific compartment thereof,

for example, as measured in serum, *i.e.*, circulating half-life, or in other tissues. In general, an increase in half-life results in an increase in mean residence time (MRT) in circulation for the administered molecule.

[00116] In some embodiments, the immunoconjugates of the present invention comprise a variant Fc Region that comprises at least one amino acid modification relative to a wild-type Fc Region, such that said molecule has an increased half-life (relative to a molecule comprising a wild-type Fc Region). In some embodiments, the immunoconjugates of the present invention comprise a variant IgG Fc Region, wherein said variant Fc Region comprises a half-life extending amino acid substitution at one or more positions selected from the group consisting of 238, 250, 252, 254, 256, 257, 256, 265, 272, 286, 288, 303, 305, 307, 308, 309, 311, 312, 317, 340, 356, 360, 362, 376, 378, 380, 382, 413, 424, 428, 433, 434, 435, and 436, wherein the numbering is that of the EU index as in Kabat. Numerous mutations capable of increasing the half-life of an Fc Region-containing molecule are known in the art and include, for example M252Y, S254T, T256E, and combinations thereof. For example, see the mutations described in U.S. Patent Nos. 6,277,375, 7,083,784; 7,217,797, 8,088,376; U.S. Publication Nos. 2002/0147311; 2007/0148164; and PCT Publication Nos. WO 98/23289; WO 2009/058492; and WO 2010/033279, which are herein incorporated by reference in their entireties. Immunoconjugates with enhanced half-life also include those possessing variant Fc Regions comprising substitutions at two or more of Fc Region residues 250, 252, 254, 256, 257, 288, 307, 308, 309, 311, 378, 428, 433, 434, 435 and 436, wherein the numbering is that of the EU index as in Kabat. In particular, two or more substitutions selected from: T250Q, M252Y, S254T, T256E, K288D, T307Q, V308P, A378V, M428L, N434A, H435K, and Y436I, wherein the numbering is that of the EU index as in Kabat.

[00117] In a specific embodiment, an immunoconjugate of the present invention possesses a variant IgG Fc Region comprising the substitutions:

(A) M252Y, S254T and T256E;

(B) M252Y and S254T;

(C) M252Y and T256E;

(D) T250Q and M428L;

(E) T307Q and N434A;

(F) A378V and N434A;

(G) N434A and Y436I;

(H) V308P and N434A; or

(I) K288D and H435K.

[00118] In a preferred embodiment, the immunoconjugate of the present invention possesses a variant IgG Fc Region comprising any 1, 2, or 3 of the substitutions: M252Y, S254T and T256E. The invention further encompasses immunoconjugates possessing variant Fc Regions comprising:

(A) one or more mutations which alter effector function and/or FcγR; and

(B) one or more mutations which extend serum half-life.

[00119] A fourth preferred IgG1 sequence for the CH2 and CH3 Domains of the Fc Region-containing immunoconjugates of the present invention comprises the M252Y, S254T and T256E substitutions (shown underlined), so as to extend the serum half-life. The amino acid sequence of such molecule is (**SEQ ID NO:147**):

APELLGGPSV FLFPPKPKDT L**Y**I**T**R**E**PEVT CVVVDVSHED PEVKFNWYVD
GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKALPA
PIEKTISKAK GQPREPQVYT LPPSREEMTK NQVSLTCLVK GFYPSDIAVE
WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE
ALHNHYTQKS LSLSPG**X**

wherein, **X** is a lysine (K) or is absent.

[00120] A fifth preferred IgG1 sequence for the CH2 and CH3 Domains of the Fc Region-containing immunoconjugates of the present invention comprises the M252Y, S254T and T256E substitutions (shown underlined), so as to extend the serum half-life, and the S442C substitution (shown underlined), so as to permit two CH3 domains to be covalently bonded to one another via a disulfide bond or to permit conjugation of a drug moiety. The amino acid sequence of such molecule is (**SEQ ID NO: 148**):

APELLGGPSV FLFPPKPKDT L**Y**I**T**R**E**PEVT CVVVDVSHED PEVKFNWYVD
GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKALPA
PIEKTISKAK GQPREPQVYT LPPSREEMTK NQVSLTCLVK GFYPSDIAVE
WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE
ALHNHYTQKS L**C**LSPG**X**

wherein, **X** is a lysine (K) or is absent.

[00121] A sixth preferred IgG1 sequence for the CH2 and CH3 Domains of the Fc Region-containing immunoconjugates of the present invention comprises the L234A/L235A substitutions (shown underlined) that reduce or abolish effector function and the M252Y,

S254T and T256E substitutions (shown underlined), so as to extend the serum half-life. The amino acid sequence of such molecule is (**SEQ ID NO: 149**):

APE**AA**GGPSV FLFPPKPKDT L**Y**I**T**R**E**PEVT CVVVDVSHED PEVKFNWYVD
GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKALPA
PIEKTISKAK GQPREPQVYT LPPSREEMTK NQVSLTCLVK GFYPSDIAVE
WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE
ALHNHYTQKS LSLSPG**X**

wherein, **X** is a lysine (K) or is absent.

[00122] A seventh preferred IgG1 sequence for the CH2 and CH3 Domains of the Fc Region-containing immunoconjugates of the present invention comprises the L234A/L235A substitutions (shown underlined) that reduce or abolish effector function and the M252Y, S254T and T256E substitutions (shown underlined), so as to extend the serum half-life and the S442C substitution (shown underlined), so as to permit two CH3 domains to be covalently bonded to one another via a disulfide bond or to permit conjugation of a drug moiety. The amino acid sequence of such molecule is (**SEQ ID NO:150**):

APE**AA**GGPSV FLFPPKPKDT L**Y**I**T**R**E**PEVT CVVVDVSHED PEVKFNWYVD
GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK CKVSNKALPA
PIEKTISKAK GQPREPQVYT LPPSREEMTK NQVSLTCLVK GFYPSDIAVE
WESNGQPENN YKTTPPVLDS DGSFFLYSKL TVDKSRWQQG NVFSCSVMHE
ALHNHYTQKS L**C**LSPG**X**

wherein, **X** is a lysine (K) or is absent.

II. Exemplary Anti-ADAM9 Antibodies

[00123] The invention provides particular antibodies and antigen-binding fragments thereof capable of specifically binding to ADAM9 useful in the generation of the immunoconjugates of the invention.

[00124] A representative human ADAM9 polypeptide (NCBI Sequence NP_003807, including a 28 amino acid residue signal sequence, shown underlined) has the amino acid sequence (**SEQ ID NO:5**):

MGSGARFPSG TLRVRWLLLL GLVGPVLGAA RPGFQQTSHL SSYEIITPWR
LTRERREAPR PYSKQVSYVI QAEGKEHIIH LERNKDLLPE DFVVYTYNKE
GTLITDHPNI QNHCHYRGYV EGVHNSSIAL SDCFGLRGLL HLENASYGIE
PLQNSSHFEH IIYRMDDVYK EPLKCGVSNK DIEKETAKDE EEEPPSMTQL
LRRRRAVLPQ TRYVELFIVV DKERYDMMGR NQTAVREEMI LLANYLDSMY
IMLNIRIVLV GLEIWTNGNL INIVGGAGDV LGNFVQWREK FLITRRRHDS
AQLVLKKGFG GTAGMAFVGT VCSRSHAGGI NVFGQITVET FASIVAHELG

HNLGMNHDDG RDCSCGAKSC IMNSGASGSR NFSSCSAEDF EKLTLNKGGN
CLLNIPKPDE AYSAPSCGNK LVDAGEECDC GTPKECELDP CCEGSTCKLK
SFAECAYGDC CKDCRFLPGG TLCRGKTSEC DVPEYCNGSS QFCQPDVFIQ
NGYPCQNNKA YCYNGMCQYY DAQCQVIFGS KAKAAPKDCF IEVNSKGDRF
GNCGFSGNEY KKCATGNALC GKLQCENVQE IPVFGIVPAI IQTPSRGTKC
WGVDFQLGSD VPDPGMVNEG TKCGAGKICR NFQCVDASVL NYDCDVQKKC
HGHGVCNSNK NCHCENGWAP PNCETKGYGG SVDSGPTYNE MNTALRDGLL
VFFFLIVPLI VCAIFIFIKR DQLWRSYFRK KRSQTYESDG KNQANPSRQP
GSVPRHVSPV TPPREVPIYA NRFAVPTYAA KQPQQFPSRP PPPQPKVSSQ
GNLIPARPAP APPLYSSLT

Of the 819 amino acid residues of ADAM9 (**SEQ ID NO:5**), residues 1-28 are a signal sequence, residues 29-697 are the Extracellular Domain, residues 698-718 are the Transmembrane Domain, and residues 719-819 are the Intracellular Domain. Three structural domains are located within the Extracellular Domain: a Reprolysin (M12B) Family Zinc Metalloprotease Domain (at approximately residues 212-406); a Disintegrin Domain (at approximately residues 423-497); and an EGF-like Domain (at approximately residues 644-697). A number of post-translational modifications and isoforms have been identified and the protein is proteolytically cleaved in the trans-Golgi network before it reaches the plasma membrane to generate a mature protein. The removal of the pro-domain occurs via cleavage at two different sites. Processed most likely by a pro-protein convertase such as furin, at the boundary between the pro-domain and the catalytic domain (Arg-205/Ala-206). An additional upstream cleavage pro-protein convertase site (Arg-56/Glu-57) has an important role in the activation of ADAM9.

[00125] A representative cynomolgus monkey ADAM9 polypeptide (NCBI Sequence XM_005563126.2, including a possible 28 amino acid residue signal sequence, shown underlined) has the amino acid sequence (**SEQ ID NO:6**):

MGSGVGSPSG TLRVRWLLLL CLVGPVLGAA RPGFQQTSHL SSYEIITPWR
LTRERREAPR PYSKQVSYLI QAEGKEHIIH LERNKDLLPE DFVVYTYNKE
GTVITDHPNI QNHCHFRGYV EGVYNSSVAL SNCFGLRGLL HLENASYGIE
PLQNSSHFEH IIYRMDDVHK EPLKCGVSNK DIEKETTKDE EEEPPSMTQL
LRRRRAVLPQ TRYVELFIVV DKERYDMMGR NQTAVREEMI LLANYLDSMY
IMLNIRIVLV GLEIWTNGNL INIAGGAGDV LGNFVQWREK FLITRRRHDS
AQLVLKKGFG GTAGMAFVGT VCSRSHAGGI NVFGHITVET FASIVAHELG
HNLGMNHDDG RDCSCGAKSC IMNSGASGSR NFSSCSAEDF EKLTLNKGGN
CLLNIPKPDE AYSAPSCGNK LVDAGEECDC GTPKECELDP CCEGSTCKLK
SFAECAYGDC CKDCRFLPGG TLCRGKTSEC DVPEYCNGSS QFCQPDVFIQ
NGYPCQNNKA YCYNGMCQYY DAQCQVIFGS KAKAAPKDCF IEVNSKGDRF
GNCGFSGNEY KKCATGNALC GKLQCENVQE IPVFGIVPAI IQTPSRGTKC

WGVDFQLGSD VPDPGMVNEG TKCGADKICR NFQCVDASVL NYDCDIQKKC
HGHGVCNSNK NCHCENGWAP PNCETKGYGG SVDSGPTYNE MNTALRDGLL
VFFFLIVPLI VCAIFIFIKR DQLWRRYFRK KRSQTYESDG KNQANPSRQP
VSVPRHVSPV TPPREVPIYA NRFPVPTYAA KQPQQFPSRP PPPQPKVSSQ
GNLIPARPAP APPLYSSLT

The Reprolysin (M12B) Family Zinc Metalloprotease Domain of the protein is at approximately residues 212-406); the Disintegrin Domain of the protein is at approximately residues 423-497.

[00126] In certain embodiments, anti-ADAM9 antibodies and ADAM9-binding fragments thereof of the invention are characterized by any one, two, three, four, five, six, seven, eight, or nine of the following criteria:

(1) the ability to immunospecifically bind human ADAM9 as endogenously expressed on the surface of a cancer cell;

(2) specifically binds human and non-human primate ADAM9 (*e.g.*, ADAM9 of cynomolgus monkey) with a similar binding affinity;

(3) specifically binds human ADAM9 with an equilibrium binding constant (K_D) of 4 nM or less;

(4) specifically binds non-human primate ADAM9 with an equilibrium binding constant (K_D) of 4 nM or less

(5) specifically binds human ADAM9 with an on rate (ka) of 5×10^5 $M^{-1}min^{-1}$ or more;

(6) specifically binds non-human primate ADAM9 with an on rate (ka) of 1×10^6 $M^{-1}min^{-1}$ or more;

(7) specifically binds human ADAM9 with an off rate (kd) of 1×10^{-3} min^{-1} or less;

(8) specifically binds non-human primate ADAM9 with an off rate (kd) of 9×10^{-4} min^{-1} or less.

(9) optimized to have at least 100-fold enhancement (e.g., at least 100-fold, at least 150-fold, at least 200-fold, at least 250-fold, at least 300-fold, at least 350-fold, at least 400-fold, at least 450-fold, at least 500-fold, at least 550-fold, or at least 600-fold enhancement) in binding affinity (e.g., as measured by BIACORE® analysis) to cyno ADAM9 and retains high affinity binding to human ADAM9 (e.g., BIACORE® analysis) as compared to the chimeric or murine parental antibody.

[00127] As described herein, the binding constants of an anti-ADAM9 antibody or ADAM9-binding fragment thereof may be determined using surface plasmon resonance *e.g.*, via a BIACORE® analysis. Surface plasmon resonance data may be fitted to a 1:1 Langmuir binding model (simultaneous ka kd) and an equilibrium binding constant K_D calculated from the ratio of rate constants kd/ka. Such binding constants may be determined for a monovalent anti-ADAM9 antibody or ADAM9-binding fragment thereof (*i.e.*, a molecule comprising a single ADAM9 epitope-binding site), a bivalent anti-ADAM9 antibody or ADAM9-binding fragment thereof (*i.e.*, a molecule comprising two ADAM9 epitope-binding sites), or anti-ADAM9 antibodies and ADAM9-binding fragments thereof having higher valency (*e.g.*, a molecule comprising three, four, or more ADAM9 epitope-binding sites).

[00128] The present invention particularly encompasses immunoconjugates possessing an anti-ADAM9 antibody or an ADAM9-binding fragment thereof comprising an anti-ADAM9 Light Chain Variable (VL) Domain and an anti-ADAM9 Heavy Chain Variable (VH) Domain that immunospecifically bind to an epitope of a human ADAM9 polypeptide. Unless otherwise stated, all such anti-ADAM9 antibodies and ADAM9-binding fragment thereof are capable of immunospecifically binding to human ADAM9. As used herein such ADAM9 Variable Domains are referred to as "**anti-ADAM9-VL**" and "**anti-ADAM9-VH**," respectively.

A. Murine Anti-Human ADAM9 Antibodies

[00129] A murine anti-ADAM9 antibody that blocks the target protein processing activity of ADAM9, is internalized and having anti-tumor activity was identified (see, *e.g.*, US Patent No. 8,361,475). This antibody, designated in US Patent Nos. 7,674,619 and 8,361,475 as an "anti-KID24" antibody produced by hybridoma clone ATCC PTA-5174, is designated herein as "**MAB-A**." MAB-A exhibits strong preferential binding to tumors over normal tissues (see, **FIGs. 7A-7C**). MAB-A exhibited little or no staining across a large panel of normal cell types (**Table 2**).

Table 2

Tissue	MAB-A **(1.25 µg/mL)**
Adrenal	Negative
Bladder	Negative

Table 2	
Tissue	MAB-A (**1.25 µg/mL**)
Bone Marrow	Negative
Breast	Negative
Cerebellum	Negative
Cerebrum	ND
Cervix	Negative
Colon	Negative
Esophagus	Smooth Muscle +/- to 1+ (gr c) <5%
Ovaduct	Negative
Heart	Negative
Kidney	Negative
Liver	Negative
Lung	Negative
Lymph Node	Negative
Ovary	Negative
Pancreas	Very rare (possible acinar) 1+ (c)
Parathyroid	Epithelium parenchymal cells 1+ (gr c), 1% Cells (favor chief cells) 2+ (m,c)5% 1+ (m,c) 10% apical primarily
Pituitary	Posterior lobe cells (possibly neural cells and/or pituicytes 1+ (c>m) <5%
Placenta	Vascular lining cells within chorionic plate 1+ (gr c>m) Mesenchymal cells of chorionic plate 1-2+ (gr c),5%
Prostate	Glandular epithelium 2+ (gr c)5% and 1+ (gr c) 5%
Retina + Ciliary Body	Favor negative (pigmented epi layer 3-4+ (gr c) due to pigment not stained)
Submandibular Gland	Ductal epi +/- (c) 10%
Skeletal Muscle	Negative
Skin	Negative
Small Intestine	Negative
Spinal Cord	Neuropil 1+ (gr c) <1%
Spleen	Negative

Table 2	
Tissue	MAB-A **(1.25 µg/mL)**
Stomach	Negative
Testis	Seminiferous tubule 1+ (gr c) <5% Interstitial cells (possibly Leydig cells) 2-3+ (gr c) <5% and 1+ (gr c) 10%
Thyroid	Negative
Tonsil	Endo cells 2-3+ (c,m) <5% and 1+ (m,c) 15%
Ureter	Transitional epithelium 1+ (m,c) <5% and 1+ (m,c) 5%; Endo cells 1+ (c) <5%
Uterus	Negative
A498 Cell Pellet	2-3+ (m,c), 50%, 1+ (m,c) 45%

[00130] As shown in **FIG. 2**, MAB-A binds human ADAM9 with high affinity, but binds non-human primate (*e.g.*, cynomolgus monkey) ADAM9 to a lesser extent.

[00131] The amino acid sequences of the VL and VH Domains of MAB-A are provided below. The VH and VL Domains of MAB-A were humanized and the CDRs optimized to improve affinity and/or to remove potential amino acid liabilities. The CDR_H3 was further optimized to enhance binding to non-human primate ADAM9 while maintaining its high affinity for human ADAM9.

[00132] The preferred immunoconjugates of the present invention comprising 1, 2 or all 3 of the CDR_Hs of a VH Domain and/or 1, 2 or all 3 of the CDR_Ls of the VL Domain of an optimized variant of MAB-A, and preferably further possess the humanized framework regions ("**FRs**") of the VH and/or VL Domains of humanized MAB-A. Other preferred immunoconjugates of the present invention possess the entire VH and/or VL Domains of a humanized/optimized variant of MAB-A.

[00133] The invention particularly relates to immunoconjugates comprising:

(A) (1) the three CDR_Hs of the VH Domain of MAB-A; and

(2) the four FRs of the VH Domain of a humanized variant of MAB-A; or

(B) (1) the three CDR_Ls of the VL Domain of MAB-A; and

(2) the four FRs of the VL Domain of a humanized variant of MAB-A; or

(C) the three CDR_Hs of the VH Domain of an optimized variant of MAB-A; and the three CDR_Ls of the VL Domain of MAB-A; or

(D) the three CDR_Hs of the VH Domain of MAB-A; and the three CDR_Ls of the VL Domain of an optimized variant MAB-A; or

(E) the three CDR_Hs of the VH Domain of an optimized variant of MAB-A; and the three CDR_Ls of the VL Domain of an optimized MAB-A; or

(F) (1) the three CDR_Hs of the VH Domain of an optimized variant of MAB-A; and

(2) the four FRs of the VH Domain of a humanized variant of MAB-A; or

(G) (1) the three CDR_Ls of the VL Domain of an optimized variant of MAB-A; and

(2) the four FRs of the VL Domain of a humanized variant of MAB-A; or

(H) (1) the VH Domain of a humanized/optimized variant of MAB-A; and

(2) the VL Domain of a humanized/optimized variant of MAB-A. Murine Antibody "MAB-A"

[00134] The amino acid sequence of the VH Domain of the murine anti-ADAM9 antibody MAB-A is **SEQ ID NO:7** (the CDR_H residues are shown underlined):

QVQLQQPGAE LVKPGASVKL SCKASGYTFT **SYWMH**WVKQR PGQGLEWIG**E**
IIPINGHTNY **NEKFKS**KATL TLDKSSSTAY MQLSSLASED SAVYYCAR**GG**
YYYYGSRDYF **DY**WGQGTTLT VSS

[00135] The amino acid sequence of the CDR_H1 Domain of MAB-A is (**SEQ ID NO:8**): SYWMH.

[00136] The amino acid sequence of the CDR_H2 Domain of MAB-A is (**SEQ ID NO:9**): EIIPINGHTNYNEKFKS.

[00137] The amino acid sequence of the CDR_H3 Domain of MAB-A is (**SEQ ID NO:10**): GGYYYYGSRDYFDY.

[00138] The amino acid sequence of the VL Domain of the murine anti-ADAM9 antibody MAB-A is **SEQ ID NO:11** (the CDR_L residues are shown underlined):

DIVLTQSPAS LAVSLGQRAT ISC**KASQSVD** **YDGDSYMN**WY QQIPGQPPKL LIY**AASDLES** GIPARFSGSG SGTDFTLNIH PVEEEDAATY YC**QQSHEDPF** **T**FGGGTKLEI K

[00139] The amino acid sequence of the CDR_L1 Domain of MAB-A is (**SEQ ID NO:12**): KASQSVDYDGDSYMN.

[00140] The amino acid sequence of the CDR_L2 Domain of MAB-A is (**SEQ ID NO:13**): AASDLES.

[00141] The amino acid sequence of the CDR_L3 Domain of MAB-A is (**SEQ ID NO:14**): QQSHEDPFT.

B. Exemplary Humanized/Optimized Anti-ADAM9-VH and VL Domains

1. Variant VH Domains of MAB-A

[00142] The amino acid sequences of certain preferred humanized/optimized anti-ADAM9-VH Domains of MAB-A are variants of the ADAM9-VH Domain of MAB-A (**SEQ ID NO:7**) and are represented by **SEQ ID NO:15** (CDR_H residues are shown underlined):

EVQLVESGGG LVKPGGSLRL SCAASGFTFS **SYWX$_1$H**WVRQA
PGKGLEWVG**E** **IIPIX$_2$GHTNY** **NEX$_3$FX$_4$X$_5$**RFTI SLDNSKNTLY
LQMGSLRAED TAVYYCAR**GG** **YYYYX$_6$X$_7$X$_8$X$_9$X$_{10}$X$_{11}$** **DY**WGQGTTVT
VSS

wherein: X_1, X_2, X_3, X_4, X_5, and X_6 are independently selected,

wherein: X_1 is M or I; X_2 is N or F;

X_3 is K or R; X_4 is K or Q;

X_5 is S or G, and X_6 is P, F, Y, W, I, L, V, T, G or D;

wherein: X_7, X_8, X_9, X_{10}, and X_{11} are selected such that:

(A) when X_6 is P:

X_7 is K or R;

X_8 is F or M;

X_9 is G;

X_{10} is W or F; and

X_{11} is M, L or K;

(B) when X_6 is F, Y or W:

X_7 is N or H;

X_8 is S or K;

X_9 is G or A;

X_{10} is T or V; and

X_{11} is M, L or K;

(C) when X_6 is I, L or V:

(D) when X_6 is T:

X_7 is G;
X_8 is K;
X_9 is G or A;
X_{10} is V; and
X_{11} is M, L or K;

X_7 is G;
X_8 is K, M or N;
X_9 is G;
X_{10} is V or T; and
X_{11} is L or M;

(E) when X_6 is G:

X_7 is G;
X_8 is S;
X_9 is G;
X_{10} is V; and
X_{11} is L;

and (F) when X_6 is D:

X_7 is S;
X_8 is N;
X_9 is A;
X_{10} is V; and
X_{11} is L.

[00143] The amino acid sequences of a preferred humanized anti-ADAM9 VH Domain of MAB-A: hMAB-A VH(1) (**SEQ ID NO:16**) and of the certain preferred humanized/optimized anti-ADAM9-VH Domains of MAB-A:

hMAB-A VH(2) (**SEQ ID NO:17**)
hMAB-A VH(3) (**SEQ ID NO:18**)
hMAB-A VH(4) (**SEQ ID NO:19**)
hMAB-A VH(2A) (**SEQ ID NO:20**)
hMAB-A VH(2B) (**SEQ ID NO:21**)
hMAB-A VH(2C) (**SEQ ID NO:22**)
hMAB-A VH(2D) (**SEQ ID NO:23**)
hMAB-A VH(2E) (**SEQ ID NO:24**)
hMAB-A VH(2F) (**SEQ ID NO:25**)
hMAB-A VH(2G) (**SEQ ID NO:26**)
hMAB-A VH(2H) (**SEQ ID NO:27**)
hMAB-A VH(2I) (**SEQ ID NO:28**)
and hMAB-A VH(2J) (**SEQ ID NO:29**)
are presented below (CDR_H residues are shown in single underline; differences relative to hMAB-A VH(1) (**SEQ ID NO:7**) are shown in double underline).

hMAB-A VH(1) (**SEQ ID NO:16**):

EVQLVESGGG LVKPGGSLRL SCAASGFTFS **SYWMH**WVRQA PGKGLEWVG**E**
IIPINGHTNY **NEKFKS**RFTI SLDNSKNTLY LQMGSLRAED TAVYYCAR**GG**
YYYYGSRDYF **DY**WGQGTTVT VSS

hMAB-A VH(2) (**SEQ ID NO:17**):

EVQLVESGGG LVKPGGSLRL SCAASGFTFS **SYWMH**WVRQA PGKGLEWVG**E**
IIPIF**GHTNY** **NEKFKS**RFTI SLDNSKNTLY LQMGSLRAED TAVYYCAR**GG**
YYYYGSRDYF **DY**WGQGTTVT VSS

hMAB-A VH(3) (**SEQ ID NO:18**):

EVQLVESGGG LVKPGGSLRL SCAASGFTFS **SYWMH**WVRQA PGKGLEWVG**E**
IIPIFGHTNY NERFQGRFTI SLDNSKNTLY LQMGSLRAED TAVYYCAR**GG**
YYYYGSRDYF DYWGQGTTVT VSS

hMAB-A VH(4) (**SEQ ID NO:19**):

EVQLVESGGG LVKPGGSLRL SCAASGFTFS **SYWIH**WVRQA PGKGLEWVG**E**
IIPIFGHTNY NERFQGRFTI SLDNSKNTLY LQMGSLRAED TAVYYCAR**GG**
YYYYGSRDYF DYWGQGTTVT VSS

hMAB-A VH(2A) (**SEQ ID NO:20**):

EVQLVESGGG LVKPGGSLRL SCAASGFTFS **SYWMH**WVRQA PGKGLEWVG**E**
IIPIFGHTNY NEKFKSRFTI SLDNSKNTLY LQMGSLRAED TAVYYCAR**GG**
YYYYFNSGTL DYWGQGTTVT VSS

hMAB-A VH(2B) (**SEQ ID NO:21**):

EVQLVESGGG LVKPGGSLRL SCAASGFTFS **SYWMH**WVRQA PGKGLEWVG**E**
IIPIFGHTNY NEKFKSRFTI SLDNSKNTLY LQMGSLRAED TAVYYCAR**GG**
YYYYIGKGVL DYWGQGTTVT VSS

hMAB-A VH(2C) (**SEQ ID NO:22**):

EVQLVESGGG LVKPGGSLRL SCAASGFTFS **SYWMH**WVRQA PGKGLEWVG**E**
IIPIFGHTNY NEKFKSRFTI SLDNSKNTLY LQMGSLRAED TAVYYCAR**GG**
YYYYPRFGWL DYWGQGTTVT VSS

hMAB-A VH(2D) (**SEQ ID NO:23**):

EVQLVESGGG LVKPGGSLRL SCAASGFTFS **SYWMH**WVRQA PGKGLEWVG**E**
IIPIFGHTNY NEKFKSRFTI SLDNSKNTLY LQMGSLRAED TAVYYCAR**GG**
YYYYTGKGVL DYWGQGTTVT VSS

hMAB-A VH(2E) (**SEQ ID NO:24**):

EVQLVESGGG LVKPGGSLRL SCAASGFTFS **SYWMH**WVRQA PGKGLEWVG**E**
IIPIFGHTNY NEKFKSRFTI SLDNSKNTLY LQMGSLRAED TAVYYCAR**GG**
YYYYDSNAVL DYWGQGTTVT VSS

hMAB-A VH(2F) (**SEQ ID NO:25**):

EVQLVESGGG LVKPGGSLRL SCAASGFTFS **SYWMH**WVRQA PGKGLEWVG**E**
IIPIFGHTNY NEKFKSRFTI SLDNSKNTLY LQMGSLRAED TAVYYCAR**GG**
YYYYFHSGTL DYWGQGTTVT VSS

hMAB-A VH(2G) (**SEQ ID NO:26**):

EVQLVESGGG LVKPGGSLRL SCAASGFTFS **SYWMH**WVRQA PGKGLEWVG**E**
IIPIFGHTNY NEKFKSRFTI SLDNSKNTLY LQMGSLRAED TAVYYCAR**GG**
YYYYFNKAVL DYWGQGTTVT VSS

hMAB-A VH(2H) (**SEQ ID NO:27**):

EVQLVESGGG LVKPGGSLRL SCAASGFTFS **SYWMH**WVRQA PGKGLEWVG**E**
IIPIFGHTNY NEKFKSRFTI SLDNSKNTLY LQMGSLRAED TAVYYCAR**GG**
YYYYGGSGVL DYWGQGTTVT VSS

hMAB-A VH(2I) (**SEQ ID NO:28**):

EVQLVESGGG LVKPGGSLRL SCAASGFTFS **SYWMH**WVRQA PGKGLEWVG**E**
IIPIFGHTNY NEKFKSRFTI SLDNSKNTLY LQMGSLRAED TAVYYCAR**GG**
YYYYPRQGFL DYWGQGTTVT VSS

hMAB-A VH(2J) (**SEQ ID NO:29**):

EVQLVESGGG LVKPGGSLRL SCAASGFTFS **SYWMH**WVRQA PGKGLEWVG**E**
IIPIFGHTNY NEKFKSRFTI SLDNSKNTLY LQMGSLRAED TAVYYCAR**GG**
YYYYYNSGTL DYWGQGTTVT VSS

[00144] Suitable amino acid sequences for the FRs of a humanized and/or optimized anti-ADAM9-VH Domain of MAB-A are:

FR_H1 Domain (**SEQ ID NO:30**): EVQLVESGGGLVKPGGSLRLSCAASGFTFS

FR_H2 Domain (**SEQ ID NO:31**): WVRQAPGKGLEWVG

FR_H3 Domain (**SEQ ID NO:32**): RFTISLDNSKNTLYLQMGSLRAEDTAVYYCAR

FR_H4 Domain (**SEQ ID NO:33**): WGQGTTVTVSS

[00145] Suitable alternative amino acid sequences for the CDR_H1 Domain of an anti-ADAM9-VH Domain include:

SEQ ID NO:8: SYWMH

SEQ ID NO:34: SYWIH

[00146] Suitable alternative amino acid sequences for the CDR_H2 Domain of an anti-ADAM9-VH Domain include:

SEQ ID NO:9: EIIPINGHTNYNEKFKS

SEQ ID NO:35: EIIPIFGHTNYNEKFKS

SEQ ID NO:36: EIIPIFGHTNYNERFQG

[00147] Suitable alternative amino acid sequences for the CDR_H3 Domain of an anti-ADAM9-VH Domain include:

SEQ ID NO:10: GGYYYYGSRDYFDY

SEQ ID NO:37: GGYYYYFNSGTLDY

SEQ ID NO:38: GGYYYYIGKGVLDY

SEQ ID NO:39: GGYYYYPRFGWLDY

SEQ ID NO:40: GGYYYYTGKGVLDY

SEQ ID NO:41: GGYYYYDSNAVLDY

SEQ ID NO:42: GGYYYYFHSGTLDY

SEQ ID NO:43: GGYYYYFNKAVLDY

SEQ ID NO:44: GGYYYYGGSGVLDY

SEQ ID NO:45: GGYYYYPRQGFLDY

SEQ ID NO:46: GGYYYYYNSGTLDY

[00148] Accordingly, the present invention encompasses ADAM9 binding molecules having a VH domain comprising:

(1) a CDR_H1 Domain having the amino acid sequence:

SEQ ID NO:47: $SYWX_1H$

wherein: $\mathbf{X_1}$ is M or I;

(2) a CDR_H2 Domain having the amino acid sequence:

SEQ ID NO:48: $EIIPIX_2GHTNYNEX_3FX_4X_5$

wherein: $\mathbf{X_2}$, $\mathbf{X_3}$, $\mathbf{X_4}$, and $\mathbf{X_5}$ are independently selected, and

wherein: $\mathbf{X_2}$ is N or F; $\mathbf{X_3}$ is K or R;

$\mathbf{X_4}$ is K or Q; and $\mathbf{X_5}$ is S or G.

and

(3) a CDR_H3 Domain having the amino acid sequence:

SEQ ID NO:49: $GGYYYYX_6X_7X_8X_9X_{10}X_{11}DY$

wherein: $\mathbf{X_6}$, is P, F, Y, W, I, L, V, T, G or D, and $\mathbf{X_7}$, $\mathbf{X_8}$, $\mathbf{X_9}$, $\mathbf{X_{10}}$, and $\mathbf{X_{11}}$ are selected such that:

(A) when $\mathbf{X_6}$ is P:
$\mathbf{X_7}$ is K or R;
$\mathbf{X_8}$ is F or M;
$\mathbf{X_9}$ is G;
$\mathbf{X_{10}}$ is W or F; and
$\mathbf{X_{11}}$ is M, L or K;

(B) when $\mathbf{X_6}$ is F, Y or W:
$\mathbf{X_7}$ is N or H;
$\mathbf{X_8}$ is S or K;
$\mathbf{X_9}$ is G or A;
$\mathbf{X_{10}}$ is T or V; and
$\mathbf{X_{11}}$ is M, L or K;

(C) when $\mathbf{X_6}$ is I, L or V:
$\mathbf{X_7}$ is G;
$\mathbf{X_8}$ is K;
$\mathbf{X_9}$ is G or A;
$\mathbf{X_{10}}$ is V; and
$\mathbf{X_{11}}$ is M, L or K;

(D) when $\mathbf{X_6}$ is T:
$\mathbf{X_7}$ is G;
$\mathbf{X_8}$ is K, M or N;
$\mathbf{X_9}$ is G;
$\mathbf{X_{10}}$ is V or T; and
$\mathbf{X_{11}}$ is L or M;

(E) when $\mathbf{X_6}$ is G:
$\mathbf{X_7}$ is G;
$\mathbf{X_8}$ is S;
$\mathbf{X_9}$ is G;
$\mathbf{X_{10}}$ is V; and
$\mathbf{X_{11}}$ is L;

and

(F) when $\mathbf{X_6}$ is D:
$\mathbf{X_7}$ is S;
$\mathbf{X_8}$ is N;
$\mathbf{X_9}$ is A;
$\mathbf{X_{10}}$ is V; and
$\mathbf{X_{11}}$ is L.

[00149] A first exemplary humanized/optimized IgG1 Heavy Chain of a derivative/variant of MAB-A contains the hMAB-A **VH (2)** Domain (**SEQ ID NO:17**), and has the amino acid sequence (**SEQ ID NO:50**):

EVQLVESGGG LVKPGGSLRL SCAASGFTFS SYWMHWVRQA PGKGLEWVGE
IIPIFGHTNY NEKFKSRFTI SLDNSKNTLY LQMGSLRAED TAVYYCARGG
YYYYGSRDYF DYWGQGTTVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG
TQTYICNVNH KPSNTKVDKR VEPKSCDKTH TCPPCPAPEL LGGPSVFLFP
PKPKDTLMIS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE
QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR
EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT
PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS
PGX

wherein X is a lysine (K) or is absent.

[00150] A second exemplary humanized/optimized IgG1 Heavy Chain of a derivative/variant of MAB-A contains the hMAB-A **VH (2C)** Domain (**SEQ ID NO:22**), and has the amino acid sequence (**SEQ ID NO:51**):

EVQLVESGGG LVKPGGSLRL SCAASGFTFS SYWMHWVRQA PGKGLEWVGE
IIPIFGHTNY NEKFKSRFTI SLDNSKNTLY LQMGSLRAED TAVYYCARGG
YYYYPRFGWL DYWGQGTTVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG
TQTYICNVNH KPSNTKVDKR VEPKSCDKTH TCPPCPAPEL LGGPSVFLFP
PKPKDTLMIS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE
QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR
EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT
PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS
PGX

wherein X is a lysine (K) or is absent.

[00151] A third exemplary humanized/optimized IgG1 Heavy Chain of a derivative/variant of MAB-A contains the hMAB-A **VH (2I)** Domain (**SEQ ID NO:28**), and has the amino acid sequence (**SEQ ID NO:52**):

EVQLVESGGG LVKPGGSLRL SCAASGFTFS SYWMHWVRQA PGKGLEWVGE
IIPIFGHTNY NEKFKSRFTI SLDNSKNTLY LQMGSLRAED TAVYYCARGG
YYYYPRQGFL DYWGQGTTVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG
TQTYICNVNH KPSNTKVDKR VEPKSCDKTH TCPPCPAPEL LGGPSVFLFP
PKPKDTLMIS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE
QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR
EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT
PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS
PGX

wherein X is a lysine (K) or is absent.

[00152] As provided above, the CH2-CH3 Domains of the Fc Region may be engineered for example, to reduce effector function and/or to introduce a conjugation site and/or to extend the serum half-life. In certain embodiments, the CH2-CH3 Domains of the exemplary humanized/optimized IgG1 Heavy Chains of the invention comprise one or more substitutions selected from: L234A, L235A, M252Y, S254T, T256E and S442C.

[00153] Thus, a fourth exemplary humanized/optimized IgG1 Heavy Chain of a derivative/variant of MAB-A contains the hMAB-A **VH (2I)** Domain (**SEQ ID NO:28**), and further comprises the substitutions L234A, and L235A in the CH2-CH3 Domains of the Fc Region (**SEQ ID NO:78**) and has the amino acid sequence (**SEQ ID NO:141**)

EVQLVESGGG LVKPGGSLRL SCAASGFTFS SYWMHWVRQA PGKGLEWVGE
IIPIFGHTNY NEKFKSRFTI SLDNSKNTLY LQMGSLRAED TAVYYCARGG
YYYYPRQGFL DYWGQGTTVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG
TQTYICNVNH KPSNTKVDKR VEPKSCDKTH TCPPCPAPE**A** **A**GGPSVFLFP
PKPKDTLMIS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE
QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR
EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT
PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS
PGX

wherein X is a lysine (K) or is absent.

[00154] A fifth exemplary humanized/optimized IgG1 Heavy Chain of a derivative/variant of MAB-A contains the hMAB-A **VH (2I)** Domain (**SEQ ID NO:28**), and further comprises the S442C substitution in the CH2-CH3 Domains of the Fc Region (**SEQ ID NO:79**) and has the amino acid sequence (**SEQ ID NO:142**):

EVQLVESGGG LVKPGGSLRL SCAASGFTFS SYWMHWVRQA PGKGLEWVGE
IIPIFGHTNY NEKFKSRFTI SLDNSKNTLY LQMGSLRAED TAVYYCARGG
YYYYPRQGFL DYWGQGTTVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG
TQTYICNVNH KPSNTKVDKR VEPKSCDKTH TCPPCPAPEL LGGPSVFLFP
PKPKDTLMIS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE
QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR
EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT
PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSL**C**LS
PGX

wherein X is a lysine (K) or is absent.

[00155] A sixth exemplary humanized/optimized IgG1 Heavy Chain of a derivative/variant of MAB-A contains the hMAB-A **VH (2I)** Domain (**SEQ ID NO:28**), and further comprises the substitutions L234A, L235A and S442C in the CH2-CH3 Domains of the Fc Region (**SEQ ID NO:80**) and has the amino acid sequence (**SEQ ID NO:143**):

EVQLVESGGG LVKPGGSLRL SCAASGFTFS SYWMHWVRQA PGKGLEWVGE
IIPIFGHTNY NEKFKSRFTI SLDNSKNTLY LQMGSLRAED TAVYYCARGG
YYYYPRQGFL DYWGQGTTVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG
TQTYICNVNH KPSNTKVDKR VEPKSCDKTH TCPPCPAPE**A** **A**GGPSVFLFP
PKPKDTLMIS RTPEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE
QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR
EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT

PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLCLS PGX

wherein X is a lysine (K) or is absent.

[00156] A seventh exemplary humanized/optimized IgG1 Heavy Chain of a derivative/variant of MAB-A contains the hMAB-A **VH (2I)** Domain (**SEQ ID NO:28**), and further comprises the substitutions M252Y, S254T and T256E in the CH2-CH3 Domains of the Fc Region (**SEQ ID NO:147**) and has the amino acid sequence (**SEQ ID NO:151**):

EVQLVESGGG LVKPGGSLRL SCAASGFTFS SYWMHWVRQA PGKGLEWVGE
IIPIFGHTNY NEKFKSRFTI SLDNSKNTLY LQMGSLRAED TAVYYCARGG
YYYYPRQGFL DYWGQGTTVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG
TQTYICNVNH KPSNTKVDKR VEPKSCDKTH TCPPCPAPEL LGGPSVFLFP
PKPKDTL**Y**I**T** R**E**PEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE
QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR
EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT
PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS
PGX

wherein **X** is a lysine (K) or is absent.

[00157] In one embodiment, the humanized/optimized IgG1 Heavy Chain of a derivative/variant of MAB-A contains the hMAB-A **VH (2I)** Domain (**SEQ ID NO:28**), and further comprises the substitutions M252Y, S254T and T256E in the CH2-CH3 Domains of the Fc Region (**SEQ ID NO:147**) and has the amino acid sequence (**SEQ ID NO:155**):

EVQLVESGGG LVKPGGSLRL SCAASGFTFS SYWMHWVRQA PGKGLEWVGE
IIPIFGHTNY NEKFKSRFTI SLDNSKNTLY LQMGSLRAED TAVYYCARGG
YYYYPRQGFL DYWGQGTTVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG
TQTYICNVNH KPSNTKVDKR VEPKSCDKTH TCPPCPAPEL LGGPSVFLFP
PKPKDTL**Y**I**T** R**E**PEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE
QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR
EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT
PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS
PG

[00158] An eighth exemplary humanized/optimized IgG1 Heavy Chain of a derivative/variant of MAB-A contains the hMAB-A **VH (2I)** Domain (**SEQ ID NO:28**), and further comprises the substitutions M252Y, S254T, T256E, and S442C in the CH2-CH3

Domains of the Fc Region (**SEQ ID NO:148**) and has the amino acid sequence (**SEQ ID NO:152**):

EVQLVESGGG LVKPGGSLRL SCAASGFTFS SYWMHWVRQA PGKGLEWVGE
IIPIFGHTNY NEKFKSRFTI SLDNSKNTLY LQMGSLRAED TAVYYCARGG
YYYYPRQGFL DYWGQGTTVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG
TQTYICNVNH KPSNTKVDKR VEPKSCDKTH TCPPCPAPEL LGGPSVFLFP
PKPKDTL**Y**I**T** R**E**PEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE
QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR
EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT
PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSL**C**LS
PGX

wherein **X** is a lysine (K) or is absent.

[00159] In one embodiment, the humanized/optimized IgG1 Heavy Chain of a derivative/variant of MAB-A contains the hMAB-A **VH (2I)** Domain (**SEQ ID NO:28**), and further comprises the substitutions M252Y, S254T, T256E, and S442C in the CH2-CH3 Domains of the Fc Region (**SEQ ID NO:148**) and has the amino acid sequence (**SEQ ID NO:156**):

EVQLVESGGG LVKPGGSLRL SCAASGFTFS SYWMHWVRQA PGKGLEWVGE
IIPIFGHTNY NEKFKSRFTI SLDNSKNTLY LQMGSLRAED TAVYYCARGG
YYYYPRQGFL DYWGQGTTVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG
TQTYICNVNH KPSNTKVDKR VEPKSCDKTH TCPPCPAPEL LGGPSVFLFP
PKPKDTL**Y**I**T** R**E**PEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE
QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR
EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT
PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSL**C**LS
PG

[00160] A ninth exemplary humanized/optimized IgG1 Heavy Chain of a derivative/variant of MAB-A contains the hMAB-A **VH (2I)** Domain (**SEQ ID NO:28**), and further comprises the substitutions L234A, L235A, M252Y, S254T and T256E in the CH2-CH3 Domains of the Fc Region (**SEQ ID NO:149**) and has the amino acid sequence (**SEQ ID NO:153**):

EVQLVESGGG LVKPGGSLRL SCAASGFTFS SYWMHWVRQA PGKGLEWVGE
IIPIFGHTNY NEKFKSRFTI SLDNSKNTLY LQMGSLRAED TAVYYCARGG
YYYYPRQGFL DYWGQGTTVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG
TQTYICNVNH KPSNTKVDKR VEPKSCDKTH TCPPCPAPE**A** **A**GGPSVFLFP
PKPKDTL**Y**I**T** R**E**PEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE

QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR
EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT
PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSLSLS
PGX

wherein **X** is a lysine (K) or is absent.

[00161] A tenth exemplary humanized/optimized IgG1 Heavy Chain of a derivative/variant of MAB-A contains the hMAB-A **VH (2I)** Domain (**SEQ ID NO:28**), and further comprises the substitutions L234A, L235A, M252Y, S254T, T256E, and S442C in the CH2-CH3 Domains of the Fc Region (**SEQ ID NO:150**) and has the amino acid sequence (**SEQ ID NO:154**):

EVQLVESGGG LVKPGGSLRL SCAASGFTFS SYWMHWVRQA PGKGLEWVGE
IIPIFGHTNY NEKFKSRFTI SLDNSKNTLY LQMGSLRAED TAVYYCARGG
YYYYPRQGFL DYWGQGTTVT VSSASTKGPS VFPLAPSSKS TSGGTAALGC
LVKDYFPEPV TVSWNSGALT SGVHTFPAVL QSSGLYSLSS VVTVPSSSLG
TQTYICNVNH KPSNTKVDKR VEPKSCDKTH TCPPCPAPE**A** **A**GGPSVFLFP
PKPKDTL**Y**I**T** R**E**PEVTCVVV DVSHEDPEVK FNWYVDGVEV HNAKTKPREE
QYNSTYRVVS VLTVLHQDWL NGKEYKCKVS NKALPAPIEK TISKAKGQPR
EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN GQPENNYKTT
PPVLDSDGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTQKSL**C**LS
PGX

wherein **X** is a lysine (K) or is absent.

2. Variant VL Domains of MAB-A

[00162] The amino acid sequences of preferred humanized/optimized anti-ADAM9-VL Domains of MAB-A are variants of the ADAM9-VL Domain of MAB-A (**SEQ ID NO:11**) and are represented by **SEQ ID NO:53** (CDR_L residues are shown underlined):

DIVMTQSPDS LAVSLGERAT ISC**X_{12}ASQSVD** **YX_{13}GDSYX_{14}N**WY
QQKPGQPPKL LIY**AASDLES** GIPARFSGSG SGTDFTLTIS
SLEPEDFATY YC**QQSX$_{15}$X$_{16}$X$_{17}$PF** **T**FGQGTKLEI K

wherein: X_{12}, X_{13}, X_{14}, X_{15}, X_{16}, and X_{17}, are independently selected, and

wherein: X_{12} is K or R; X_{13} is D or S;
X_{14} is M or L; X_{15} is H or Y;
X_{16} is E or S; and X_{17} is D or T.

[00163] The amino acid sequences of a preferred humanized anti-ADAM9-VL Domain of MAB-A**:** hMAB-A VL(1) (**SEQ ID NO:54**), and of certain preferred humanized/optimized anti-ADAM9-VL Domains of MAB-A: hMAB-A VL(2) (**SEQ ID**

NO:55), hMAB-A VL(3) (**SEQ ID NO:56**), and hMAB-A VL(4) (**SEQ ID NO:57**), are presented below (CDR_L residues are shown in single underline; differences relative to hMAB-A VL(1) (**SEQ ID NO:54**) are shown in double underline).

hMAB-A VL(1) (**SEQ ID NO:54**):

DIVMTQSPDS LAVSLGERAT ISC**KASQSVD YDGDSYMN**WY QQKPGQPPKL
LIY**AASDLES** GIPARFSGSG SGTDFTLTIS SLEPEDFATY YC**QQSHEDPF**
TFGQGTKLEI K

hMAB-A VL(2) (**SEQ ID NO:55**):

DIVMTQSPDS LAVSLGERAT ISC**KASQSVD YSGDSYMN**WY QQKPGQPPKL
LIY**AASDLES** GIPARFSGSG SGTDFTLTIS SLEPEDFATY YC**QQSHEDPF**
TFGQGTKLEI K

hMAB-A VL(3) (**SEQ ID NO:56**):

DIVMTQSPDS LAVSLGERAT ISC**RASQSVD YSGDSYMN**WY QQKPGQPPKL
LIY**AASDLES** GIPARFSGSG SGTDFTLTIS SLEPEDFATY YC**QQSHEDPF**
TFGQGTKLEI K

hMAB-A VL(4) (**SEQ ID NO:57**):

DIVMTQSPDS LAVSLGERAT ISC**RASQSVD YSGDSYLN**WY QQKPGQPPKL
LIY**AASDLES** GIPARFSGSG SGTDFTLTIS SLEPEDFATY YC**QQSYSTPF**
TFGQGTKLEI K

[00164] Accordingly, suitable amino acid sequences for the FRs of a humanized and/or optimized anti-ADAM9-VL Domain of MAB-A are:

FR_L1 Domain (**SEQ ID NO:58**): DIVMTQSPDSLAVSLGERATISC

FR_L2 Domain (**SEQ ID NO:59**): WYQQKPGQPPKLLIY

FR_L3 Domain (**SEQ ID NO:60**): GIPARFSGSGSGTDFTLTISSLEPEDFATYYC

FR_L4 Domain (**SEQ ID NO:61**): FGQGTKLEIK

[00165] Suitable alternative amino acid sequences for the CDR_L1 Domain of an anti-ADAM9-VL Domain include:

SEQ ID NO:12: KASQSVDYDGDSYMN

SEQ ID NO:62: KASQSVDYSGDSYMN

SEQ ID NO:63: RASQSVDYSGDSYMN

SEQ ID NO:64: RASQSVDYSGDSYLN

[00166] Suitable alternative amino acid sequences for the CDR_L3 Domain of an anti-ADAM9-VL Domain include:

SEQ ID NO:14: QQSHEDPFT

SEQ ID NO:65: QQSYSTPFT

[00167] Accordingly, the present invention encompasses anti-ADAM9 antibody VL Domain comprising:

(1) a CDR_L1 Domain having the amino acid sequence:

SEQ ID NO:66: X_{12}ASQSVDYX_{13}GDSYX_{14}N

wherein: $\mathbf{X_{12}}$, $\mathbf{X_{13}}$, $\mathbf{X_{14}}$, are independently selected, and

wherein: $\mathbf{X_{12}}$ is K or R; $\mathbf{X_{13}}$ is D or S; and $\mathbf{X_{14}}$ is M or L;

(2) a CDR_L2 Domain having the amino acid sequence:

SEQ ID NO:13: AASDLES

and

(3) a CDR_L3 Domain having the amino acid sequence:

SEQ ID NO:67: QQS$X_{15}X_{16}X_{17}$PFT

wherein: $\mathbf{X_{15}}$, $\mathbf{X_{16}}$, and $\mathbf{X_{17}}$, are independently selected, and

wherein: $\mathbf{X_{15}}$ is H or Y; $\mathbf{X_{16}}$ is E or S; and $\mathbf{X_{17}}$ is D or T.

[00168] An exemplary humanized/optimized IgG1 Light Chain of a derivative/variant of MAB-A contains the hMAB-A VL (2) Domain (**SEQ ID NO:55**), and has the amino acid sequence (**SEQ ID NO:68**):

DIVMTQSPDS LAVSLGERAT ISCKASQSVD YSGDSYMNWY QQKPGQPPKL
LIYAASDLES GIPARFSGSG SGTDFTLTIS SLEPEDFATY YCQQSHEDPF
TFGQGTKLEI KRTVAAPSVF IFPPSDEQLK SGTASVVCLL NNFYPREAKV
QWKVDNALQS GNSQESVTEQ DSKDSTYSLS STLTLSKADY EKHKVYACEV
THQGLSSPVT KSFNRGEC

[00169] The present invention additionally expressly contemplates immunoconjugates that immunospecifically bind to an epitope of a human ADAM9 polypeptide, and that comprise any of the above-provided MAB-A CDR_H1, CDR_H2, CDR_H3, CDR_L1, CDR_L2, or CDR_L3, and particularly contemplates such immunoconjugates that comprise one of the

above-provided MAB-A CDR_H1, one of the above-provided MAB-A CDR_H2, one of the above-provided MAB-A CDR_H3, one of the above-provided MAB-A CDR_L1, one of the above-provided MAB-A CDR_L2, and one of the above-provided MAB-A CDR_L3. The invention further contemplates such immunoconjugates that further comprise any of the above-provided humanized MAB-A FR_H1, FR_H2, FR_H3, or FR_H4, FR_L1, FR_L2, FR_L3, or FR_L4, and particularly contemplates such immunoconjugates that comprise FR_H1, FR_H2, FR_H3, and FR_H4, and/or that comprise FR_L1, FR_L2, FR_L3, FR_L4 and FR_H1.

[00170] In some embodiments, the humanized/optimized anti-ADAM9 antibody or ADAM9-binding fragment thereof includes a CDR_H1 domain, a CDR_H2 domain, and a CDR_H3 domain and a CDR_L1 domain, a CDR_L2 domain, and a CDR_L3 domain having the sequences selected from the group consisting of:

(a) SEQ ID NOs: 8, 35, and 10 and SEQ ID NOs: 62, 13, 14, respectively;

(b) SEQ ID NOs: 8, 35, and 10 and SEQ ID NOs: 63, 13, 14, respectively;

(c) SEQ ID NOs: 8, 36, and 10 and SEQ ID NOs: 63, 13, 14, respectively;

(d) SEQ ID NOs: 34, 36, and 10 and SEQ ID NO:64, 13, 65, respectively

(e) SEQ ID NOs: 8, 35, and 37 and SEQ ID NOs: 62, 13, 14, respectively;

(f) SEQ ID NOs: 8, 35, and 38 and SEQ ID NOs: 62, 13, 14, respectively;

(g) SEQ ID NOs: 8, 35, and 39 and SEQ ID NOs: 62, 13, 14, respectively;

(h) SEQ ID NOs: 8, 35, and 40 and SEQ ID NOs: 62, 13, 14, respectively;

(i) SEQ ID NOs: 8, 35, and 41 and SEQ ID NOs: 62, 13, 14, respectively;

(j) SEQ ID NOs: 8, 35, and 42 and SEQ ID NOs: 62, 13, 14, respectively;

(k) SEQ ID NOs: 8, 35, and 43 and SEQ ID NOs: 62, 13, 14, respectively;

(l) SEQ ID NOs: 8, 35, and 44 and SEQ ID NOs: 62, 13, 14, respectively;

(m) SEQ ID NOs: 8, 35, and 45 and SEQ ID NOs: 62, 13, 14, respectively; and

(n) SEQ ID NOs: 8, 35, and 46 and SEQ ID NOs: 62, 13, 14, respectively.

[00171] In particular embodiments, the humanized/optimized anti-ADAM9 antibody or ADAM9-binding fragment thereof includes a CDR_H1 domain, a CDR_H2 domain, and a CDR_H3 domain and a CDR_L1 domain, a CDR_L2 domain, and a CDR_L3 domain having the sequences of SEQ ID NOs: 8, 35, and 45 and SEQ ID NOs: 62, 13, 14, respectively.

[00172] In some embodiments, the humanized/optimized anti-ADAM9 antibody or ADAM9-binding fragment thereof includes a heavy chain variable domain (VH) and a light chain variable domain (VL) having sequences that are at least 90%, at least 95%, at least 99%, or are 100% identical to the sequences as follows:

(a) SEQ ID NO:17 and SEQ ID NO:55, respectively;
(b) SEQ ID NO:17 and SEQ ID NO:56, respectively;
(c) SEQ ID NO:18 and SEQ ID NO:56, respectively;
(d) SEQ ID NO:19 and SEQ ID NO:57, respectively
(e) SEQ ID NO:20 and SEQ ID NO:55, respectively;
(f) SEQ ID NO:21 and SEQ ID NO:55, respectively;
(g) SEQ ID NO:22 and SEQ ID NO:55, respectively;
(h) SEQ ID NO:23 and SEQ ID NO:55, respectively;
(i) SEQ ID NO:24 and SEQ ID NO:55, respectively;
(j) SEQ ID NO:25 and SEQ ID NO:55, respectively;
(k) SEQ ID NO:26 and SEQ ID NO:55, respectively;
(l) SEQ ID NO:27 and SEQ ID NO:55, respectively;
(m) SEQ ID NO:28 and SEQ ID NO:55, respectively; and
(n) SEQ ID NO:29 and SEQ ID NO:55, respectively

[00173] By "substantially identical" or “identical” is meant a polypeptide exhibiting at least 50% identity to a reference amino acid sequence (for example, any one of the amino acid sequences described herein). Preferably, such a sequence is at least 60%, more preferably at least 80% or at least 85%, and more preferably at least 90%, at least 95% at least 99%, or even 100% identical at the amino acid level or nucleic acid to the sequence used for comparison.

[00174] Sequence identity is typically measured using sequence analysis software (for example, Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, Wis. 53705, BLAST, BESTFIT, GAP, or PILEUP/PRETTYBOX programs). Such software matches identical or similar sequences by assigning degrees of homology to various substitutions, deletions, and/or other modifications. Conservative substitutions typically include substitutions within the following groups: glycine, alanine; valine, isoleucine, leucine; aspartic acid, glutamic acid, asparagine, glutamine; serine, threonine; lysine, arginine; and

phenylalanine, tyrosine. In an exemplary approach to determining the degree of identity, a BLAST program may be used, with a probability score between e^{-3} and e^{-100} indicating a closely related sequence.

[00175] In particular embodiments, the humanized/optimized anti-ADAM9 antibody or ADAM9-binding fragment thereof includes a heavy chain variable domain (VH) and a light chain variable domain (VL) having sequences that are at least 90%, at least 95%, at least 99%, or are 100% identical to the sequences of SEQ ID NO:28 and SEQ ID NO:55, respectively.

[00176] In certain embodiments, the humanized/optimized anti-ADAM9 antibody comprises a heavy chain and a light chain sequence as follows:

(a) SEQ ID NO:50 and SEQ ID NO:68, respectively;
(b) SEQ ID NO:51 and SEQ ID NO:68, respectively;
(c) SEQ ID NO:52 and SEQ ID NO:68, respectively
(d) SEQ ID NO:141 and SEQ ID NO:68, respectively;
(e) SEQ ID NO:142 and SEQ ID NO:68, respectively;
(f) SEQ ID NO:143 and SEQ ID NO:68, respectively;
(g) SEQ ID NO:151 and SEQ ID NO:68, respectively;
(h) SEQ ID NO:152 and SEQ ID NO:68, respectively;
(i) SEQ ID NO:153 and SEQ ID NO:68, respectively; and
(j) SEQ ID NO:154 and SEQ ID NO:68, respectively.

[00177] In particular embodiments, the humanized/optimized anti-ADAM9 antibody comprises a heavy chain having the sequence of SEQ ID NO:52 and a light chain having the sequence of SEQ ID NO:68. In other particular embodiments, the humanized/optimized anti-ADAM9 antibody comprises a heavy chain having the sequence of SEQ ID NO:142 and a light chain having the sequence of SEQ ID NO:68. In other embodiments, the humanized/optimized anti-ADAM9 antibody is engineered for extended serum half life and comprises a heavy chain having the sequence of SEQ ID NO:151 and a light chain having the sequence of SEQ ID NO:68. In other particular embodiments, the humanized/optimized anti-ADAM9 antibody is engineered for extended serum half life and comprises a heavy chain having the sequence of SEQ ID NO:155 and a light chain having the sequence of SEQ ID NO:68. In other particular embodiments, the humanized/optimized anti-ADAM9 antibody is engineered for extended serum half life and for site specific conjugation and

comprises a heavy chain having the sequence of SEQ ID NO:152 and a light chain having the sequence of SEQ ID NO:68. In other particular embodiments, the humanized/optimized anti-ADAM9 antibody is engineered for extended serum half life and for site specific conjugation and comprises a heavy chain having the sequence of SEQ ID NO:156 and a light chain having the sequence of SEQ ID NO:68.

[00178] The present invention also expressly contemplates immunoconjugates that immunospecifically bind to an epitope of a human ADAM9 polypeptide, and that comprise any of the above-provided humanized/optimized anti-ADAM9 MAB-A VL or VH Domains. The present invention particularly contemplates such anti-ADAM9 antibodies and ADAM9-binding fragments thereof that comprise any of the following combinations of humanized/optimized anti-ADAM9 VL or VH Domains:

hMAB-A **VH** / hMAB-A **VL Combinations**	
hMAB-A VH(1) / hMAB-A VL(1)	hMAB-A VH(2D) / hMAB-A VL(1)
hMAB-A VH(1) / hMAB-A VL(2)	hMAB-A VH(2D) / hMAB-A VL(2)
hMAB-A VH(1) / hMAB-A VL(3)	hMAB-A VH(2D) / hMAB-A VL(3)
hMAB-A VH(1) / hMAB-A VL(4)	hMAB-A VH(2D) / hMAB-A VL(4)
hMAB-A VH(2) / hMAB-A VL(1)	hMAB-A VH(2E) / hMAB-A VL(1)
hMAB-A VH(2) / hMAB-A VL(2)	hMAB-A VH(2E) / hMAB-A VL(2)
hMAB-A VH(2) / hMAB-A VL(3)	hMAB-A VH(2E) / hMAB-A VL(3)
hMAB-A VH(2) / hMAB-A VL(4)	hMAB-A VH(2E) / hMAB-A VL(4)
hMAB-A VH(3) / hMAB-A VL(1)	hMAB-A VH(2F) / hMAB-A VL(1)
hMAB-A VH(3) / hMAB-A VL(2)	hMAB-A VH(2F) / hMAB-A VL(2)
hMAB-A VH(3) / hMAB-A VL(3)	hMAB-A VH(2F) / hMAB-A VL(3)
hMAB-A VH(3) / hMAB-A VL(4)	hMAB-A VH(2F) / hMAB-A VL(4)
hMAB-A VH(4) / hMAB-A VL(1)	hMAB-A VH(2G) / hMAB-A VL(1)
hMAB-A VH(4) / hMAB-A VL(2)	hMAB-A VH(2G) / hMAB-A VL(2)
hMAB-A VH(4) / hMAB-A VL(3)	hMAB-A VH(2G) / hMAB-A VL(3)
hMAB-A VH(4) / hMAB-A VL(4)	hMAB-A VH(2G) / hMAB-A VL(4)
hMAB-A VH(2A) / hMAB-A VL(1)	hMAB-A VH(2H) / hMAB-A VL(1)
hMAB-A VH(2A) / hMAB-A VL(2)	hMAB-A VH(2H) / hMAB-A VL(2)
hMAB-A VH(2A) / hMAB-A VL(3)	hMAB-A VH(2H) / hMAB-A VL(3)
hMAB-A VH(2A) / hMAB-A VL(4)	hMAB-A VH(2H) / hMAB-A VL(4)
hMAB-A VH(2B) / hMAB-A VL(1)	hMAB-A VH(2I) / hMAB-A VL(1)
hMAB-A VH(2B) / hMAB-A VL(2)	hMAB-A VH(2I) / hMAB-A VL(2)
hMAB-A VH(2B) / hMAB-A VL(3)	hMAB-A VH(2I) / hMAB-A VL(3)
hMAB-A VH(2B) / hMAB-A VL(4)	hMAB-A VH(2I) / hMAB-A VL(4)
hMAB-A VH(2C) / hMAB-A VL(1)	hMAB-A VH(2J) / hMAB-A VL(1)
hMAB-A VH(2C) / hMAB-A VL(2)	hMAB-A VH(2J) / hMAB-A VL(2)
hMAB-A VH(2C) / hMAB-A VL(3)	hMAB-A VH(2J) / hMAB-A VL(3)
hMAB-A VH(2C) / hMAB-A VL(4)	hMAB-A VH(2J) / hMAB-A VL(4)

[00179] The present invention specifically encompasses immunoconjugates comprising a humanized/optimized anti-ADAM9-VL and/or VH Domain as provided above. In particular embodiments, the immunoconjugates of the present invention comprise (i) a humanized/optimized anti-ADAM9-VL and/or VH Domain as provided above, and (ii) an Fc Region.

[00180] Although particular modifications to anti-ADAM9 VH and VL Domains are summarized above and compared in **FIGs. 3A-3B**, it is not necessary to modify all or most of these residues when engineering a humanized and/or optimized anti-ADAM9-VH or VL Domain of the invention. The present invention also encompasses minor variations of these VH and VL sequences including, for example, amino acid substitutions of the C-terminal and/or N-terminal amino acid residues which may be introduced to facilitate subcloning.

III. Antibody Drug Conjugates

Definitions

[00181] The term "**immunoconjugate**," "**conjugate**," or "**ADC**" as used herein refers to a maytansinoid compound described herein that is linked to or conjugated to a cell binding agent (*e.g.*, an anti-ADAM9 antibody or ADAM9-binding fragment thereof described herein).

[00182] A "**linker**" is any chemical moiety that is capable of linking a maytansinoid compound described herein, to a cell-binding agent, such as an anti-ADAM9 antibody or ADAM9-binding fragment thereof in a stable, covalent manner. Linkers can be susceptible to or be substantially resistant to acid-induced cleavage, light-induced cleavage, peptidase-induced cleavage, esterase-induced cleavage, and disulfide bond cleavage, at conditions under which the compound or the antibody remains active. Suitable linkers are well known in the art and include, for example, disulfide groups, thioether groups, acid labile groups, photolabile groups, peptidase labile groups and esterase labile groups. Linkers also include charged linkers, and hydrophilic forms thereof as described herein and know in the art.

[00183] "**Alkyl**" as used herein refers to a saturated linear or branched-chain monovalent hydrocarbon radical of one to twenty carbon atoms. Examples of alkyl include, but are not limited to, methyl, ethyl, 1-propyl, 2-propyl, 1-butyl, 2-methyl-1-propyl, -$CH_2CH(CH_3)_2$), 2-butyl, 2-methyl-2-propyl, 1-pentyl, 2-pentyl 3-pentyl, 2-methyl-2-butyl,

3-methyl-2-butyl, 3-methyl-1-butyl, 2-methyl-1-butyl, 1-hexyl), 2-hexyl, 3-hexyl, 2-methyl-2-pentyl, 3-methyl-2-pentyl, 4-methyl-2-pentyl, 3-methyl-3-pentyl, 2-methyl-3-pentyl, 2,3-dimethyl-2-butyl, 3,3-dimethyl-2-butyl, 1-heptyl, 1-octyl, and the like. Preferably, the alkyl has one to ten carbon atoms. More preferably, the alkyl has one to four carbon atoms.

[00184] The number of carbon atoms in a group can be specified herein by the prefix "C_{x-xx}", wherein x and xx are integers. For example, "C_{1-4}alkyl" is an alkyl group having from 1 to 4 carbon atoms.

[00185] The term "**compound**" or "**cytotoxic compound**," or "**cytotoxic agent**" are used interchangeably. They are intended to include compounds for which a structure or formula or any derivative thereof has been disclosed in the present invention or a structure or formula or any derivative thereof that has been incorporated by reference. The term also includes, stereoisomers, geometric isomers, tautomers, solvates, metabolites, and salts (*e.g.*, pharmaceutically acceptable salts) of a compound of all the formulae disclosed in the present invention. The term also includes any solvates, hydrates, and polymorphs of any of the foregoing. The specific recitation of "stereoisomers," "geometric isomers," "tautomers," "solvates," "metabolites," "salt", "conjugates," "conjugates salt," "solvate," "hydrate," or "polymorph" in certain aspects of the invention described in this application shall not be interpreted as an intended omission of these forms in other aspects of the invention where the term "compound" is used without recitation of these other forms.

[00186] The term "**chiral**" refers to molecules that have the property of non-superimposability of the mirror image partner, while the term "achiral" refers to molecules that are superimposable on their mirror image partner.

[00187] The term "**stereoisomer**" refers to compounds that have identical chemical constitution and connectivity, but different orientations of their atoms in space that cannot be interconverted by rotation about single bonds.

[00188] "**Diastereomer**" refers to a stereoisomer with two or more centers of chirality and whose molecules are not mirror images of one another. Diastereomers have different physical properties, *e.g.* melting points, boiling points, spectral properties, and reactivities. Mixtures of diastereomers can separate under high resolution analytical procedures such as crystallization, electrophoresis and chromatography.

[00189] "**Enantiomers**" refer to two stereoisomers of a compound that are non-superimposable mirror images of one another.

[00190] Stereochemical definitions and conventions used herein generally follow S. P. Parker, Ed., McGraw-Hill, *Dictionary of Chemical Terms* (1984) McGraw-Hill Book Company, New York; and Eliel, E. and Wilen, S., *Stereochemistry of Organic Compounds*, John Wiley & Sons, Inc., New York, 1994. The compounds of the invention can contain asymmetric or chiral centers, and therefore exist in different stereoisomeric forms. It is intended that all stereoisomeric forms of the compounds of the invention, including but not limited to, diastereomers, enantiomers and atropisomers, as well as mixtures thereof such as racemic mixtures, form part of the present invention. Many organic compounds exist in optically active forms, *i.e.*, they have the ability to rotate the plane of plane-polarized light. In describing an optically active compound, the prefixes D and L, or R and S, are used to denote the absolute configuration of the molecule about its chiral center(s). The prefixes d and l or (+) and (-) are employed to designate the sign of rotation of plane-polarized light by the compound, with (-) or l meaning that the compound is levorotatory. A compound prefixed with (+) or d is dextrorotatory. For a given chemical structure, these stereoisomers are identical except that they are mirror images of one another. A specific stereoisomer can also be referred to as an enantiomer, and a mixture of such isomers is often called an enantiomeric mixture. A 50:50 mixture of enantiomers is referred to as a racemic mixture or a racemate, which can occur where there has been no stereoselection or stereospecificity in a chemical reaction or process. The terms "racemic mixture" and "racemate" refer to an equimolar mixture of two enantiomeric species, devoid of optical activity.

[00191] The term "**tautomer**" or "**tautomeric form**" refers to structural isomers of different energies that are interconvertible via a low energy barrier. For example, proton tautomers (also known as prototropic tautomers) include interconversions via migration of a proton, such as keto-enol and imine-enamine isomerizations. Valence tautomers include interconversions by reorganization of some of the bonding electrons.

[00192] The term "**cation**" refers to an ion with positive charge. The cation can be monovalent (e.g., Na^+, K^+, NH_4^+ etc.), bi-valent (e.g., Ca^{2+}, Mg^{2+}, etc.) or multi-valent (e.g., Al^{3+} etc.). Preferably, the cation is monovalent

[00193] The phrase "**pharmaceutically acceptable salt**" as used herein, refers to pharmaceutically acceptable organic or inorganic salts of a compound of the invention. Exemplary salts include, but are not limited, to sulfate, citrate, acetate, oxalate, chloride, bromide, iodide, nitrate, bisulfate, phosphate, acid phosphate, isonicotinate, lactate, salicylate, acid citrate, tartrate, oleate, tannate, pantothenate, bitartrate, ascorbate, succinate, maleate, gentisinate, fumarate, gluconate, glucuronate, saccharate, formate, benzoate, glutamate, methanesulfonate "mesylate," ethanesulfonate, benzenesulfonate, p-toluenesulfonate, pamoate (*i.e.*, 1,1'-methylene-bis-(2-hydroxy-3-naphthoate)) salts, alkali metal (*e.g.*, sodium and potassium) salts, alkaline earth metal (*e.g.*, magnesium) salts, and ammonium salts. A pharmaceutically acceptable salt can involve the inclusion of another molecule such as an acetate ion, a succinate ion or other counter ion. The counter ion can be any organic or inorganic moiety that stabilizes the charge on the parent compound. Furthermore, a pharmaceutically acceptable salt can have more than one charged atom in its structure. Instances where multiple charged atoms are part of the pharmaceutically acceptable salt can have multiple counter ions. Hence, a pharmaceutically acceptable salt can have one or more charged atoms and/or one or more counter ion.

[00194] If the compound of the invention is a base, the desired pharmaceutically acceptable salt can be prepared by any suitable method available in the art, for example, treatment of the free base with an inorganic acid, such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, methanesulfonic acid, phosphoric acid and the like, or with an organic acid, such as acetic acid, maleic acid, succinic acid, mandelic acid, fumaric acid, malonic acid, pyruvic acid, oxalic acid, glycolic acid, salicylic acid, a pyranosidyl acid, such as glucuronic acid or galacturonic acid, an alpha hydroxy acid, such as citric acid or tartaric acid, an amino acid, such as aspartic acid or glutamic acid, an aromatic acid, such as benzoic acid or cinnamic acid, a sulfonic acid, such as p-toluenesulfonic acid or ethanesulfonic acid, or the like.

[00195] If the compound of the invention is an acid, the desired pharmaceutically acceptable salt can be prepared by any suitable method, for example, treatment of the free acid with an inorganic or organic base, such as an amine (primary, secondary or tertiary), an alkali metal hydroxide or alkaline earth metal hydroxide, or the like. Illustrative examples of suitable salts include, but are not limited to, organic salts derived from amino acids, such as glycine and arginine, ammonia, primary, secondary, and tertiary amines, and cyclic

amines, such as piperidine, morpholine and piperazine, and inorganic salts derived from sodium, calcium, potassium, magnesium, manganese, iron, copper, zinc, aluminum and lithium.

[00196] As used herein, the term "**solvate**" means a compound that further includes a stoichiometric or non-stoichiometric amount of solvent such as water, isopropanol, acetone, ethanol, methanol, DMSO, ethyl acetate, acetic acid, and ethanolamine dichloromethane, 2-propanol, or the like, bound by non-covalent intermolecular forces. Solvates or hydrates of the compounds are readily prepared by addition of at least one molar equivalent of a hydroxylic solvent such as methanol, ethanol, 1-propanol, 2-propanol or water to the compound to result in solvation or hydration of the imine moiety.

[00197] A "**metabolite**" or "**catabolite**" is a product produced through metabolism or catabolism in the body of a specified compound, a derivative thereof, or a conjugate thereof, or salt thereof. Metabolites of a compound, a derivative thereof, or a conjugate thereof, can be identified using routine techniques known in the art and their activities determined using tests such as those described herein. Such products can result for example from the oxidation, hydroxylation, reduction, hydrolysis, amidation, deamidation, esterification, deesterification, enzymatic cleavage, and the like, of the administered compound. Accordingly, the invention includes metabolites of compounds, a derivative thereof, or a conjugate thereof, of the invention, including compounds, a derivative thereof, or a conjugate thereof, produced by a process comprising contacting a compound, a derivative thereof, or a conjugate thereof, of this invention with a mammal for a period of time sufficient to yield a metabolic product thereof.

[00198] The phrase "**pharmaceutically acceptable**" indicates that the substance or composition must be compatible chemically and/or toxicologically, with the other ingredients comprising a formulation, and/or the mammal being treated therewith.

[00199] The term "**protecting group**" or "**protecting moiety**" refers to a substituent that is commonly employed to block or protect a particular functionality while reacting other functional groups on the compound, a derivative thereof, or a conjugate thereof. For example, an "amine-protecting group" or an "amino-protecting moiety" is a substituent attached to an amino group that blocks or protects the amino functionality in the compound. Such groups are well known in the art (see for example P. Wuts and T. Greene, 2007,

Protective Groups in Organic Synthesis, Chapter 7, J. Wiley & Sons, NJ) and exemplified by carbamates such as methyl and ethyl carbamate, FMOC, substituted ethyl carbamates, carbamates cleaved by 1,6-β-elimination (also termed "self immolative"), ureas, amides, peptides, alkyl and aryl derivatives. Suitable amino-protecting groups include acetyl, trifluoroacetyl, t-butoxycarbonyl (BOC), benzyloxycarbonyl (CBZ) and 9-fluorenylmethylenoxycarbonyl (Fmoc). For a general description of protecting groups and their use, *see* P. G.M. Wuts & T. W. Greene, *Protective Groups in Organic Synthesis*, John Wiley & Sons, New York, 2007.

[00200] The term "**amino acid**" refers to naturally occurring amino acids or non-naturally occurring amino acid. In one embodiment, the amino acid is represented by NH_2-$C(R^{aa'}R^{aa})$-C(=O)OH, wherein R^{aa} and $R^{aa'}$ are each independently H, an optionally substituted linear, branched or cyclic alkyl, alkenyl or alkynyl having 1 to 10 carbon atoms, aryl, heteroaryl or heterocyclyl or R^{aa} and the N-terminal nitrogen atom can together form a heterocycyclic ring (*e.g.*, as in proline). The term "**amino acid residue**" refers to the corresponding residue when one hydrogen atom is removed from the amine end of the amino acid and/or the hydroxyl group is removed from the carboxy end of the amino acid, such as -NH-$C(R^{aa'}R^{aa})$-C(=O)-. When an amino acid or an amino acid residue is referenced without indicating the specific stererochemistry of the alpha carbon, it is meant to include both the L- and R-isomers. For example, "Ala" includes both L-alanine and R-alanine.

[00201] The term "**peptide**" refers to short chains of amino acid monomers linked by peptide (amide) bonds. In some embodiments, the peptides contain 2 to 20 amino acid residues. In other embodiments, the peptides contain 2 to 10 amino acid residus. In yet other embodiments, the peptides contain 2 to 5 amino acid residues. As used herein, when a peptide is a portion of a cytotoxic agent or a linker described herein represented by a specific sequence of amino acids, the peptide can be connected to the rest of the cytotoxic agent or the linker in both directions. For example, a dipeptide X1-X2 includes X1-X2 and X2-X1. Similarly, a tripeptide X1-X2-X3 includes X1-X2-X3 and X3-X2-X1 and a tetrapeptide X1-X2-X3-X4 includes X1-X2-X3-X4 and X4-X2-X3-X1. X1, X2, X3 and X4 represents an amino acid residue. When a peptide or a peptide residue is referenced without indicating the stereochemistry of each amino acid or amino acid redidue, it meant to include both L- and R-isomers. However, when the stereochemistry of one or more amino acid or

amino acid residue in the peptide or peptide residue is specified as D-isomer, the other amino acid or aminod acid residue in the peptide or peptide residue without specified stereochemistry is meant to include only the natural L-isomer. For example, "Ala-Ala-Ala" meant to include peptides or peptide residues, in which each of the Ala can be either L- or R-isomer; while "Ala-D-Ala-Ala" meant to include L-Ala-D-Ala-L-Ala.

[00202] The term "**reactive ester group**" refers to a group an ester group that can readily react with an amine group to form amide bond. Exemplary reactive ester groups include, but are not limited to, N-hydroxysuccinimide esters, N-hydroxyphthalimide esters, N-hydroxy sulfo-succinimide esters, para-nitrophenyl esters, dinitrophenyl esters, pentafluorophenyl esters and their derivatives, wherein said derivatives facilitate amide bond formation. In certain embodiments, the reactive ester group is a N-hydroxysuccinimide ester or a N-hydroxy sulfo-succinimide ester.

[00203] The term "**amine-reactive group**" refers to a group that can react with an amine group to form a covalent bond. Exemplary amine-reactive groups include, but are not limited to, reactive ester groups, acyl halides, sulfonyl halide, imidoester, or a reactive thioester groups. In certain embodiments, the amine reactive group is a reactive ester group. In one embodiment, the amine reactive group is a N-hydroxysuccinimide ester or a N-hydroxy sulfo-succinimide ester.

[00204] The term "**thiol-reactive group**" refers to a group that can react with a thiol (-SH) group to form a covalent bond. Exemplary thiol-reactive groups include, but are not limited to, maleimide, haloacetyl, aloacetamide, vinyl sulfone, vinyl sulfonamide or vinyal pyridine. In one embodiment, the thiol-reactive group is maleimide.

[00205] As used in the present disclosure and claims, the singular forms "**a**," "**an**," and "**the**" include plural forms unless the context clearly dictates otherwise.

[00206] It is understood that wherever embodiments are described herein with the language "**comprising**," otherwise analogous embodiments described in terms of "**consisting of**" and/or "**consisting essentially of**" are also provided.

A. Exemplary Immunoconjugates

[00207] The maytansinoid compounds of the present invention may be coupled or conjugated either directly to the anti-ADAM9 antibody or ADAM9-binding fragment thereof or indirectly, through a linker using techniques known in the art to produce an "immunoconjugate," "conjugate," or "ADC."

[00208] In a first embodiment, the immunoconjugate of the present invention comprises an anti-ADAM9 antibody or an ADAM9-binding fragment thereof described herein covalently linked to a maytansinod compound described herein through the ε-amino group of one or more lysine residues located on the anti-ADAM9 antibody or an ADAM9-binding fragment thereof or through the thiol group of one or more cysteine residues located on the anti-ADAM9 antibody or an ADAM9-binding fragment thereof.

[00209] In a 1st specific embodiment of the first embodiment, the immunoconjugate of the present invention is represented by formula (I) described above, wherein R^x, R^y, $R^{x'}$ and $R^{y'}$ are all H; and l and k are each independently an integer an integer from 2 to 6; and the remaining variables are as described above for formula (I).

[00210] In a 2nd specific embodiment of the first embodiment, the immunoconjugate of the present invention is represented by formula (I) described above, wherein A is a peptide containing 2 to 5 amino acid residues; and the remaining variables are as described above for formula (I) or in the 1st specific embodiment. In some embodiments, A is a peptide cleavable by a protease. In some embodiments, a peptide cleavable by a protease expressed in tumor tissue. In some embodiments, A is a peptide having an amino acid that is covalent linked with –NH-CR^1R^2-S-L_1-D selected from the group consisting of Ala, Arg, Asn, Asp, Cit, Cys, selino-Cys, Gln, Glu, Gly, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr and Val, each independently as L or D isomer. In some embodiments, the amino acid connected to –NH-CR^1R^2-S-L_1-D is an L amino acid.

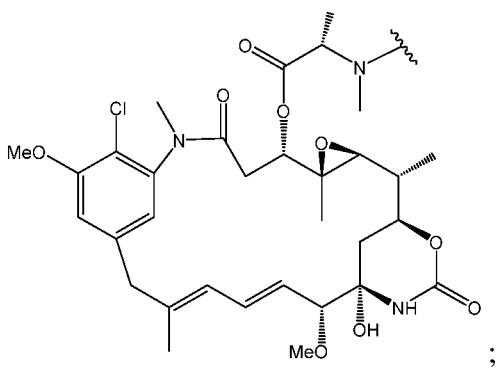
[00211] In a 3rd specific embodiment of the first embodiment, the immunoconjugate of the present invention is represented by formula (I) described above, wherein A is selected from the group consisting of Gly-Gly-Gly, Ala-Val, Val-Ala, D-Val-Ala, Val-Cit, D-Val-Cit, Val-Lys, Phe-Lys, Lys-Lys, Ala-Lys, Phe-Cit, Leu-Cit, Ile-Cit, Phe-Ala, Phe-N9-tosyl-Arg, Phe-N9-nitro-Arg, Phe-Phe-Lys, D-Phe-Phe-Lys, Gly-Phe-Lys, Leu-Ala-Leu, Ile-Ala-Leu, Val-Ala-Val, Ala-Ala-Ala, D-Ala-Ala-Ala, Ala-D-Ala-Ala, Ala-Ala-D-Ala, Ala-Leu-

Ala-Leu (SEQ ID NO: 144), β-Ala-Leu-Ala-Leu (SEQ ID NO: 145), Gly-Phe-Leu-Gly (SEQ ID NO: 146), Val-Arg, Arg-Arg, Val-D-Cit, Val-D-Lys, Val-D-Arg, D-Val-Cit, D-Val-Lys, D-Val-Arg, D-Val-D-Cit, D-Val-D-Lys, D-Val-D-Arg, D-Arg-D-Arg, Ala-Ala, Ala-D-Ala, D-Ala-Ala, D-Ala-D-Ala, Ala-Met, Gln-Val, Asn-Ala, Gln-Phe, Gln-Ala, D-Ala-Pro, and D-Ala-tBu-Gly, wherein the first amino acid in each peptide is connected to L2 group and the last amino acid in each peptide is connected to –NH-CR1R2-S-L1-D; and the remaining variables are as described for formula (I) or in the 1st specific embodiment.

[00212] In a 4th specific embodiment of the first embodiment, the immunoconjugate of the present invention is represented by formula (I) described above, wherein R^1 and R^2 are both H; and the remaining variables are as described for formula (I) or in the 1st, 2nd, or 3rd specific embodiment.

[00213] In a 5th specific embodiment of the first embodiment, the immunoconjugate of the present invention is represented by formula (I) described above, wherein L_1 is $-(CH_2)_{4-6}$-C(=O)-; and the remaining variables are as described for formula (I) or in the 1st, 2nd, 3rd or 4th specific embodiment.

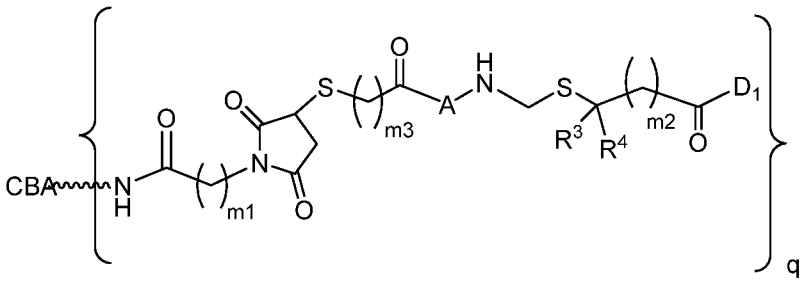
[00214] In a 6th specific embodiment of the first embodiment, the immunoconjugate of the present invention is represented by formula (I) described above, wherein D is represented by the following formula:



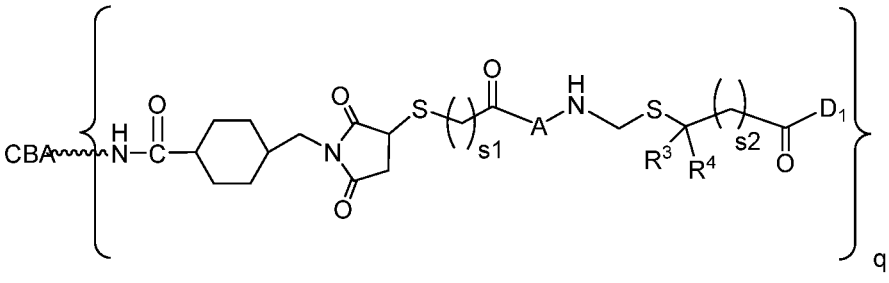
;

and the remaining variables are as described for formula (I) or in the 1st, 2nd, 3rd, 4th or 5th specific embodiment.

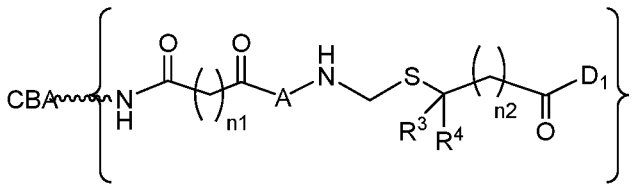
[00215] In a 7th specific embodiment, the immunoconjugate of the present invention is represented by the following formula:



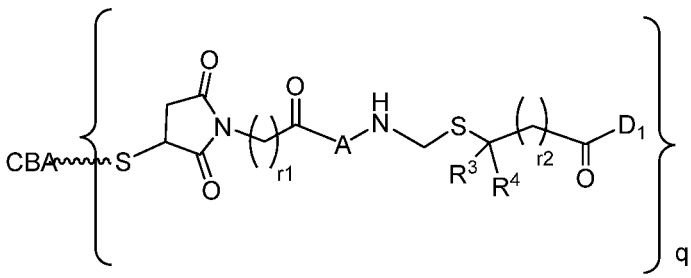
(Ia);



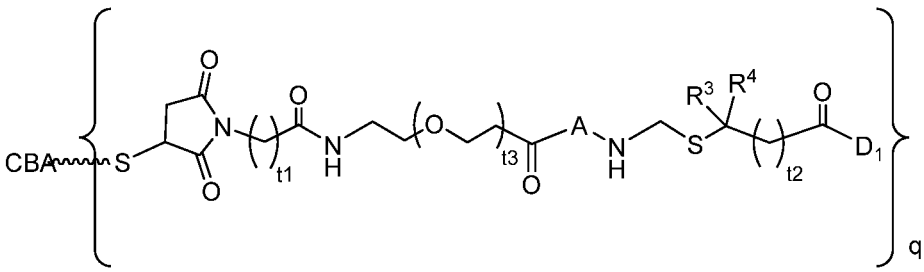
(Ib);



(Ic);



(Id); or



(Ie);

or a pharmaceutically acceptable salt thereof, wherein:

CBA–N(H)– is the anti-ADAM9 antibody or ADAM9-binding fragment thereof connected to the L_2 group through a Lys amine group;

CBA~S— is the anti-ADAM9 antibody or ADAM9-binding fragment thereof connected to the L_2 group through a Cys thiol group;

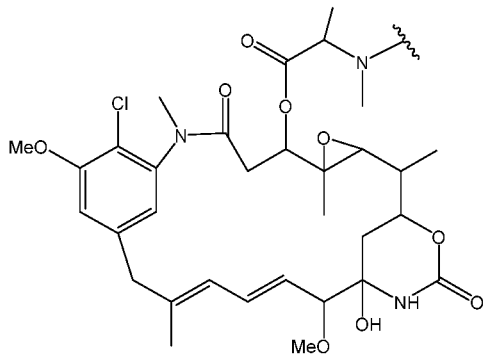
R^3 and R^4 are each independently H or Me;

m1, m3, n1, r1, s1 and t1 are each independently an integer from 1 to 6;

m2, n2, r2, s2 and t2 are each independently an integer from 1 to 7;

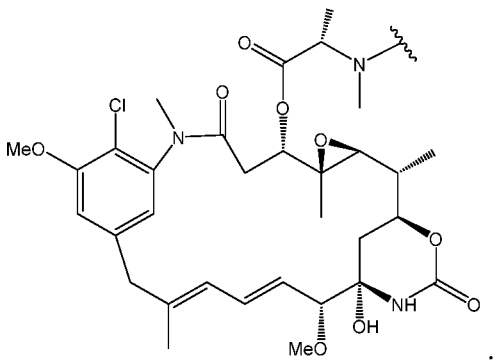
t3 is an integer from 1 to 12;

D_1 is represented by the following formula:



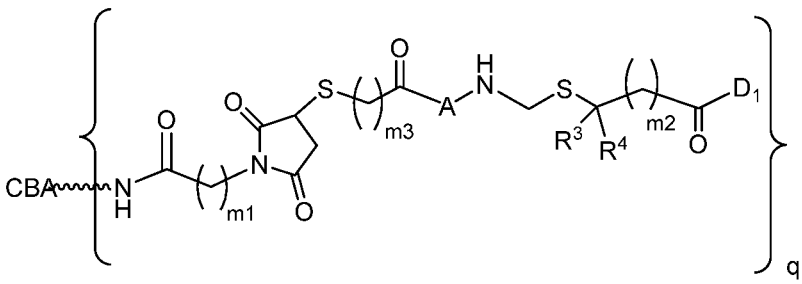
; and

q is an integer from 1 to 20. In a more specific embodiment, D_1 is represented by the following formula:

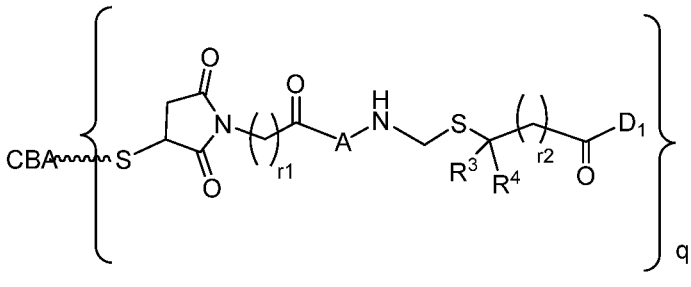


.

[00216] In an 8th specific embodiment, the immunoconjugate of the present invention is represented by the following formula:



q (Ia), or



(Id);

wherein:

m1 and m3 are each independently an integer from 2 to 4;

m2 is an integer from 2 to 5;

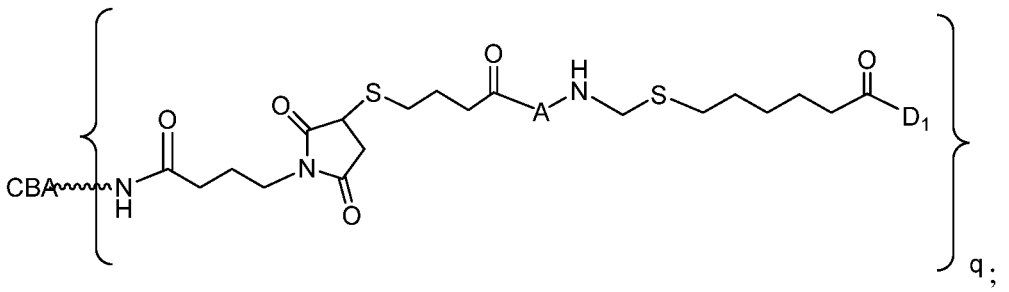
r1 is an integer from 2 to 6;

r2 is an integer from 2 to 5; and

the remaining variables are as described in the 7th specific embodiment.

[00217] In a 9th specific embodiment, for the immunoconjugates described in the 7th or 8th specific embodiment, A is Ala-Ala-Ala, Ala-D-Ala-Ala, Ala-Ala, D-Ala-Ala, Val-Ala, D-Val-Ala, D-Ala-Pro, or D-Ala-tBu-Gly. In a more specific embodiment, for the immunoconjugates described in the 7th or 8th specific embodiment, A is L-Ala-D-Ala-L-Ala.

[00218] In a 10th specific embodiment, the immunoconjugate of the present invention is represented by the following formula:



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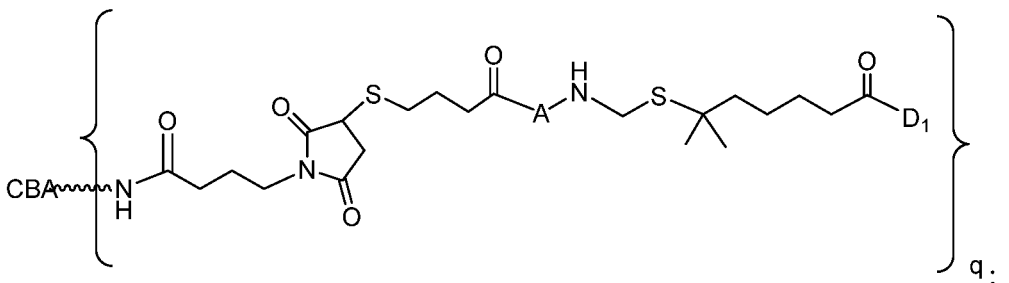

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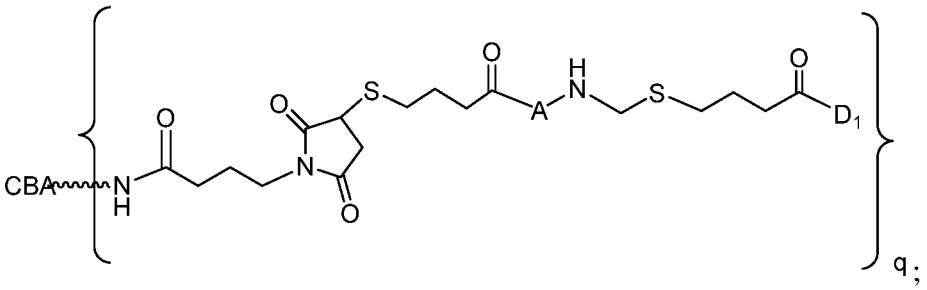

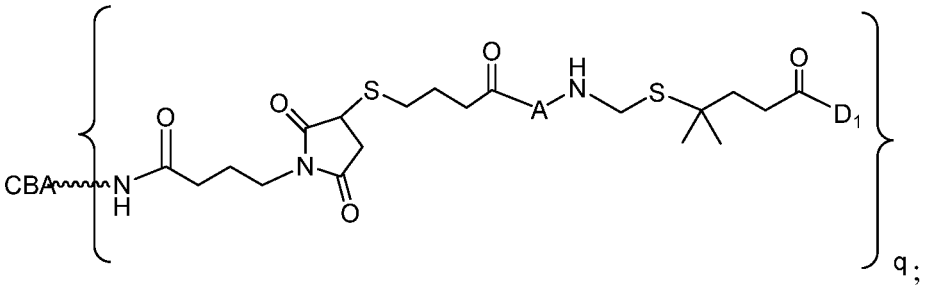

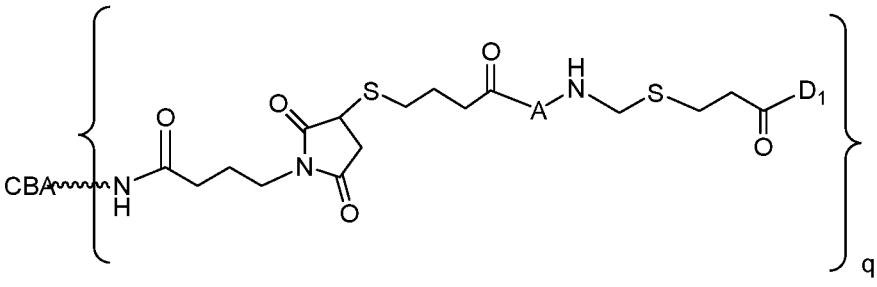

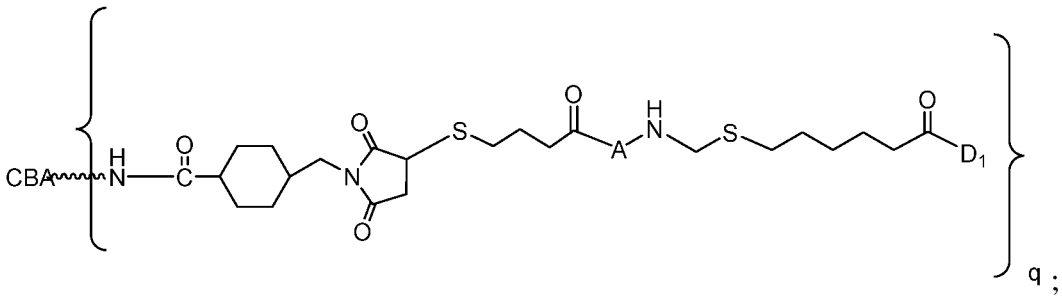

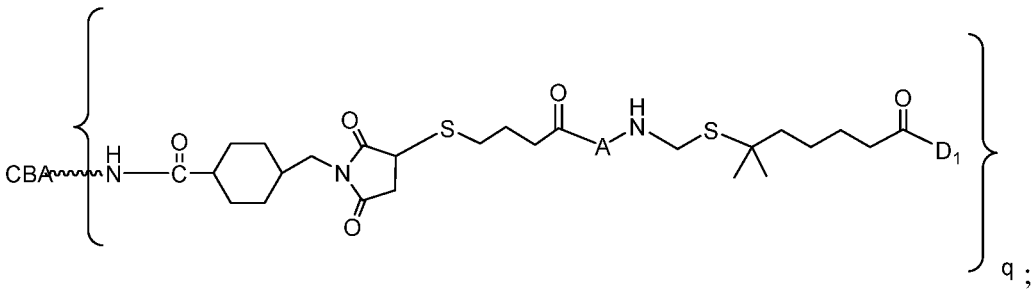

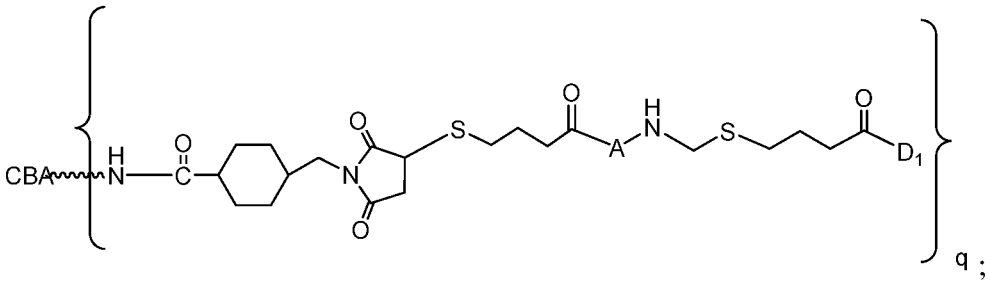

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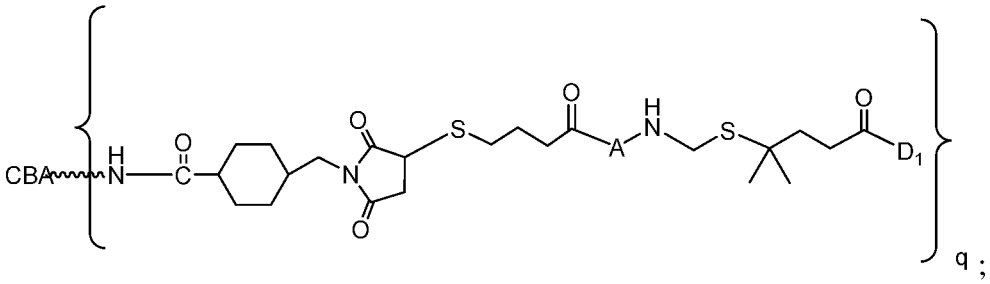

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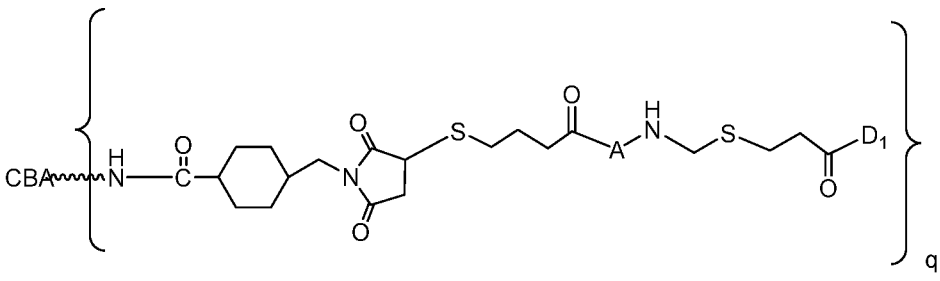

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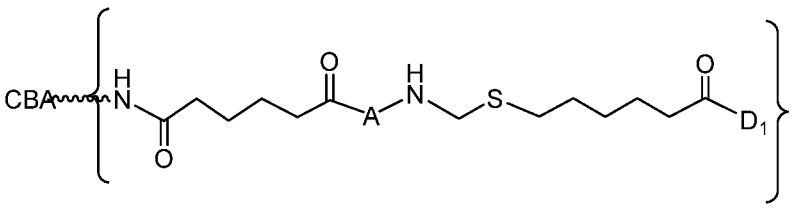

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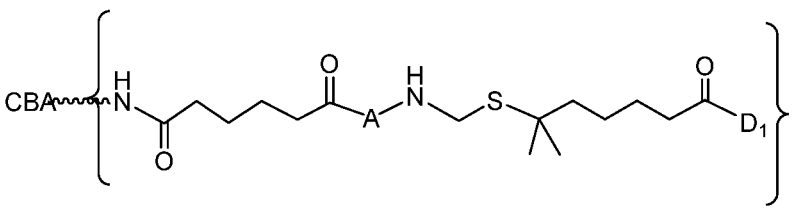

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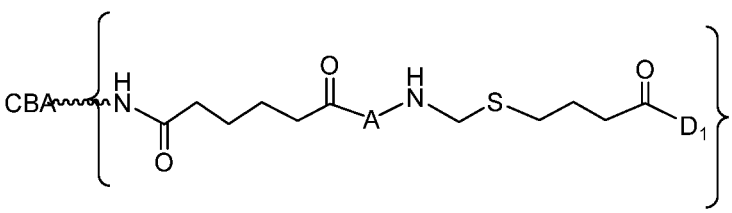

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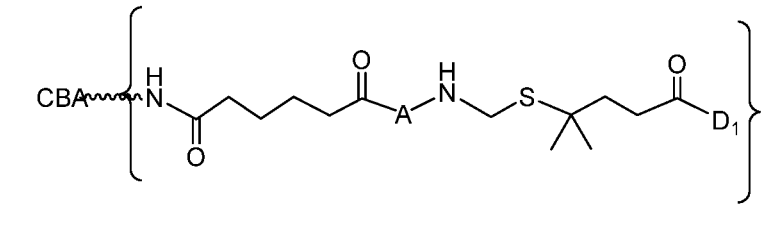
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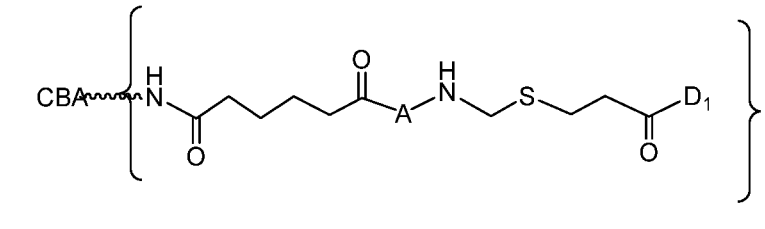
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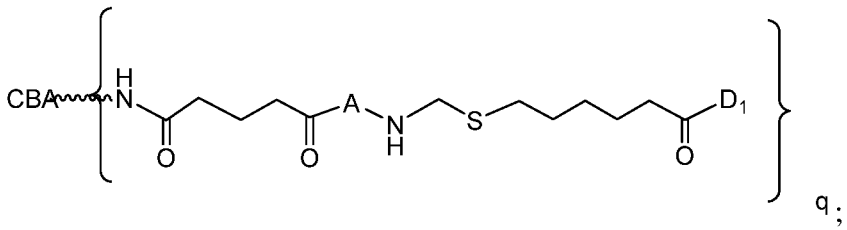
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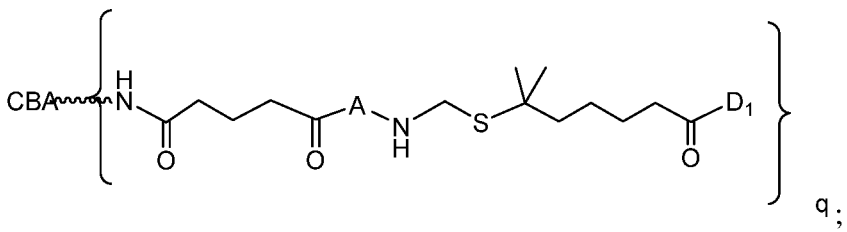
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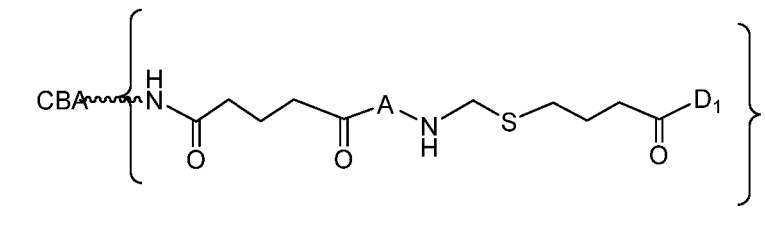
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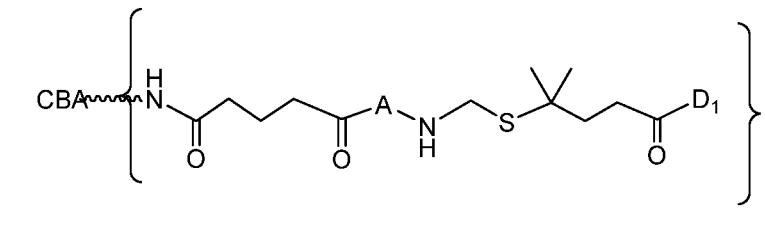
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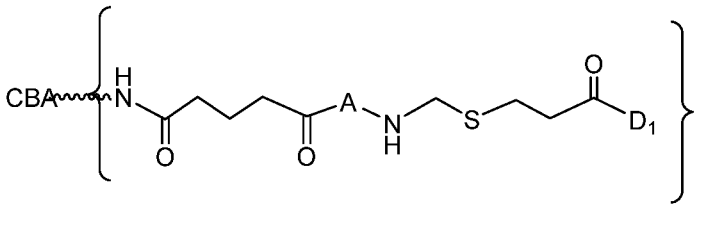

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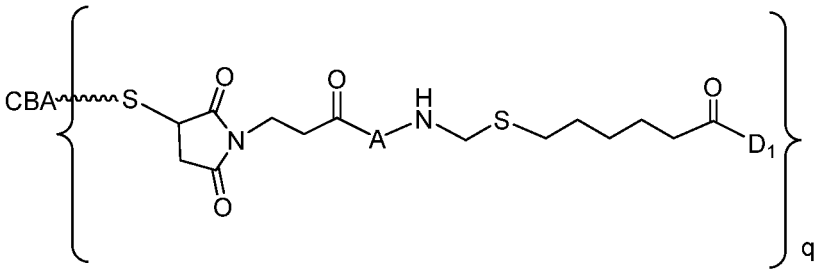

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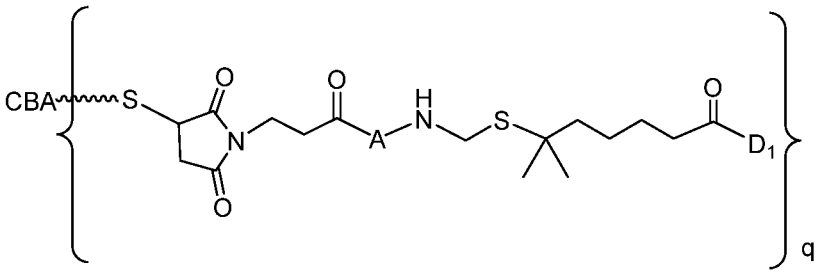

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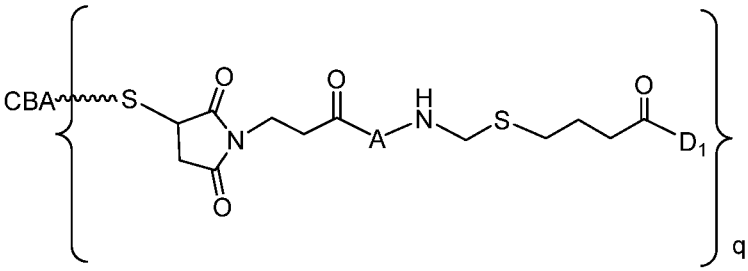

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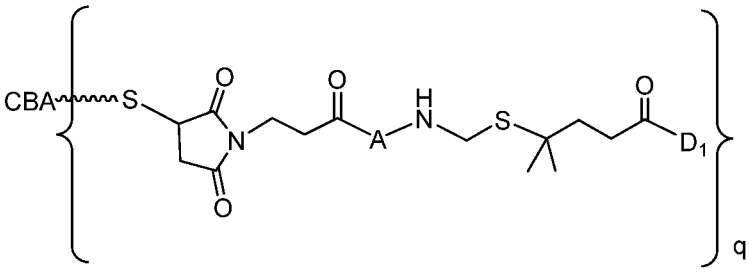
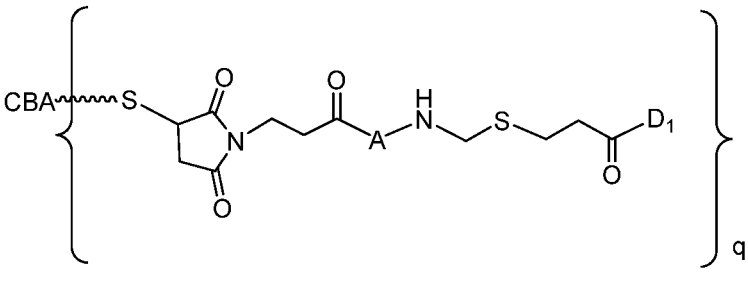
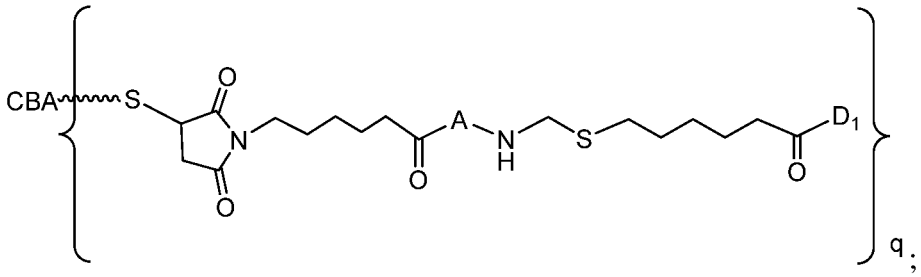
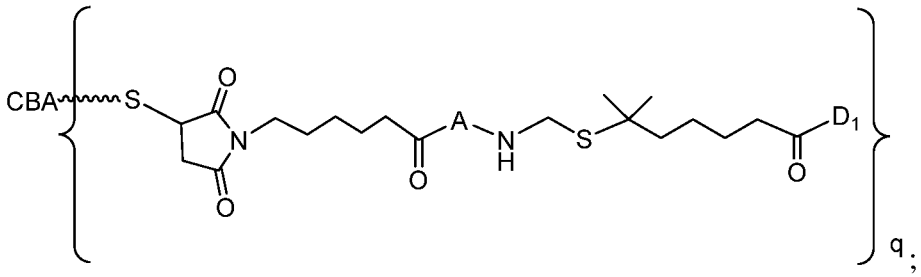
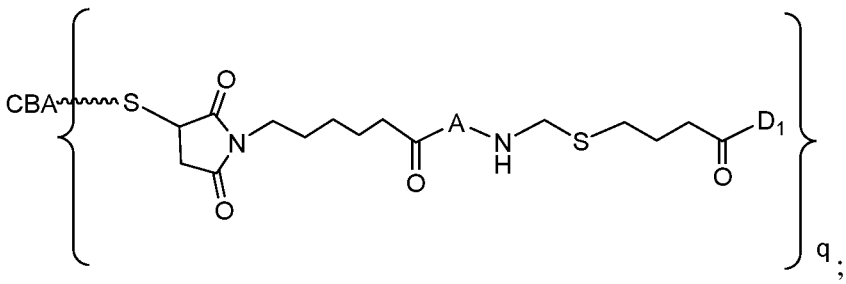


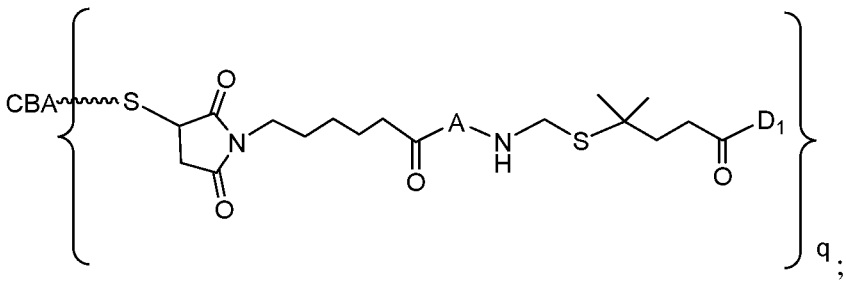
q; or

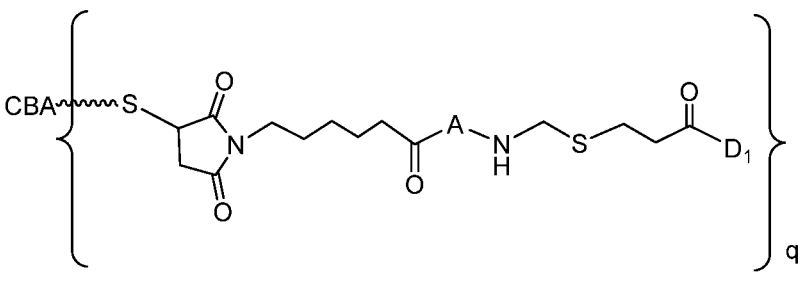


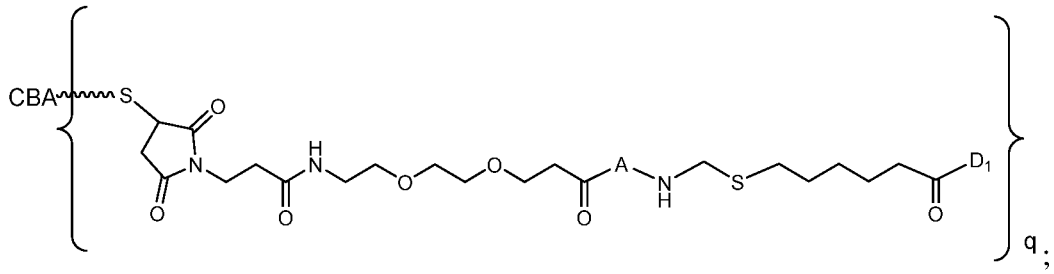


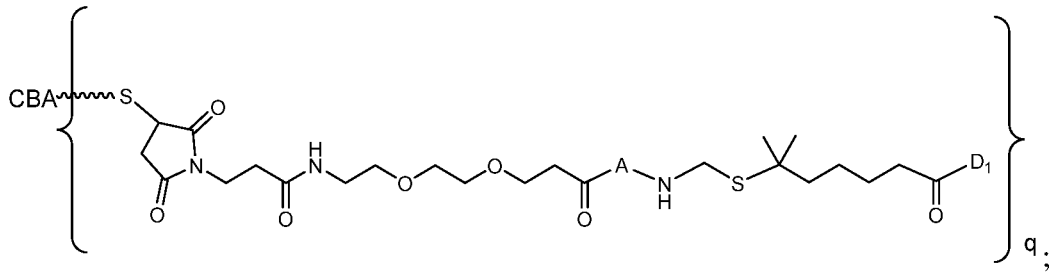


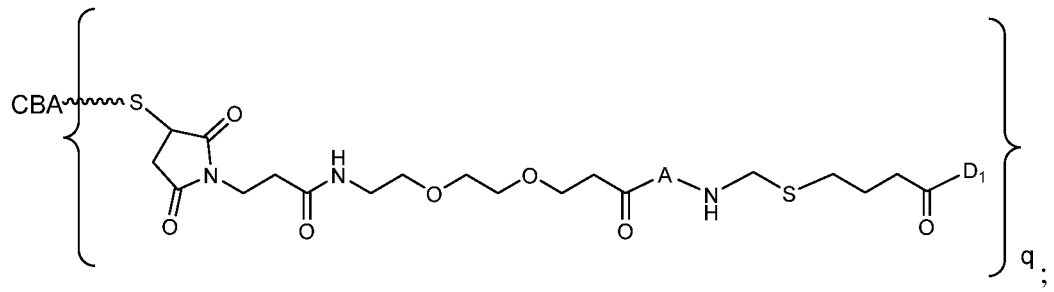


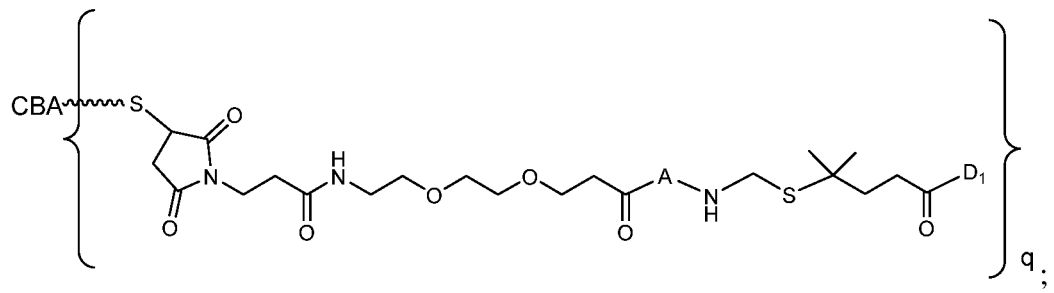


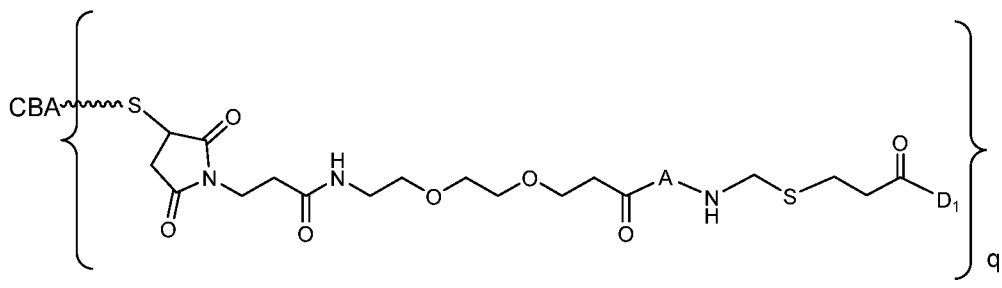


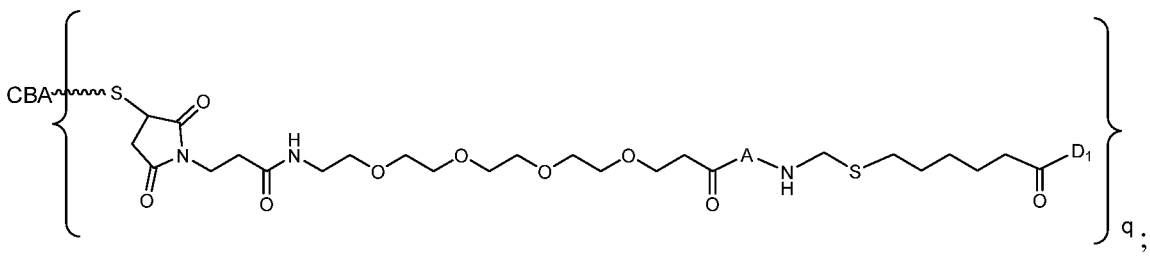


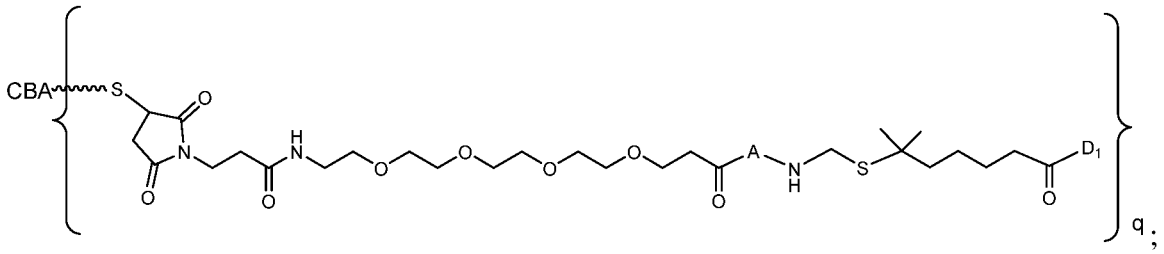


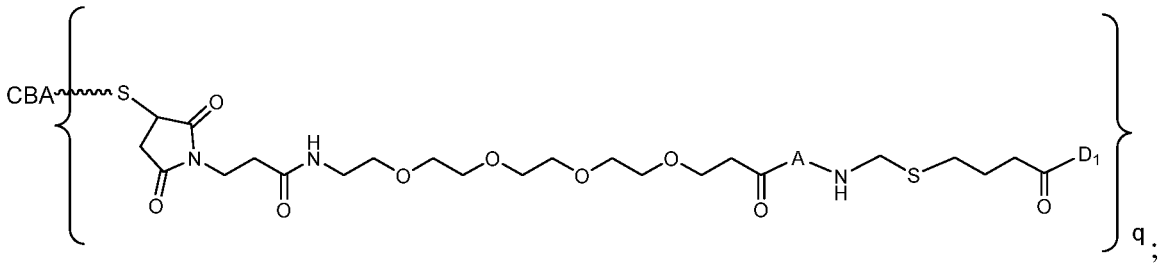


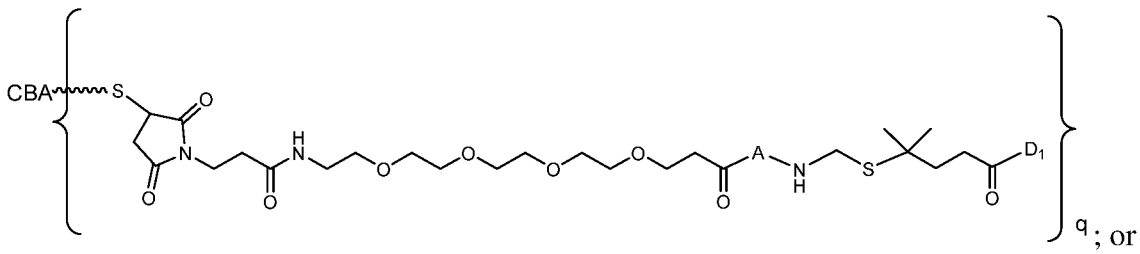


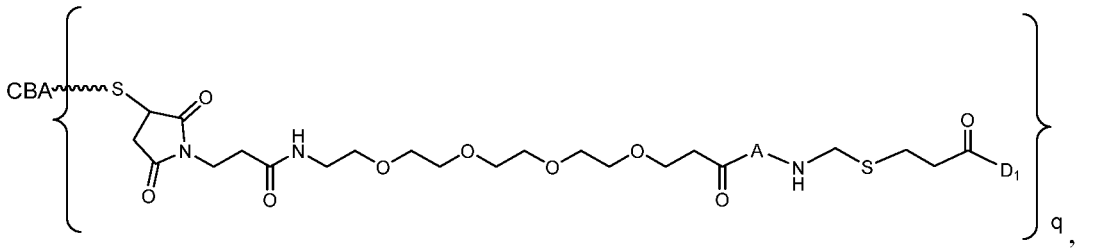








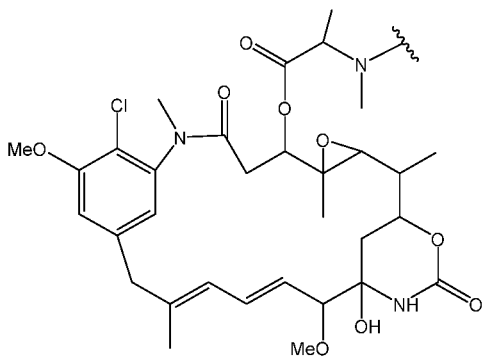




or a pharmaceutically acceptable salt thereof, wherein:

A is Ala-Ala-Ala, Ala-D-Ala-Ala, Ala-Ala, D-Ala-Ala, Val-Ala, D-Val-Ala, D-Ala-Pro, or D-Ala-tBu-Gly, and

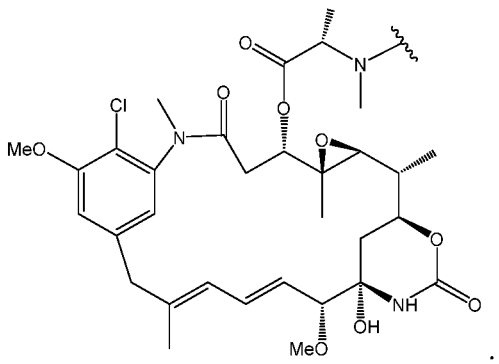
D_1 is represented by the following formula:



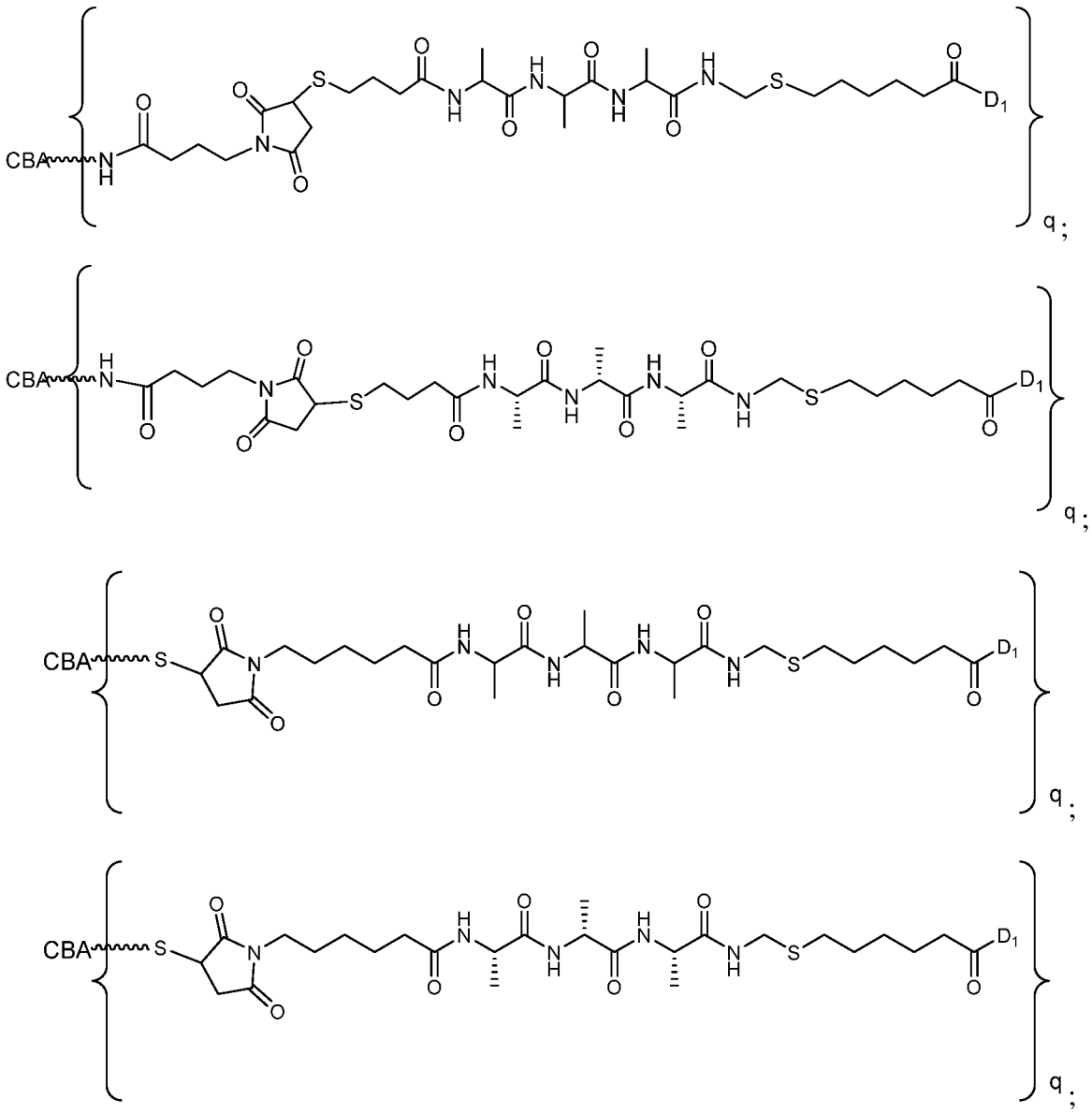
;

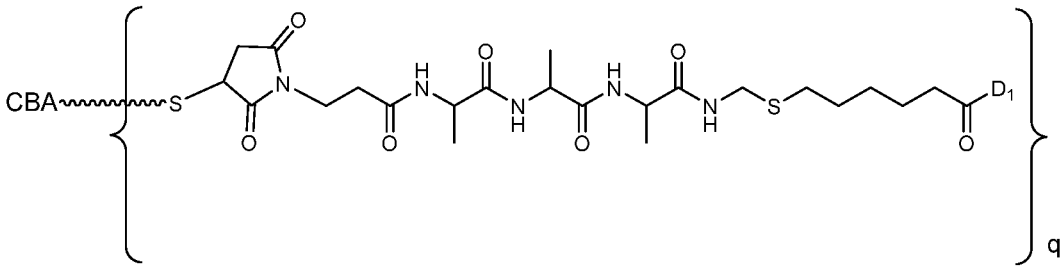
and the remaining variables are as described in the 7th, 8th or 9th specific embodiment. In a more specific embodiment, A is L-Ala-D-Ala-L-Ala. In a more specific

embodiment, D_1 is represented by the following formula:

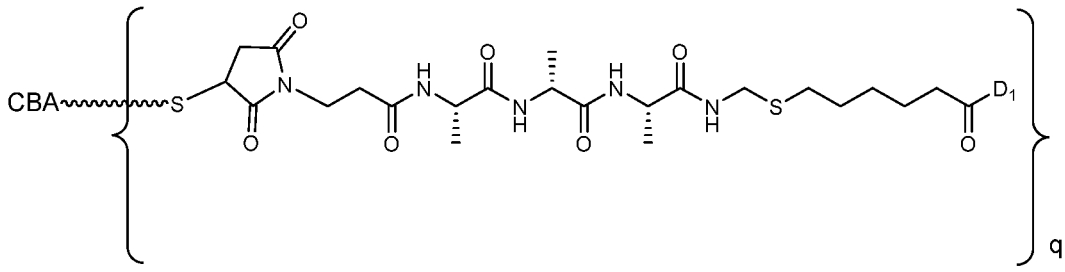


[00219] In a 11th specific embodiment, the immunoconjugate of the present invention is represented by the following formula:



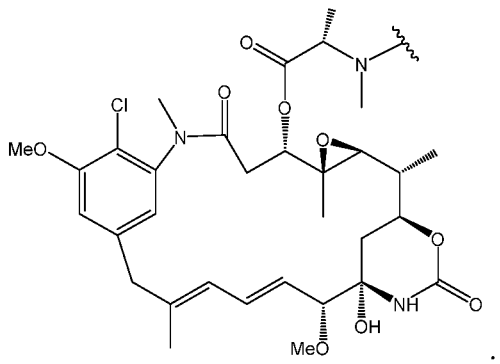


; or



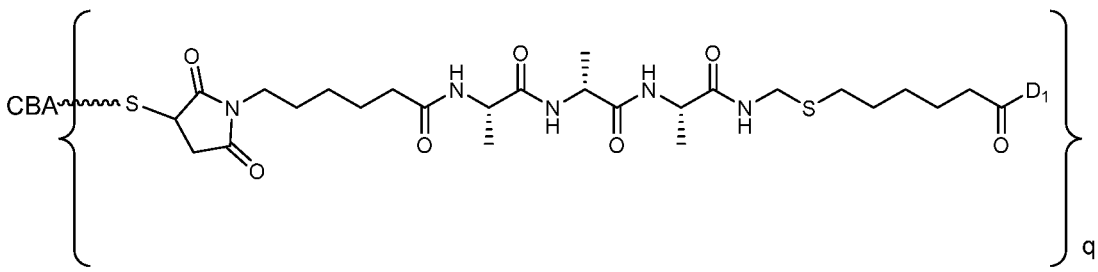
,

wherein D_1 is represented by the following formula:

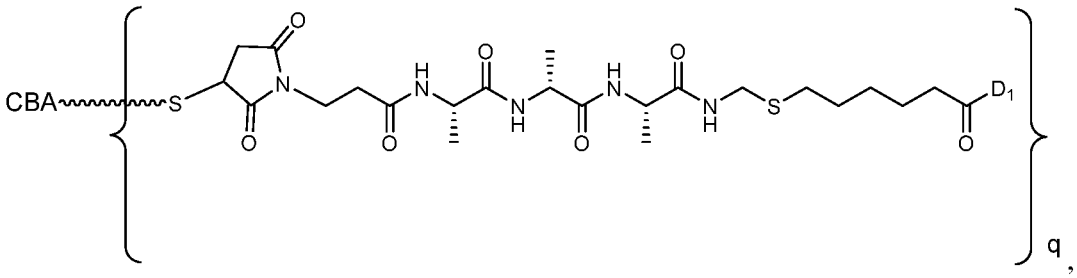


.

[00220] In a 12th specific embodiment, the immunoconjugate of the present invention is represented by the following formula:



,

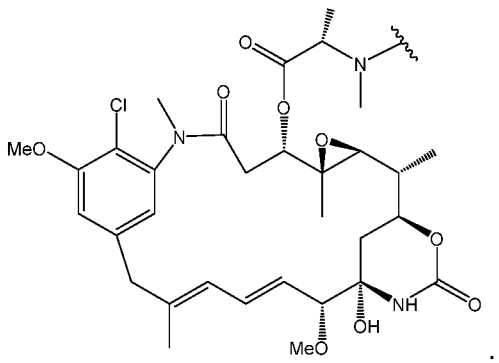


wherein:

CBA is an humanized anti-ADAM9 antibody or ADAM9-binding fragment thereof comprising a CDR_H1 domain, a CDR_H2 domain, and a CDR_H3 domain and a CDR_L1 domain, a CDR_L2 domain, and a CDR_L3 domain having the sequences of SEQ ID NOs: 8, 35, and 45 and SEQ ID NOs: 62, 13, 14, respectively;

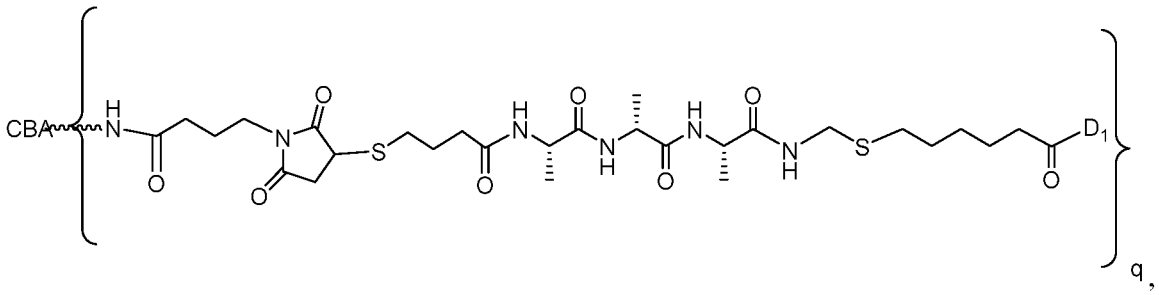
q is 1 or 2;

D_1 is represented by the following formula:



[00221] In some embodiments, the humanized anti-ADAM9 antibody or ADAM9-binding fragment thereof comprises a heavy chain variable domain (VH) and a light chain variable domain (VL) having sequences of SEQ ID NO:28 and SEQ ID NO:55, respectively. In some embodiments, the humanized anti-ADAM9 antibody comprises a heavy chain and a light chain having the sequences of SEQ ID NO:142 and SEQ ID NO:68, respectively. In some embodiments, the humanized anti-ADAM9 antibody comprises a heavy chain and a light chain having the sequences of SEQ ID NO:152 and SEQ ID NO:68, respectively. In some embodiments, X in SEQ ID NO:142 or SEQ ID NO:152 is lysine. In some embodiments, X in SEQ ID NO:142 or SEQ ID NO:152 is absent. In some embodiments, the humanized anti-ADAM9 antibody comprises a heavy chain and a light chain having the sequences of SEQ ID NO:156 and SEQ ID NO:68, respectively.

[00222] In a 13th specific embodiment, the immunoconjugate of the present invention is represented by the following formula:

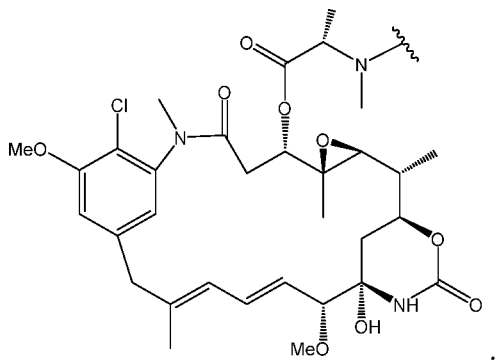


wherein:

CBA is an humanized anti-ADAM9 antibody or ADAM9-binding fragment thereof comprising a CDR_H1 domain, a CDR_H2 domain, and a CDR_H3 domain and a CDR_L1 domain, a CDR_L2 domain, and a CDR_L3 domain having the sequences of SEQ ID NOs: 8, 35, and 45 and SEQ ID NOs: 62, 13, 14, respectively;

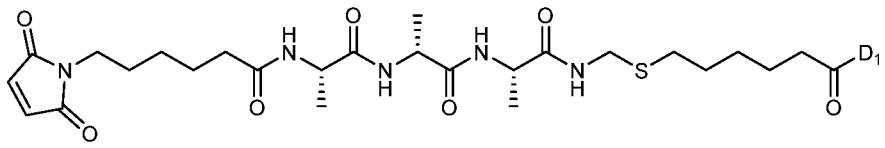
q is an integer from 1 or 10;

D_1 is represented by the following formula:



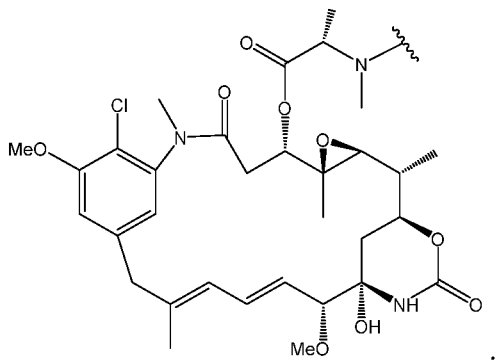
[00223] In certain embodiments, the anti-ADAM9 antibody or ADAM9-binding fragment thereof comprises a heavy chain variable domain (VH) and a light chain variable domain (VL) having sequences of SEQ ID NO:28 and SEQ ID NO:55, respectively. In some embodiments, the humanized anti-ADAM9 antibody comprises a heavy chain and a light chain having the sequences of SEQ ID NO:52 and SEQ ID NO:68, respectively. In some embodiments, the humanized anti-ADAM9 antibody comprises a heavy chain and a light chain having the sequences of SEQ ID NO:151 and SEQ ID NO:68, respectively. In some embodiment, X in SEQ ID NO:52 or SEQ ID NO:151 is lysine. In some embodiments, X in SEQ ID NO:52 or SEQ ID NO:151 is absent. In certain embodiments, the humanized anti-ADAM9 antibody comprises a heavy chain and a light chain having the sequences of SEQ ID NO:155 and SEQ ID NO:68, respectively.

[00224] In a 14th embodiment, the immunoconjugate of the present invention comprises an anti-ADAM9 antibody, hMAB-A(2I.2)(YTE/C/-K)), coupled to a maytansinoid compound DM21C (also referred to as Mal-LDL-DM or MalC5-LDL-DM or compound 17a) represented by the following structural formula:



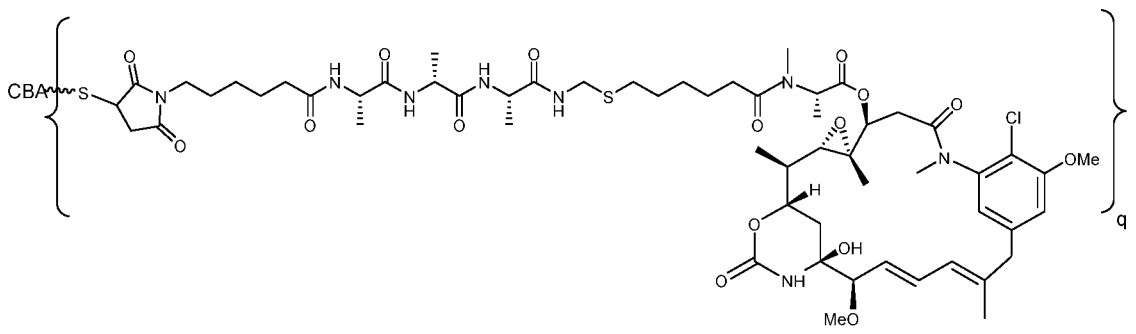
(D-4),

wherein D_1 is represented by the following formula:



The anti-ADAM9 antibody hMAB-A(2I.2)(YTE/C/-K)) has a heavy chain and a light chain having the sequences of SEQ ID NO:156 and SEQ ID NO:68, respectfully. In some embodiments, the immunoconjugate is referenced herein as hMAB-A(2I.2)(YTE/C/-K)-Mal-LDL-DM.

[00225] In one embodiment, the immunoconjugate hMAB-A(2I.2)(YTE/C/-K)-Mal-LDL-DM is represented by the following structural formula:



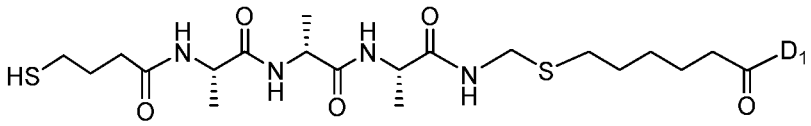
wherein:

CBA is the anti-ADAM9 antibody hMAB-A(2I.2)(YTE/C/-K) connected to the maytansinoid compound through a Cys thiol group; and

q is 1 or 2.

[00226] In certain embodiments, for compositions (*e.g.*, pharmaceutical compositions) comprising immunoconjugates of the 14th specific embodiment, DAR is in the range of 1.5 to 2.2, 1.7 to 2.2 or 1.9 to 2.1. In some embodiment, the DAR is 1.7, 1.8, 1.9, 2.0 or 2.1.

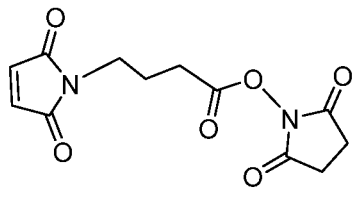
[00227] In a 15th specific embodiment, the immunoconjugate of the present invention comprises an anti-ADAM9 antibody, hMAB-A(2I.2)(YTE/-K)), coupled to a maytansinoid compound DM21L (also referred to as LDL-DM or compound 14c) represented by the following structural formula:



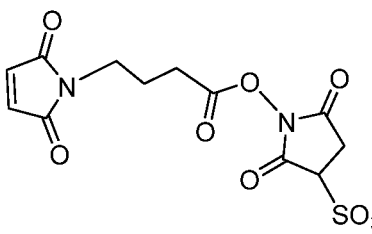
(D-2);

via γ-maleimidobutyric acid N-succinimidyl ester (GMBS) or a N-(γ-maleimidobutryloxy)sulfosuccinimide ester (sulfo-GMBS or sGMBS) linker. The anti-ADAM9 antibody hMAB-A(2I.2)(YTE/-K))has a heavy chain and a light chain having the sequences of SEQ ID NO:155 and SEQ ID NO:68, respectfully. In some embodiments, the conjugate is referenced herein as hMAB-A(2I.2)(YTE/-K)-sGMBS-LDL-DM. The conjugate can also be referred to as hMAB-A(2I.2)(YTE/-K)-GMBS-LDL-DM, which can be used interchangeably with hMAB-A(2I.2)(YTE/-K)-sGMBS-LDL-DM.

[00228] The GMBS and sulfo-GMBS (or sGMBS) linkers are known in the art and can be presented by the following structural formula:



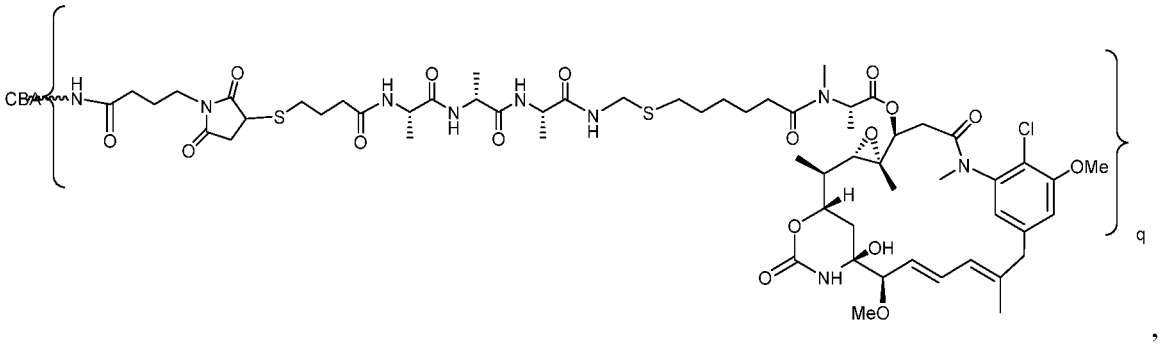
GMBS



sulfo-GMBS

.

[00229] In one embodiment, the immunoconjugate is represented by the following structural formula:



,

wherein:

CBA is the anti-ADAM9 antibody hMAB-A(2I.2)(YTE/-K)) connected to the maytansinoid compound through a Lys amine group; and

q is an integer from 1 or 10.

[00230] In certain embodiments, for compositions (*e.g.*, pharmaceutical compositions) comprising immunoconjugates of the 15th specific embodiment, DAR is in the range of 3.0 to 4.0, 3.2 to 3.8, or 3.4 to 3.7. In some embodiments, the DAR is 3.2, 3.3, 3.4, 3.5, 3.5, 3.7, or 3.8.

[00231] In certain embodiments, for compositions (*e.g.*, pharmaceutical compositions) comprising immunoconjugates of the first embodiment, or the 1st, 2nd, 3rd, 4th, 5th, 6th, 7th, 8th, 9th, 10th, 11th, 12th, 13th, 14th or 15th specific embodiment, the average number of the cytotoxic agent per antibody molecule (*i.e.*, average value of q), also known as Drug-Antibody Ratio (DAR) in the composition is in the range of 1.0 to 8.0. In some embodiments, DAR is in the range of 1.0 to 5.0, 1.0 to 4.0, 1.5 to 4.0, 2.0 to 4.0, 2.5 to 4.0, 1.0 to 3.4, 1.0 to 3.0, 2.9 to 3.3, 3.3 to 3.8, 1.5 to 2.5, 2.0 to 2.5, 1.7 to 2.3, or 1.8 to 2.2. In some embodiments, the DAR is less than 4.0, less than 3.8, less than 3.6, less than 3.5, less than 3.0 or less than 2.5. In some embodiments, the DAR is in the range of 3.2 to 3.4. In some embodiments, the DAR is in the range of 3.0 to 3.2. In some embodiments, the DAR is in the range of 3.5 to 3.7. In some embodiments, the DAR is 3.1, 3.2, 3.3, 3.4, 3.5, 3.6 or 3.7. In some embodiments, the DAR is in the range of 1.8 to 2.0. In some embodiments, the DAR is in the range of 1.7 to 1.9. In some embodiments, the DAR is in the range of 1.9 to 2.1. In some embodiments, the DAR is 1.9, 2.0 or 2.1. In some embodiments, for the immunoconjugates of the present invention comprising an anti-ADAM9 antibody or an anti-ADAM9-binding fragment thereof linked to the maytansinoid compound through one or

more cysteine thiol group, the DAR is in the range of 1.5 to 2.5, 1.8 to 2.2, 1.1 to 1.9 or 1.9 to 2.1. In some embodiments, the DAR is 1.8, 1.9, 2.0 or 2.1.

C. Exemplary Linker Molecules

[00232] Any suitable linkers known in the art can be used in preparing the immunoconjugates of the present invention. In certain embodiments, the linkers are bifunctional linkers. As used herein, the term "**bifunctional linker**" refers to modifying agents that possess two reactive groups; one of which is capable of reacting with a cell binding agent while the other one reacts with the maytansinoid compound to link the two moieties together. Such bifunctional crosslinkers are well known in the art (see, for example, Isalm and Dent in *Bioconjugation* chapter 5, p218-363, Groves Dictionaries Inc. New York, 1999). For example, bifunctional crosslinking agents that enable linkage via a thioether bond include *N*-succinimidyl-4-(N-maleimidomethyl)-cyclohexane-1-carboxylate (SMCC) to introduce maleimido groups, or with *N*-succinimidyl-4-(iodoacetyl)-aminobenzoate (SIAB) to introduce iodoacetyl groups. Other bifunctional crosslinking agents that introduce maleimido groups or haloacetyl groups on to a cell binding agent are well known in the art (see US Patent Publication Nos. 2008/0050310, 20050169933, available from Pierce Biotechnology Inc. P.O. Box 117, Rockland, IL 61105, USA) and include, but not limited to, bis-maleimidopolyethyleneglycol (BMPEO), $BM(PEO)_2$, $BM(PEO)_3$, N-(β-maleimidopropyloxy)succinimide ester (BMPS), γ-maleimidobutyric acid N-succinimidyl ester (GMBS), ε-maleimidocaproic acid N-hydroxysuccinimide ester (EMCS), 5-maleimidovaleric acid NHS, HBVS, N-succinimidyl-4-(N-maleimidomethyl)-cyclohexane-1-carboxy-(6-amidocaproate), which is a "long chain" analog of SMCC (LC-SMCC), m-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS), 4-(4-N-maleimidophenyl)-butyric acid hydrazide or HCl salt (MPBH), N-succinimidyl 3-(bromoacetamido)propionate (SBAP), N-succinimidyl iodoacetate (SIA), κ-maleimidoundecanoic acid N-succinimidyl ester (KMUA), N-succinimidyl 4-(p-maleimidophenyl)-butyrate (SMPB), succinimidyl-6-(β-maleimidopropionamido)hexanoate (SMPH), succinimidyl-(4-vinylsulfonyl)benzoate (SVSB), dithiobis-maleimidoethane (DTME), 1,4-bis-maleimidobutane (BMB), 1,4-bismaleimidyl-2,3-dihydroxybutane (BMDB), bis-maleimidohexane (BMH), bis-maleimidoethane (BMOE), sulfosuccinimidyl 4-(N-maleimido-methyl)cyclohexane-1-carboxylate (sulfo-SMCC), sulfosuccinimidyl(4-iodo-acetyl)aminobenzoate (sulfo-SIAB), m-maleimidobenzoyl-N-hydroxysulfosuccinimide

ester (sulfo-MBS), N-(γ-maleimidobutryloxy)sulfosuccinimide ester (sulfo-GMBS or sGMBS), N-(ε-maleimidocaproyloxy)sulfosuccimido ester (sulfo-EMCS), N-(κ-maleimidoundecanoyloxy)sulfosuccinimide ester (sulfo-KMUS), and sulfosuccinimidyl 4-(p-maleimidophenyl)butyrate (sulfo-SMPB).

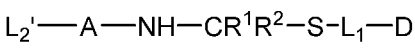
[00233] Heterobifunctional crosslinking agents are bifunctional crosslinking agents having two different reactive groups. Heterobifunctional crosslinking agents containing both an amine-reactive *N*-hydroxysuccinimide group (NHS group) and a carbonyl-reactive hydrazine group can also be used to link the cytotoxic compounds described herein with a cell-binding agent (*e.g.*, antibody). Examples of such commercially available heterobifunctional crosslinking agents include succinimidyl 6-hydrazinonicotinamide acetone hydrazone (SANH), succinimidyl 4-hydrazidoterephthalate hydrochloride (SHTH) and succinimidyl hydrazinium nicotinate hydrochloride (SHNH). Conjugates bearing an acid-labile linkage can also be prepared using a hydrazine-bearing benzodiazepine derivative of the present invention. Examples of bifunctional crosslinking agents that can be used include succinimidyl-p-formyl benzoate (SFB) and succinimidyl-p-formylphenoxyacetate (SFPA).

[00234] Bifunctional crosslinking agents that enable the linkage of cell binding agent with cytotoxic compounds via disulfide bonds are known in the art and include *N*-succinimidyl-3-(2-pyridyldithio)propionate (SPDP), *N*-succinimidyl-4-(2-pyridyldithio)pentanoate (SPP), *N*-succinimidyl-4-(2-pyridyldithio)butanoate (SPDB), *N*-succinimidyl-4-(2-pyridyldithio)2-sulfo butanoate (sulfo-SPDB or sSPDB) to introduce dithiopyridyl groups. Other bifunctional crosslinking agents that can be used to introduce disulfide groups are known in the art and are disclosed in U.S. Patents 6,913,748, 6,716,821 and US Patent Publications 20090274713 and 20100129314, all of which are incorporated herein by reference. Alternatively, crosslinking agents such as 2-iminothiolane, homocysteine thiolactone or S-acetylsuccinic anhydride that introduce thiol groups can also be used.

D. Exemplary Maytansinoids

[00235] In a second embodiment, the present invention provides the maytansinoid compounds that can be used for making the immunoconjugates of the present invention.

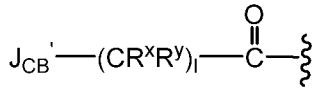
[00236] In some embodiments, the maytansinoid compound is represented by the following formula:



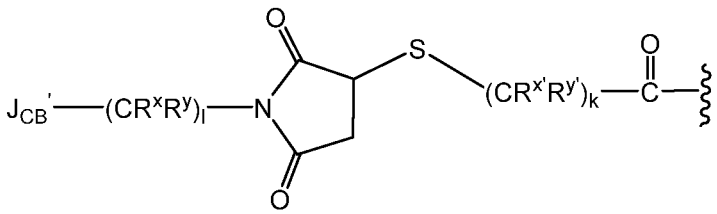
$$L_2'—A—NH—CR^1R^2—S—L_1—D \quad (II)$$

or a pharmaceutically acceptable salt thereof, wherein:

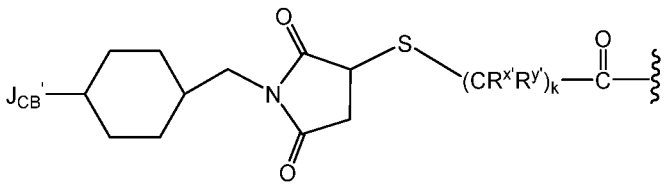
L_2' is represented by the following structural formulas:



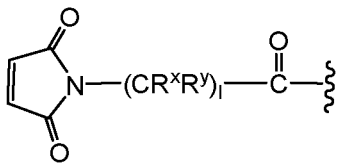
(L2a');



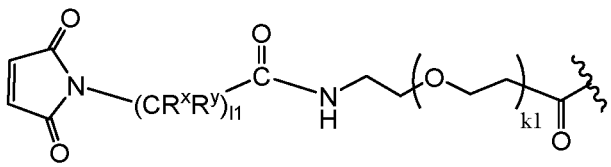
(L2b');



(L2c');



(L2d'); or



(L2e');

wherein:

R^x, R^y, $R^{x'}$ and $R^{y'}$, for each occurrence, are independently H, -OH, halogen, -O-(C_{1-4} alkyl), -SO_3H, -$NR_{40}R_{41}R_{42}^+$, or a C_{1-4} alkyl optionally substituted with -OH, halogen, -SO_3H or $NR_{40}R_{41}R_{42}^+$, wherein R_{40}, R_{41} and R_{42} are each independently H or a C_{1-4} alkyl;

l and k are each independently an integer from 1 to 10;

J_{CB}' is -C(=O)OH or –COE, wherein –COE is a reactive ester;

A is an amino acid or a peptide comprising 2 to 20 amino acids;

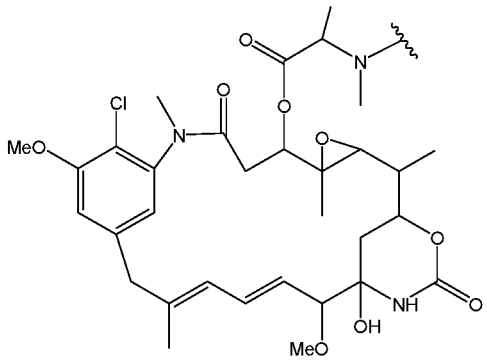
R^1 and R^2 are each independently H or a C_{1-3}alkyl;

L_1 is represented by the following formula:

$-CR^3R^4-(CH_2)_{1-8}-C(=O)-$;

wherein R^3 and R^4 are each independently H or Me, and the –C(=O)- moiety in L_1 is connected to D;

D is represented by the following formula:



and

q is an integer from 1 to 20.

[00237] In some embodiments, the maytansinoid of the present invention is represented by the following formula:

$$A'—NH—CR^1R^2—S-L_1—D \quad (III)$$

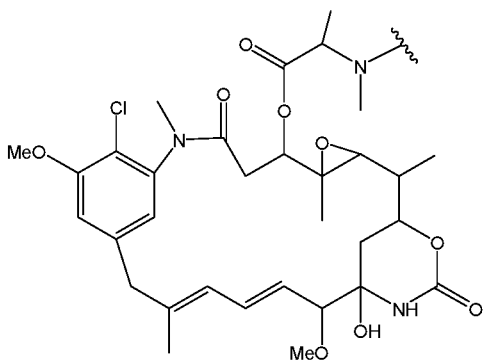
or a pharmaceutically acceptable salt thereof, wherein:

A' is an amino acid or a peptide comprising 2 to 20 amino acids (*i.e.*, A-NH_2);

R^1 and R^2 are each independently H or a C_{1-3}alkyl;

L_1 is $-CR^3R^4-(CH_2)_{1-8}-C(=O)-$; R^3 and R^4 are each independently H or Me;

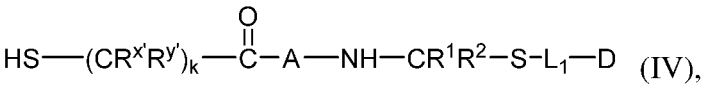
D is is represented by the following formula:



; and

q is an integer from 1 to 20.

[00238] In some embodiments, the maytansinoid of the present invention is represented by the following formula:



(IV),

or a pharmaceutically acceptable salt thereof, wherein:

$R^{x'}$ and $R^{y'}$, for each occurrence, are independently H, -OH, halogen, -O-(C_{1-4} alkyl), -SO_3H, -$NR_{40}R_{41}R_{42}^+$, or a C_{1-4} alkyl optionally substituted with -OH, halogen, SO_3H or $NR_{40}R_{41}R_{42}^+$, wherein R_{40}, R_{41} and R_{42} are each independently H or a C_{1-4} alkyl;

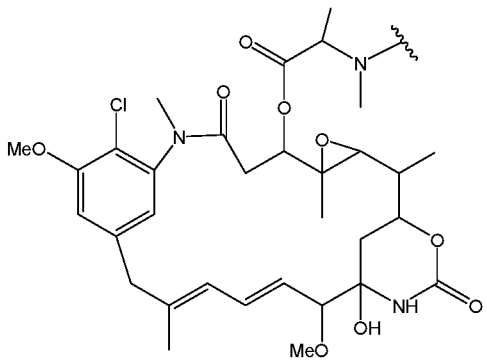
k is an integer from 1 to 10

A is an amino acid residue or a peptide comprising 2 to 20 amino acid residues;

R^1 and R^2 are each independently H or a C_{1-3}alkyl;

L_1 is –CR^3R^4-$(CH_2)_{1-8}$-C(=O)-; R^3 and R^4 are each independently H or Me;

D is represented by the following formula:

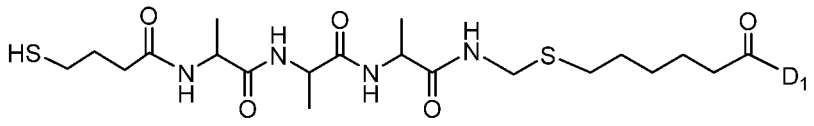


; and

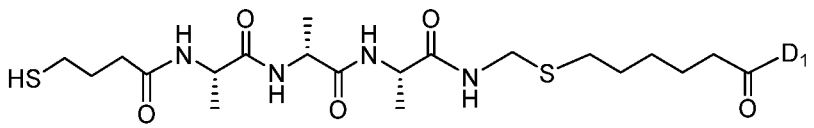
q is an integer from 1 to 20.

[00239] In some embodiments, for maytansinoid compounds of formulas (II), (III) or (IV), the variables are as described in the first embodiment, or the 1st, 2nd, 3rd, 4th, 5th, 6th, 7th, 8th, 9th, 10th or 11th specific embodiment in the first embodiment.

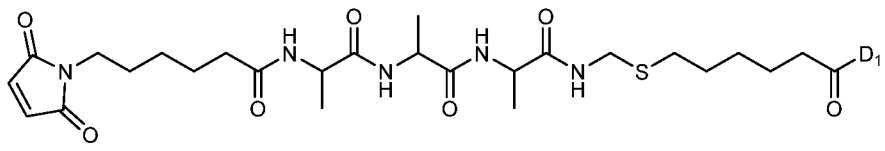
[00240] In a specific embodiment, the maytansinoid compound is represented by the following formula:



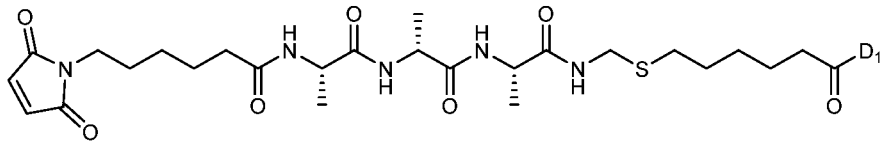
(D-1);



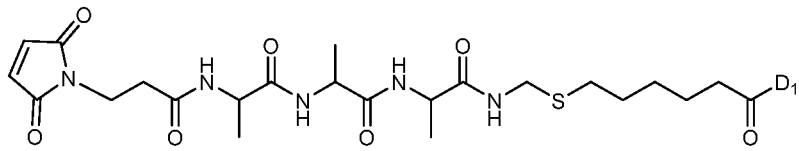
(D-2);



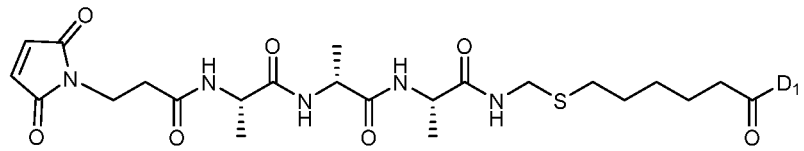
(D-3);



(D-4);

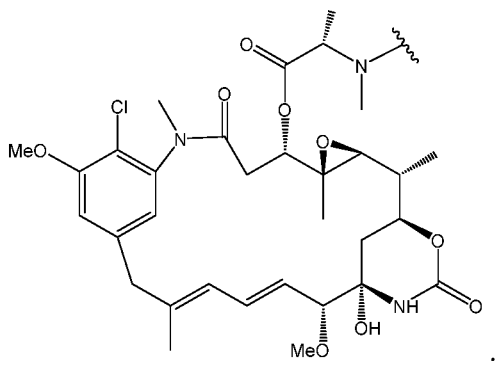


(D-5); or



(D-6),

wherein D_1 is represented by the following formula:



IV. Methods of Production

[00241] The anti-ADAM9 antibodies and ADAM9-binding fragments thereof of the present invention are most preferably produced through the recombinant expression of nucleic acid molecules that encode such polypeptides, as is well-known in the art.

[00242] Polypeptides of the invention may be conveniently prepared using solid phase peptide synthesis (Merrifield, B. (1986) "S*olid Phase Synthesis*," Science 232(4748):341-347; Houghten, R.A. (1985) "*General Method For The Rapid Solid-Phase Synthesis Of Large Numbers Of Peptides: Specificity Of Antigen-Antibody Interaction At The Level Of Individual Amino Acids*," Proc. Natl. Acad. Sci. (U.S.A.) 82(15):5131-5135; Ganesan, A.

(2006) "*Solid-Phase Synthesis In The Twenty-First Century*," Mini Rev. Med. Chem. 6(1):3-10).

[00243] In an alternative, antibodies may be made recombinantly and expressed using any method known in the art. Antibodies may be made recombinantly by first isolating the antibodies made from host animals, obtaining the gene sequence, and using the gene sequence to express the antibody recombinantly in host cells (*e.g.*, CHO cells). Another method that may be employed is to express the antibody sequence in plants {*e.g.*, tobacco) or transgenic milk. Suitable methods for expressing antibodies recombinantly in plants or milk have been disclosed (see, for example, Peeters *et al.* (2001) "*Production Of Antibodies And Antibody Fragments In Plants*," Vaccine 19:2756; Lonberg, N. *et al.* (1995) "*Human Antibodies From Transgenic Mice*," Int. Rev. Immunol 13:65-93; and Pollock *et al.* (1999) "*Transgenic Milk As A Method For The Production Of Recombinant Antibodies*," J. Immunol Methods 231:147-157). Suitable methods for making derivatives of antibodies, *e.g.*, humanized, single-chain, *etc.* are known in the art, and have been described above. In another alternative, antibodies may be made recombinantly by phage display technology (see, for example, U.S. Patent Nos. 5,565,332; 5,580,717; 5,733,743; 6,265,150; and Winter, G. *et al.* (1994) "*Making Antibodies By Phage Display Technology*," Annu. Rev. Immunol. 12.433-455).

[00244] Vectors containing polynucleotides of interest (*e.g.*, polynucleotides encoding the polypeptide chains of the anti-ADAM9 antibodies and ADAM9-binding fragments thereof of the present invention) can be introduced into the host cell by any of a number of appropriate means, including electroporation, transfection employing calcium chloride, rubidium chloride, calcium phosphate, DEAE- dextran, or other substances; microprojectile bombardment; lipofection; and infection (*e.g.*, where the vector is an infectious agent such as vaccinia virus). The choice of introducing vectors or polynucleotides will often depend on features of the host cell.

[00245] Any host cell capable of overexpressing heterologous DNAs can be used for the purpose of expressing a polypeptide or protein of interest. Non-limiting examples of suitable mammalian host cells include but are not limited to COS, HeLa, and CHO cells.

[00246] The invention includes immunoconjugates comprising an amino acid sequence of an anti-ADAM9 antibody or ADAM9-binding fragment thereof of this invention. The polypeptides of this invention can be made by procedures known in the art. The polypeptides can be produced by proteolytic or other degradation of the antibodies, by recombinant methods (*i.e.*, single or fusion polypeptides) as described above or by chemical synthesis. Polypeptides of the antibodies, especially shorter polypeptides up to about 50 amino acids, are conveniently made by chemical synthesis. Methods of chemical synthesis are known in the art and are commercially available.

[00247] The invention includes immunoconjugates comprising variants of anti-ADAM9 antibodies and fragments thereof, including functionally equivalent polypeptides that do not significantly affect the properties of such molecules as well as variants that have enhanced or decreased activity. Modification of polypeptides is routine practice in the art and need not be described in detail herein. Examples of modified polypeptides include polypeptides with conservative substitutions of amino acid residues, one or more deletions or additions of amino acids which do not significantly deleteriously change the functional activity, or use of chemical analogs. Amino acid residues that can be conservatively substituted for one another include but are not limited to: glycine/alanine; serine/threonine; valine/isoleucine/leucine; asparagine/glutamine; aspartic acid/glutamic acid; lysine/arginine; and phenylalanine/tyrosine. These polypeptides also include glycosylated and non-glycosylated polypeptides, as well as polypeptides with other post-translational modifications, such as, for example, glycosylation with different sugars, acetylation, and phosphorylation. Preferably, the amino acid substitutions would be conservative, *i.e.*, the substituted amino acid would possess similar chemical properties as that of the original amino acid. Such conservative substitutions are known in the art, and examples have been provided above. Amino acid modifications can range from changing or modifying one or more amino acids to complete redesign of a region, such as the Variable Domain. Changes in the Variable Domain can alter binding affinity and/or specificity. Other methods of modification include using coupling techniques known in the art, including, but not limited to, enzymatic means, oxidative substitution and chelation. Modifications can be used, for example, for attachment of labels for immunoassay, such as the attachment of radioactive moieties for radioimmunoassay. Modified polypeptides are made using established procedures in the art and can be screened using standard assays known in the art.

[00248] The invention encompasses immunoconjugates comprising fusion proteins possessing one or more of the anti-ADAM9-VL and/or VH of this invention. In one embodiment, a fusion polypeptide is provided that comprises a light chain, a heavy chain or both a light and heavy chain. In another embodiment, the fusion polypeptide contains a heterologous immunoglobulin constant region. In another embodiment, the fusion polypeptide contains a Light Chain Variable Domain and a Heavy Chain Variable Domain of an antibody produced from a publicly-deposited hybridoma. For purposes of this invention, an antibody fusion protein contains one or more polypeptide domains that specifically bind to ADAM9 and another amino acid sequence to which it is not attached in the native molecule, for example, a heterologous sequence or a homologous sequence from another region.

[00249] The present invention also provides polynucleotides comprising a nucleotide sequence encoding an anti-ADAM9 antibody or ADAM9-binding fragment thereof of this invention.

[00250] In certain embodiments, the invention provides a polynucleotide encoding hMAB-A VL (2) light chain having the amino acid sequence of SEQ ID NO:68, wherein the polynucleotide has the nucleotide sequence of **SEQ ID NO:157**:

gacattgtgatgacccaatctccagattctttggctgtgtctctaggggagagggccacc
atctcctgcaaggccagccaaagtgttgattactctggtgatagttatatgaactggtac
caacagaaaccaggacagccacccaaactcctcatctatgctgcatccgacctagaatct
ggaatcccagccaggtttagtggcagtgggtctgggacagacttcaccctcactatctct
agcctggagcctgaggatttcgcaacctattactgtcagcaaagtcatgaagacccgttc
acgttcggacaagggaccaagctcgaaatcaaacgtacggtggctgcaccatctgtcttc
atcttcccgccatctgatgagcagttgaaatctggaactgcctctgttgtgtgcctgctg
aataacttctatcccagagaggccaaagtacagtggaaggtggataacgccctccaatcg
ggtaactcccaggagagtgtcacagagcaggacagcaaggacagcacctacagcctcagc
agcaccctgacgctgagcaaagcagactacgagaaacacaaagtctacgcctgcgaagtc
acccatcagggcctgagctcgcccgtcacaaagagcttcaacaggggagagtgt

[00251] In certain embodiments, the invention provides a polynucleotide encoding hMAB-A VL (2) light chain having the amino acid sequence of SEQ ID NO:68, wherein the polynucleotide is codon optimized and has the nucleotide sequence of **SEQ ID NO:158:**

gacattgtgatgacgcagtcccccgactccctggccgtgtccttgggcgaaagggccac
aatcagctgcaaggcatcacagagcgtggactactctggggacagctacatgaattggt
accagcagaagcccgggcagcctccaaagctgctgatctacgccgcatccgacctggag
tccggcatcccggcgcggttctcgggttcgggatccggcactgacttcaccctgaccat
ctcaagcctggagcccgaggactttgcgacctactactgccaacagtcccacgaagatc
cgtttaccttcggacaaggcaccaagctcgagatcaagagaactgtggccgccccgagc
gtgttcattttcccgccatcggatgagcaactgaagtccggaactgcgagcgtggtctg
cctcctcaacaacttctatcctcgggaagccaaagtgcagtggaaggtcgacaacgctc
tgcagtccggaaactcccaagagagcgtgaccgaacaggattccaaggactcgacctac
tcgctgtcatccactctgaccctgagcaaggccgattacgaaaagcacaaagtgtacgc
ttgcgaagtgacccaccagggactgtcatcccctgtgaccaagtcgttcaaccgcggcg
aatgc

[00252] In certain embodiments, the invention provides a polynucleotide encoding hMAB-A VH (2I) heavy chain having the amino acid sequence of SEQ ID NO:151, wherein the polynucleotide has the nucleotide sequence of **SEQ ID NO:159:**

gaggtccaactggtggaatctgggggaggcctggtgaagcctgggggctcactgagact
gtcttgcgctgcttctggttttaccttctctagctactggatgcactgggtgagacagg
cacctggaaagggccttgagtgggttggagagattattcctatctttggtcatactaac
tacaatgagaagttcaagagcaggttcacaatttctttagacaactccaagaatacact
gtacctccaaatgggaagcctgagggcagaggacacagcggtctattactgtgcaagag
ggggttattattattacccccggcagggcttcctggactactggggccaaggcaccact
gtgacagtctcctcagcctccaccaagggcccatcggtcttcccctggcaccctcctc
caagagcacctctgggggcacagcggccctgggctgcctggtcaaggactacttccccg
aaccggtgacggtgtcgtggaactcaggcgccctgaccagcggcgtgcacaccttcccg
gctgtcctacagtcctcaggactctactccctcagcagcgtggtgaccgtgccctccag
cagcttgggcacccagacctacatctgcaacgtgaatcacaagcccagcaacaccaagg
tggacaagagagttgagcccaaatcttgtgacaaaactcacacatgcccaccgtgccca
gcacctgaactcctgggggggaccgtcagtcttcctcttcccccaaaacccaaggacac
cctctatatcacccgggagcctgaggtcacatgcgtggtggtggacgtgagccacgaag
accctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagaca
aagccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcct
gcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcc
cagccccatcgagaaaaccatctccaaagccaaagggcagccccgagaaccacaggtg
tacaccctgcccccatcccgggaggagatgaccaagaaccaggtcagcctgacctgcct
ggtcaaaggcttctatcccagcgacatcgccgtggagtgggagagcaatgggcagccgg
agaacaactacaagaccacgcctcccgtgctggactccgacggctccttcttcctctac
agcaagctcaccgtggacaagagcaggtggcagcaggggaacgtcttctcatgctccgt
gatgcatgaggctctgcacaaccactacacgcagaagagcctctccctgtctccgggt**x**
xx

wherein xxx are aaa or are absent.

[00253] In certain embodiments, the invention provides a polynucleotide encoding hMAB-A VH (2I) heavy chain having the amino acid sequence of SEQ ID NO:155, wherein the polynucleotide has the nucleotide sequence of **SEQ ID NO:160:**

gaggtccaactggtggaatctgggggaggcctggtgaagcctgggggctcactgagact
gtcttgcgctgcttctggttttaccttctctagctactggatgcactgggtgagacagg
cacctggaaagggccttgagtgggttggagagattattcctatctttggtcatactaac
tacaatgagaagttcaagagcaggttcacaatttctttagacaactccaagaatacact
gtacctccaaatgggaagcctgagggcagaggacacagcggtctattactgtgcaagag
ggggttattattattacccccggcagggcttcctggactactggggccaaggcaccact
gtgacagtctcctcagcctccaccaagggcccatcggtcttcccccctggcaccctcctc
caagagcacctctgggggcacagcggccctgggctgcctggtcaaggactacttccccg
aaccggtgacggtgtcgtggaactcaggcgccctgaccagcggcgtgcacaccttcccg
gctgtcctacagtcctcaggactctactccctcagcagcgtggtgaccgtgccctccag
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gcacctgaactcctgggggggaccgtcagtcttcctcttccccccaaaacccaaggacac
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accctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagaca
aagccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcct
gcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcc
cagccccccatcgagaaaaccatctccaaagccaaagggcagccccgagaaccacaggtg
tacaccctgcccccatcccgggaggagatgaccaagaaccaggtcagcctgacctgcct
ggtcaaaggcttctatcccagcgacatcgccgtggagtgggagagcaatgggcagccgg
agaacaactacaagaccacgcctcccgtgctggactccgacggctccttcttcctctac
agcaagctcaccgtggacaagagcaggtggcagcaggggaacgtcttctcatgctccgt
gatgcatgaggctctgcacaaccactacacgcagaagagcctctccctgtctccgggt

[00254] In certain embodiments, the invention provides a polynucleotide encoding hMAB-A VH (2I) heavy chain having the amino acid sequence of SEQ ID NO:156, wherein the polynucleotide has the nucleotide sequence of **SEQ ID NO:161:**

gaggtccaactggtggaatctgggggaggcctggtgaagcctgggggctcactgagactg
tcttgcgctgcttctggttttaccttctctagctactggatgcactgggtgagacaggca
cctggaaagggccttgagtgggttggagagattattcctatctttggtcatactaactac
aatgagaagttcaagagcaggttcacaatttctttagacaactccaagaatacactgtac
ctccaaatgggaagcctgagggcagaggacacagcggtctattactgtgcaagaggggt
tattattattaccccggcagggcttcctggactactggggccaaggcaccactgtgaca
gtctcctcagcctccaccaagggcccatcggtcttcccccctggcaccctcctccaagagc
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acggtgtcgtggaactcaggcgccctgaccagcggcgtgcacaccttcccggctgtccta
cagtcctcaggactctactccctcagcagcgtggtgaccgtgccctccagcagcttgggc

acccagacctacatctgcaacgtgaatcacaagcccagcaacaccaaggtggacaagaga
gttgagcccaaatcttgtgacaaaactcacacatgcccaccgtgcccagcacctgaactc
ctgggggggaccgtcagtcttcctcttccccccaaaacccaaggacaccctctatatcacc
cgggagcctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtcaag
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cagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctg
aatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgagaaa
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cgggaggagatgaccaagaaccaggtcagcctgacctgcctggtcaaaggcttctatccc
agcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacg
cctcccgtgctggactccgacggctccttcttcctctacagcaagctcaccgtggacaag
agcaggtggcagcaggggaacgtcttctcatgctccgtgatgcatgaggctctgcacaac
cactacacgcagaagagcctctgcctgtctccgggt

[00255] In certain embodiments, the invention provides a polynucleotide encoding hMAB-A VH (2I) heavy chain having the amino acid sequence of SEQ ID NO:156, wherein the polynucleotide is codon optimized and has the nucleotide sequence of **SEQ ID NO:162:**

gaagtccaactggtggaatcgggggcggcctcgtgaagcccggaggatccctgaggctc
tcctgcgccgcctccgggttcacttttcgtcatactggatgcattgggtccgccaggcc
ccggggaagggactggaatgggtcggagagatcatccccattttcggccacacaaactac
aacgaaaagttcaagagccgctttactatttccttggacaattcaaagaacaccctgtat
ctgcaaatgggaagcctgcgggccgaggacaccgctgtgtactactgcgcccggggtggc
tactattactacccgagacagggtttcctcgattactggggccagggaaccaccgtgacc
gtgtcctctgcctcgaccaaaggcccctcggtgttcccgcttgcgccatcctccaaatcc
acctccggcggcaccgccgctctgggatgcctggtcaaagattacttcccggagcctgtg
acggtgtcgtggaactctggagccctcacgagcggagtgcataccttccctgcggtgctc
caatcgtccggactgtacagcctgagcagcgtcgtcactgtgcctagctcgtccctgggc
acccagacctacatttgcaacgtgaaccataagccttcaaacactaaggtcgacaaacgg
gtggaacccaagtcgtgcgataagactcatacttgcccgccttgccccgcgcctgaactt
ttgggagggccgtccgtgttcctgttcccgccaaagccaaaggacactctgtacatcact
cgcgaacccgaagtgacctgtgtggtcgtggacgtgtcccacgaggatccggaagtcaag
ttcaattggtacgtggacggtgtcgaggtgcacaacgcaaagaccaagccgcgcgaggaa
cagtacaactccacataccgggtggtgtcagtgctgaccgtgttgcaccaggactggctc
aacggaaaggagtacaagtgcaaagtgtccaacaaggccctgcctgcaccaatcgaaaag
accattagcaaggccaaggggcagccccgggagccccaagtgtacactctgcccccgtca
cgggaagaaatgaccaagaaccaagtgtcactgacctgtcttgtgaagggtttctacccc
tccgacatcgccgtggagtgggagtccaacggacagccggagaacaattacaagactacc

ccgccggtgctggatagcgacggctccttcttcctgtactccaagctgaccgtggacaag
tcgagatggcagcaggggaacgtgttctcgtgctccgtgatgcacgaagcgctgcacaac
cactatacccagaagtccctgtgcctgtcccctgga

V. Drug Conjugation

[00256] The immunoconjugates comprising an anti-ADAM9 antibody or an ADAM9-binding fragment thereof covalently linked to a maytansinoid compound described herein can be prepared according to any suitable methods known in the art.

[00257] In certain embodiments, the immunoconjugates of the first embodiment can be prepared by a first method comprising the steps of reacting the anti-ADAM9 antibody or an ADAM9-binding fragment thereof with the maytansinoid compound of formula (II) described in the second embodiment.

[00258] In certain embodiments, the immunoconjugates of the first embodiment can be prepared by a second method comprising the steps of:

(a) reacting the maytansinoid compound of formula (III) or (IV) with a linker compound described herein to form a cytotoxic agent-maytansinoid compound having an amine-reactive group or a thiol-reactive group bound thereto that can be covalently linked to the anti-ADAM9 antibody or an ADAM9-binding fragment thereof (or CBA); and

(b) reacting the anti-ADAM9 antibody or an ADAM9-binding fragment thereof with the maytansinoid-linker compound to form the immunoconjugate.

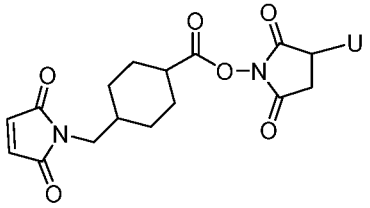
[00259] In certain embodiments, the immunoconjugates of the first embodiment can be prepared by a third method comprising the steps of:

(a) reacting the anti-ADAM9 antibody or an ADAM9-binding fragment thereof with a linker compound described herein to form a modified anti-ADAM9 antibody or an ADAM9-binding fragment thereof having an amine-reactive group or a thiol-reactive group bound thereto (*e.g.*, compound of formula (II)) that can be covalently linked to the maytansinoid compound of formula (III) or (IV); and

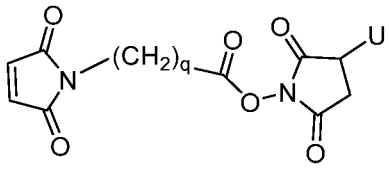
(b) reacting the modified anti-ADAM9 antibody or an ADAM9-binding fragment thereof with the maytansinoid compound of formula (III) or (IV) to form the immunoconjugate.

[00260] In certain embodiments, the immunoconjugates of the first embodiment can be prepared by a third method comprising reacting an anti-ADAM9 antibody or an ADAM9-binding fragment thereof, a linker compound and a maytansinoid compound of formula (III) or (IV) to form the immunoconjugates. In one embodiment, the anti-ADAM9 antibody or ADAM9-binding fragment thereof and the maytansinoid compound of formula (III) or (IV) are mixed first, followed by the addition of the linker compound.

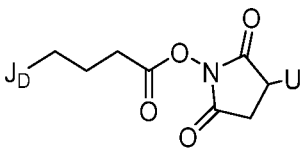
[00261] In certain embodiments, for the second, third or fourth methods described above, the linker compound is represented by any one of the formula (a1L) – (a10L):



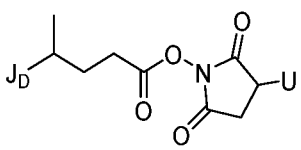
(a1L);



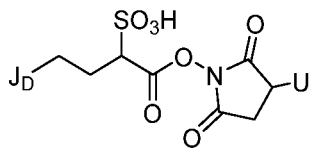
(a2L);



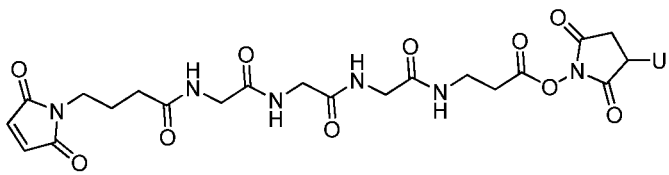
(a3L);



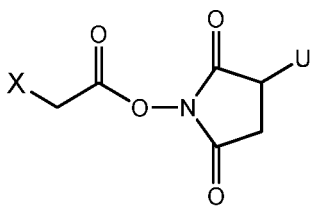
(a4L);



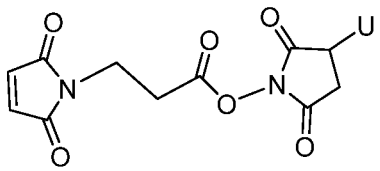
(a5L),



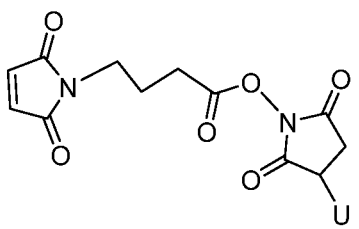
(a6L),



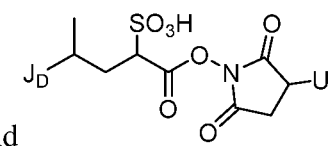
(a7L);



(a8L);



(a9L); and

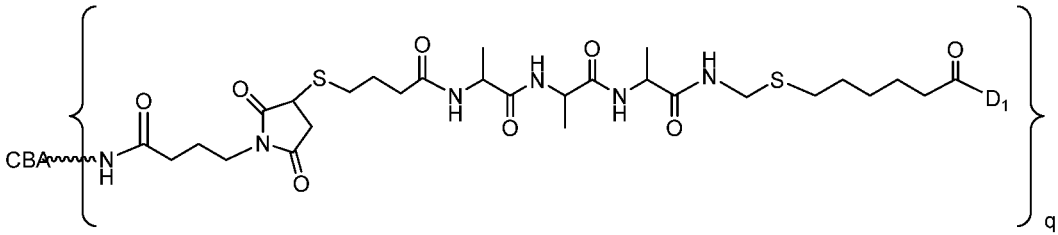


(a10L),

wherein X is halogen; J_D –SH, or –SSR^d; R^d is phenyl, nitrophenyl, dinitrophenyl, carboxynitrophenyl, pyridyl or nitropyridyl; R^g is an alkyl; and U is –H or SO_3H or a pharmaceutically acceptable salt thereof.

[00262] In one embodiment, the linker compound is GMBS or sulfo-GMBS represented by represented by formula (a9L), wherein U is –H or SO_3H or a pharmaceutically acceptable salt thereof.

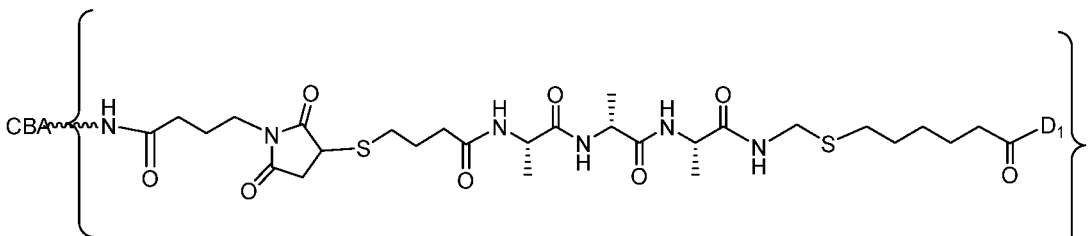
[00263] In a specific embodiment, the immunoconjugate of the present invention is represented by the following formula:



q (I-1); and

the immunoconjugate can be prepared by the second, third or fourth method described above, wherein the linker compound is GMBS or sulfo-GMBS represented by represented by formula (a9L), wherein U is –H or SO_3H or a pharmaceutically acceptable salt thereof; and the maytansinoid compound is represented by formula (D-1) described above. In a more specific embodiment, the immunoconjugate of formula (I-1) is prepared by reacting the maytansinoid compound of formula (D-1) with the linker compound GMBS or sulfo-GMBS to form a maytansinoid-linker compound, followed by reacting the anti-ADAM9 antibody or ADAM9-binding fragment thereof with the maytansinoid-linker compound. In an even more specific embodiment, the maytansinoid linker compound is not purified before reacting with the anti-ADAM9 antibody or an ADAM9-binding fragment thereof.

[00264] In another specific embodiment, the immunoconjugate is represented by the following formula:

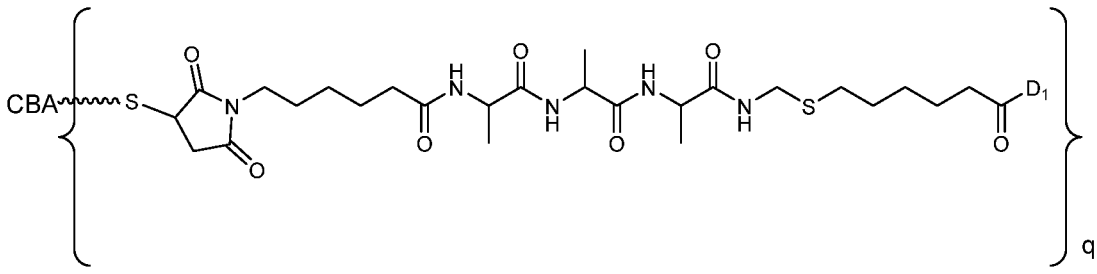


q (I-2);

and the immunoconjugate can be prepared by the second, third or fourth method described

above, wherein the linker compound is GMBS or sulfo-GMBS represented by represented by formula (a9L), wherein U is –H or SO_3H or a pharmaceutically acceptable salt thereof; and the maytansinoid compound is represented by formula (D-2) described above. In a more specific embodiment, the immunoconjugate of formula (I-2) is prepared by reacting the maytansinoid compound of formula (D-2) with the linker compound GMBS or sulfo-GMBS to form a maytansinoid-linker compound, followed by reacting the anti-ADAM9 antibody or ADAM9-binding fragment thereof with the maytansinoid-linker compound. In a even more specific embodiment, the maytansinoid linker compound is not purified before reacting with the anti-ADAM9 antibody or an ADAM9-binding fragment thereof.

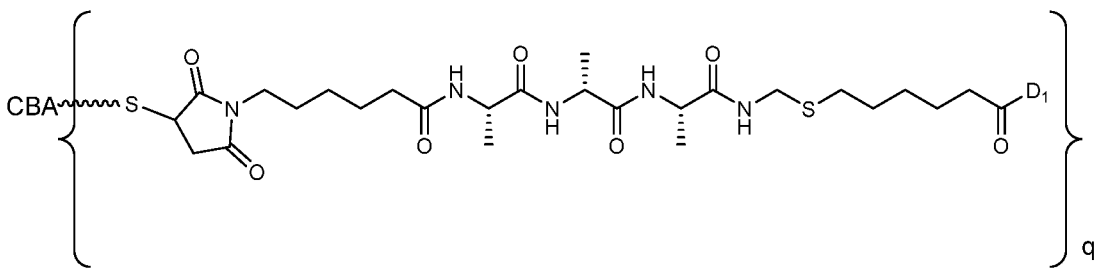
[00265] In another specific embodiment, the immunoconjugate is represented by the following formula:



(I-3);

and the immunoconjugate is prepared according to the first method described above by reacting the anti-ADAM9 antibody or ADAM9-binding fragment thereof with the maytansinoid compound of formula (D-3) described above.

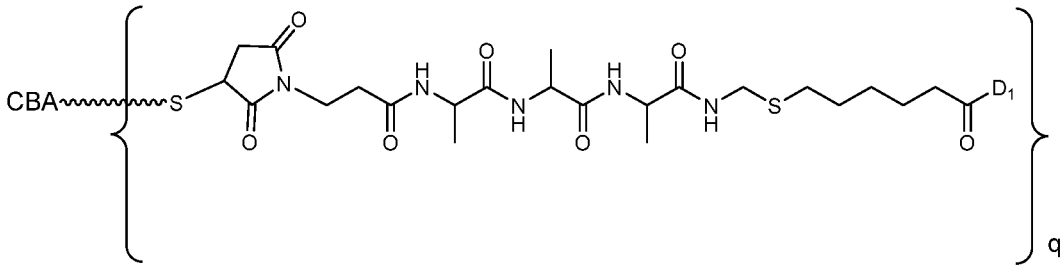
[00266] In another specific embodiment, the immunoconjugate is represented by the following formula:



(I-4);

and the immunoconjugate is prepared according to the first method described above by reacting the anti-ADAM9 antibody or ADAM9-binding fragment thereof with the maytansinoid compound of formula (D-4) described above.

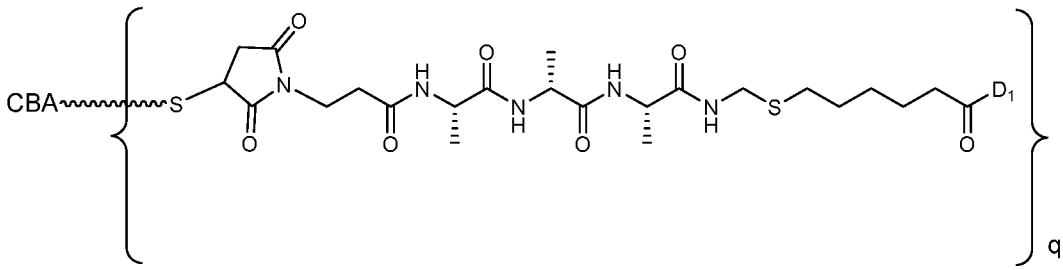
[00267] In another specific embodiment, the immunoconjugate is represented by the following formula:



(I-5); and

the immunoconjugate is prepared according to the first method described above by reacting the anti-ADAM9 antibody or ADAM9-binding fragment thereof with the maytansinoid compound of formula (D-5) described above.

[00268] In another specific embodiment, the immunoconjugate is represented by the following formula:



(I-6); and

the immunoconjugate is prepared according to the first method described above by reacting the anti-ADAM9 antibody or ADAM9-binding fragment thereof with the maytansinoid compound of formula (D-6) described above

[00269] In some embodiments, the immunoconjugates prepared by any methods described above is subject to a purification step. In this regard, the immunoconjugate can be purified from the other components of the mixture using tangential flow filtration (TFF), non-adsorptive chromatography, adsorptive chromatography, adsorptive filtration, selective precipitation, or any other suitable purification process, as well as combinations thereof.

[00270] In some embodiments, the immunoconjugate is purified using a single purification step (e.g., TFF). Preferably, the conjugate is purified and exchanged into the appropriate formulation using a single purification step (e.g., TFF). In other embodiments of the invention, the immunoconjugate is purified using two sequential purification steps. For example, the immunoconjugate can be first purified by selective precipitation, adsorptive

filtration, absorptive chromatography or non-absorptive chromatography, followed by purification with TFF. One of ordinary skill in the art will appreciate that purification of the immunoconjugate enables the isolation of a stable conjugate comprising the cell-binding agent chemically coupled to the cytotoxic agent.

[00271] Any suitable TFF systems may be utilized for purification, including a Pellicon type system (Millipore, Billerica, Mass.), a Sartocon Cassette system (Sartorius AG, Edgewood, N.Y.), and a Centrasette type system (Pall Corp., East Hills, N.Y.)

[00272] Any suitable adsorptive chromatography resin may be utilized for purification. Preferred adsorptive chromatography resins include hydroxyapatite chromatography, hydrophobic charge induction chromatography (HCIC), hydrophobic interaction chromatography (HIC), ion exchange chromatography, mixed mode ion exchange chromatography, immobilized metal affinity chromatography (IMAC), dye ligand chromatography, affinity chromatography, reversed phase chromatography, and combinations thereof. Examples of suitable hydroxyapatite resins include ceramic hydroxyapatite (CHT Type I and Type II, Bio-Rad Laboratories, Hercules, Calif.), HA Ultrogel hydroxyapatite (Pall Corp., East Hills, N.Y.), and ceramic fluoroapatite (CFT Type I and Type II, Bio-Rad Laboratories, Hercules, Calif.). An example of a suitable HCIC resin is MEP Hypercel resin (Pall Corp., East Hills, N.Y.). Examples of suitable HIC resins include Butyl-Sepharose, Hexyl-Sepharose, Phenyl-Sepharose, and Octyl Sepharose resins (all from GE Healthcare, Piscataway, N.J.), as well as Macro-prep Methyl and Macro-Prep t-Butyl resins (Biorad Laboratories, Hercules, Calif.). Examples of suitable ion exchange resins include SP-Sepharose, CM-Sepharose, and Q-Sepharose resins (all from GE Healthcare, Piscataway, N.J.), and Unosphere S resin (Bio-Rad Laboratories, Hercules, Calif.). Examples of suitable mixed mode ion exchangers include Bakerbond ABx resin (JT Baker, Phillipsburg N.J.) Examples of suitable IMAC resins include Chelating Sepharose resin (GE Healthcare, Piscataway, N.J.) and Profinity IMAC resin (Bio-Rad Laboratories, Hercules, Calif.). Examples of suitable dye ligand resins include Blue Sepharose resin (GE Healthcare, Piscataway, N.J.) and Affi-gel Blue resin (Bio-Rad Laboratories, Hercules, Calif.). Examples of suitable affinity resins include Protein A Sepharose resin (e.g., MabSelect, GE Healthcare, Piscataway, N.J.), where the cell-binding agent is an antibody, and lectin affinity resins, e.g. Lentil Lectin Sepharose resin (GE Healthcare, Piscataway, N.J.), where the cell-binding agent bears appropriate lectin binding sites. Alternatively an

antibody specific to the cell-binding agent may be used. Such an antibody can be immobilized to, for instance, Sepharose 4 Fast Flow resin (GE Healthcare, Piscataway, N.J.). Examples of suitable reversed phase resins include C4, C8, and C18 resins (Grace Vydac, Hesperia, Calif.).

[00273] Any suitable non-adsorptive chromatography resin may be utilized for purification. Examples of suitable non-adsorptive chromatography resins include, but are not limited to, SEPHADEXTM G-25, G-50, G-100, SEPHACRYLTM resins (e.g., S-200 and S-300), SUPERDEXTM resins (e.g., SUPERDEXTM 75 and SUPERDEXTM 200), BIO-GEL® resins (e.g., P-6, P-10, P-30, P-60, and P-100), and others known to those of ordinary skill in the art.

VI. Uses of the Immunoconjugates of the Present Invention

[00274] The present invention encompasses compositions, including pharmaceutical compositions, comprising the immunoconjugates of the present invention.

[00275] As provided herein, the immunoconjugates of the present invention, comprising the humanized/optimized anti-ADAM9-VL and/or VH Domains provided herein, have the ability to bind ADAM9 present on the surface of a cell and mediate cell killing. In particular, the immunoconjugates of the present invention comprising a pharmacological agent, are internalized and mediate cell killing via the activity of the pharmacological agent. Such cell killing activity may be augmented by the immunoconjugate inducing antibody-dependent cell-mediated cytotoxicity (ADCC) and/or complement dependent cytotoxicity (CDC)

[00276] Thus, immunoconjugates of the present invention, comprising the humanized/optimized anti-ADAM9-VL and/or VH Domains provided herein, have the ability to treat any disease or condition associated with or characterized by the expression of ADAM9. As discussed above, ADAM9 is an onco-embryonic antigen expressed in numerous blood and solid malignancies that is associated with high-grade tumors exhibiting a less-differentiated morphology, and is correlated with poor clinical outcomes. Thus, without limitation, the immunoconjugates of the present invention may be employed in the treatment of cancer, particularly a cancer characterized by the expression of ADAM9.

[00277] In other particular embodiments, immunoconjugates of the present invention may be useful in the treatment of lung cancer (e.g., non-small-cell lung cancer), colorectal cancer, bladder cancer, gastric cancer, pancreatic cancer, renal cell carcinoma, prostate cancer, esophageal cancer, breast cancer, head and neck cancer, uterine cancer, ovarian cancer, liver cancer, cervical cancer, thyroid cancer, testicular cancer, myeloid cancer, melanoma, and lymphoid cancer. In other particular embodiments, immunoconjugates of the present invention may be useful in the treatment of non-small-cell lung cancer, colorectal cancer, gastric cancer, breast cancer (*e.g.*, triple negative breast cancer (TNBC)), or pancreatic cancer.

[00278] In further embodiments, immunoconjugates of the present invention may be useful in the treatment of non-small-cell lung cancer (squamous cell, nonsquamous cell, adenocarcinoma, or large-cell undifferentiated carcinoma), colorectal cancer (adenocarcinoma, gastrointestinal carcinoid tumors, gastrointestinal stromal tumors, primary colorectal lymphoma, leiomyosarcoma, or squamous cell carcinoma) or breast cancer (*e.g.*, triple negative breast cancer (TNBC)).

[00279] In addition to their utility in therapy, the immunoconjugates of the present invention may be detectably labeled and used in the diagnosis of cancer or in the imaging of tumors and tumor cells.

VII. Pharmaceutical Compositions

[00280] The compositions of the invention include bulk drug compositions useful in the manufacture of pharmaceutical compositions (*e.g.*, impure or non-sterile compositions) and pharmaceutical compositions (*i.e.*, compositions that are suitable for administration to a subject or patient) that can be used in the preparation of unit dosage forms. Such compositions comprise a prophylactically or therapeutically effective amount of the immunoconjugates of the present invention, or a combination of such agents and a pharmaceutically acceptable carrier. Preferably, compositions of the invention comprise a prophylactically or therapeutically effective amount of immunoconjugates of the present invention and a pharmaceutically acceptable carrier. The invention also encompasses such pharmaceutical compositions that additionally include a second therapeutic antibody (*e.g.*, tumor-specific monoclonal antibody) that is specific for a particular cancer antigen, and a pharmaceutically acceptable carrier.

[00281] In a specific embodiment, the term "**pharmaceutically acceptable**" means approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeia for use in animals, and more particularly in humans. The term "**carrier**" refers to a diluent, adjuvant (*e.g.*, Freund's adjuvant (complete and incomplete), excipient, or vehicle with which the therapeutic is administered. Generally, the ingredients of compositions of the invention are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a hermetically sealed container such as an ampoule or sachette indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water or saline. Where the composition is administered by injection, an ampoule of sterile water for injection or saline can be provided so that the ingredients may be mixed prior to administration.

[00282] The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with an immunoconjugates of the present invention, alone or with such pharmaceutically acceptable carrier. Additionally, one or more other prophylactic or therapeutic agents useful for the treatment of a disease can also be included in the pharmaceutical pack or kit. The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

[00283] The present invention provides kits that can be used in the above methods. A kit can comprise any of the immunoconjugates of the present invention. The kit can further comprise one or more other prophylactic and/or therapeutic agents useful for the treatment of cancer, in one or more containers.

VIII. Methods of Administration

[00284] The compositions of the present invention may be provided for the treatment, prophylaxis, and amelioration of one or more symptoms associated with a disease, disorder by administering to a subject an effective amount an immunoconjugate of the invention. In

a preferred aspect, such compositions are substantially purified (*i.e.*, substantially free from substances that limit its effect or produce undesired side effects). In a specific embodiment, the subject is an animal, preferably a mammal such as non-primate (*e.g.*, bovine, equine, feline, canine, rodent, *etc.*) or a primate (*e.g.*, monkey such as, a cynomolgus monkey, human, *etc.*). In a preferred embodiment, the subject is a human.

[00285] Various delivery systems are known and can be used to administer the compositions of the invention, *e.g.*, encapsulation in liposomes, microparticles, microcapsules, recombinant cells capable of expressing the antibody or fusion protein, receptor-mediated endocytosis (See, *e.g.*, Wu *et al.* (1987) *"Receptor-Mediated In Vitro Gene Transformation By A Soluble DNA Carrier System,"* J. Biol. Chem. 262:4429-4432), construction of a nucleic acid as part of a retroviral or other vector, *etc.*

[00286] Methods of administering an immunoconjugate of the invention include, but are not limited to, parenteral administration (*e.g.*, intradermal, intramuscular, intraperitoneal, intravenous and subcutaneous), epidural, and mucosal (*e.g.*, intranasal and oral routes). In a specific embodiment, the immunoconjugates of the present invention are administered intramuscularly, intravenously, or subcutaneously. The compositions may be administered by any convenient route, for example, by infusion or bolus injection, and may be administered together with other biologically active agents. Administration can be systemic or local.

[00287] The invention also provides that preparations of the immunoconjugates of the present invention are packaged in a hermetically sealed container such as an ampoule or sachette indicating the quantity of the molecule. In one embodiment, such molecules are supplied as a dry sterilized lyophilized powder or water free concentrate in a hermetically sealed container and can be reconstituted, *e.g.*, with water or saline to the appropriate concentration for administration to a subject. Preferably, the immunoconjugates of the present invention are supplied as a dry sterile lyophilized powder in a hermetically sealed container.

[00288] The lyophilized preparations of the immunoconjugates of the present invention should be stored at between 2°C and 8°C in their original container and the molecules should be administered within 12 hours, preferably within 6 hours, within 5 hours, within 3 hours, or within 1 hour after being reconstituted. In an alternative embodiment, such

molecules are supplied in liquid form in a hermetically sealed container indicating the quantity and concentration of the molecule, fusion protein, or conjugated molecule. Preferably, such immunoconjugates when provided in liquid form are supplied in a hermetically sealed container.

[00289] As used herein, an "**effective amount**" of a pharmaceutical composition is an amount sufficient to effect beneficial or desired results including, without limitation, clinical results such as decreasing symptoms resulting from the disease, attenuating a symptom of infection (*e.g.*, viral load, fever, pain, sepsis, etc.) or a symptom of cancer (e.g., the proliferation, of cancer cells, tumor presence, tumor metastases, *etc.*), thereby increasing the quality of life of those suffering from the disease, decreasing the dose of other medications required to treat the disease, enhancing the effect of another medication such as via targeting and/or internalization, delaying the progression of the disease, and/ or prolonging survival of individuals. An effective amount can be administered in one or more administrations. For purposes of this invention, an effective amount of drug, compound, or pharmaceutical composition is an amount sufficient: to kill and/or reduce the proliferation of cancer cells, and/or to eliminate, reduce and/or delay the development of metastasis from a primary site of cancer.

[00290] The pharmaceutical compositions of the invention may be administered locally to the area in need of treatment; this may be achieved by, for example, and not by way of limitation, local infusion, by injection, or by means of an implant, said implant being of a porous, non-porous, or gelatinous material, including membranes, such as sialastic membranes, or fibers. Preferably, when administering an immunoconjugate of the invention, care must be taken to use materials to which the molecule does not absorb.

[00291] The compositions of the invention can be delivered in a vesicle, in particular a liposome (*See* Langer (1990) *"New Methods Of Drug Delivery,"* Science 249:1527-1533); Treat *et al.*, in LIPOSOMES IN THE THERAPY OF INFECTIOUS DISEASE AND CANCER, Lopez-Berestein and Fidler (eds.), Liss, New York, pp. 353- 365 (1989); Lopez-Berestein, ibid., pp. 3 17-327).

EXAMPLES

[00292] Having now generally described the invention, the same will be more readily understood through reference to the following Examples. The following examples illustrate various methods for compositions in the diagnostic or treatment methods of the invention. The examples are intended to illustrate, but in no way limit, the scope of the invention.

Example 1
Tumor Cell Specificity of the Anti-ADAM9 Antibody MAB-A

[00293] A murine anti-ADAM9 antibody (designated herein as MAB-A) was identified that: (1) blocks the target protein processing activity of ADAM9; (2) is internalized; and (3) has anti-tumor activity (see, *e.g.*, US Patent No. 8361475). The tumor cell specificity of MAB-A was investigated by IHC. Tumor tissue was contacted with MAB-A (0.4 μg/mL) or an isotype control (0.4 μg/mL) and the extent of staining was visualized. MAB-A was found to strongly label a variety of large cell carcinoma, squamous cell carcinoma, and adenocarcinoma non-small cell lung cancer cell types (**FIG. 1A**), breast cancer cells, prostate cancer cells, gastric cancer cells (**FIG. 1B**), as well as colon cancer samples (**FIG. 1C**). Normal tissue was contacted with MAB-A (1.25 μg/mL) and the extent of staining was visualized. As summarized in **Table 2** above, MAB-A exhibited little or no staining of a wide variety of normal tissues. It will be noted that the concentration of MAB-A used in these studies was nearly 3-times that used for staining of tumor cells. The results of these IHC studies indicate that MAB-A exhibits strong preferential binding to tumor cells over normal cells.

Example 2
Species Cross Reactivity

[00294] The binding of MAB-A to human ADAM9 (huADAM9) and cynomolgus monkey ADAM9 (cynoADAM9) was examined. Briefly, 293-FT and CHO-K cells transiently expressing huADAM9, cynoADAM9, an unrelated antigen, or the untransfected parental cells were incubated with MAB-A followed by goat anti-murine-PE secondary antibody and analyzed by FACS. As shown in **FIG. 2**, MAB-A exhibits strong binding to huADAM9 transiently expressed on both cells types. MAB-A exhibits poor binding to cynoADAM9. MAB-A did not bind to the parental cells or cells expressing an irrelevant antigen. Similar low levels of binding to cynoADAM were seen in ELISA assays.

Example 3
Humanization and Initial Optimization

[00295] Humanization of MAB-A yielded a humanized VH Domain, designated herein as **"hMAB-A VH(1)"** and a humanized VL Domain designated herein as "hMAB-A VL(1)." The humanized Variable Domains were then optimized to enhance binding activity and/or to remove potentially labile amino acid residues as described in more detail below. This first round of optimization yielded three additional humanized VH Domains, designated herein as "**hMAB-A VH(2)**," "**hMAB-A VH(3)**," and "**hMAB-A VH(4)**," and three additional humanized VL Domains designated herein as "**hMAB-A VL(2)**," "**hMAB-A VL(3)**," and "**hMAB-A VL(4)**." In addition, a chimeric version of MAB-A ("**chMAB-A**") having the murine VH and VL Domains and human constant regions was generated. The amino acid sequences of the murine and the humanized/optimized VH and VL Domains are provided above, an alignment is provided in **FIGs. 3A** and **3B**. The consensus sequence of these humanized/optimized VH and VL Domains is provided above. Where multiple humanized Variable Domains were generated the humanized heavy and light chain Variable Domains of a particular anti-ADAM9 antibody (*e.g.*, MAB-A) may be used in any combination and particular combinations of humanized chains are referred to by reference to the specific VH/VL Domains, for example an antibody comprising hMAB-A VH(1) and hMAB-A VL(2) is specifically referred to as "hMAB-A (1.2)."

[00296] hMAB-A VH(1) was generated having framework regions derived from human germlines VH3-21 and VH3-64, and hMAB-A VL(1) was generated having framework regions derived from human germlines B3 and L6. The murine CDRs were retained in these humanized variable domains.

[00297] A potential deamidation site was identified in the CDR_H2 (shown in single underlining in **FIG. 3A**) and a potential aspartic acid isomerization site was identified in CDR_L1 (shown in single underlining in **FIG. 3B**). Amino acid substitutions at these positions were examined to identify substitutions to remove these sites while maintaining binding affinity. A substitution of phenylalanine at position 54 (N54F) of CDR_H2 (present in hMAB-A VH(2)) and at serine at position 28 (D28S) of CDR_L1 (present in hMAB-A VL(2)) were selected, wherein the numbering is accordingly to Kabat. The identified substitutions may be used separately or in combination. Surprisingly, antibodies comprising

the N54F substitution were found to exhibit about a 2-fold increase in affinity for human ADAM9 (see, *e.g.*, **Table 3**, below) and slightly improved binding to cynomolgus ADAM9.

[00298] Additional, optimized variants were generated to minimize the number of lysine residues present in the CDRs. Two lysine residues are present in CDR_H2 (indicated with a double underline in **FIG. 3A**), and one lysine is present in CDR_L1 (indicated with a double underline in **FIG. 3B**). Amino acid substitutions at these positions were examined to identify substitutions that maintained binding affinity. Substitutions of arginine at position 62 (K62R), of glutamine at position 64 (K64Q), and serine at position 65 (S65G) were selected for CDR_H2 (present in hMAB-A VH(3)), wherein the numbering is accordingly to Kabat. A substitution of an arginine at position 24 (K24R) was selected for CDR_L1 (present in hMAB-A VL(3)). The identified substitutions may be used separately or in combination.

[00299] Other potentially labile resides present in the CDRs were identified (indicated with a dotted underline in **FIGs. 3A-3B**), one methionine residue within CDR_H1 at position 34 (M34), one methionine residue within CDR_L1 at position 33 (M33), and histidine, glutamic acid, and aspartic acid residues at positions 92 (H93), 93 (E93), and 94 (D94), within CDR_L3, wherein the numbering is accordingly to Kabat. Amino acid substitutions at these positions were examined to identify substitutions that maintained binding affinity. Substitution of isoleucine at position 34 (M34I) was selected for CDR_H1 and substitutions of leucine, tyrosine, serine and threonine were selected for positions 33 (M33L), 92 (H93Y), 93 (E93S), and 94 (D94T) of CDR_L3, wherein the numbering is according to Kabat. Each of these positions could readily be substituted in combination with all of the substitutions detailed above to yield hMAB-A VH(4) and hMAB-A VL(4), which when paired together generate an antibody that retained a small improvement in affinity as compared to the parental murine antibody, and that has a greatly reduced potential for deamidation or oxidation and no lysine residues in the CDRs.

[00300] The relative binding affinity of the humanized/optimized antibodies hMAB-A (1.1), hMAB-A (2.2), hMAB-A (2.3), hMAB-A (3.3), hMAB-A (4.4) and the chimeric **c**hMAB-A (having murine VH/VL Domains) to huADAM was investigated using BIACORE® analysis, in which His-tagged soluble human ADAM9 ("**shADAM9-His**," containing an extracellular portion of human ADAM9 fused to a histidine-containing protein) was passed over a surface coated with immobilized antibody. Briefly, each antibody was captured on a Fab2 goat anti-human Fc surface and then incubated in the

presence of different concentrations (6.25-100 nM) of the shADAM9-His protein. The kinetics of binding were determined via BIACORE® analysis binding (normalized 1:1 Langmuir binding model). The calculated k_a, k_d and K_D from these studies are presented in **Table 3**. Binding to cynoADAM9 was examined by FACS as described above and by ELISA.

Table 3.

Antibody	pI	huADAM9		
		$\mathbf{k_a}$ ($\times 10^{6}$)	$\mathbf{k_d}$ ($\times 10^{-3}$)	**KD** (nM)
chMAB-A	6.61	1.3	4.7	3.6
hMAB-A (1.1)	6.44	1.5	5.2	3.5
hMAB-A (2.2)	6.58	1.1	1.5	1.4
hMAB-A (2.3)	6.58	1.3	1.7	1.3
hMAB-A (3.3)	6.44	1.1	1.5	1.4
hMAB-A (4.4)	6.73	1.0	2.0	2.0

[00301] The results of these studies demonstrate that the humanized/optimized antibodies have the same or higher binding affinity to human ADAM9 than the parental murine antibody. In particular, it was observed that the introduction of the N54F mutation in the humanized antibodies resulted in improved binding to huADAM9 (i.e., hMAB-A (2.2), hMAB-A (2.3), and hMAB-A (3.3)). This mutation also provided a slight improvement in binding to cynoADAM9 as determined by FACS and ELISA, however, these antibodies continued to exhibit poor binding to cynoADAM9. These studies also identified additional substitutions that could be introduced to remove lysine residues from the CDRs without reducing affinity. Additional substitutions were identified to remove other potentially labile residues with a minimal impact on affinity.

Example 4
Optimization of Binding to Non-Human Primate ADAM9

[00302] Random mutagenesis was used to introduce substitutions within the Heavy Chain CDR_H2 (Kabat positions 53-58) and CDR_H3 (Kabat positions 95-100 and 100a-100f) domains of hMAB-A (2.2). The mutants were screened to identify clones having enhanced binding to non-human primate ADAM9 (*e.g.*, cynoADAM9) and that retained high affinity binding to huADAM9. 48 clones were selected from two independent screens of mutations within CDR_H3 (Kabat positions 100a-100f). **Table 4** provides an alignment of the amino acid sequence of CDR_H3 Kabat residues 100a-f from hMAB-A **(2.2)** clones selected for enhanced binding to cynoADAM9 from two independent screens. Additional clone alignments are provided in **Table 5**. As indicated in such Tables, similar clones emerged in each experiment, which fell into discrete substitution patterns.

Table 4
Substitutions within Sub-Domain of the Heavy Chain CDRH3 of MAB-A (Kabat Positions 100a-100f)

Screen 1			Screen 2		
Clone ID	**SEQ ID NO**	**CDR_H3 Sub-Domain Sequence**	**Clone ID**	**SEQ ID NO**	**CDR_H3 Sub-Domain Sequence**
MAB-A	81	GSRDYF	MAB-A	81	GSRDYF
1	82	DGEGVM	1	112	DGKAVL
2	82	DGEGVM	2	113	FNKAVL
3	83	FHSGLL	3	84	FNSATL
4	84	FNSATL	4	114	FNSGTW
5	85	FNSGTL	5	115	FNTGVF
6	86	FNSSTL	6	116	GKSRFH
7	87	GKSKWL	7	91	IGKGVF
8	88	GMGGTL	8	92	IGKGVL
9	89	HAKGGM	9	117	IGKNVY
10	90	IGEAVL	10	118	MGKGVM
11	91	IGKGVF	11	119	NGESVF
12	91	IGKGVF	12	120	PDFGWM
13	92	IGKGVL	13	121	PGSGVM
14	93	KHDSVL	14	122	PKDAWL
15	94	LNTAVM	15	99	PKFGWK
16	95	NGEGTL	16	99	PKFGWK
17	96	NGKNTL	17	123	PKFGWL
18	97	NSAGIL	18	124	PKIGWH
19	98	PKEGWM	19	124	PKIGWH
20	99	PKFGWK	20	124	PKIGWH
21	100	PKMGWV	21	125	PKMGWA

22	101	PRLGHL	22	126	PKMGWM
23	102	PSFGWA	23	126	PKMGWM
24	103	QAKGTM	24	126	PKMGWM
25	104	RGMGVM	25	126	PKMGWM
26	105	RKEGWM	26	127	PQMGWL
27	106	TGKGVL	27	128	PRFGWL
28	107	TGMGTL	28	128	PRFGWL
29	108	TGNGVM	29	128	PRFGWL
30	108	TGNGVM	30	129	PRMGFL
31	109	WNAGTF	31	130	PRMGFM
32	110	YHHTPL	32	131	PSFGWM
33	110	YHHTPL	33	132	RREGWM
34	111	YQSATL	34	133	SGEGVL
			35	134	SGNGVM
			36	135	VGKAVL

Table 5
Substitutions within Sub-Domain of the Heavy Chain CDRH3 of MAB-A
(Kabat Positions 100a-100f)

Clone ID	SEQ ID NO	CDR_H3 Sub-Domain Sequence
MAB-A **VH (2A)**	85	FNSGTL
MAB-A **VH (2B)**	92	IGKGVL
MAB-A **VH (2C)**	128	PRFGWL
MAB-A **VH (2D)**	106	TGKGVL
MAB-A **VH (2E)**	136	DSNAVL
MAB-A **VH (2F)**	137	FHSGTL
MAB-A **VH (2G)**	113	FNKAVL
MAB-A **VH (2H)**	138	GGSGVL
MAB-A **VH (2I)**	139	PRQGFL
MAB-A **VH (2J)**	140	YNSGTL

[00303] For all the clones examined, Gly and Ala are the preferred amino acid residues at positon 4 (P4) and Leu, Met, and Phe are the preferred amino acid residues at position 6 (P6). The preferred amino acid residues at other positions (*e.g.*, position 2 (P2), position 3 (P3) and position 5 (P5)) depend on the amino acid residue found at P1. For clones having a Pro residue at position 1 (P1), Lys and Arg were preferred at P2, Phe and Met at P3, Gly at P4, and Trp or Phe at P5. For clones having a Phe, Tyr or Trp at P1, Asn and His were preferred at P2, Ser and His at P3, and Leu at P6. For clones having Ile, Leu or Val at P1, Gly was preferred at P2, Lys at P3, Val at P5 and hydrophobic at P6. In addition, as can be seen in **Table 4**, for clones having a Thr residue at P1, Gly was preferred at P2, Lys, Met, and Asn were preferred at P3, Gly was preferred at P4, Val or Thr were preferred at P5 and

Leu and Met at P6. Additional clones having an Asp, Gly, Arg, His, or Ser residue at P1 were also identified at lower frequencies (see **Table 4** and **Table 5**).

[00304] The VH Domain of the ten clones shown in **Table 5** were used to generate further optimized variants of hMAB-A (2.2) designated hMAB-A (2A.2)-(2J.2). The binding of the selected clones was examined by ELISA assay. Briefly, antibodies that bind to histidine-containing peptides, and that had been coated onto microtiter plates, were used to capture His peptide-tagged soluble cynoADAM9 ("**cynoADAM9-His**") (1 μg/mL) or His peptide-tagged soluble huADAM9 (1 μg/mL), and the binding of serial dilutions of the parental hMAB-A (2.2) and the ten CDR_H3 hMAB-A (2A.2) variants was examined. The binding curves cynoADAM9 and huADAM9 are presented in **FIG. 4A** and **FIG. 4B**, respectively. hMAB-A (2A.2) variants comprising each of the selected VH Domains exhibited improved binding to cynoADAM9 with MAB-A VH(2B), MAB-A VH(2C), MAB-A VH(2D), and MAB-A VH(2I), showing the greatest enhancement in cynoADAM9 binding while maintaining similar binding to huADAM9 as the parental hMAB-A (2.2) antibody.

[00305] The relative binding affinity of the humanized/further optimized antibodies MAB-A VH(2B.2), MAB-A VH(2C.2), MAB-A VH(2D.2), and MAB-A VH(2I.2), and the parental hMAB-A (2.2), to huADAM9-His and cynoADAM9-His was investigated using BIACORE® analysis essentially as described above. The calculated k_a, k_d and K_D from these studies are presented in **Table 6**.

Table 6

Antibody	huADAM9			cynoADAM9		
	$\mathbf{k_a}$ ($x10^5$) ($M^{-1}s^{-1}$)	$\mathbf{k_d}$ ($x10^{-4}$) (s^{-1})	KD (nM)	$\mathbf{k_a}$ ($x10^5$) ($M^{-1}s^{-1}$)	$\mathbf{k_d}$ ($x10^{-4}$) (s^{-1})	KD (nM)
hMAB-A (2.2)	9.0	5.5	0.6	2.0	220	110
hMAB-A (2B.2)	6.1	3.9	0.6	3.4	0.66	0.2
hMAB-A (2C.2)	5.9	8.1	1.4	3.5	<0.1	<0.3

hMAB-A (2D.2)	6.9	5.8	0.8	4.2	3.0	0.7
hMAB-A (2I.2)	6.6	2.3	0.4	4.0	0.85	0.2

[00306] The binding studies demonstrate that the four top clones exhibited between 150-550-fold enhancement in binding affinity to cynoADAM9 while maintaining the same high affinity binding to huADAM9 as the parental antibody. hMAB-A (2C.2) and hMAB-A (2I.2) was selected for further studies.

Example 5
Immunohistochemistry Study of Antibody hMAB-A (2I.2)

[00307] The cell specificity of hMAB-A (2I.2) was investigated by IHC. Positive and negative control cells, and normal human and cynomolgus monkey tissues were contacted with hMAB-A (2I.2) (2.5 µg/mL) or an isotype control (2.5 µg/mL) and the extent of staining was visualized. The results of the study are summarized in **Table 7**.

Table 7

Cell/Tissue	hMAB-A (2I.2) (2.5 µg/ml)	IgG1 Negative Control (2.5 µg/ml)
Cho-K parental cells	-	-
Cho-K/huADAM9 medium expression P:1	2-4+ (gr c > m) rare to occasional and 1+ (gr c > m) occasional	-
Cho-K/huADAM9 high expression	2-4+ (gr c > m) frequent	-
Cho-K/ cynoADAM9 clone 2	2-4+ (gr c > m) frequent	-
Cho-K/cynoADAM9 clone #16	2-4+ (gr c > m) frequent	-
A498 cells	2-4+ (gr c > m) rare to occasional and 1+ (gr c > m) occasional to frequent	-
Colon MG06-CHTN-96 B	-	numerous 2-4+ (gr c) cells consistent with macrophages
Lung MG06-CHtN-162B1 A	-	occasional 2-4+ (gr c) cells consistent with macrophages
Liver ILS11103 B	-	hepatocytes 1+ (gr c) rare to occasional
Pancreas ILS10266	-	-
Heart Life Legacy 0910035D	-	cardiac muscle cells with numerous 1-3+ small foci of (gr c) consistent with lipofuscin pigment
Kidney ILS10241 B	-	tubule epi 1+ (gr c) rare
Bladder ILSD8011 J	-	occasional 2-4+ (gr c) cells consistent with macrophages
Cyno Colon #1	-	mucosal epi (luminal m) 2-4+ rare to occasional and 1+ rare to occasional; numerous 2-3+ (gr c) cells consistent with macrophages predominantly within LP
Cyno Lung #1	-	very rare 2-4+ (gr c) cells consistent with macrophages

Table 7		
Cell/Tissue	hMAB-A (**2I.2**) (**2.5 µg/ml**)	**IgG1 Negative Control (2.5 µg/ml)**
Cyno Liver #1	-	-
Cyno Pancreas #1	-	-
Cyno Heart #1	-	-
Cyno Kidney #070368M	-	tubule epi 2+ (gr c) rare and 1+ (gr c) rare to occasional
Cyno Bladder #1	transitional cell epi ± (gr c) rare	rare 1-4+ (gr c) cells consistent with macrophages
Lung CA ILS10108	H score 150	tu -
Lung CA ILS7223	H score 180	tu -
Lung CA ILS2156 A	H score 80	tu -
Lung CA ILS7295 A	H score 60	tu -

[00308] IHC studies were also conducted to assess binding of humanized/optimized hMAB-A (2I.2) at a concentration of 12.5 µg/mL (5x optimal staining concentration). Positive and negative control cells, and normal human and cynomolgus monkey tissues were employed in this study. The results of the study are summarized in **Table 8**.

Table 8		
Cell/Tissue	hMAB-A (**2I.2**) (**12.5 µg/ml**)	**IgG1 Negative Control (12.5 µg/ml)**
Cho-K parental cells	-	-
Cho-K/huADAM9 medium expression P:1	2-4+ (gr c > m) occasional to frequent	-
Cho-K/huADAM9 high expression	3-4+ (gr c > m) occasional to frequent	-
Cho-K/cynoADAM9 clone 2	3-4+ (gr c > m) frequent	-
Cho-K/cynoADAM9 clone #16	3-4+ (gr c > m) frequent	-
A498 cells	2-4+ (gr c > m) occasional to frequent	-
Colon MG06-CHTN-96 B	epi ± - 1+ rare to occasional	numerous 2-4+ (gr c) cells consistent with macrophages predominantly within LP in test article and negative control
Lung MG06-CHtN-162B1 A	alveolar cells (favor pneumocytes) 2-3+ (gr c > m) rare, 1+ (gr c > m) rare to occasional; EC 2-4+ (c,m) rare, 1+ (c,m) rare	occasional scattered 2-4+ (gr c) cells consistent with macrophages in test article and negative control
Liver ILS11103 B	-	occasional scattered 2-4+ (gr c) cells consistent with macrophages in test article and negative control
Pancreas ILS10266	ductal epi 1+ (gr c > m) very rare	cells (favor acinar cells) 1+ (gr c) very rare; occasional scattered 2-4+ (gr c) cells consistent with macrophages in test article and negative
Heart Life Legacy 0910035D	-	numerous small foci 1-3+ granular staining with cardiac muscle cells consistent with lipofuscin pigment consistent with artifact in test article and negative control
Kidney ILS10241 B	tubule epi 1+ (gr c) rare to occasional	tubule epi ± (gr c) rare
Bladder ILSD8011 J	transitional cell epi 1+ (gr c) rare	rare 2-4+ (gr c) cells consistent with

Table 8		
Cell/Tissue	hMAB-A **(2I.2) (12.5 µg/ml)**	**IgG1 Negative Control (12.5 µg/ml)**
		macrophages in test article and negative control
Cyno Colon #1	-	mucosal epi (luminal m) 2-4+ occasional and 1+ rare to occasional
Cyno Lung #1	bronchial epi 1+ (gr c > m) rare to occasional and ± (gr c > m) occasional to frequent	-
Cyno Liver #1	-	-
Cyno Pancreas #1	-	-
Cyno Heart #1	-	-
Cyno Kidney #070368M	-	tubule epi 1+ (gr c) rare and ± (gr c) rare
Cyno Bladder #1	transitional cell epi 2+ (gr c > m) rare and 1+ (gr c > m) rare to occasional	-
Lung CA ILS10108	H score 180	tu -
Lung CA ILS7223	H score 180	tu -
Lung CA ILS2156 A	H score 115	tu -
Lung CA ILS7295 A	H score 115	tu -

[00309] A comparative IHC study was conducted in order to assess differences in binding by hMAB-A (2.2), hMAB-A (2.3), hMAB-A (2C.2), and hMAB-A (2I.2) at 2.5 µg/mL or 5 µg/mL. Positive and negative control cells, and normal human and cynomolgus monkey tissues were employed in this study. The results of the study are summarized in **Table 9**.

Table 9					
Tissue	hMAB-A **(2.3) 5 ug/mL**	hMAB-A **(2.2) 2.5 µg/mL**	hMAB-A **(2C.2) 2.5 µg/mL**	hMAB-A **(2I.2) 2.5 µg/mL**	**Isotype control 5 µg/mL**
Cho-K parental P:3	-	-	-	-	-
Cho-K/hu ADAM9.2 medium expression P:1	1+ (c) occasional	2-4+ (gr c > m) rare and 1+ (gr c > m) rare to occasional	2-4+ (gr c > m) rare to occasional and 1+ (gr c > m) rare to occasional	2-4+ (gr c > m) rare to occasional and 1+ (gr c > m) occasional	-
Cho-K/hu ADAM9.18 high expression P:1	3+ (m,c) frequent	2-4+ (gr c > m) occasional to frequent and 1+ (gr c > m) occasional	2-4+ (gr c > m) occasional to frequent and 1+ (gr c > m) occasional	2-4+ (gr c > m) frequent	-
Cho-K Cyno #2	1+ (c) occasional	-	3-4+ (gr c > m) frequent	2-4+ (gr c > m) frequent	-
Cho-K Cyno #16	2+ (c,m) occasional to frequent	2-4+ (gr c > m) rare and 1+ (gr c > m) rare to occasional	3-4+ (gr c > m) frequent	2-4+ (gr c > m) frequent	-
A498 072210	3-4+ (c,m) frequent	2-4+ (gr c > m) rare and 1+ (gr c > m) occasional to frequent	2-4+ (gr c > m) rare and 1+ (gr c > m) occasional	2-4+ (gr c > m) rare to occasional and 1+ (gr c > m) occasional to	-

Table 9					
Tissue	hMAB-A (**2.3**) **5 ug/mL**	hMAB-A (**2.2**) **2.5 µg/mL**	hMAB-A (**2C.2**) **2.5 µg/mL**	hMAB-A (**2I.2**) **2.5 µg/mL**	**Isotype control 5 µg/mL**
				frequent	
Lung CA ILS10108	IHC score 3	H Score 55	H Score 17	H score 150	-
Lung CA ILS7223	IHC score 3	H Score 205	H Score 160	H score 180	-
Lung CA ILS2156 A	IHC score 1	H Score 5	H Score 0	H score 80	-
Lung CA ILS7295 A	IHC score 1	H Score 1	H Score 0	H score 60	-

[00310] A further comparative IHC study was conducted in order to assess differences in binding by hMAB-A (2.2), hMAB-A (2.3), hMAB-A (2C.2), and hMAB-A (2I.2) and murine MAB-A at 2.5 µg/mL 5 µg/mL or 12.5 µg/mL. Positive and negative control cells, and normal human and cynomolgus monkey tissues were employed in this study. The results of the study are summarized in **Table 10**.

Table 10					
Tissue	hMAB-A (**2.3**) **5 ug/mL**	hMAB-A (**2.2**) **2.5 µg/mL**	hMAB-A (**2C.2**) **2.5 µg/mL**	hMAB-A (**2I.2**) **12.5 µg/ml**	MAB-A **5 µg/mL**
Colon MG06-CHTN-96 B	epi 1+ (c,m) rare; sm negative	-	-	epi ± - 1+ rare to occasional	Epithelium 1-3+ [m, c] (occas to freq); Others (Neg)
Lung MG06-CHtN-162B1 A	pneumocytes/macrophages 2+ (c,m) occasional	-	-	alveolar cells (favor pneumocytes) 2-3+ (gr c > m) rare, 1+ (gr c > m) rare to occasional; EC 2-4+ (c,m) rare, 1+ (c,m) rare	Monoctyes 1+ [c] (rare to occas); Others (Neg)
Liver ILS11103 B	hepatocytes 1+ (c) rare to occasional	hepatocytes 1+ (gr c) frequent	hepatocytes 2+ (gr c) rare and 1+ (gr c) frequent	-	Kupffer cells 3+ [c] (occas); Others (Neg)
Pancreas ILS10266	epi 1+ (c) rare; Islet Cells 1+ (c) very rare	-	-	ductal epi 1+ (gr c > m) very rare	Ductal epithelium 1-2+ [c, m] (rare to occas); Fibril 2+ (rare); Others (Neg)
Heart Life Legacy 0910035D	±	-	-	-	Neg
Kidney ILS10241 B	epi 2-3+ (c,m) frequent	tubule epi 2+ (gr c) rare to occasional and 1+ (gr c) occasional to frequent	tubule epi 2+ (gr c) rare to occasional and 1+ (gr c) occasional to frequent	tubule epi 1+ (gr c) rare to occasional	Epithelium 1+ [c] (rare); Others (Neg)

Table 10

Tissue	hMAB-A (2.3) 5 ug/mL	hMAB-A (2.2) 2.5 µg/mL	hMAB-A (2C.2) 2.5 µg/mL	hMAB-A (2I.2) 12.5 µg/ml	MAB-A 5 µg/mL
Bladder ILSD8011 J	transitional epi 1+ (c) rare to occasional	-	-	transitional cell epi 1+ (gr c) rare	Transitional epithelium 2+ [c, m] (occas to freq); Stromal cells 3+ [c] (rare); Others (Neg)
Cyno Colon #1	epi 1+ (c,m) rare	-	-	-	
Cyno Lung #1	Macrophage and pneumocytes 1+ (c) very rare	-	bronchial epi 3-4+ (gr c) rare, 2+ (gr c) occasional, and 1+ (gr c) occasional	bronchial epi 1+ (gr c > m) rare to occasional and ± (gr c > m) occasional to frequent	
Cyno Liver #1	hepatocytes 1+ (c) frequent	hepatocytes 2+ (gr c) rare to occasional and 1+ (gr c) rare to occasional	hepatocytes 2+ (gr c) rare to occasional and 1+ (gr c) occasional; ductal epi 1+ (gr c) occasional	-	
Cyno Pancreas #1	epi and Islet Cells 1+ (c) very rare	-	islet cells ± (gr c) frequent; ductal epi 1+ (gr c) rare to occasional	-	positive
Cyno Heart #1	myocardium 1+ (c) frequent	-	-	-	
Cyno Kidney #070368M	epi 2+ (c) frequent	tubule epi 2+ (gr c) rare to occasional and 1+ (gr c) rare to occasional	tubule epi 2+ (gr c) rare to occasional and 1+ (gr c) occasional to frequent	-	positive
Cyno Bladder #1	transitional epi ± (c); macrophages very rare	-	transitional cell epi 2-3+ (gr c > m) rare and 1+ (gr c > m) occasional	transitional cell epi 2+ (gr c > m) rare and 1+ (gr c > m) rare to occasional	

[00311] The results thus demonstrate that hMAB-A (2.2) exhibited an overall low level staining of human hepatocytes and kidney tubules at optimal concentration, with a lower staining intensity/frequency of reactivity in hepatocytes and kidney tubules observed in the negative control. hMAB-A (2.2) exhibited similar low level staining of cyno hepatocytes and kidney tubules at optimal concentration, with lower staining intensity/frequency of reactivity in kidney tubules observed in the negative control.

[00312] The results also demonstrate that hMAB-A (2C.2) exhibited an overall low level staining of human hepatocytes and kidney tubules at optimal concentration, with lower staining intensity/frequency of reactivity in hepatocytes and kidney tubules observed in the negative control. hMAB-A (2C.2) exhibited similar low level staining in cyno hepatocytes

and kidney tubules at optimal concentration. Additional minimal findings in cyno lung epithelium, pancreas islets/ epithelium and bladder epithelium for hMAB-A (2C.2) was not observed in the corresponding human tissue; lower staining intensity/frequency of reactivity was observed in lung epithelium, kidney tubules, bladder epithelium in negative control. The results also demonstrate that hMAB-A (2I.2) exhibited no staining of human or cyno tissues at optimal concentration, with rare +/- bladder transitional cell epithelium staining. hMAB-A (2I.2) also exhibited overall low level and frequency staining of human lung alveolar cells, pancreas ductal epithelium, kidney tubule, bladder transitional cell epithelium at 5x optimal concentration, and overall low level staining of cyno bronchial epithelium and bladder transitional cell epithelium at 5x optimal concentration. hMAB-A (2I.2) exhibits an overall favorable IHC profile on the human normal tissues tested and a similar profile on corresponding cynomolgus monkey tissues.

Example 6
hMAB-A (2I.2) Comprising Variant Fc Regions

[00313] hMAB-A(2I.2) comprises a light chain (**SEQ ID NO:68**) having a kappa light chain constant region and a heavy chain (**SEQ ID NO:52**) having wild-type IgG heavy chain constant regions. Fc variants were generated by introducing the following substitutions into the Fc Region: L234A/L235A (see, *e.g.*, **SEQ ID NO: 78**) designated hMAB-A (2I.2)(AA); S442C (see, *e.g.*, **SEQ ID NO: 79**) designated hMAB-A (2I.2)(C); and L234A/L235A/S442C (see, *e.g.*, **SEQ ID NO: 80**) designated hMAB-A (2I.2)(AA/C). The binding of each Fc variant to huADAM9-His and cynoADAM9-His was examined by ELISA assay. Briefly, antibodies that bind to histidine-containing peptides, and that had been coated onto microtiter plates, were used to capture His peptide-tagged soluble cynoADAM9 or His peptide-tagged soluble huADAM9 (0.5 μg/mL), and the binding of serial dilutions of the parental hMAB-A (2.2) and the Fc variants was examined. The binding curves huADAM9 and cynoADAM9 are presented in **FIG. 5A** and **FIG. 5B**, respectively and show that each of the Fc variants retained the binding affinity of hMAB-A (2I.2) having a wild-type Fc region.

Example 7
Target Expression Analysis

[00314] To evaluate ADAM9 expression across different indications, a tissue microarray (TMA) with 20 different tumor types was first evaluated using an ADAM9 IHC assay developed at ImmunoGen for preliminary research use.

[00315] All samples analyzed were FFPE (Formalin fixed & paraffin embedded) samples. The 500 core 20 carcinoma TMA was purchased from Folio Biosciences (Cat# ARY-HH0212). The NSCLC TMA with 80 cores for adenocarcinoma and 80 cores for squamous cell carcinoma was purchased from US Biomax (Cat# LC1921A). The colorectal cancer TMA with 80 cores for adenocarcinoma was purchased from Pantomics Inc. (Cat# COC1261). The gastric cancer samples were purchased from Avaden Biosciences.

[00316] Immunohistochemical staining for ADAM9 was carried out using the Ventana Discovery Ultra autostainer. The primary antibody for ADAM9 was a commercially available rabbit monoclonal antibody. All samples were evaluated and scored by a board certified pathologist trained in the scoring algorithm. The presence of at least 100 viable tumor cells was required for scoring. Staining intensity was scored on a semi-quantitative integer scale from 0 to 3, with 0 representing no staining, 1 representing weak staining, 2 representing moderate and 3 representing strong staining. The percentage of cells staining positively at each intensity level was recorded. Scoring was based on localization of Adam9 to the cell membrane only, as well as evaluation of localization to both cytoplasm and membrane. The staining results were analyzed by H score, which combines components of staining intensity with the percentage of positive cells. It has a value between 0 and 300 and is defined as:

1 * (percentage of cells staining at 1+ intensity)
+ 2 * (percentage of cells staining at 2+ intensity)
+ 3 * (percentage of cells staining at 3+ intensity)
= H score.

[00317] The 500 core 20 carcinoma TMA with 5 normal tissue controls for each tumor type was stained and scored in two different ways: (1) based on membrane staining alone or (2) based on membrane and cytoplasmic staining. Table 11 below and FIG. 6A summarize the prevalence of ADAM9 based on membrane staining for all twenty

indications and Table 12 and FIG. 6B summarize the results of membrane and cytoplasmic staining for eight selected indications.

[00318] Based on the results from the multi carcinoma TMA, three indications for an expanded prevalence analysis were chosen: non-small cell lung cancer (NSCLC), colorectal cancer (CRC) and gastric cancer. For NSCLC, one TMA with 80 cores for adenocarcinoma and 80 cores for squamous cell carcinoma was stained and evaluated. For CRC, one TMA with 80 cores for adenocarcinoma was analyzed, of which 78 were evaluable. For gastric cancer, 15 whole tissue sections of adenocarcinoma were analyzed. All of these samples were scored for membrane and cytoplasmic staining, and the results are summarized in Table 13. The results of these preliminary studies show that ADAM9 is expressed in a wide range of solid cancers and support the use of anti-ADAM9 drug conjugates in many different ADAM9-expressing solid tumors.

Table 11: Prevalence of ADAM9 in 20 different indications based on membrane staining

Tumor type	% Positive (H score >=1)	H score: 1-100	H score: 101-200
Pancreas (n=17)	95%	24%	71%
Uterus (n=18)	89%	67%	22%
Thyroid (n=17)	88%	88%	0%
Kidney (n=17)	88%	59%	29%
Testis (n=17)	83%	65%	18%
Prostate (n=20)	80%	45%	35%
Colon (n=16)	76%	38%	38%
Bladder (n=16)	76%	63%	13%
Breast(n=20)	75%	65%	10%
Brain (n=19)	68%	63%	5%
Stomach (n=17)	59%	24%	35%
Lung (n=19)	58%	58%	0%
Esophagus (n=19)	43%	32%	11%
Cervix (n=20)	40%	40%	0%
Ovary (n=18)	39%	33%	6%
Head and Neck (n=20)	35%	30%	2%
Liver (n=19)	32%	32%	0%
Skin (n=20)	10%	10%	0%
Soft Tissue (n=20)	0%	0%	0%
Lymphoma (n=20)	0%	0%	0%

Table 12: Prevalence of ADAM9 in 8 selected indications based on membrane and cytoplasmic staining

Tumor type	% Positive (H score >=1)	H score: 1-100	H score: 101-200	H score: 201-300
Colon	100%	31%	63%	6%
Lung	100%	58%	42%	0%
Pancreas	100%	18%	76%	6%
Prostate	95%	25%	55%	15%
Esophagus	95%	58%	37%	0%
Stomach	94%	18%	71%	6%
Breast	70%	50%	20%	0%
Ovarian	61%	44%	17%	0%

Table 13: Prevalence of ADAM9 in additional samples for NSCLC, CRC and Gastric Cancer based on membrane and cytoplasmic staining

Tumor Type	Number of Samples	% positive (H score >=1)	H-Score Distribution		
			1-100	101-200	201-300
NSCLC Adenocarcinoma	80	90%	46%	39%	5%
NSCLC Squamous	80	81%	65%	13%	3%
CRC Adenocarcinoma	78	91%	51%	41%	0%
Gastric Adenocarcinoma	15	100%	27%	53%	20%

Example 8
Anti-ADAM9 Antibody Internalization Studies

[00319] To assess the internalization of the anti-ADAM9 antibodies of the invention, flow cytometry-based internalization experiments were performed on hMAB-A(2.2), hMAB-A(2I.2), and hMAB-A(2I.2)-S442C antibodies conjugated to Alexa Fluor 488.

[00320] Anti-ADAM9 Alexa488 antibody conjugates for hMAB-A(2.2), hMAB-A(2I.2), hMAB-A(2I.2)-S442C were generated using Alexa Fluor 488 tetrafluorophenyl ester according to the manufacturer's instructions (Thermofisher). The conjugates were eluted in sodium azide free PBS, pH7.2 to enable internalization assays. The concentration and degree of labeling were calculated from absorption measurements at 280 nm and 494 nm. FACS binding assays were performed to ensure that Alexa488-labeling did not adversely affect target binding.

[00321] The internalization of anti-ADAM9-Alexa488 conjugates was determined following both continuous and pulse exposure to the fluorescent conjugates. For continuous experiments, NCI-H1703 cells were treated with a saturating concentration of the indicated Alexa488-labeled antibody on ice or at 37°C for the entire time indicated. While for pulse experiments anti-ADAM9-Alexa488 conjugates were prebound to the cells on ice and the excess conjugate washed away before shifting to 37°C and monitoring internalization. At the indicated time points following either continuous or pulse exposure, cells were lifted with versene (Thermofisher) and washed with ice-cold PBS twice, and replicate wells were resuspended in ice-cold PBS without (unquenched samples) or with 300nM anti-A488 antibody (quenched samples). All samples were incubated for 30 m on ice. Cells were then pelleted, fixed in 1% paraformaldehyde and analyzed by flow cytometry. The fluorescence of cells incubated on ice for 30 minutes and then incubated with anti-Alexa488 antibody represents the unquenchable fluorescent fraction and was subtracted from all other samples prior to calculating internalization. The percent internalization was calculated as fluorescence of quenched samples corrected for incomplete surface quenching (intracellular fluorescence) divided by that of unquenched cells (total fluorescence). The internalization of anti-ADAM9 antibody conjugates were graphed and the data was fitted using a single-phase exponential decay equation (GraphPad Prism, ver. 5.01).

[00322] The internalization of surface bound Alexa488-labeled anti-ADAM9 antibodies was evaluated after both pulse and continuous treatment in NCI-H1703 cells. All three anti-ADAM9-Alexa488 conjugates tested showed rapid internalization, with ~39% of the conjugates internalized in the first 15 minutes and a total of ~77% internalized after 6 hours (FIG. 7A). Interestingly, after continuous exposure for 24 hours, the internalized fluorescent signal was ~7-fold greater than the total initial fluorescent signal bound to the cell surface after 30 minutes (FIG. 7B). Thus, ADAM9 is likely replenished at the cell surface from an intracellular pool during incubations at 37°C, allowing for multiple rounds of anti-ADAM9 antibody conjugate internalization. The efficacy of anti-ADAM9 immunoconjugates rely on of the internalization, intracellular trafficking, and degradation of the immunoconjugates. The potency of anti-ADAM9 immunoconjugates can in part be explained by the high internalization of anti-ADAM9 immunoconjugates which likely leads to generation of high amounts of cytotoxic catabolites.

Example 9
Anti-ADAM9 Antibody Cell Processing Studies

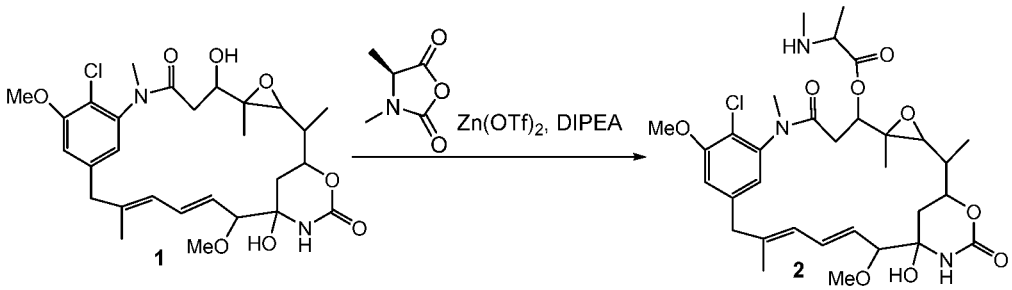
[00323] To assess the on-cell target binding, uptake and lysosomal degradation of chMAB-A, a previously-described ^{3}H-propionamide-labeled antibody processing method was used (Lai et al., Pharm Res. 2015 Nov; 32(11):3593-603). Using this method, the ADAM9-targeting chMAB-A antibody was trace labeled with tritiated propionate via lysine residues. It has previously been shown that upon cellular binding, uptake, and trafficking to the lysosome, [^{3}H]propionate labeled-Ab (^{3}H-Ab) is degraded and lysine-[^{3}H]propionamide is released into the cell growth medium. Addition of organic solvent precipitates the intact, labeled antibody and leaves the lysine-[^{3}H]propinoamide in solution, allowing convenient and accurate measurement of the extent of antibody processing.

[00324] chMAB-A was labeled with [^{3}H]-propionate as previously described. The NSCLC line, NCI-H1703, and the CRC line, DLD-1, were treated with 10 nM ^{3}H-chMAB-A antibody after determination of antigen saturation via binding curve. Some cell samples were treated with the non-targeting, tritiated isotype control antibody, ^{3}H-chKTI, while others were untreated. Cells were plated and grown overnight in 6-well plates and then pulse-treated with reagent(s) as previously described. Briefly, cells were incubated with either ^{3}H-chMAB-A antibody or ^{3}H-chKTI for 20 minutes before washing 3 times in fresh media. Cells were incubated overnight at 37°C with 5% CO_2. After a 20-24 hour incubation cells were harvested and protein precipitated with 4:3 volume acetone: media/cell mixture. Samples were frozen at -80 °C for a minimum of 1 hour before thawing and separating by centrifuge. Pellets were treated to solubilize protein prior to counting for 5 minutes in a Tri-Carb liquid scintillation counter (LSC). Per manufacturer's protocol, 1 mL of SOLVABLE (Perkin Elmer) was added to each pellet sample and incubated in a 50 °C water bath overnight. Samples were removed from the water bath, transferred to 20 mL glass scintillation vials and EDTA and H_2O_2 were added to samples followed by an additional 1 hour 50 °C incubation. Samples were quenched with HCl, 15 mL of Optima Gold liquid scintillation fluid (Perkin Elmer) was added, and samples were vortexed thoroughly. Samples were kept in the dark for a minimum of 4 hour before counting by LSC. Protein-free acetone extract samples were dried to <1 mL volumes under vacuum and processed using Solvable as described above prior to LSC. The amount of bound, degraded, and intact labeled antibody were calculated from the resulting sample CPM values.

[00325] The level of processing of ^{3}H-chMAB-A antibody was determined after pulse-treatment and overnight incubation at 37 °C. NCI-H1703 cells showed 93% of ^{3}H-chMAB-A processed within 24 hours, and DLD-1 cells showed 92% of ^{3}H-chMAB-A processed in the same time period. Binding and processing of ^{3}H-chKTI was negligible (>100-fold lower total CPM than for targeted antibody). The processing values for these cell lines are high, especially compared to the 24 hour pulse processing values previously reported for other ADC targets/antibodies supporting the anti-ADAM9 antibodies of the invention as effective drug conjugates.

Example 10.
Synthesis of Maytansinoid Derivatives of The Invention

Example 10a. Preparation of DM-H (7) stock solution

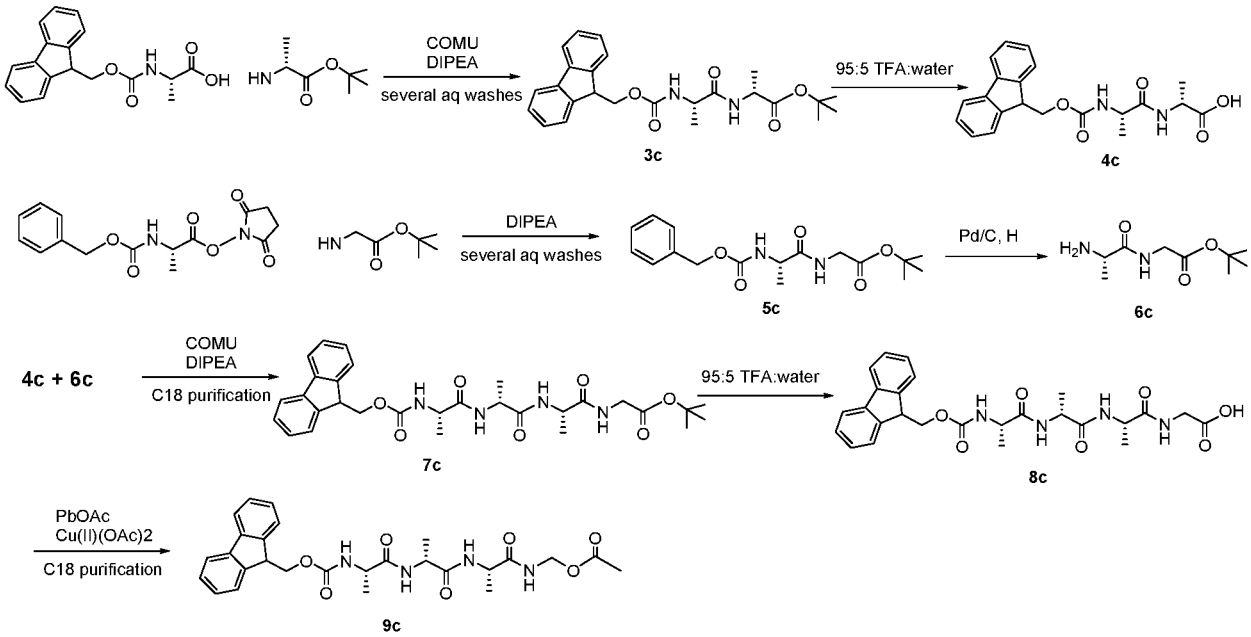


Maytansinol (5.0 g, 8.85 mmol) was dissolved in anhydrous DMF (125 mL) then cooled in an ice bath. The N-carboxy anhydride of N-methyl alanine (5.7 g, 44.25 mmol), anhydrous DIPEA (7.70 mL, 44.25 mmol) and zinc trifluoromethane sulfonate (22.5 g, 62 mmol) were then added with magnetic stirring under an argon atmosphere. The ice bath was removed and the reaction was allowed to warm with stirring. After 16 h, deionized water (10 mL) was added. After 30 min a 1:1 solution of saturated aqueous sodium bicarbonate : saturated aqueous sodium chloride (190 mL) and ethyl acetate (250 mL)were added with vigorous stirring. The mixture was transferred to a separatory funnel and the organic layer was retained. The aqueous layer was extracted with ethyl acetate (100 mL) then the organic layers were combined and washed with saturated aqueous sodium chloride (50 mL). The organic layer was concentrated to approximately 1/4th its volume by rotary evaporation under vacuum without heating the evaporator bath, no purification was conducted. The concentration of the solution was estimated by dividing the mmoles of maytansinol used in the reaction (1.77 mmol) by the volume (150 mL) giving DM-H stock solution (0.06 mmol/mL). Aliqouts of the stock solution were immediately dispensed then used in reactions or stored in a -80 C freezer then thawed when needed.

Example 10b. Synthesis of thio-peptide-maytansinoids

1. FMoc-Peptide-NH-CH_2-OAc compounds (Compound 9a-j)

Synthesis of FMoc-L-Ala-D-Ala-L-Ala-NH-CH_2-OAc (9c):



*Step 1: FMoc-L-Ala-D-Ala-OtBu (**3c**):*

FMoc-L-alanine (10g, 32.1 mmol) and D-Ala-OtBu, HCl (7.00 g, 38.5 mmol) were dissolved in CH2Cl2 (100 ml), treated with COMU (20.63 g, 48.2 mmol) and DIPEA (11.22 ml, 64.2 mmol). The reaction was allowed to proceed for under argon at room temperature. After 2 hours the reaction showed completion by UPLC, was diluted with 2-MeTHF (50ml), washed with 10% aqueous citric acid (2x 100mL), water (100mL), followed by brine (100mL). The organic layer was dried over magnesium sulfate, filter and concentrate to yield crude FMoc-L-Ala-D-Ala-OtBu, assume 100% yield.

*Step 2: FMoc-L-Ala-D-Ala (**4c**)*

FMoc-LAla-DAla-OtBu (11.25g, 25.7 mmol) was treated with TFA:Water (95:5) (50ml). The reaction was allowed to proceed at room temerpature under argon atmosphere. After 4 hours the reaction showed completion by UPLC, diluted with toluene (25mL) and coevaporated 3x. to yield FMoc-L-Ala-D-Ala, assume 100% yield.

Step 3: FMoc-L-Ala-Gly-OtBu (**5c**)

Z-L-Ala-ONHS (10 g, 31.2 mmol) and tert-butyl glycinate, (6.28 g, 37.5 mmol) were dissolved in CH2Cl2 (100 ml), treated with DIPEA (10.91 ml, 62.4 mmol). The reaction was allowed to proceed under argon at room temperature. After 2 hours, UPLC showed

completion, the reaction was diluted with 2-MeTHF (50mL), awashed with 10% aqueous citric acid (100mL), sat'd sodium bicarbonate (2x100mL), water (100mL), brine (100mL). The organic layer dried over magnesium sulfate, filtered and concentrated to yield Z-L-Ala-Gly-OtBu, assume 100% yield.

*Step 4. L-Ala-Gly-OtBu (**6c**)*

Z-Ala-Gly-OtBu (10.05 g, 29.9 mmol) was dissolved in 95:5 MeOH:Water (50 ml), transfered to hydrogenator flask, treated with Pd/C (1.272 g, 11.95 mmol). The hydrogenator flask was placed on the shaker, air was removed by vaccum while flask was shook. Hydrogen filled flask to 30psi, flask was shaken for 2 minutes and hydrogen was removed by vaccum. This was repeated 2 additional times. Hydrogen was allowed to fill flask to 30psi and was allowed to shake. After 4 hr, UPLC showed completion, reaction was filtered through a celite plug, *en vucuo*, redissolved in 2-MeTHF, concentrated to yield LAla-Gly-OtBu, assume 100% yield.

*Step 5: FMoc-L-Ala-D-Ala-L-Ala-Gly-OtBu (**7c**)*

FMoc-LAla-D-ALa-OH (0.959 g, 2.508 mmol) and L-Ala-Gly-OtBu (0.718 g, 3.01 mmol) were dissolved in CH2Cl2 (10 ml), treated with COMU (1.181 g, 2.76 mmol) and DIPEA (0.876 ml, 5.02 mmol). The reaction was allowed to proceed under argon at room temperature. After 2 hours reaction showed completion. The reaction was concentrated to remove CH2Cl2, redissolved in 2mL DMF and purified by C18 combiflash using a linear gradient, product was combined to yield FMoc-L-Ala-D-Ala-L-Ala-Gly-OtBu (660mg, 46% yield).

*Step 6. FMoc-L-Ala-D-Ala-L-Ala-Gly-OH (**8c**)*

FMoc-LAla-DAla-LAla-GlyOtBu (200mg, 0.353 mmol) was treated with TFA: Water (95:5) (2 ml). The reaction was allowed to proceed under argon at room temperature. After 1 hr the reaction showed completion by UPLC. The crude product was diluted with toluene (1mL), coevaporated 2x with toluene to yield FMoc-L-Ala-D-Ala-L-Ala-Gly-OH, assume 100% yield.

*Step 7. FMoc-L-Ala-D-Ala-L-Ala-CH_2-OAc (**9c**)*

FMoc-L-Ala-D-Ala-L-Ala-Gly-OH (2.65 g, 5.19 mmol) was dissolved in DMF (20mL), treated with copper (II) acetate (0.094 g, 0.519 mmol) and acetic acid (0.446 ml, 7.79 mmol)

once all reagants were dissolved the reaction was treated lead tetraacetate (3.45 g, 7.785 mmol). The reaction was allowed to proceed under argon at 60°C for 30 minutes. The crude reaction was purified via Combiflash Rf 200i using C18 450g column with a flow rate of 125mL/min with deionized water containing 0.1% formic acid and acetonitrile as solvents using a gradient as follows (time in minutes, percent acetonitrile) (0,5) (8,50) (26, 55). The desired product having a retention time of 11 minutes, product fractions were immediatley froze and lypholized to yield FMoc-L-Ala-D-Ala-L-Ala-CH2-OAc (843mg, 1.607 mmol, 31.0 % yield). HRMS $(M+Na)^+$ calcd 547.2163, found 547.2167. ^{1}H NMR (400 MHz, DMSO-d6) δ 1.23 (dd, J = 12.5, 7.4 Hz, 9H), 1.95 (s, 2H), 4.00 – 4.13 (m, 1H), 4.17 – 4.38 (m, 6H), 5.06 (q, J = 8.8 Hz, 2H), 7.33 (t, J = 7.3 Hz, 2H), 7.42 (t, J = 7.4 Hz, 2H), 7.62 (d, J = 6.8 Hz, 1H), 7.71 (t, J = 8.6 Hz, 2H), 7.85 – 8.01 (m, 3H), 8.21 (d, J = 7.0 Hz, 1H), 8.69 (d, J = 6.9 Hz, 1H).

The following compounds of the type FMoc-Peptide-NH-CH_2-OAc were prepared as shown in FIG. 9A and as exemplified for FMoc-L-Ala-D-Ala-L-Ala-NH-CH_2-OAc (9c) above.

FMoc-L-Ala-L-Ala-L-Ala-NH-CH_2-OAc (9a): FMoc-L-Ala-L-Ala-L-Ala-Gly-OH (SEQ ID NO:163) (500 mg, 0.979 mmol) was dissolved in DMF (2 mL), to which was added copper (II) acetate (17.8 mg, 0.098 mmol) and acetic acid (84 μL, 1.47 mmol) with magnetic stirring under argon. Once solids were dissolved, lead tetraacetate (434 mg, 0.979 mmol) was added, The reaction was allowed to proceed at 60°C for 20 min then purified on a C18, 30 micron 450 g column cartridge, eluting with deionized water containing 0.1% formic acid and an linear acetonitrile gradient of 5% to 55% over 26 min at a flow rate of 125 mL/min. Fractions containing pure desired product were frozen and lypholized to give 178 mg (34 % yield) of a white solid. HRMS $(M + Na)^+$ calcd. 547.2163; found 547.2160. ^{1}H NMR (400 MHz, DMSO-*d*6) δ 1.20 (qd, *J* = 7.5, 6.9, 4.2 Hz, 9H), 1.91 – 2.05 (m, 3H), 3.26 – 3.38 (m, 1H), 4.05 (q, *J* = 7.3 Hz, 1H), 4.23 (td, *J* = 11.9, 10.7, 6.4 Hz, 5H), 5.07(ddd, *J* = 11.2, 6.9, 4.3 Hz, 2H), 7.32 (q, *J* = 7.5 Hz, 2H), 7.41 (q, *J* = 7.4 Hz, 2H), 7.52 (t, *J* = 6.8 Hz, 1H), 7.71 (q, *J* = 7.5, 7.0 Hz, 2H), 7.82 – 8.08 (m, 4H), 8.84 (q, *J* = 7.1 Hz, 1H).

FMoc-D-Ala-L-Ala-L-Ala-NH-CH_2-OAc (9b): HRMS $(M+Na)^+$ calcd. 547.2163, found 547.2167. ^{1}H NMR (400 MHz, DMSO-d6) δ 1.23 (dd, *J* = 12.5, 7.4 Hz, 9H), 1.95 (s, 2H), 4.00 – 4.13 (m, 1H), 4.17 – 4.38 (m, 6H), 5.06 (q, *J* = 8.8 Hz, 2H), 7.33 (t, *J* = 7.3 Hz, 2H),

7.42 (t, *J* = 7.4 Hz, 2H), 7.62 (d, *J* = 6.8 Hz, 1H), 7.71 (t, *J* = 8.6 Hz, 2H), 7.85 – 8.01 (m, 3H), 8.21 (d, *J* = 7.0 Hz, 1H), 8.69 (d, *J* = 6.9 Hz, 1H).

FMoc-L-Ala-L-Ala-D-Ala-NH-CH_2-OAc (9d): HRMS $(M+Na)^+$ calcd. 547.2163, found 547.2167. ^{1}H NMR (400 MHz, DMSO-d6) δ 1.18 – 1.25 (m, 9H), 1.97 (s, 3H), 3.96 – 4.15 (m, 1H), 4.17 – 4.36 (m, 5H), 5.09 (d, *J* = 6.9 Hz, 2H), 7.34 (t, *J* = 7.4 Hz, 2H), 7.42 (t, *J* = 7.4 Hz, 2H), 7.57 (d, *J* = 7.2 Hz, 1H), 7.71 (d, *J* = 7.3 Hz, 2H), 7.90 (d, *J* = 7.5 Hz, 2H), 8.07 (s, 2H), 8.86 (s, 1H).

FMoc-L-Ala-D-Ala-NH-CH_2-OAc (9f): HRMS $(M+Na)^+$ calcd. 476.1792, found 476.1786.^{1}H NMR (400 MHz, DMSO-d6) δ 1.13 (dd, *J* = 7.1, 1.4 Hz, 6H), 1.89 (s, 3H), 3.99 (q, *J* = 7.1 Hz, 1H), 4.10 – 4.29 (m, 4H), 4.95 – 5.08 (m, 2H), 7.26 (t, *J* = 7.4, 1.3 Hz, 2H), 7.35 (t, *J* = 7.4 Hz, 2H), 7.49 (d, *J* = 7.2 Hz, 1H), 7.66 (t, *J* = 7.6 Hz, 2H), 7.82 (d, *J* = 7.5 Hz, 2H), 8.11 (d, *J* = 7.7 Hz, 1H), 8.76 (t, *J* = 7.0 Hz, 1H).

FMoc-D-Ala-L-Ala-NH-CH_2-OAc (9g): HRMS $(M+Na)^+$ calcd. 476.1792, found 476.1788. ^{1}H NMR (400 MHz, DMSO-d6) δ 1.21 (dd, *J* = 7.1, 1.4 Hz, 6H), 1.96 (s, 3H), 4.08 (t, *J* = 7.1 Hz, 1H), 4.17 – 4.36 (m, 4H), 5.05 – 5.14 (m, 2H), 7.26 – 7.38 (m, 2H), 7.42 (t, *J* = 7.4 Hz, 2H), 7.56 (d, *J* = 7.3 Hz, 1H), 7.73 (t, *J* = 7.6 Hz, 2H), 7.90 (d, *J* = 7.6 Hz, 2H), 8.18 (d, *J* = 7.8 Hz, 1H), 8.83 (t, *J* = 6.9 Hz, 1H).

FMoc-D-Ala-D-Ala-NH-CH_2-OAc (9h): HRMS $(M+H)^+$ calcd. 455.4877, found 455.2051 ^{1}H NMR (400 MHz, DMSO-d6) δ 1.14 (dd, *J* = 7.1, 3.3 Hz, 6H), 1.21 (d, *J* = 7.2 Hz, 1H), 1.81 (s, 1H), 1.91 (s, 2H), 4.01 (q, *J* = 7.7 Hz, 1H), 4.09 – 4.27 (m, 5H), 4.95 – 5.10 (m, 1H), 7.26 (td, *J* = 7.4, 1.2 Hz, 3H), 7.35 (t, *J* = 7.4 Hz, 3H), 7.45 (d, *J* = 7.6 Hz, 1H), 7.65 (t, *J* = 7.1 Hz, 3H), 7.82 (d, *J* = 6.4 Hz, 2H), 7.96 (d, *J* = 7.4 Hz, 1H), 8.78 (t, *J* = 7.0 Hz, 1H).

2. FMoc-peptide-COOH compounds (Compound 10a-10j)

Compounds of the type FMoc-Peptide-NH-CH_2-S-$(CH_2)_n$-CO_2H were prepared as shown in FIG. 9A and as exemplified by FMoc-L-Ala-L-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO_2H.

FMoc-L-Ala-L-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO_2H (10a) : 6-mercaptohexanoic acid (287 μL, 2.07 mmol) was dissolved in a solution of 1:4 TFA: dichloromethane (5 mL), then added to a vial containing FMoc-L-Ala-L-Ala-L-Ala-NH-CH_2-OAc (178 mg, 0.339 mmol). The reaction was allowed to proceed with magnetic stirring under an argon atmosphere at room temperature for 20 min. The crude material was concentrated *en vacuo,* redissolved in a minimum volume of DMF and purified on a C18 30 micron, 30g cartridge eluting with deionized water containing 0.1% formic acid with a linear gradient of acetonitrile from 5%

to 95% over 13 min at 35 mL/min. Fractions containing pure desired product were frozen and lypholized to give 200 mg (96 % yield) of a white solid. HRMS $(M + H)^+$ calcd. 613.2690; found 613.2686. ^{1}H NMR (400 MHz, DMSO-*d*6) δ 1.20 (dt, *J* = 7.1, 4.9 Hz, 10H), 1.31 (tt, *J* = 10.1, 6.0 Hz, 2H), 1.49 (dq, *J* = 12.5, 7.4 Hz, 4H), 2.18 (t, *J* = 7.3 Hz, 2H),4.05 (t, *J* = 7.3 Hz, 1H), 4.16 – 4.30 (m, 7H), 7.33 (td, *J* = 7.4, 1.2 Hz, 2H), 7.42 (td, *J* = 7.3, 1.1 Hz, 2H), 7.54 (d, *J* = 7.4 Hz, 1H), 7.72 (t, *J* = 7.0 Hz, 2H), 7.89 (d, *J* = 7.5 Hz, 2H), 7.94 – 8.07 (m, 2H), 8.44 (t, *J* = 6.1 Hz, 1H).

FMoc-D-Ala-L-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO_2H (10b): HRMS $(M+Na)^+$ calcd. 635.2510, found 635.2515. ^{1}H NMR (400 MHz, DMSO-d6) δ 1.15 (d, *J* = 6.8 Hz, 3H), 1.18 – 1.25 (m, 10H), 2.18 (q, *J* = 7.5 Hz, 4H), 2.40 – 2.48 (m, 1H), 2.70 (t, *J* = 7.2 Hz, 1H), 4.15 – 4.30 (m, 6H), 6.29 (s, 2H), 7.34 (q, *J* = 7.3 Hz, 3H), 7.42 (t, *J* = 7.4 Hz, 3H), 7.63 – 7.78 (m, 1H), 7.85 (d, *J* = 7.3 Hz, 2H), 7.89 (d, *J* = 7.5 Hz, 3H), 8.37 – 8.46 (m, 1H).

FMoc-L-Ala-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO_2H (10c) : HRMS $(M+Na)^+$ calcd. 635.2510, found 635.2514. ^{1}H NMR (400 MHz, DMSO-d6) δ 1.18 – 1.23 (m, 10H), 1.34 (q, *J* = 3.4 Hz, 5H), 2.24 (s, 2H), 2.44 (s, 2H), 4.05 (t, *J* = 7.1 Hz, 1H), 4.16 – 4.35 (m, 8H), 7.33 (t, *J* = 7.4 Hz, 2H), 7.42 (t, *J* = 7.5 Hz, 2H), 7.58 (d, *J* = 7.0 Hz, 1H), 7.71 (t, *J* = 8.4 Hz, 2H), 7.90 (s, 1H), 7.98 (d, *J* = 7.5 Hz, 1H), 8.15 (d, *J* = 7.3 Hz, 1H), 8.39 (t, *J* = 6.2 Hz, 1H), 11.98 (s, 1H).

FMoc-L-Ala-L-Ala-D-Ala-NH-CH_2-S-$(CH_2)_5$-CO_2H (10d) : HRMS $(M+Na)^+$ calcd. 635.2510, found 635.2510. ^{1}H NMR (400 MHz, DMSO-d6) δ 1.15 (d, *J* = 6.9 Hz, 3H), 1.21 (d, *J* = 7.1 Hz, 9H), 1.28 – 1.38 (m, 3H), 1.44 – 1.60 (m, 5H), 2.13 – 2.22 (m, 3H), 3.33 (q, *J* = 6.9 Hz, 1H), 4.20 (s, 2H), 6.29 (s, 2H), 7.29 – 7.40 (m, 3H), 7.38 – 7.47 (m, 3H), 7.85 (d, *J* = 7.5 Hz, 2H), 7.89 (d, *J* = 7.5 Hz, 2H), 8.26 (d, *J* = 7.6 Hz, 1H), 8.48 (d, *J* = 6.2 Hz, 1H).

FMoc-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO_2H (10g): HRMS $(M+H)^+$ calcd. 542.2319, found 542.2316. ^{1}H NMR (400 MHz, DMSO-d6) δ 1.13 (dd, *J* = 7.1, 1.7 Hz, 6H), 1.16 – 1.25 (m, 2H), 1.32 – 1.47 (m, 4H), 2.08 (t, *J* = 7.3 Hz, 2H), 3.25 (s, 2H), 3.99 (p, *J* = 7.0 Hz, 1H), 4.07 – 4.27 (m, 6H), 7.26 (t, *J* = 7.4, 1.2 Hz, 2H), 7.35 (t, *J* = 7.4 Hz, 2H), 7.52 (d, *J* = 7.0 Hz, 1H), 7.65 (t, *J* = 7.3 Hz, 2H), 7.82 (d, *J* = 7.5 Hz, 2H), 8.08 (d, *J* = 7.7 Hz, 1H), 8.27 (t, *J* = 6.2 Hz, 1H), 11.82 (s, 1H).

FMoc-L-Ala-D-Ala-NH-CH_2-S-$(CH_2)_5$-CO_2H (10f): HRMS $(M+H)^+$ calcd. 542.2319, found 542.2321. ^{1}H NMR (400 MHz, DMSO-d6) δ 1.13 (dd, *J* = 7.1, 1.8 Hz, 7H), 1.17 – 1.26 (m, 2H), 1.32 – 1.48 (m, 5H), 2.08 (t, *J* = 7.3 Hz, 2H), 3.99 (p, *J* = 7.1 Hz, 1H), 4.07 – 4.26 (m, 7H), 7.26 (t, *J* = 7.4 Hz, 2H), 7.35 (t, *J* = 7.4 Hz, 2H), 7.53 (d, *J* = 7.1 Hz, 1H),

7.65 (t, *J* = 7.3 Hz, 2H), 7.82 (d, *J* = 7.4 Hz, 2H), 8.10 (d, *J* = 7.7 Hz, 1H), 8.28 (t, *J* = 6.3 Hz, 1H).

FMoc-D-Ala-D-Ala-NH-CH_2-S-$(CH_2)_5$-CO_2H (10h): (16.7 mg, 0.031 mmol, 70 % yield). HRMS $(M+H)^+$ calcd. 542.2319, found 542.2318.

FMoc-L-Ala-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_3$-CO_2H(10j) : HRMS $(M+H)^+$ calcd. 585.2377, found 585.2367. ^1H NMR (400 MHz, DMSO-d6) δ 1.14 – 1.26 (m, 9H), 1.75 (p, *J* = 7.3 Hz, 2H), 2.27 (t, *J* = 7.3 Hz, 2H), 2.54 (d, *J* = 7.7 Hz, 2H), 3.97 – 4.10 (m, 1H), 4.13 – 4.34 (m, 7H), 7.33 (t, *J* = 7.5 Hz, 2H), 7.42 (t, *J* = 7.5 Hz, 2H), 7.57 (d, *J* = 6.9 Hz, 1H), 7.71 (t, *J* = 8.4 Hz, 2H), 7.89 (d, *J* = 7.6 Hz, 2H), 7.97 (d, *J* = 7.5 Hz, 1H), 8.14 (d, *J* = 7.0 Hz, 1H), 8.41 (s, 1H), 12.06 (s, 1H).

FMoc-D-Ala-L-Ala-NH-CH_2-S-$(CH)_2$-CO_2H (10i): HRMS $(M+H)^+$ calcd. 500.1850, found 500.1843. ^1H NMR (400 MHz, DMSO-*d*6) δ 1.20 (dd, *J* = 7.2, 1.9 Hz, 6H), 2.53 (d, *J* = 7.1 Hz, 2H), 2.70 (t, *J* = 7.1 Hz, 2H), 4.07 (q, *J* = 7.0 Hz, 1H), 4.17 – 4.26 (m, 4H), 4.29 (d, *J* = 6.8 Hz, 2H), 7.33 (t, *J* = 7.4 Hz, 2H), 7.41 (t, *J* = 7.5 Hz, 2H), 7.56 (d, *J* = 7.1 Hz, 1H), 7.72 (t, *J* = 7.7 Hz, 2H), 7.89 (d, *J* = 7.5 Hz, 2H), 8.14 (d, *J* = 7.6 Hz, 1H), 8.42 (t, *J* = 6.3 Hz, 1H), 12.22 (s, 1H).

3. FMoc-Peptide-May-NMA Compounds (Compound 11a-11j)

Compounds of the type FMoc-Peptide-NH-CH_2-S-$(CH_2)_n$-CO_2-DM were prepared as shown in FIG. 9A and as exemplified by FMoc-L-Ala-L-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM.

FMoc-L-Ala-L-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (11a): To DM-H stock solution (8.2 mL, 0.49 mmol) was added FMoc-L-Ala-L-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-COOH (300 mg, 0.49 mmol), EDC (94 mg, 0.490 mmol) and DIPEA (90 µL, 0.49 mmol). The reaction was allowed to proceed with magnetic stirring at room temperature under argon atmosphere for 2 h. The crude material was concentrated by rotary evaporation under vacuum and residue was taken up in a minimum volume of DMF then purified on a C18, 30 micron, 30 g cartridge eluting with deionized water containing 0.1% formic acid and a linear gradient of acetonitrile from 5% to 50% over 25 min. Fractions containing pure desired product were frozen and lypholized to yield 151 mg, (37.2 % yield) of white solid. HRMS $(M + Na)^+$ calcd. 1266.5170; found 1266.5141. ^1H NMR (400 MHz, DMSO-*d*6) δ 0.77 (s, 3H), 1.12 (d, *J* = 6.4 Hz, 3H), 1.14 – 1.22 (m, 12H), 1.22 – 1.30 (m, 3H), 1.35 – 1.49 (m, 4H), 1.50 – 1.55 (m, 1H), 1.59 (s, 3H), 2.00 – 2.07 (m, 1H), 2.14 (ddd, *J* = 15.6, 8.7, 5.9 Hz, 1H), 2.40

(dtd, *J* = 17.0, 7.9, 7.0, 4.9 Hz, 3H), 2.69 (s, 3H), 2.79 (d, *J* = 9.6 Hz, 1H), 3.08 (s, 3H), 3.20 (d, *J* = 12.6 Hz, 1H), 3.24 (s, 3H), 3.43 (d, *J* = 12.4 Hz, 2H), 3.48 (d, *J* = 8.9 Hz, 1H), 3.92 (s, 3H), 4.08 (ddd, *J* = 20.8, 10.8, 5.0 Hz, 3H), 4.14 – 4.24 (m, 4H), 4.26 (d, *J* = 6.0 Hz, 3H), 4.52 (dd, *J* = 12.0, 2.8 Hz, 1H), 5.34 (q, *J* = 6.7 Hz, 1H), 5.56 (dd, *J* = 14.7, 9.0 Hz, 1H), 5.91 (s, 1H), 6.50 – 6.66 (m, 3H), 6.88 (s, 1H), 7.17 (d, *J* = 1.8 Hz, 1H), 7.33 (td, *J* = 7.5, 1.2 Hz, 2H), 7.41 (t, *J* = 7.4 Hz, 2H), 7.53 (d, *J* = 7.4 Hz, 1H), 7.72 (t, *J* = 7.0 Hz, 2H), 7.89 (d, *J* = 7.5 Hz, 3H), 7.99 (d, *J* = 7.3 Hz, 1H), 8.36 (t, *J* = 6.3 Hz, 1H).

FMoc-D-Ala-L-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (11b): HRMS $(M+Na)^+$ calcd. 1266.5170, found 1266.5164. ^{1}H NMR (400 MHz, DMSO-d6) δ 0.78 (s, 3H), 1.14 (dd, *J* = 14.6, 6.5 Hz, 6H), 1.22 (t, *J* = 6.8 Hz, 10H), 1.33 – 1.57 (m, 4H), 1.59 (s, 3H), 2.04 (d, *J* = 13.5 Hz, 1H), 2.27 – 2.44 (m, 1H), 2.69 (s, 3H), 2.80 (d, *J* = 9.7 Hz, 1H), 3.08 (s, 3H), 3.14 – 3.28 (m, 5H), 3.37 – 3.55 (m, 3H), 3.92 (s, 3H), 3.98 – 4.16 (m, 3H), 4.20 (dd, *J* = 15.6, 7.6 Hz, 7H), 4.52 (d, *J* = 12.7 Hz, 1H), 5.34 (d, *J* = 6.9 Hz, 1H), 5.57 (dd, *J* = 14.7, 9.0 Hz, 1H), 5.92 (s, 1H), 6.46 – 6.72 (m, 4H), 6.88 (s, 1H), 7.17 (s, 1H), 7.33 (t, *J* = 7.5 Hz, 3H), 7.41 (t, *J* = 7.4 Hz, 3H), 7.60 – 7.75 (m, 4H), 7.80 – 7.93 (m, 4H), 8.12 (t, 1H), 8.29 (d, *J* = 6.9 Hz, 1H).

FMoc-L-Ala-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (11c): HRMS $(M+Na)^+$ calcd. 1266.5170, found 1266.5170. ^{1}H NMR (400 MHz, DMSO-d6) δ 0.71 (s, 3H), 0.96 – 1.16 (m, 10H), 1.16 – 1.51 (m, 10H), 1.52 (s, 4H), 1.82 – 2.16 (m, 1H), 2.17 – 2.56 (m, 11H), 2.62 (d, *J* = 5.8 Hz, 4H), 2.68 – 2.87 (m, 3H), 2.92 – 3.04 (m, 4H), 3.09 – 3.22 (m, 7H), 3.24 (d, *J* = 7.4 Hz, 1H), 3.33 – 3.50 (m, 2H), 3.73 – 3.89 (m, 4H), 3.92 – 4.07 (m, 2H), 4.07 – 4.25 (m, 2H), 4.45 (dd, *J* = 12.0, 2.8 Hz, 1H), 5.27 (q, *J* = 6.7 Hz, 1H), 5.40 – 5.55 (m, 1H), 5.85 (s, 1H), 6.33 – 6.66 (m, 4H), 6.81 (s, 2H), 7.03 – 7.19 (m, 1H), 7.19 – 7.43 (m, 2H), 7.62 (d, *J* = 11.6 Hz, 1H), 7.73 – 7.85 (m, 1H).

FMoc-L-Ala-L-Ala-D-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (11d): HRMS $(M+Na)^+$ calcd. 1266.5170, found 1266.5158. ^{1}H NMR (400 MHz, DMSO-d6) δ 0.78 (s, 3H), 1.06 – 1.33 (m, 16H), 1.44 (d, *J* = 10.3 Hz, 11H), 1.59 (s, 3H), 1.99 – 2.22 (m, 3H), 2.35 – 2.45 (m, 2H), 2.55 (d, *J* = 1.8 Hz, 1H), 2.69 (s, 3H), 2.80 (d, J = 9.6 Hz, 1H), 3.08 (s, 2H), 3.25 (s, 3H), 3.39 – 3.52 (m, 3H), 3.92 (s, 3H), 3.99 – 4.40 (m, 4H), 4.52 (d, *J* = 11.1 Hz, 1H), 5.34 (d, *J* = 6.8 Hz, 1H), 5.57 (dd, *J* = 14.5, 9.2 Hz, 1H), 5.92 (s, 1H), 6.53 – 6.64 (m, 2H), 6.88 (s, 2H), 7.17 (d, *J* = 1.9 Hz, 1H), 7.33 (t, *J* = 7.3 Hz, 3H), 7.42 (t, *J* = 7.4 Hz, 3H), 7.57 (d, *J* = 7.4 Hz, 1H), 7.72 (s, 3H), 7.89 (d, *J* = 7.6 Hz, 3H), 7.99 (d, *J* = 7.6 Hz, 1H), 8.07 (s, 1H), 8.35 (s, 1H).

FMoc-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (11g): HRMS $(M+H)^+$ calcd. 1173.4980, found 1173.4964. ^{1}H NMR (400 MHz, DMSO-d6) δ 0.79 (s, 3H), 1.06 – 1.34 (m, 13H), 1.36 – 1.54 (m, 4H), 1.60 (s, 2H), 1.88 – 2.10 (m, 1H), 2.10 – 2.23 (m, 1H), 2.31 – 2.51 (m, 13H), 2.71 (s, 3H), 2.80 (d, *J* = 9.6 Hz, 1H), 3.10 (s, 3H), 3.26 (s, 4H), 3.33 – 3.66 (m, 3H), 3.98 – 4.32 (m, 4H), 4.53 (dd, *J* = 12.0, 2.8 Hz, 1H), 5.35 (q, *J* = 6.7 Hz, 1H), 5.49 – 5.65 (m, 1H), 6.51 – 6.67 (m, 3H), 6.89 (s, 1H), 7.19 (d, *J* = 1.8 Hz, 1H), 8.25 (s, 2H), 8.34 (d, *J* = 7.1 Hz, 1H), 8.58 (t, *J* = 6.3 Hz, 1H).

FMoc-L-Ala-D-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (11f): HRMS $(M+H)^+$ calcd. 1173.4980, found 1173.4969.

FMoc-D-Ala-D-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (11h): HRMS $(M+Na)^+$ calcd. 1195.4907, found 1195.4799. ^{1}H NMR (400 MHz, DMSO-d_6) δ 0.71 (s, 3H), 1.00 – 1.22 (m, 13H), 1.28 – 1.45 (m, 2H), 1.52 (s, 3H), 1.91 – 2.14 (m, 1H), 2.26 (t, *J* = 1.9 Hz, 5H), 2.48 (t, *J* = 1.8 Hz, 2H), 2.62 (s, 3H), 2.66 – 2.77 (m, 2H), 3.01 (s, 2H), 3.10 – 3.21 (m, 5H), 3.28 – 3.47 (m, 2H), 3.86 (d, *J* = 6.7 Hz, 4H), 3.93 – 4.25 (m, 10H), 4.37 – 4.54 (m, 1H), 5.27 (d, *J* = 6.7 Hz, 1H), 5.40 – 5.56 (m, 1H), 5.85 (s, 1H), 6.31 – 6.66 (m, 3H), 6.81 (s, 1H), 7.11 (d, *J* = 1.8 Hz, 1H), 7.26 (t, *J* = 7.4 Hz, 2H), 7.35 (t, *J* = 7.4 Hz, 2H), 7.45 (d, *J* = 7.5 Hz, 1H), 7.65 (t, *J* = 7.1 Hz, 2H), 7.82 (d, *J* = 7.5 Hz, 2H), 7.89 (d, *J* = 7.3 Hz, 1H).

FMoc-L-Ala-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_3$-CO-DM (11j): HRMS $(M+H)^+$ calcd. 1216.5038, found 1216.4999. ^{1}H NMR (400 MHz, DMSO-d6) δ 0.78 (s, 3H), 0.95 – 1.29 (m, 16H), 1.37 (d, *J* = 3.4 Hz, 1H), 1.46 (t, *J* = 12.5 Hz, 2H), 1.59 (s, 3H), 1.62 – 1.90 (m, 1H), 1.99 – 2.07 (m, 1H), 2.08 (s, 2H), 2.18 – 2.43 (m, 1H), 2.50 – 2.59 (m, 1H), 2.69 (s, 3H), 2.73 – 2.83 (m, 1H), 3.10 (s, 2H), 3.25 (s, 3H), 3.38 – 3.55 (m, 2H), 3.91 (s, 3H), 3.99 – 4.13 (m, 4H), 4.12 – 4.35 (m, 7H), 4.52 (dd, *J* = 12.0, 2.9 Hz, 1H), 5.34 (q, *J* = 6.7 Hz, 1H), 5.48 – 5.65 (m, 1H), 5.92 (s, 1H), 6.48 – 6.70 (m, 3H), 6.88 (s, 1H), 7.17 (d, *J* = 1.7 Hz, 1H), 7.33 (t, *J* = 7.5 Hz, 2H), 7.41 (t, *J* = 7.4 Hz, 2H), 7.58 (d, *J* = 7.0 Hz, 1H), 7.71 (t, *J* = 8.3 Hz, 2H), 7.89 (d, *J* = 7.5 Hz, 3H), 7.95 (d, *J* = 7.6 Hz, 1H), 8.15 (d, *J* = 7.2 Hz, 1H), 8.29 – 8.38 (m, 1H), 8.41 (s, 1H).

FMoc-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_2$-CO-DM (11i): HRMS $(M+H)^+$ calcd. 1131.4510, found 1131.4507.^{1}H NMR (400 MHz, DMSO-*d*6) δ 0.76 (s, 3H), 1.08 - 1.21 (m, 12H), 1.24 (d, *J* = 13.9 Hz, 1H), 1.38 – 1.52 (m, 2H), 1.58 (s, 3H), 1.99 – 2.09 (m, 1H), 2.33 – 2.44 (m, 1H), 2.68 (s, 3H), 2.80 (dd, *J* = 14.4, 8.6 Hz, 2H), 3.08 (s, 3H), 3.17 (d, *J* = 12.5 Hz, 1H), 3.23 (s, 3H), 3.46 (t, *J* = 10.3 Hz, 2H), 3.91 (s, 3H), 4.00 – 4.13 (m, 3H), 4.13 – 4.34 (m, 5H), 4.52 (dd, *J* = 12.0, 2.9 Hz, 1H), 5.30 (q, *J* = 6.8 Hz, 1H), 5.55 (dd, *J* = 13.4, 9.1 Hz, 1H), 5.91 (s, 1H), 6.55 (dd, *J* = 7.4, 5.7 Hz, 3H), 6.87 (s, 1H), 7.16 (d, *J* = 1.8 Hz, 1H), 7.32

(tt, *J* = 7.4, 1.5 Hz, 2H), 7.41 (tt, *J* = 7.5, 1.5 Hz, 2H), 7.57 (d, *J* = 7.0 Hz, 1H), 7.71 (dd, *J* = 10.5, 7.5 Hz, 2H), 7.88 (d, *J* = 7.5 Hz, 2H), 8.14 (d, *J* = 7.6 Hz, 1H), 8.37 (t, *J* = 6.3 Hz, 1H).

4. Amino-Peptide-Maytansinoids (Compound 12a-12j)

Compounds of the type H_2N-Peptide-NH-CH_2-S-$(CH_2)_n$-CO_2-DM were prepared as shown in FIG. 9A and as exemplified by H_2N-L-Ala-L-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM.

H_2N-L-Ala-L-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (12a): FMoc-L-Ala-L-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (151 mg, 0.121 mmol) was treated with 20% morpholine in DMF (2 mL). The reaction was allowed to proceed with magnetic stirring under argon at room temperature for 1 h. The crude material was purified on a C18, 30 micro, 150 g column cartridge eluting with deionized water containing 0.1% formic acid and a linear gradient of acetonitrile from 5% to 50% over 26 min. Fractions containing desired product were immediately frozen and lypholized to give 46 mg (37.1 % yield) of a colorless oil. HRMS $(M + H)^+$ calcd. 1022.4670; found 1022.4669. ^{1}H NMR (400 MHz, DMSO-*d*6) δ 0.78 (s, 3H), 1.12 (d, *J* = 6.3 Hz, 3H), 1.13 – 1.21 (m, 10H), 1.21 – 1.31 (m, 3H), 1.37 – 1.50 (m, 4H), 1.51 – 1.57 (m, 1H), 1.59 (s, 3H), 2.04 (dd, *J* = 14.4, 2.8 Hz, 1H), 2.15 (ddd, *J* = 15.9, 8.7, 6.0 Hz, 1H), 2.38 (td, *J* = 7.0, 3.6 Hz, 2H), 2.70 (s, 3H), 2.79 (d, *J* = 9.6 Hz, 1H), 3.09 (s, 3H), 3.21 (d, *J* = 12.5 Hz, 1H), 3.25 (s, 3H), 3.33-3.55 (m, 8H), 3.93 (s, 3H), 4.01 – 4.33 (m, 5H), 4.52 (dd, *J* = 12.0, 2.8 Hz, 1H), 5.34 (q, *J* = 6.7 Hz, 1H), 5.57 (dd, *J* = 14.6, 9.0 Hz, 1H), 5.95 (s, 1H), 6.48 – 6.65 (m, 3H), 6.89 (s, 1H), 7.18 (d, *J* = 1.8 Hz, 1H), 8.07 (d, *J* = 7.5 Hz, 1H), 8.13 (s, 1H), 8.31 (s, 1H), 8.40 (t, *J* = 6.3 Hz, 1H).

H_2N-D-Ala-L-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (12b): HRMS $(M+H)^+$ calcd. 1022.4670, found 1022.4675. ^{1}H NMR (400 MHz, DMSO-d6) δ 0.71 (s, 3H), 1.05 (dd, *J* = 6.7, 3.1 Hz, 7H), 1.08 – 1.16 (m, 10H), 1.19 (t, *J* = 8.1 Hz, 3H), 1.30 – 1.50 (m, 6H), 1.52 (s, 3H), 1.97 (d, *J* = 13.3 Hz, 1H), 2.01 – 2.21 (m, 2H), 2.34 (s, 3H), 2.63 (s, 3H), 2.73 (d, *J* = 9.8 Hz, 1H), 3.02 (s, 3H), 3.14 (d, *J* = 12.5 Hz, 1H), 3.33 – 3.48 (m, 2H), 3.86 (s, 3H), 3.95 – 4.23 (m, 7H), 4.45 (dd, *J* = 13.1 Hz, 1H), 5.27 (q, *J* = 6.8 Hz, 1H), 5.41 – 5.58 (m, 1H), 5.85 (s, 1H), 6.39 – 6.63 (m, 4H), 6.81 (s, 1H), 7.12 (d, *J* = 1.8 Hz, 1H), 8.02 (s, 1H), 8.13 (d, *J* = 7.7 Hz, 1H), 8.26 (s, 1H), 8.36 (t, *J* = 6.2 Hz, 1H).

H_2N-L-Ala-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (12c): HRMS $(M+H)^+$ calcd. 1022.4670, found 1022.4680. ^{1}H NMR (400 MHz, DMSO-d6) δ 0.71 (s, 3H), 1.01 – 1.26 (m, 19H), 1.25 – 1.50 (m, 6H), 1.52 (s, 3H), 1.97 (d, *J* = 13.7 Hz, 1H), 2.02 – 2.22 (m, 1H),

2.35 (dd, *J* = 17.2, 9.5 Hz, 2H), 2.47 (d, *J* = 11.5 Hz, 1H), 2.63 (s, 4H), 2.73 (d, J = 9.6 Hz, 1H), 3.02 (s, 3H), 3.10 – 3.24 (m, 6H), 3.32 – 3.50 (m, 2H), 3.86 (s, 3H), 3.95 – 4.18 (m, 4H), 4.45 (dd, *J* = 12.1, 2.6 Hz, 1H), 5.27 (q, *J* = 6.9 Hz, 1H), 5.44 – 5.55 (m, 1H), 5.85 (s, 1H), 6.42 – 6.59 (m, 4H), 6.81 (s, 1H), 7.12 (d, *J* = 1.7 Hz, 1H), 8.02 (s, 1H), 8.13 (d, *J* = 7.7 Hz, 1H), 8.36 (t, *J* = 6.3 Hz, 1H).

H_2N-L-Ala-L-Ala-D-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (12d): HRMS $(M+H)^+$ calcd. 1022.4670, found 1022.4675. ^{1}H NMR (400 MHz, DMSO-d6) δ 0.71 (s, 3H), 0.98 – 1.14 (m, 13H), 1.14 – 1.26 (m, 2H), 1.30 – 1.49 (m, 4H), 1.52 (s, 3H), 2.24 – 2.41 (m, 2H), 2.44 (d, *J* = 1.8 Hz, 16H), 2.63 (s, 2H), 2.73 (d, *J* = 9.6 Hz, 1H), 3.02 (s, 2H), 3.08 – 3.21 (m, 4H), 3.32 – 3.49 (m, 2H), 3.86 (s, 3H), 3.92 – 4.23 (m, 3H), 4.45 (d, *J* = 11.8 Hz, 1H), 5.26 (t, *J* = 6.7 Hz, 1H), 5.40 – 5.57 (m, 1H), 5.86 (s, 1H), 6.41 – 6.66 (m, 3H), 6.81 (s, 1H), 7.12 (d, *J* = 1.7 Hz, 1H), 8.02 (s, 1H), 8.10 (d, *J* = 7.7 Hz, 1H), 8.35 (t, *J* = 6.3 Hz, 1H).

H_2N-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (12g): HRMS $(M+H)^+$ calcd. 951.4299, found 951.4289. ^{1}H NMR (400 MHz, DMSO-d6) δ 0.79 (s, 3H), 1.06 – 1.34 (m, 13H), 1.36 – 1.54 (m, 4H), 1.60 (s, 2H), 1.88 – 2.10 (m, 1H), 2.10 – 2.23 (m, 1H), 2.31 – 2.51 (m, 13H), 2.71 (s, 3H), 2.80 (d, *J* = 9.6 Hz, 1H), 3.10 (s, 3H), 3.26 (s, 4H), 3.33 – 3.66 (m, 3H), 3.98 – 4.32 (m, 4H), 4.53 (dd, *J* = 12.0, 2.8 Hz, 1H), 5.35 (q, *J* = 6.7 Hz, 1H), 5.49 – 5.65 (m, 1H), 6.51 – 6.67 (m, 3H), 6.89 (s, 1H), 7.19 (d, *J* = 1.8 Hz, 1H), 8.25 (s, 2H), 8.34 (d, *J* = 7.1 Hz, 1H), 8.58 (t, *J* = 6.3 Hz, 1H).

H_2N-L-Ala-D-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (12f): HRMS $(M+H)^+$ calcd. 951.4226, found 951.1299. ^{1}H NMR (400 MHz, DMSO-d6) δ 0.71 (s, 3H), 1.00 – 1.13 (m, 11H), 1.19 (t, *J* = 8.9 Hz, 3H), 1.29 – 1.45 (m, 4H), 1.52 (s, 3H), 1.92 – 2.03 (m, 1H), 2.07 (dd, *J* = 15.7, 8.7 Hz, 1H), 2.23 – 2.39 (m, 1H), 2.63 (s, 3H), 2.73 (d, *J* = 9.7 Hz, 1H), 3.02 (s, 3H), 3.07 – 3.32 (m, 14H), 3.34 – 3.47 (m, 2H), 3.86 (s, 3H), 3.95 – 4.21 (m, 4H), 4.45 (dd, *J* = 11.9, 2.8 Hz, 1H), 5.27 (q, *J* = 6.8 Hz, 1H), 5.50 (dd, *J* = 14.7, 9.0 Hz, 1H), 5.85 (s, 1H), 6.40 – 6.61 (m, 3H), 6.81 (s, 1H), 7.12 (d, *J* = 1.8 Hz, 1H), 8.41 (t, *J* = 6.1 Hz, 1H).

H_2N-D-Ala-D-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (12h): HRMS $(M+H)^+$ calcd. 950.4226, found 951.4299. ^{1}H NMR (400 MHz, DMSO-d6) δ 0.71 (s, 3H), 0.96 – 1.14 (m, 14H), 1.19 (t, *J* = 8.9 Hz, 3H), 1.38 (q, *J* = 10.5, 7.0 Hz, 5H), 1.52 (s, 3H), 1.88 – 2.02 (m, 1H), 2.02 – 2.18 (m, 1H), 2.22 – 2.41 (m, 2H), 2.48 (s, 1H), 2.63 (s, 3H), 2.73 (d, *J* = 9.6 Hz, 1H), 3.02 (s, 3H), 3.08 – 3.22 (m, 4H), 3.34 – 3.48 (m, 2H), 3.86 (s, 4H), 3.95 – 4.23 (m, 5H), 4.45 (dd, *J* = 11.9, 2.8 Hz, 1H), 5.27 (q, *J* = 6.7 Hz, 1H), 5.41 – 5.60 (m, 1H), 5.85 (s, 1H), 6.40 – 6.65 (m, 4H), 6.81 (s, 1H), 7.12 (d, *J* = 1.8 Hz, 1H), 8.44 (t, *J* = 6.1 Hz, 1H).

H_2N-L-Ala-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_3$-CO-DM (12j): HRMS $(M+H)^+$ calcd. 994.4357, found 994.4330.

H_2N-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_2$-CO-DM (12i): HRMS $(M+H)^+$ calcd. 909.3830, found 909.3826. ^{1}H NMR (400 MHz, DMSO-*d*6) δ 0.77 (s, 3H), 1.12 (d, *J* = 6.7 Hz, 6H), 1.17 (dd, *J* = 7.0, 5.2 Hz, 6H), 1.25 (d, *J* = 13.3 Hz, 1H), 1.40 – 1.51 (m, 2H), 1.59 (s, 3H), 2.04 (dd, *J* = 14.4, 2.9 Hz, 1H), 2.41 (ddt, *J* = 18.6, 10.1, 5.4 Hz, 1H), 2.61 – 2.70 (m, 1H), 2.72 (s, 3H), 2.76 – 2.90 (m, 3H), 3.09 (s, 3H), 3.20 (d, *J* = 12.4 Hz, 1H), 3.25 (s, 3H), 3.33 (q, *J* = 6.9 Hz, 1H), 3.39 – 3.64 (m, 3H), 3.93 (s, 3H), 4.03 – 4.16 (m, 2H), 4.24 (dt, *J* = 15.1, 7.6 Hz, 2H), 4.53 (dd, *J* = 12.0, 2.9 Hz, 1H), 5.32 (q, *J* = 6.8 Hz, 1H), 5.51 – 5.64 (m, 1H), 5.93 (s, 1H), 6.49 – 6.62 (m, 2H), 6.88 (s, 1H), 7.19 (d, *J* = 1.8 Hz, 1H), 8.10 (s, 1H), 8.55 (t, *J* = 6.3 Hz, 1H).

5. SPDB-Peptide-Maytansinoids (Compound 13a-13j)

Compounds of the type SPDB-Peptide-NH-CH_2-S-$(CH_2)_n$-CO_2-DM were prepared as shown in FIG. 9A and as exemplified by SPDB-L-Ala-L-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM.

SPDB-L-Ala-L-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (13a): H_2N-L-Ala-L-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (46 mg, 0.045 mmol) was dissolved in DMF (2 mL), to which was added SPDB (14.7 mg, 0.045 mmol) and reacted at room temperature with magnetic stirring under an argon atmosphere for 1 h. The crude material was purified on a C18, 430 micro, 30g cartridge eluting with deionized water containing 0.1% formic acid and a linear gradient of acetonitrile from 5% to 95% over 35 min. Fractions containing pure desired product were frozen and lypholized to give 38 mg, (68.5 % yield) of white solid. HRMS $(M + H)^+$ calcd. 1233.4796; found 1233.4783. ^{1}H NMR (400 MHz, DMSO-*d*6) δ 0.78 (s, 3H), 1.12 (d, *J* = 6.4 Hz, 3H), 1.14 – 1.21 (m, 10H), 1.22 – 1.30 (m, 3H), 1.44 (qd, *J* = 10.2, 4.5 Hz, 5H), 1.50 – 1.56 (m, 1H), 1.59 (s, 3H), 1.84 (p, *J* = 7.3 Hz, 2H), 2.04 (dd, *J* = 14.4, 2.7 Hz, 1H), 2.15 (ddd, *J* = 15.8, 8.6, 5.9 Hz, 2H), 2.24 (t, *J* = 7.2 Hz, 2H), 2.39 (dtdd, *J* = 18.1, 13.2, 8.1, 4.7 Hz, 3H), 2.70 (s, 3H), 2.76 – 2.86 (m, 3H), 3.09 (s, 3H), 3.21 (d, *J* = 12.5 Hz, 1H), 3.25 (s, 3H), 3.43 (d, *J* = 12.4 Hz, 1H), 3.48 (d, *J* = 9.0 Hz, 1H), 3.92 (s, 3H), 4.13 (s, 2H), 4.19 (h, *J* = 6.6 Hz, 4H), 4.52 (dd, *J* = 12.1, 2.8 Hz, 1H), 5.34 (q, *J* = 6.8 Hz, 1H), 5.56 (dd, *J* = 14.7, 9.0 Hz, 1H), 5.92 (s, 1H), 6.49 – 6.66 (m, 3H), 6.85 – 6.97 (m, 2H), 7.18 (d, *J* = 1.8 Hz, 1H), 7.23 (ddd, *J* = 7.3, 4.8, 1.2 Hz, 1H), 7.76 (dt, *J* = 8.1, 1.2 Hz, 1H), 7.78 – 7.91 (m, 2H), 8.00 (d, *J* = 7.1 Hz, 1H), 8.09 (d, *J* = 7.0 Hz, 1H), 8.33 (t, *J* = 6.3 Hz, 1H), 8.44 (dt, *J* = 4.7, 1.3 Hz, 1H), 8.50 (s, 1H).

SPDB-D-Ala-L-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (13b): HRMS $(M+H)^+$ calcd. 1233.4796, found 1233.4799. ^{1}H NMR (400 MHz, DMSO-d6) δ 0.71 (s, 3H), 1.01 – 1.22 (m, 13H), 1.27 – 1.45 (m, 2H), 1.52 (s, 3H), 1.91 – 2.16 (m, 1H), 2.26 (d, *J* = 7.4 Hz, 7H), 2.26 (t, *J* = 1.9 Hz, 4H), 2.48 (t, *J* = 1.8 Hz, 2H), 2.57 – 2.65 (m, 3H), 2.65 – 2.77 (m, 2H), 3.01 (s, 2H), 3.13 (d, *J* = 12.2 Hz, 1H), 3.18 (s, 3H), 3.32 – 3.47 (m, 2H), 3.86 (d, *J* = 6.7 Hz, 4H), 3.93 – 4.11 (m, 3H), 4.18 (t, *J* = 11.2 Hz, 7H), 4.39 – 4.50 (m, 1H), 5.27 (d, *J* = 6.7 Hz, 1H), 5.50 (dd, *J* = 14.7, 8.8 Hz, 1H), 5.85 (s, 1H), 6.37 – 6.61 (m, 3H), 6.81 (s, 1H), 7.11 (d, *J* = 1.8 Hz, 1H), 7.26 (t, *J* = 7.4 Hz, 2H), 7.35 (t, *J* = 7.4 Hz, 2H), 7.45 (d, *J* = 7.5 Hz, 1H), 7.65 (t, *J* = 7.1 Hz, 2H), 7.82 (d, *J* = 7.5 Hz, 2H), 7.89 (d, *J* = 7.3 Hz, 1H).

SPDB- L-Ala-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (13c): HRMS $(M+H)^+$ calcd. 1233.4796, found 1233.4795. ^{1}H NMR (400 MHz, DMSO-d6) δ 0.71 (s, 3H), 1.02 – 1.25 (m, 18H), 1.29 – 1.50 (m, 6H), 1.52 (s, 3H), 1.70 – 1.87 (m, 2H), 1.87 – 2.14 (m, 2H), 2.13 – 2.22 (m, 2H), 2.27 – 2.40 (m, 3H), 2.63 (s, 3H), 2.69 – 2.84 (m, 4H), 3.02 (s, 3H), 3.14 (d, *J* = 12.3 Hz, 1H), 3.18 (s, 3H), 3.32 – 3.45 (m, 2H), 3.85 (s, 3H), 3.95 – 4.07 (m, 2H), 4.07 – 4.19 (m, 4H), 4.45 (dd, *J* = 11.9, 2.7 Hz, 1H), 5.27 (q, *J* = 6.7 Hz, 1H), 5.44 – 5.55 (m, 1H), 5.85 (s, 1H), 6.42 – 6.59 (m, 3H), 6.81 (s, 1H), 7.11 (s, 1H), 7.13 – 7.19 (m, 1H), 7.68 (d, *J* = 8.2, 2.7 Hz, 1H), 7.72 – 7.80 (m, 1H), 7.88 (t, *J* = 6.6 Hz, 1H), 8.04 (d, *J* = 6.4 Hz, 1H), 8.09 (d, *J* = 7.4 Hz, 1H), 8.25 (t, *J* = 6.3 Hz, 1H), 8.37 (dd, *J* = 5.0, 1.9 Hz, 1H).

SPDB- L-Ala-L-Ala-D-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (13d): HRMS $(M+H)^+$ calcd. 1233.4796, found 1233.4797. ^{1}H NMR (400 MHz, DMSO-d6) δ 0.72 (d, *J* = 3.3 Hz, 3H), 0.98 – 1.28 (m, 22H), 1.30 – 1.46 (m, 3H), 1.53 (s, 3H), 1.78 (q, *J* = 7.1 Hz, 2H), 1.86 – 2.16 (m, 2H), 2.19 (q, *J* = 7.4, 5.6 Hz, 2H), 2.26 – 2.41 (m, 2H), 2.41 – 2.55 (m, 4H), 2.64 (d, *J* = 3.2 Hz, 2H), 2.81 – 2.92 (m, 1H), 3.02 (s, 2H), 3.14 (d, *J* = 12.0 Hz, 1H), 3.26 (s, 1H), 3.31 – 3.48 (m, 2H), 3.86 (s, 3H), 3.97 – 4.30 (m, 7H), 4.46 (dd, *J* = 11.8, 3.2 Hz, 1H), 5.24 – 5.36 (m, 1H), 5.45 – 5.62 (m, 1H), 5.86 (s, 1H), 6.40 – 6.65 (m, 3H), 6.82 (d, *J* = 3.4 Hz, 1H), 7.11 (d, *J* = 3.2 Hz, 1H), 7.18 (d, *J* = 12.1, 6.1, 4.9 Hz, 2H), 7.69 (d, *J* = 8.1 Hz, 1H), 7.75 (t, *J* = 7.6 Hz, 2H), 7.89 (d, *J* = 7.8, 3.2 Hz, 1H), 7.95 – 8.04 (m, 2H), 8.26 (d, *J* = 6.1 Hz, 1H), 8.33 – 8.47 (m, 1H).

SPDB-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (13g): HRMS $(M+H)^+$ calcd. 1162.4425, found 1162.4405. ^{1}H NMR (400 MHz, DMSO-d6) δ 0.71 (s, 3H), 1.08 (dt, *J* = 13.9, 6.9 Hz, 15H), 1.15 – 1.25 (m, 3H), 1.28 – 1.44 (m, 5H), 1.52 (s, 3H), 1.77 (p, *J* = 7.2 Hz, 2H), 1.91 – 2.02 (m, 1H), 2.02 – 2.13 (m, 1H), 2.17 (t, *J* = 7.2 Hz, 2H), 2.22 – 2.40 (m, 2H), 2.63 (s, 3H), 2.68 – 2.80 (m, 3H), 3.02 (s, 3H), 3.13 (d, *J* = 12.3 Hz, 1H), 3.18 (s, 3H), 3.33 – 3.45 (m, 2H), 3.85 (s, 3H), 3.95 – 4.16 (m, 5H), 4.45 (dd, *J* = 12.1, 2.8 Hz, 1H), 5.27 (q, *J* = 6.7

Hz, 1H), 5.44 – 5.56 (m, 1H), 5.85 (s, 1H), 6.43 – 6.60 (m, 3H), 6.82 (s, 1H), 7.11 (d, *J* = 1.8 Hz, 1H), 7.12 – 7.18 (m, 1H), 7.65 – 7.79 (m, 2H), 8.06 – 8.16 (m, 2H), 8.30 (t, *J* = 6.3 Hz, 1H), 8.35 – 8.40 (m, 1H).

SPDB-L-Ala-D-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (13f): HRMS $(M+H)^+$ calcd. 1162.4399, found 1162.455. ^{1}H NMR (400 MHz, DMSO-d6) δ 0.71 (s, 3H), 1.02 – 1.13 (m, 12H), 1.14 – 1.25 (m, 3H), 1.31 – 1.44 (m, 5H), 1.52 (s, 3H), 1.77 (p, *J* = 7.3 Hz, 2H), 1.97 (d, *J* = 14.3, 2.7 Hz, 1H), 2.02 – 2.13 (m, 1H), 2.17 (t, *J* = 7.2 Hz, 2H), 2.28 – 2.40 (m, 3H), 2.43 (m, *J* = 3.2 Hz, 3H), 2.63 (s, 3H), 2.69 – 2.80 (m, 3H), 3.02 (s, 3H), 3.13 (d, *J* = 12.4 Hz, 1H), 3.18 (s, 3H), 3.39 (dd, *J* = 21.0, 10.7 Hz, 2H), 3.85 (s, 3H), 3.96 – 4.18 (m, 5H), 4.45 (dd, *J* = 12.1, 2.8 Hz, 1H), 5.27 (q, *J* = 6.7 Hz, 1H), 5.45 – 5.55 (m, 1H), 5.85 (s, 1H), 6.43 – 6.60 (m, 3H), 6.81 (s, 1H), 7.10 (d, *J* = 1.8 Hz, 1H), 7.16 (t, *J* = 7.2, 4.9 Hz, 1H), 7.68 (d, *J* = 8.1 Hz, 1H), 7.71 – 7.79 (m, 1H), 8.02 – 8.15 (m, 2H), 8.28 (t, *J* = 6.3 Hz, 1H), 8.37 (d, *J* = 4.8, 1.7 Hz, 1H).

SPDB-D-Ala-D-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (13h): HRMS $(M+H)^+$ calcd. 1162.4399, found 1162.455. ^{1}H NMR (400 MHz, DMSO-d6) δ 0.71 (s, 3H), 1.02 – 1.16 (m, 13H), 1.14 – 1.25 (m, 3H), 1.28 – 1.49 (m, 5H), 1.52 (s, 3H), 1.77 (p, *J* = 7.2 Hz, 2H), 1.92 – 2.14 (m, 2H), 2.17 (t, *J* = 7.2 Hz, 2H), 2.23 – 2.40 (m, 2H), 2.46 – 2.54 (m, 1H), 2.63 (s, 3H), 2.65 – 2.85 (m, 4H), 3.02 (s, 3H), 3.03 – 3.16 (m, 2H), 3.18 (s, 3H), 3.28 – 3.45 (m, 2H), 3.85 (s, 3H), 3.95 – 4.20 (m, 5H), 4.45 (dd, *J* = 12.1, 2.8 Hz, 1H), 5.27 (q, *J* = 6.7 Hz, 1H), 5.44 – 5.55 (m, 1H), 5.82 – 5.88 (m, 1H), 6.42 – 6.59 (m, 3H), 6.81 (s, 1H), 7.11 (d, *J* = 1.9 Hz, 1H), 7.14 – 7.20 (m, 1H), 7.67 – 7.72 (m, 1H), 7.72 – 7.80 (m, 1H), 7.88 (d, J = 7.6 Hz, 1H), 7.99 (d, *J* = 7.1 Hz, 1H), 8.28 (t, *J* = 6.3 Hz, 1H), 8.35 – 8.40 (m, 1H).

SPDB-L-Ala-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_3$-CO-DM (13j): HRMS $(M+H)^+$ calcd. 1203.4337, found 1203.4315. ^{1}H NMR (400 MHz, DMSO-d6) δ 0.71 (s, 3H), 0.94 – 1.24 (m, 20H), 1.38 (s, 3H), 1.52 (s, 3H), 1.57 – 1.87 (m, 1H), 1.89 – 2.08 (m, 1H), 2.26 (t, *J* = 15.1 Hz, 1H), 2.50 (d, *J* = 5.2 Hz, 2H), 2.54 – 2.79 (m, 7H), 3.05 (d, *J* = 3.8 Hz, 3H), 3.18 (s, 5H), 3.29 – 3.46 (m, 3H), 3.86 (d, *J* = 6.1 Hz, 4H), 4.00 (s, 3H), 4.05 – 4.24 (m, 4H), 4.33 – 4.54 (m, 1H), 5.17 – 5.38 (m, 1H), 5.39 – 5.58 (m, 1H), 5.85 (s, 1H), 6.29 – 6.58 (m, 4H), 6.63 (s, 1H), 6.81 (s, 1H), 7.04 – 7.19 (m, 1H), 7.90 (s, 1H), 8.14 – 8.39 (m, 1H), 8.45 (s, 1H).

SPDB-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_2$-CO-DM (13i): HRMS $(M+H)^+$ calcd. 1120.3955, found 1120.3951. ^{1}H NMR (400 MHz, DMSO-*d*6) δ 0.74 – 0.82 (m, 3H), 1.10 – 1.22 (m, 13H), 1.25 (d, *J* = 14.1 Hz, 1H), 1.46 (t, *J* = 10.9 Hz, 2H), 1.56 – 1.63 (m, 3H), 1.85 (ddd, *J* = 14.4, 9.0, 5.1 Hz, 2H), 2.00 (ddd, *J* = 14.7, 9.3, 5.4 Hz, 9H), 2.24 (dt, *J* = 10.8, 5.0 Hz,

2H), 2.72 (d, *J* = 3.6 Hz, 2H), 2.94 (dq, *J* = 10.7, 7.2, 5.7 Hz, 9H), 3.10 (d, *J* = 3.7 Hz, 3H), 3.20 (d, *J* = 3.4 Hz, 1H), 3.25 (d, *J* = 3.6 Hz, 3H), 3.32 (d, *J* = 3.7 Hz, 1H), 3.47 (td, *J* = 10.7, 10.0, 3.8 Hz, 2H), 3.93 (t, *J* = 4.6 Hz, 3H), 4.02 – 4.25 (m, 6H), 4.49 – 4.57 (m, 1H), 5.28 – 5.37 (m, 1H), 5.53 – 5.62 (m, 1H), 5.92 (d, *J* = 3.6 Hz, 1H), 6.57 (q, *J* = 5.4, 4.5 Hz, 3H), 6.85 – 6.93 (m, 1H), 7.17 (d, *J* = 3.3 Hz, 1H), 7.25 (dq, *J* = 8.0, 4.9 Hz, 6H), 7.72 – 7.87 (m, 11H), 8.16 (dt, *J* = 15.4, 4.9 Hz, 2H), 8.45 (tt, *J* = 9.9, 5.9 Hz, 6H).

6. Thio-Peptide-Maytansinoids (Compounds 14a-14j)

Compounds of the type HS-$(CH_2)_3$CO-Peptide-NH-CH_2-S-$(CH_2)_n$-CO_2-DM were prepared as shown in FIG. 9A and as exemplified by HS-$(CH_2)_3$CO-L-Ala-L-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM.

HS-$(CH_2)_3$CO-L-Ala-L-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (14a): SPDB-L-Ala-L-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (38 mg, 0.031 mmol) was dissolved in DMSO (1 mL) to which a solution of DTT (19 mg, 0.12 mmol) in 100 mM potassium phosphate, 2mM EDTA pH 7.5 buffer (1mL) was added. The reaction was allowed to proceed at room temperature with magnetic stirring under an argon for 1 h. The crude reaction was purified on a C18, 30 micron, 30g cartridge eluting with deionized water containing 0.1% formic acid and a linear gradient of acetonitrile of 5% to 95% over 35 min. Fractions containing desired product were immediatley frozen and lypholized to give 18.2 mg, (52.5 % yield) of a white solid. HRMS (M + H)+ calcd. 1124.4809; found 1124.4798. ^{1}H NMR (400 MHz, DMSO-*d*6) δ 0.78 (s, 3H), 1.12 (d, *J* = 6.4 Hz, 3H), 1.14 – 1.21 (m, 10H), 1.22 – 1.30 (m, 3H), 1.37 – 1.50 (m, 5H), 1.51 – 1.57 (m, 1H), 1.59 (s, 3H), 1.74 (p, *J* = 7.2 Hz, 2H), 2.04 (dd, *J* = 14.4, 2.8 Hz, 1H), 2.09 – 2.18 (m, 1H), 2.18 – 2.24 (m, 2H), 2.27 (t, *J* = 7.6 Hz, 1H), 2.38 (td, *J* = 7.1, 4.7 Hz, 2H), 2.44 (t, *J* = 7.3 Hz, 2H), 2.70 (s, 3H), 2.79 (d, *J* = 9.6 Hz, 1H), 3.09 (s, 3H), 3.21 (d, *J* = 12.6 Hz, 1H), 3.25 (s, 3H), 3.43 (d, *J* = 12.4 Hz, 1H), 3.49 (d, *J* = 9.0 Hz, 1H), 3.93 (s, 3H), 4.08 (ddd, *J* = 21.6, 11.4, 4.1 Hz, 2H), 4.13 – 4.28 (m, 4H), 4.52 (dd, *J* = 12.1, 2.8 Hz, 1H), 5.34 (q, *J* = 6.7 Hz, 1H), 5.56 (dd, *J* = 14.7, 9.0 Hz, 1H), 5.91 (d, *J* = 1.4 Hz, 1H), 6.48 – 6.66 (m, 3H), 6.88 (s, 1H), 7.18 (d, *J* = 1.8 Hz, 1H), 7.86 (d, *J* = 7.5 Hz, 1H), 7.96 (d, *J* = 7.3 Hz, 1H), 8.05 (d, *J* = 7.1 Hz, 1H), 8.33 (t, *J* = 6.3 Hz, 1H).

HS-$(CH_2)_3$CO-D-Ala-L-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (14b): HRMS $(M+Na)^+$ calcd. 1146.4629, found 1146.4591. ^{1}H NMR (400 MHz, DMSO-d6) δ 0.71 (s, 3H), 1.03 – 1.25 (m, 19H), 1.30 – 1.45 (m, 6H), 1.52 (s, 4H), 1.65 (p, *J* = 7.3 Hz, 2H), 1.91 – 2.02 (m,

1H), 2.02 – 2.13 (m, 1H), 2.12 – 2.19 (m, 4H), 2.29 – 2.39 (m, 4H), 2.63 (s, 3H), 2.73 (d, *J* = 9.6 Hz, 1H), 3.02 (s, 3H), 3.14 (d, *J* = 12.5 Hz, 1H), 3.33 – 3.47 (m, 2H), 3.86 (s, 3H), 4.01 (td, *J* = 10.4, 9.7, 4.3 Hz, 2H), 4.04 – 4.16 (m, 5H), 4.45 (dd, *J* = 12.0, 2.9 Hz, 1H), 5.27 (q, *J* = 6.7 Hz, 1H), 5.43 – 5.56 (m, 1H), 5.85 (s, 1H), 6.38 – 6.61 (m, 4H), 6.81 (s, 1H), 7.11 (d, *J* = 1.8 Hz, 1H), 7.82 (d, *J* = 7.7 Hz, 1H), 7.97 (t, *J* = 6.3 Hz, 1H), 8.10 (d, *J* = 6.0 Hz, 1H), 8.25 (d, *J* = 6.9 Hz, 1H).

HS-$(CH_2)_3$CO-L-Ala-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (14c) : HRMS $(M+Na)^+$ calcd. 1146.4629, found 1146.4553. ^{1}H NMR (400 MHz, DMSO-d6) δ 0.71 (s, 3H), 0.99 – 1.26 (m, 21H), 1.31 – 1.45 (m, 5H), 1.52 (s, 3H), 1.67 (p, *J* = 7.2 Hz, 2H), 1.89 – 2.02 (m, 1H), 2.02 – 2.24 (m, 4H), 2.25 – 2.46 (m, 3H), 2.63 (s, 3H), 2.73 (d, *J* = 9.7 Hz, 1H), 3.02 (s, 3H), 3.18 (s, 3H), 3.32 – 3.51 (m, 2H), 3.86 (s, 3H), 3.96 – 4.18 (m, 7H), 4.45 (dd, *J* = 12.0, 2.9 Hz, 1H), 5.27 (q, J = 6.8 Hz, 1H), 5.44 – 5.63 (m, 1H), 5.85 (s, 1H), 6.37 – 6.59 (m, 4H), 6.81 (s, 1H), 7.11 (d, *J* = 1.8 Hz, 1H), 7.89 (d, *J* = 7.7 Hz, 1H), 8.03 (d, *J* = 6.5 Hz, 1H), 8.08 (d, *J* = 7.3 Hz, 1H), 8.27 (t, *J* = 6.3 Hz, 1H).

HS-$(CH_2)_3$CO-L-Ala-L-Ala-D-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (14d): HRMS $(M+Na)^+$ calcd. 1146.4629, found 1146.4519. ^{1}H NMR (400 MHz, DMSO-d6) δ 0.71 (s, 3H), 0.95 – 1.24 (m, 20H), 1.27 – 1.45 (m, 5H), 1.52 (s, 3H), 1.67 (p, *J* = 7.3 Hz, 2H), 1.93 – 2.01 (m, 1H), 2.02 – 2.22 (m, 4H), 2.22 – 2.41 (m, 5H), 2.63 (s, 3H), 2.73 (d, *J* = 9.6 Hz, 1H), 3.02 (s, 3H), 3.18 (s, 4H), 3.39 (dd, *J* = 21.4, 10.7 Hz, 2H), 3.86 (s, 3H), 3.94 – 4.24 (m, 6H), 4.45 (dd, *J* = 12.0, 2.8 Hz, 1H), 5.27 (q, *J* = 6.7 Hz, 1H), 5.44 – 5.57 (m, 1H), 5.85 (s, 1H), 6.37 – 6.65 (m, 3H), 6.81 (s, 1H), 7.11 (d, *J* = 1.8 Hz, 1H), 7.89 (d, *J* = 7.6 Hz, 1H), 7.93 – 8.05 (m, 2H), 8.26 (t, *J* = 6.4 Hz, 1H).

HS-$(CH_2)_3$CO-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (14g): HRMS $(M+H)^+$ calcd. 1053.4438, found 1053.4426. ^{1}H NMR (400 MHz, DMSO-d6) δ 0.71 (s, 3H), 1.01 – 1.15 (m, 13H), 1.15 – 1.27 (m, 3H), 1.31 – 1.44 (m, 5H), 1.53 (s, 3H), 1.67 (p, *J* = 7.1 Hz, 2H), 1.93 – 2.03 (m, 1H), 2.03 – 2.23 (m, 4H), 2.22 – 2.41 (m, 5H), 2.63 (s, 3H), 2.73 (d, *J* = 9.7 Hz, 1H), 3.02 (s, 3H), 3.14 (d, *J* = 12.5 Hz, 1H), 3.18 (s, 3H), 3.32 – 3.46 (m, 2H), 3.86 (s, 3H), 3.92 – 4.20 (m, 6H), 4.45 (dd, *J* = 11.9, 2.8 Hz, 1H), 5.27 (q, *J* = 6.7 Hz, 1H), 5.42 – 5.58 (m, 1H), 5.85 (s, 1H), 6.42 – 6.60 (m, 3H), 6.81 (s, 1H), 7.12 (d, *J* = 1.8 Hz, 1H), 8.05 (d, *J* = 6.5 Hz, 1H), 8.10 (d, *J* = 7.8 Hz, 1H), 8.30 (t, *J* = 6.3 Hz, 1H).

HS-$(CH_2)_3$CO-L-Ala-D-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (14f): HRMS $(M+H)^+$ calcd. 1053.4366, found 1053.4438. ^{1}H NMR (400 MHz, DMSO-d6) δ 0.71 (s, 3H), 1.02 – 1.14 (m, 13H), 1.19 (t, *J* = 9.7 Hz, 3H), 1.31 – 1.43 (m, 6H), 1.53 (s, 3H), 1.67 (p, *J* = 7.3 Hz, 2H), 1.91 – 2.02 (m, 1H), 2.02 – 2.22 (m, 4H), 2.34 – 2.39 (m, 4H), 2.63 (s, 3H), 2.73 (d, *J*

= 9.5 Hz, 1H), 3.02 (s, 3H), 3.19 (d, *J* = 4.2 Hz, 4H), 3.30 – 3.47 (m, 2H), 3.86 (s, 3H), 3.94 – 4.20 (m, 6H), 4.45 (d, *J* = 11.8, 2.8 Hz, 1H), 5.27 (q, *J* = 6.7 Hz, 1H), 5.44 – 5.56 (m, 1H), 5.85 (s, 1H), 6.40 – 6.61 (m, 3H), 6.81 (s, 1H), 7.12 (s, 1H), 8.03 (d, *J* = 6.5 Hz, 1H), 8.08 (d, *J* = 7.8 Hz, 1H), 8.29 (t, *J* = 6.2 Hz, 1H).

HS-$(CH_2)_3$CO-D-Ala-D-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (14h): HRMS $(M+H)^+$ calcd. 1053.4366, found 1053.4438. ^{1}H NMR (400 MHz, DMSFO-d6) δ 0.71 (s, 3H), 1.02 – 1.15 (m, 13H), 1.14 – 1.24 (m, 3H), 1.30 – 1.45 (m, 5H), 1.53 (s, 3H), 1.67 (p, J = 7.1 Hz, 2H), 1.90 – 2.01 (m, 1H), 2.01 – 2.24 (m, 4H), 2.27 – 2.33 (m, 1H), 2.33 – 2.42 (m, 4H), 2.63 (s, 3H), 2.73 (d, *J* = 9.7 Hz, 1H), 3.02 (s, 3H), 3.10 – 3.21 (m, 4H), 3.33 – 3.46 (m, 2H), 3.86 (s, 3H), 3.95 – 4.18 (m, 6H), 4.45 (dd, *J* = 11.9, 2.8 Hz, 1H), 5.27 (q, *J* = 6.7 Hz, 1H), 5.44 – 5.55 (m, 1H), 5.85 (s, 1H), 6.42 – 6.59 (m, 3H), 6.81 (s, 1H), 7.12 (d, *J* = 1.8 Hz, 1H), 8.05 (d, *J* = 6.5 Hz, 1H), 8.10 (d, *J* = 7.8 Hz, 1H), 8.30 (t, *J* = 6.3 Hz, 1H).

HS-$(CH_2)_3$CO-L-Ala-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_3$-CO-DM (14j): HRMS $(M+H)^+$ calcd. 1096.4496, found 1096.4464. 1H NMR (400 MHz, DMSO-*d*6) δ 0.78 (s, 3H), 1.02 – 1.31 (m, 19H), 1.35 – 1.55 (m, 2H), 1.60 (s, 3H), 1.74 (p, *J* = 7.4 Hz, 3H), 1.78 – 1.93 (m, 1H), 2.14 – 2.33 (m, 4H), 2.41 – 2.49 (m, 2H), 2.71 (s, 3H), 2.80 (d, *J* = 9.6 Hz, 1H), 3.12 (s, 3H), 3.22 (d, *J* = 12.7 Hz, 1H), 3.26 (s, 3H), 3.47 (dd, *J* = 21.3, 10.6 Hz, 2H), 3.93 (s, 4H), 4.03 – 4.13 (m, 3H), 4.13 – 4.25 (m, 3H), 4.52 (dd, *J* = 12.0, 2.8 Hz, 1H), 5.35 (q, *J* = 6.8 Hz, 1H), 5.50 – 5.64 (m, 1H), 5.92 (s, 1H), 6.47 – 6.69 (m, 4H), 6.88 (s, 1H), 7.18 (d, *J* = 1.7 Hz, 1H), 7.94 (d, *J* = 7.3 Hz, 1H), 8.09 (d, *J* = 6.4 Hz, 1H), 8.15 (d, *J* = 7.3 Hz, 1H), 8.32 (t, *J* = 6.3 Hz, 1H).

HS-$(CH_2)_3$CO-$(CH_2)_3$-CO-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_2$-CO-DM (14i): HRMS $(M+H)^+$ calcd. 1011.3969, found 1011.3961. ^{1}H NMR (400 MHz, DMSO-*d*6) δ 0.77 (s, 3H), 1.12 (d, *J* = 6.4 Hz, 3H), 1.17 (dd, *J* = 7.0, 5.1 Hz, 9H), 1.25 (d, *J* = 13.0 Hz, 1H), 1.40 – 1.51 (m, 2H), 1.59 (s, 3H), 1.74 (q, *J* = 7.2 Hz, 2H), 2.00 – 2.08 (m, 1H), 2.23 (dt, *J* = 16.8, 7.6 Hz, 3H), 2.43 (q, *J* = 7.4 Hz, 2H), 2.62 – 2.69 (m, 1H), 2.72 (s, 3H), 2.76 – 2.88 (m, 2H), 3.10 (s, 3H), 3.20 (d, *J* = 12.6 Hz, 1H), 3.25 (s, 3H), 3.31 (s, 3H), 3.39 – 3.54 (m, 2H), 3.93 (s, 3H), 4.01 – 4.26 (m, 5H), 4.53 (dd, *J* = 12.0, 2.8 Hz, 1H), 5.32 (q, *J* = 6.8 Hz, 1H), 5.49 – 5.63 (m, 1H), 5.92 (d, *J* = 1.4 Hz, 1H), 6.48 – 6.62 (m, 3H), 6.88 (s, 1H), 7.18 (d, *J* = 1.8 Hz, 1H), 8.10 (d, *J* = 6.5 Hz, 1H), 8.16 (d, *J* = 7.7 Hz, 1H), 8.41 (t, *J* = 6.3 Hz, 1H).

7. HOOC-$(CH_2)_3$-CO-Peptide-NH-CH_2-S-$(CH_2)_n$-CO_2-DM (Compounds 19a-19j)

Compounds of the type HOOC-$(CH_2)_3$-CO-Peptide-NH-CH_2-S-$(CH_2)_n$-CO_2-DM were prepared as shown in FIG. 9B and as exemplified by HOOC-$(CH_2)_3$-CO-L-Ala-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM.

HOOC-$(CH_2)_3$-CO-L-Ala-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM(19a): L-Ala-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (17.25 mg, 0.017 mmol) was treated with glutaric anhydride (38.5 mg, 0.337 mmol) and reacted at room temperature with magnetic stirring under argon overnight. The crude reaction was purified by HPLC using a XDB-C18, 21.2 x 5 mm, 5 micron column eluting with deionized water containing 0.1% formic acid and a linear gradient of acetonitrile from 5% to 95% over 30 min at 20 ml/min. Fractions containing pure desired product were immediately combined, frozen and lypholized to give 3 mg, (15 % yield) of white solid. HRMS $(M+H)^+$ calcd. 1136.4987, found 1136.4954. ^{1}H NMR (400 MHz, DMSO-d6) δ 0.71 (s, 3H), 0.92 – 1.27 (m, 20H), 1.26 – 1.48 (m, 5H), 1.52 (s, 3H), 1.63 (q, *J* = 7.1 Hz, 2H), 1.83 – 2.20 (m, 7H), 2.23 – 2.41 (m, 5H), 2.63 (s, 4H), 2.73 (d, *J* = 9.5 Hz, 1H), 3.02 (s, 3H), 3.36 – 3.50 (m, 2H), 3.86 (s, 3H), 3.91 – 4.24 (m, 7H), 4.45 (d, *J* = 11.8 Hz, 1H), 5.27 (q, *J* = 6.7 Hz, 1H), 5.41 – 5.57 (m, 1H), 5.86 (s, 1H), 6.32 – 6.66 (m, 3H), 6.81 (s, 1H), 7.12 (s, 1H), 8.06 (t, *J* = 9.1 Hz, 2H), 8.35 (d, *J* = 11.6 Hz, 1H), 8.62 (s, 1H).

HOOC-$(CH_2)_3$-CO-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (19g): HRMS $(M+H)^+$ calcd. 1136.4987, found 1136.4962.^{1}H NMR (400 MHz, DMSO-d6) δ 0.71 (s, 3H), 0.97 – 1.14 (m, 13H), 1.14 – 1.26 (m, 3H), 1.28 – 1.45 (m, 5H), 1.52 (s, 3H), 1.62 (p, *J* = 7.5 Hz, 2H), 1.93 – 2.00 (m, 1H), 2.08 (dt, *J* = 13.1, 7.4 Hz, 6H), 2.25 – 2.41 (m, 3H), 2.63 (s, 3H), 2.73 (d, *J* = 9.5 Hz, 1H), 3.02 (s, 3H), 3.18 (s, 3H), 3.31 – 3.48 (m, 2H), 3.86 (s, 3H), 3.93 – 4.19 (m, 6H), 4.45 (dd, *J* = 12.0, 2.8 Hz, 1H), 5.27 (q, *J* = 6.8 Hz, 1H), 5.43 – 5.58 (m, 1H), 5.85 (s, 1H), 6.40 – 6.61 (m, 3H), 6.81 (s, 1H), 7.11 (d, *J* = 1.8 Hz, 1H), 8.03 (d, *J* = 6.5 Hz, 1H), 8.13 (d, *J* = 7.8 Hz, 1H), 8.34 (t, *J* = 6.3 Hz, 1H), 11.94 (s, 1H).

HOOC-$(CH_2)_3$-CO-L-Ala-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_3$-CO-DM (19i): HRMS $(M+H)^+$ calcd. 1108.4674, found 1108.4634. ^{1}H NMR (400 MHz, DMSO-d6) δ 0.78 (s, 3H), 1.04 – 1.32 (m, 16H), 1.45 (d, *J* = 12.6 Hz, 2H), 1.60 (s, 3H), 1.69 (p, *J* = 7.2 Hz, 3H), 1.77 – 1.95 (m, 1H), 1.99 – 2.07 (m, 1H), 2.11 – 2.20 (m, 4H), 2.20 – 2.39 (m, 1H), 2.55 (s, 1H), 2.71 (s, 3H), 2.80 (d, *J* = 9.5 Hz, 1H), 3.12 (s, 3H), 3.40 (d, *J* = 21.0 Hz, 8H), 3.49 (d, *J* = 9.1 Hz, 1H), 3.93 (s, 3H), 4.02 – 4.27 (m, 6H), 4.48 – 4.61 (m, 1H), 5.34 (q, J = 6.6 Hz,

1H), 5.48 – 5.65 (m, 1H), 5.92 (s, 1H), 6.50 – 6.71 (m, 3H), 6.88 (s, 1H), 7.18 (s, 1H), 7.99 (d, *J* = 7.6 Hz, 1H), 8.08 (d, *J* = 6.5 Hz, 1H), 8.22 (d, *J* = 7.4 Hz, 1H), 8.30 (s, 1H), 8.42 (s, 1H).

8. NHS-OOC-$(CH_2)_3$-CO-Peptide-NH-CH_2-S-$(CH_2)_n$-CO_2-DM (Compound 20a-20j)

Compounds of the type NHS-OOC-$(CH_2)_3$-CO-Peptide-NH-CH_2-S-$(CH_2)_n$-CO_2-DM were prepared as shown in FIG. 9B and as exemplified by NHS-OOC-$(CH_2)_3$-CO-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM.

NHS-OOC-$(CH_2)_3$-CO-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (20g): HOOC-$(CH_2)_3$-CO-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (8 mg 7.5 µmol) was dissolved in DMSO (1 mL), treated with NHS (0.9 mg, 7.51 µmol) and EDC (1.4 mg, 7.51 µmol). The reaction was allowed to proceed at room temperature with magnetic stirring under an argon atmosphere for 2 hours. The crude material was purified via HPLC using a XDB-C18, 21.2 x 5mm, 5 µm column eluting with deionized water containing 0.1% formic acid and a linear gradient of acetonitrile from 5% to 95% over 30 min at 20 ml/min. Fractions containing desired product were combined and immediatley frozen then lypholized to give 6.5 mg (74 % yield) of white solid. ^{1}H NMR (400 MHz, DMSO-d6) δ 0.71 (s, 3H), 1.00 – 1.14 (m, 13H), 1.14 – 1.25 (m, 3H), 1.29 – 1.46 (m, 5H), 1.52 (s, 3H), 1.75 (p, *J* = 7.5 Hz, 2H), 1.92 – 2.12 (m, 2H), 2.16 (t, *J* = 7.3 Hz, 2H), 2.22 – 2.39 (m, 3H), 2.62 (d, *J* = 10.8 Hz, 5H), 2.73 (d, *J* = 10.5 Hz, 5H), 3.02 (s, 3H), 3.18 (s, 3H), 3.32 – 3.47 (m, 2H), 3.86 (s, 3H), 3.95 – 4.19 (m, 6H), 4.45 (dd, *J* = 12.0, 2.8 Hz, 1H), 5.27 (q, *J* = 6.8 Hz, 1H), 5.42 – 5.57 (m, 1H), 5.82 – 5.87 (m, 1H), 6.41 – 6.60 (m, 4H), 6.81 (s, 1H), 7.11 (d, *J* = 1.7 Hz, 1H), 8.05 (d, *J* = 6.5 Hz, 1H), 8.10 (d, *J* = 7.7 Hz, 1H), 8.20 (d, J = 4.8 Hz, 1H), 8.29 (t, *J* = 6.3 Hz, 1H).

NHS-OOC-$(CH_2)_3$-CO -L-Ala-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM (20g): HRMS $(M+H)^+$ calcd. 1233.5151, found 1233.5135.

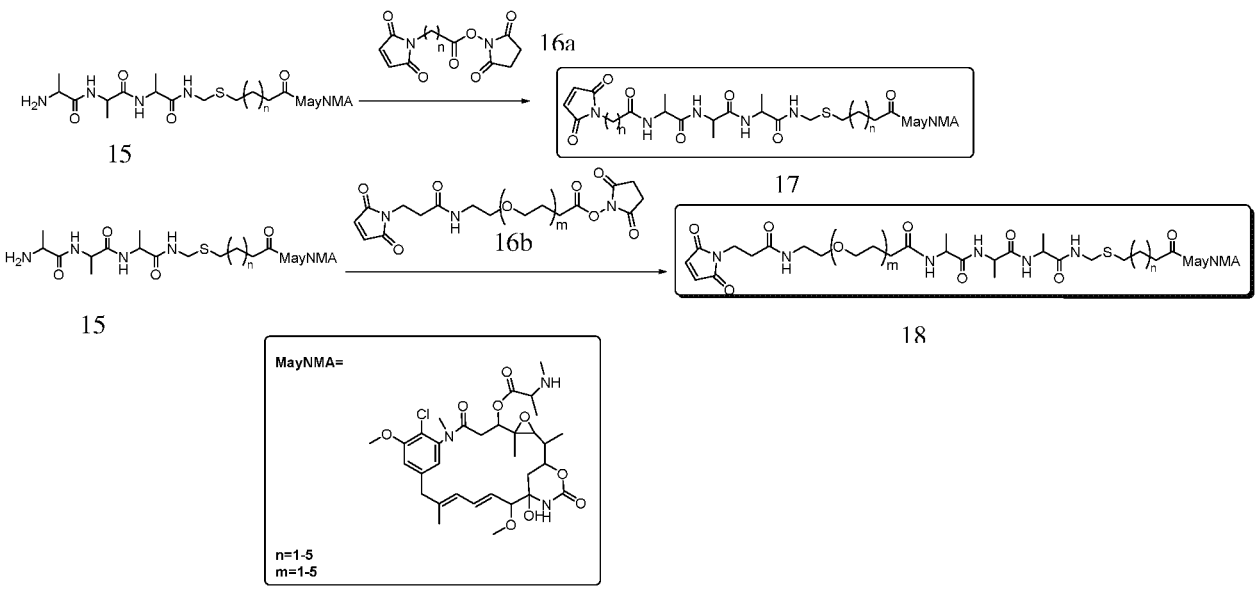
NHS-OOC-$(CH_2)_3$-CO -L-Ala-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_3$-CO-DM (20i): HRMS $(M+H)^+$ calcd. 1205.4838, found 1205.4808.

9. Mal-$(CH_2)_3$-CO-Peptide-NH-CH_2-S-$(CH_2)_n$-CO-DM (Compounds 23a-23j)

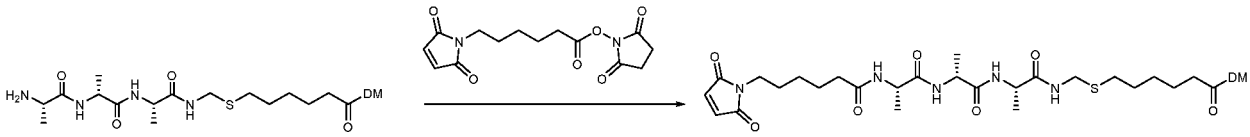
Compounds 23a-23j can be prepared as shown in FIG. 9B and as exemplified for compound 23c.

Mal-$(CH_2)_3$-CO-L-Ala-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-DM or Mal-LDL-DM (23c): H_2N-L-Ala-D-Ala-L-Ala-CH_2-S-$(CH_2)_5$-CO-DM (8 mg, 7.82 µmol), was dissolved in DMF (2 mL), treated with 3-maleimidopropanoic acid (1.32 mg, 7.82 µmol), EDC (2.25 mg, 0.012 mmol) and HOBt (1.198 mg, 7.82 µmol). The reaction was allowed to proceed at room temperature with magnetic stirring under an argron atmosphere for 2 h. The crude material was purified via semi-prep HPLC using a XDB-C18, 21.2x5mm, 5 µm eluting with deionized water containing 0.1% formic acid and a linear gradient of acetonitrile from 5% to 95% over 30 min at 20 ml/min. Fractions containing desired product were immediately combined and frozen then lypholized to give 1.8 mg (19.60 % yield) of white solid. HRMS $(M+H)^+$ calcd. 1173.4940, found 1173.4931. ^{1}H NMR (400 MHz, DMSO-d6) δ 0.71 (s, 3H), 1.02 – 1.14 (m, 15H), 1.16 – 1.25 (m, 3H), 1.30 – 1.44 (m, 5H), 1.52 (s, 3H), 1.92 – 2.03 (m, 1H), 2.03 – 2.17 (m, 1H), 2.23 – 2.39 (m, 4H), 2.63 (s, 3H), 2.73 (d, *J* = 9.6 Hz, 1H), 3.02 (s, 3H), 3.18 (s, 4H), 3.33 – 3.46 (m, 2H), 3.52 (t, *J* = 7.3 Hz, 2H), 3.86 (s, 3H), 3.95 – 4.17 (m, 7H), 4.45 (dd, *J* = 12.0, 2.9 Hz, 1H), 5.27 (q, *J* = 6.7 Hz, 1H), 5.44 – 5.56 (m, 1H), 5.85 (s, 1H), 6.39 – 6.64 (m, 3H), 6.81 (s, 1H), 6.86 (s, 1H), 6.92 (s, 2H), 7.11 (d, *J* = 1.7 Hz, 1H), 7.89 (d, *J* = 7.4 Hz, 1H), 8.10 (d, J = 7.3 Hz, 1H), 8.17 (d, *J* = 6.7 Hz, 1H), 8.28 (t, *J* = 6.3 Hz, 1H), 8.43 (s, 1H).

10. Other compounds



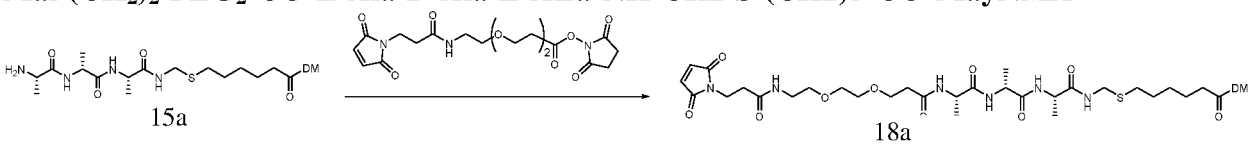
Mal2-LAla-D-Ala-L-Ala-Imm-C6-May



15a 17a

Mal-C5-L-Ala-D-Ala-L-Ala-Imm-C6-May: Reaction between L-Ala-D-Ala-L-Ala-CH_2-S-$(CH_2)_5$-CO-MayNMA (compound I-1a) (25mg, 0.024 mmol), and 2,5-dioxopyrrolidin-1-yl 6-(2,5-dioxo-2,5-dihydro-1H-pyrrol-1-yl)hexanoate (7.54 mg, 0.024 mmol) yielded Mal-C5-L-Ala-D-Ala-L-Ala-Imm-C6-May (compound I-2a) (20.8mg, 0.017 mmol, 70.0 % yield). LRMS $(M+H)^+$ calcd 1215.52, found 1216.4. ^{1}H NMR (400 MHz, DMSO-*d*6) δ 0.71 (s, 3H), 1.05 (d, *J* = 6.4 Hz, 3H), 1.07 – 1.14 (m, 14H), 1.15 – 1.25 (m, 3H), 1.39 (t, *J* = 9.2 Hz, 10H), 1.52 (s, 3H), 2.01 (t, *J* = 7.6 Hz, 3H), 2.26 (t, *J* = 1.9 Hz, 1H), 2.28 – 2.38 (m, 2H), 2.57 – 2.62 (m, 1H), 2.63 (s, 3H), 2.73 (d, *J* = 9.6 Hz, 1H), 3.02 (s, 3H), 3.14 (d, *J* = 12.5 Hz, 1H), 3.18 (s, 3H), 3.29 (t, *J* = 7.1 Hz, 2H), 3.36 (d, *J* = 12.5 Hz, 1H), 3.42 (d, *J* = 9.0 Hz, 1H), 3.86 (s, 3H), 3.96 – 4.05 (m, 1H), 4.04 – 4.15 (m, 4H), 4.41 – 4.48 (m, 1H), 5.27 (q, *J* = 6.7 Hz, 1H), 5.46 – 5.54 (m, 1H), 5.82 – 5.88 (m, 1H), 6.47 – 6.50 (m, 2H), 6.54 (t, *J* = 11.4 Hz, 2H), 6.82 (s, 1H), 6.92 (s, 2H), 7.11 (d, *J* = 1.8 Hz, 1H), 7.86 – 7.93 (m, 2H), 7.95 (s, 1H), 8.05 (d, *J* = 7.4 Hz, 1H), 8.24 (t, *J* = 6.2 Hz, 1H).

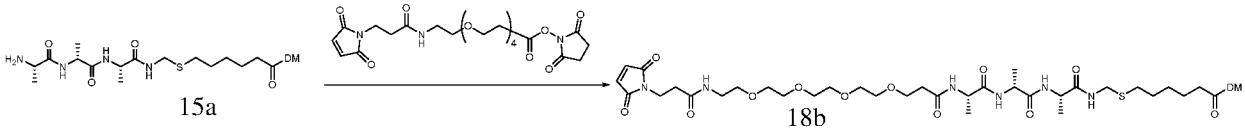
Mal-$(CH_2)_2$-PEG_2-CO-L-Ala-D-Ala-L-ALa-NH-CH2-S-(CH2)5-CO-MayNMA



15a 18a

Mal-$(CH_2)_2$-PEG_2-CO-L-Ala-D-Ala-L-ALa-NH-CH_2-S-$(CH_2)_5$-CO-MayNMA: Reaction between L-Ala-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-MayNMA (compound I-1a) (25mg, 0.024 mmol) and Mal-amido-PEG_2-NHS (10.40 mg, 0.024 mmol) yielded Mal-$(CH2)_2$-PEG_2-CO2-L-Ala-D-Ala-L-ALa-NH-CH_2-S-$(CH_2)_5$-CO-MayNMA (compound I-3a) (14.1mg, 10.58 µmol, 43.3 % yield). LRMS $(M+H)^+$ calcd 1332.58, found 1332.95. ^{1}H NMR (400 MHz, DMSO-*d*6) δ 0.71 (s, 4H), 1.05 (d, *J* = 6.3 Hz, 4H), 1.07 – 1.14 (m, 15H), 1.18 (d, *J* = 9.0 Hz, 2H), 1.37 (d, *J* = 11.8 Hz, 6H), 1.52 (s, 3H), 2.23 – 2.38 (m, 5H), 2.63 (s, 4H), 2.72 (d, *J* = 9.7 Hz, 1H), 3.02 (s, 3H), 3.07 (q, *J* = 5.7 Hz, 2H), 3.18 (s, 3H), 3.39 (s, 4H), 3.41 (d, *J* = 9.9 Hz, 2H), 3.47 – 3.56 (m, 4H), 3.86 (s, 4H), 3.95 – 4.08 (m, 2H), 4.08 – 4.19 (m, 3H), 4.41 – 4.51 (m, 1H), 5.23 – 5.31 (m, 1H), 5.44 – 5.54 (m, 1H), 5.85 (s, 1H), 6.46 – 6.50 (m, 2H), 6.54 (t, *J* = 11.3 Hz, 2H), 6.83 (s, 1H), 6.93 (s, 2H), 7.12 (s, 1H), 7.88 – 8.00 (m, 2H), 8.01 – 8.08 (m, 2H), 8.27 (t, *J* = 6.2 Hz, 1H).

Mal-$(CH_2)_2$-PEG_4-CO-L-Ala-D-Ala-L-ALa-NH-CH_2-S-$(CH_2)_5$-CO-MayNMA



15a 18b

Mal-$(CH_2)_2$-PEG_4-CO_2-L-Ala-D-Ala-L-ALa-NH-CH_2-S-$(CH_2)_5$-CO-MayNMA:

Reaction between L-Ala-D-Ala-L-Ala-NH-CH_2-S-$(CH_2)_5$-CO-MayNMA (compound I-1a) (25mg, 0.024 mmol) and Mal-amido-PEG4-NHS (12.55 mg, 0.024 mmol) yielded Mal-$(CH_2)_2$-PEG_4-CO2-L-Ala-D-Ala-L-ALa-NH-CH_2-S-$(CH_2)_5$-CO-MayNMA Mal-PEG4-CO2-C6-LDL-DM (compound I-3b) (22.3mg, 0.016 mmol, 64.2 % yield).

LRMS $(M+H)^+$ calcd 1420.63, found 1420.06

^{1}H NMR (400 MHz, DMSO-*d*6) δ 0.71 (s, 4H), 1.05 (d, *J* = 6.4 Hz, 3H), 1.07 – 1.16 (m, 14H), 1.19 (t, *J* = 8.1 Hz, 2H), 1.31 – 1.50 (m, 2H), 1.52 (s, 4H), 1.98 (s, 1H), 2.02 – 2.17 (m, 2H), 2.20 – 2.40 (m, 7H), 2.63 (s, 4H), 2.73 (d, *J* = 9.6 Hz, 1H), 3.02 (s, 3H), 3.05 – 3.12 (m, 2H), 3.18 (s, 3H), 3.28 – 3.36 (m, 1H), 3.37 – 3.45 (m, 15H), 3.47 – 3.57 (m, 4H), 3.86 (s, 4H), 3.94 – 4.08 (m, 2H), 4.12 (ddt, *J* = 14.5, 7.3, 3.6 Hz, 4H), 4.41 – 4.49 (m, 1H), 5.27 (q, *J* = 6.7 Hz, 1H), 5.45 – 5.55 (m, 1H), 5.86 (s, 1H), 6.42 – 6.60 (m, 4H), 6.83 (s, 1H), 6.94 (s, 1H), 7.12 (d, *J* = 1.8 Hz, 1H), 7.89 – 8.00 (m, 2H), 8.00 – 8.09 (m, 2H), 8.26 (t, *J* = 6.2 Hz, 1H).

Example 11
Preparation of Lysine-Linked DM Conjugates of anti-ADAM9 Antibodies

a. Preparation of hMAB-A(2I.2)-sSPDB-DM4

[00326] hMAB-A(2I.2) is a humanized/optimized antibody with a light chain sequence of SEQ ID NO:68 and a heavy chain sequence of SEQ ID NO:52 (X in SEQ ID NO:52 is K).

[00327] To prepare the hMAB-A(2I.2)-sSPDB-DM4 conjugate, sulfo-SPDB (sSPDB) and DM4 additions were performed in a step-wise manner. First, a solution containing hMAB-A(2I.2) antibody buffered at pH 8.1 with 50 mM 4-(2-hydroxyethyl)-1-piperazinepropanesulfonic acid (EPPS), 50 mM sodium chloride was mixed with DMA and 11.5 equivalents of sSPDB from a DMA stock solution such that the final solvent composition was 10% (v/v) DMA and 90% (v/v) aqueous buffer. After allowing the first reaction step to proceed for 4 hr. at 25°C, 17.3 equivalents of DM4 from a DMA stock solution, DMA, and 500 mM EPPS/500 mM sodium chloride pH 8.1 buffer were added to the reaction mixture such that the final solvent composition of 10% (v/v) DMA and

90% (v/v) aqueous buffer from the first reaction step was maintained. The second reaction step was allowed to proceed overnight at 25°C.

[00328] The conjugate was purified into 10 mM succinate, 250 mM glycine, 0.5% sucrose, 0.01% Tween-20, pH 5.5 over Sephadex G-25 desalting columns, dialzyed against this buffer using a membrane with a 10 kDa molecular weight cutoff, and filtered through a 0.22 μm syringe filter.

[00329] The conjugate had an average of 3.5 mol DM4/mol antibody by UV-vis, 99.2% monomer by SEC, and ≤ 1.7% unconjugated DM4 by mixed-mode HPLC. LC-MS of the deglycosylated conjugate is not shown.

b. Preparation of hMAB-A(2I.2)-S442C-Mal-LDL-DM

[00330] hMAB-A(2I.2)-S442C is a humanized/optimized antibody with a light chain sequence of SEQ ID NO:68 and a heavy chain sequence of SEQ ID NO:142 (wherein X is K).

[00331] hMAB-A(2I.2)-S442C antibody bearing two unpaired cysteine residues (at the C442 position of the heavy chain CH3 region) in the reduced state was prepared using standard procedures and purified into phosphate buffered saline (PBS) pH 7.4, 2 mM EDTA. The reduced and re-oxidized antibody solution was used immediately for conjugation to Mal-LDL-DM (compound 17a).

[00332] The re-oxidized hMAB-A(2I.2)-S442C antibody was spiked with PBS pH 6.0, 2 mM EDTA and the conjugation was carried out in 90% aqueous solution with 10% N-N-dimethylacetamide (DMA, SAFC) and 5 equivalents of Mal-LDL-DM (compound 17a). The reaction was incubated overnight at 25 °C.

[00333] Post-reaction, the conjugate was purified into 10 mM Acetate, 9% sucrose, 0.01% Tween-20, pH 5.0 formulation buffer using NAP desalting columns (GE Healthcare) and filtered through a syringe filter with a 0.22 μm PVDF membrane.

[00334] The purified conjugate was found to have 2.1 mol LDL-DM/mol antibody by UV-Vis, 95% monomer by SEC, and below 1% free drug by SEC/reverse-phase HPLC dual column analysis.

c. Preparation of hMAB-A(2I.2)-sGMBS-LDL-DM, 3.1 DAR

[00335] Prior to conjugation, sGMBS-LDL-DM was prepared by mixing a stock solution of sGMBS (FIG. 9C) in N-N-dimethylacetamide (DMA, SAFC) with a stock solution of LDL-DM (compound 14c in FIG. 9A) in DMA in presence of succinate buffer pH 5.0 to obtain a 60:40 organic:aqueous solution and final concentrations of 3 mM sulfo-GMBS and 3.9 mM LDL-DM. The reaction was incubated for 2h at 25 °C. The crude sGMBS-LDL-DM mixture was added to a solution containing hMAB-A(2I.2) antibody in phosphate buffered saline (PBS) pH 7.4 spiked with 5x solution of 300 mM 4-(2-hydroxyethyl)-1-piperazinepropanesulfonic acid (EPPS) pH 8.5 and 10% DMA (v/v) to a final ratio of 7.8 mol sulfo-GMBS-LDL-DM to 1 mol of hMAB-A (2I.2)antibody. The reaction was incubated overnight at 25 °C.

[00336] The reaction was purified into 10 mM Histidine, 250 mM Glycine, 1 % Sucrose, 0.01% Tween20, pH 5.5 formulation buffer using NAP desalting columns (GE Healthcare) and filtered through a syringe filter with a 0.22 μm PVDF membrane.

[00337] The purified conjugate was found to have 3.1 mol LDL-DM/mol antibody by UV-Vis, 97% monomer by SEC, and below 4 % free drug by SEC/reverse-phase HPLC dual column analysis.

d. Preparation of hMAB-A(2I.2)-sGMBS-LDL-DM, 2.0 DAR

[00338] Prior to conjugation, sGMBS-LDL-DM was prepared by mixing a stock solution of sGMBS in N-N-dimethylacetamide (DMA, SAFC) with a stock solution of LDL-DM (compound 14c in FIG. 9A) in DMA in presence of succinate buffer pH 5.0 to obtain a 60/40 organic/ aqueous solution and final concentrations of 3 mM sulfo-GMBS and 3.9 mM LDL-DM. The reaction was incubated for 2h at 25 °C. The crude sGMBS-LDL-DM mixture was added to a solution containing hMAB-A(2I.2)antibody in phosphate buffered saline (PBS) pH 7.4 spiked with 5x solution of 300 mM 4-(2-hydroxyethyl)-1-piperazinepropanesulfonic acid (EPPS) pH 8.5 and 10% DMA (v/v) to a final ratio of 3 mol sGMBS-LDL-DM to 1 mol of hMAB-A (2I.2) antibody. The reaction was incubated overnight at 25 °C.

[00339] The reaction was purified into 10 mM Acetate, 9 % Sucrose, 0.01% Tween20, pH 5.0 formulation buffer using NAP desalting columns (GE Healthcare) and filtered through a syringe filter with a 0.22 µm PVDF membrane.

[00340] The purified conjugate was found to have 2.0 mol LDL-DM/mol antibody by UV-Vis, 99% monomer by SEC, and below 1 % free drug by SEC/reverse-phase HPLC dual column analysis.

e. Preparation of hMAB-A(2I.2)(YTE/C/-K)-Mal-LDL-DM

[00341] hMAB-A(2I.2)(YTE/C/-K) is a humanized antibody with a light chain sequence of SEQ ID NO:68 and a heavy chain sequence of SEQ ID NO:156.

[00342] hMAB-A(2I.2)(YTE/C/-K) antibody bearing two unpaired cysteine residues (at the C442 position of the heavy chain CH3 region) in the reduced state was prepared using standard procedures and purified into phosphate buffered saline (PBS) pH 7.4, 2 mM EDTA. The reduced and re-oxidized antibody solution was used immediately for conjugation to Mal-LDL-DM.

[00343] The re-oxidized hMAB-A(2I.2)(YTE/C/-K) antibody was spiked with PBS pH 6.0, 2 mM EDTA and the conjugation was carried out in 90% aqueous solution with 10% N-N-dimethylacetamide (DMA, SAFC) and 5 equivalents of Mal-LDL-DM (compound 17a). The reaction was incubated over night at 25 °C.

[00344] Post-reaction, the conjugate was purified into 10 mM Acetate, 9% sucrose, 0.01% Tween-20, pH 5.0 formulation buffer using NAP desalting columns (GE Healthcare) and filtered through a syringe filter with a 0.22 µm PVDF membrane.

[00345] The purified conjugate was found to have 2.0 mol LDL-DM/mol antibody by UV-Vis, 99% monomer by SEC, and below 5% free drug by SEC/reverse-phase HPLC dual column analysis.

f. Preparation of hMAB-A(2I.2)(YTE/-K)-sGMBS-LDL-DM

[00346] hMAB-A(2I.2)(YTE/-K) antibody is a humanized antibody with a light chain sequence of SEQ ID NO:68 and a heavy chain sequence of SEQ ID NO:155.

[00347] Prior to conjugation, sGMBS-LDL-DM was prepared by mixing a stock solution of sulfo-GMBS in N-N-dimethylacetamide (DMA, SAFC) with a stock solution of LDL-DM in DMA in presence of succinate buffer pH 5.0 to obtain a 60/40 organic/ aqueous solution and final concentrations of 3 mM sulfo-GMBS and 3.9 mM LDL-DM (compound 14c). The reaction was incubated for 2h at 25 °C. The crude sGMBS-LDL-DM mixture was added to a solution containing hMAB-A(2I.2)(YTE/-K) antibody in phosphate buffered saline (PBS) pH 7.4 spiked with 5x solution of 300 mM 4-(2-Hydroxyethyl)-1-piperazinepropanesulfonic acid (EPPS) pH 8.5 and 10% DMA (v/v) to a final ratio of 5 mol sGMBS-LDL-DM to 1 mol of hMAB-A(2I.2)(YTE/-K)antibody. The reaction was incubated overnight at 25 °C.

[00348] The reaction was purified into 10 mM Acetate, 9 % Sucrose, 0.01% Tween20, pH 5.0 formulation buffer using NAP desalting columns (GE Healthcare) and filtered through a syringe filter with a 0.22 µm PVDF membrane.

[00349] The purified conjugate was found to have 3.6 mol LDL-DM/mol antibody by UV-Vis, 99% monomer by SEC, and below 4 % free drug by SEC/reverse-phase HPLC dual column analysis.

Example 12
Binding affinity of anti-ADAM9 Antibody Drug Conjugates

[00350] To evaluate the consequence of conjugation on antigen binding, the relative binding affinity of each anti-ADAM9 ADC and its respective unconjugated antibody to ADAM9 was determined by FACS analysis on NCI-H1703 cells endogenously expressing human ADAM9. Briefly, the ADAM9-expressing NCI-H1703 cells were incubated with dilution series of anti-ADAM9 antibodies or ADCs for 30 min @ 4°C in FACS buffer (PBS, 0.1% BSA, 0.01% NaN3). Samples were then washed and incubated with fluorescently-labeled secondary antibody for 30 minutes at 4°C. The normalized mean of fluorescence intensity at each concentration was plotted and the EC50 of binding was calculated using a nonlinear regression analysis (GraphPad Prism 7.0). The results from these studies are summarized in Table 14.

[00351] All of the anti-ADAM9 antibodies and ADCs bound with similar affinity to human ADAM9 with an EC_{50} of approximately 0.3 nM measured by flow cytometry, indicating that conjugation did not appreciably alter antibody binding affinity FIG. 10.

Table 14.

Antibody/ADC	EC_{50} (nM)
	NCI-H1703
hMAB-A(2I.2)	0.37
hMAB-A(2I.2)-sSPDB-DM4	0.33
hMAB-A(2I.2)(YTE/-K)-sGMBS-LDL-DM	0.31
hMAB-A(2I.2)(YTE/C/-K)-Mal-LDL-DM	0.33

Example 13
In vitro Cytotoxicity of anti-ADAM9 Antibody Drug Conjugates

[00352] The *in vitro* cytotoxicty of anti-ADAM9 ADCs using the LDL-DM linker/payload against three ADAM9-expressing lung cancer cell lines was compared to either non-targeting IgG1 ADCs or cells first blocked with unconjugated antibody. An anti-ADAM9 ADC using the DM4 payload was included for comparison. Specifically, 500 to 2000 cells/well were plated in 96-well plates 24 hours prior to treatment. Conjugates were diluted into the culture medium using 3-fold dilution series and 100µL were added per well. Control wells containing cells but lacking conjugate, along with wells contained medium only, were included in each assay plate. Assays were performed in triplicate for each data point. Plates were incubated at 37°C in a humidified 5% CO_2 incubator for 5 days. Then the relative number of viable cells in each well was determined using the WST-8 based Cell Counting Kit-8. The surviving fraction of cells in each well was calculated by first correcting for the medium background absorbance, and then dividing each value by the average of the values in the control wells (non-treated cells). The percentage of surviving cells was plotted against conjugate concentration and the EC_{50} of activity was calculated using a nonlinear regression analysis (GraphPad Prism 7.0). These results are shown in Table 15 and FIGs. 11A and 11B. The LDL-DM conjugates were potent and show a greater specificity window as compared to the DM4 conjugate.

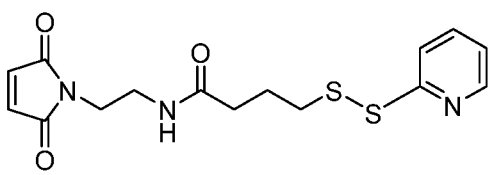
Table 15

Cell Line	Disease Type	anti-ADAM9 ADC	In Vitro Cytotoxicity by drug (IC_{50} M)	Fold-specificity (IC50 control ADC/ IC50 anti-ADAM9 ADC) Or (IC50 blocked anti-ADAM9 ADC/ IC50 anti-ADAM9 ADC)
NCI-H1703	NSCLC – Squamous Cell Carcinoma	hMAB-A(2I.2)-sSPDB-DM4	7.13E-11	134
		hMAB-A(2I.2)-sGMBS-LDL-DM	2.56E-10	>1000
		hMAB-A(2I.2)(YTE/-K)-sGMBS-LDL-DM	3.73E-10	>1000
		hMAB-A(2I.2)(YTE/C/-K)-Mal-LDL-DM	3.10E-10	>1000
NCI-H2110	NSCLC – Adenocarcinoma	hMAB-A(2I.2)-sSPDB-DM4	1.65E-09	4.4
		hMAB-A(2I.2)-sGMBS-LDL-DM	1.20E-08	>1000
Calu-3	NSCLC – Adenocarcinoma	hMAB-A(2I.2)-sSPDB-DM4	3.07E-09	13
		hMAB-A(2I.2)-sGMBS-LDL-DM	1.42E-09	>1000

Example 14

Anti-tumor Activity of anti-ADAM9 Antibody Drug Conjugates in SCID Mice Bearing Calu-3 Human Non-Small Cell Lung Adenocarcinoma Xenografts

[00353] The anti-tumor activity of 50 μg/kg of DM (maytansinoid) payload of hMAB-A(2I.2)-sSPDB-DM4 (3.6 DAR), hMAB-A(2I.2)-sGMBS-LDL-DM (3.3 DAR), hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR), hMAB-A(2I.2)-sGMBS-LDL-DM (1.9 DAR), hMAB-A(2I.2)-S442C-Mal-SPBD-DM4 (1.8 DAR), and hMAB-A(2I.2)-S442C-Mal-LDL-DM (1.8 DAR) conjugates were evaluated in female SCID mice bearing Calu-3 cells, a human lung adenocarcinoma xenograft model. Immunoconjugate hMAB-A(2I.2)-S442C-Mal-SPBD-DM4 comprises hMAB-A(2I.2)-S442C antibody coupled to DM4 via the Mal-SPDB linker:



(Mal-SPDB)..

[00354] Calu-3 cells were harvested for inoculation, with 100% viability determined by trypan blue exclusion. Mice were inoculated with 5 x 106 Calu-3 cells in 0.2ml 50% Matrigel/ 50% serum free medium by subcutaneous injection in the area on the right hind flank. Eighty-eight female CB.17 SCID Mice (6 weeks of age) were obtained. Upon receipt, the animals were observed for 7 days prior to study initiation. Animals showed no sign of disease or illness upon arrival, or prior to treatment.

[00355] Fifty-six mice were randomized into 7 groups (8 mice per group) by tumor volume. The tumor volumes ranged from 78.92 to 123.62 (98.60 ± 12.90, Mean ± SD) mm3. The mice were measured and randomized based on the tumor volume on day 7 post implantation. The mice were dosed on day 7 post implantation (12/19/17). Body weight of the mice ranged from 16.99 to 21.57 (18.89 ± 0.93, Mean ± SD) grams. Mice in each group were identified by punch method. Administration of the test agents and vehicle were carried out intravenously by using a 1.0 ml syringe fitted with a 27 gauge, ½ inch needle. Antibody drug conjugate test agents were dosed qdx1 at 50 μg/kg DM payload, which is ~2.5 mg/kg antibody for the DAR ~3.5 conjugates and ~4.3 mg/kg antibody for the DAR ~2.0 conjugates. The groups included: a control group dosed with vehicle (PBS, 150 μL), hMAB-A(2I.2)-sSPDB-DM4 (3.6 DAR) at 2.6 mg/kg antibody, hMAB-A(2I.2)-sGMBS-LDL-DM (3.3 DAR) at 2.9 mg/kg antibody, hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR) at 4.3 mg/kg antibody, hMAB-A(2I.2)-sGMBS-LDL-DM (1.9 DAR) at 5.1 mg/kg antibody, hMAB-A(2I.2)-S442C-Mal-SPBD-DM4 (1.8 DAR) at 5.3 mg/kg antibody, and hMAB-A(2I.2)-S442C-Mal-LDL-DM (1.8 DAR) at 5.3 mg/kg antibody.

[00356] Tumor size was measured two times per week in three dimensions using a caliper. The tumor volume was expressed in mm3 using the formula Volume = Length x Width x Height x ½. A mouse was considered to have a partial regression (PR) when tumor volume was reduced by 50% or greater, a complete tumor regression (CR) when no palpable tumor could be detected, and to be a tumor-free survivor (TFS) if no palpable tumor was detected at the end of the study. Tumor volume was determined by StudyLog software.

[00357] Tumor growth inhibition (%T/C) is the ratio of the median tumor volume (TV) of the treatment group (T) to the median TV of the control group (C) at a predetermined time (e.g. the time when the median TV for control tumors reach a maximum tumor volume ~1000mm^3, which is when the mice are euthanized). %T/C was calculated on day 58 post inoculation, when the median TV of the control group reached 953 mm^3. According to NCI

standards, a T/C ≤ 42% is the minimum level of anti-tumor activity and a T/C <10% is considered a high anti-tumor activity level. Tumor growth delay (T-C), is the difference between the median time (in days) for the treatment group (T) and control group tumors (C) to reach a predetermined size of 1000 mm^3 (tumor-free survivors excluded). Tumor doubling time (Td) is estimated from nonlinear exponential curve fit of daily median of control tumor growth and determined by StudyLog software. Td was 16.9 days with an R2=0.998. Log10 cell kill (LCK) is calculated with the formula LCK = (T – C) / Td x 3.32, where 3.32 is the number of cell doublings per log of cell growth. The Southern Research Institute (SRI) activity criteria for LCK are <0.7: - (inactive), 0.7-1.2: +, 1.3-1.9: ++, 2.0-2.8: +++, >2.8: ++++ (highly active).

[00358] Body weight (BW) of all the mice was measured two times per week as a rough index of drug toxicity and was determined by StudyLog software. Body weights of mice were expressed as percent change in body weight from the pre-treatment body weight as follows: % BW change = [(BWpost / BWpre) – 1] x 100, where BWpost is weight after treatment and BWpre is the starting body weight prior to treatment. Percent body weight loss (BWL) was expressed as the mean change in body weight post treatment. Animals were euthanized if the tumor volume became larger than 1000 mm^3, the tumors became necrotic, the mice lost >20% of their initial body weight, or the mice become moribund at any time during the study.

[00359] The results of the study are shown in FIG. 12. The LDL-DM ADCs were all more active than their SPDB-DM4 counterparts. The hMAB-A(2I.2)-sSPDB-DM4 (3.6 DAR) conjugate had a tumor growth inhibition (T/C) value of 30% (active), tumor growth delay (T-C) value of 34 days, and a log10 cell kill (LCK) value of 6.7 (++++), with 1 partial tumor regression out of 8 mice and no complete regressions. The hMAB-A(2I.2)-sGMBS-LDL-DM (3.3 DAR) conjugate had a T/C value of 7% (highly active), T-C value of >66 days, and a LCK value of >13.0 (++++), with 6 partial tumor regressions out of 8 mice and no complete regressions. This demonstrates that hMAB-A(2I.2)-sGMBS-LDL-DM is more active than hMAB-A(2I.2)-sSPDB-DM4 at ~3.5 DAR. The hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR) had a T/C value of 58% (inactive), T-C value of 20 days, and a LCK value of 4.0 (++++), with 0 partial tumor regressions out of 8 mice and no complete regressions. hMAB-A(2I.2)-sGMBS-LDL-DM (1.9 DAR) had a T/C value of 15% (active), T-C value of 47 days, and a LCK value of 9.2 (++++), with 6 partial tumor regressions out of 8 mice and 1

complete regression. This demonstrates that hMAB-A(2I.2)-sGMBS-LDL-DM is more active than hMAB-A(2I.2)-sSPDB-DM4 at ~2.0 DAR. hMAB-A(2I.2)-S442C-Mal-SPBD-DM4 (1.8 DAR) had a T/C value of 97% (inactive), T-C value of 3 days, and a LCK value of 0.6 (-), with 0 partial tumor regressions out of 8 mice and no complete regressions. hMAB-A(2I.2)-S442C-Mal-LDL-DM (1.8 DAR) had a T/C value of 15% (active), T-C value of 39 days, and a LCK value of 7.7 (++++), with 6 partial tumor regressions out of 8 mice and 2 complete regressions. This demonstrates that the hMAB-A(2I.2)-S442C-Mal-LDL-DM is more active than the hMAB-A(2I.2)-S442C-Mal-SPBD-DM4 at a DAR ~2.0 with site specific conjugation.. No significant body weight loss was observed with any of the ADCs at the indicated doses, and thus all six conjugates were well tolerated in mice in this study.

[00360] In addition, DAR ~2.0 ADCs were comparably active as their DAR ~3.5 counterparts. Specifically, hMAB-A(2I.2)-sGMBS-LDL-DM (3.3 DAR) was about as active as hMAB-A(2I.2)-sGMBS-LDL-DM (1.9 DAR) and hMAB-A(2I.2)-S442C-Mal-LDL-DM (1.8 DAR). Since tolerability and toxicity are determined by the payload concentration, an ADC with DAR 2.0 can be dosed at a higher antibody concentration than an ADC with DAR 3.5. The increased exposure of the DAR 2.0 ADC may improve efficacy by saturating target-mediated drug disposition (TMDD) and/or increasing tumor penetration. The results from this study suggest that the hMAB-A(2I.2)-S442C-Mal-LDL-DM (1.8 DAR) conjugate demonstrated compelling anti-tumor activity and is highly efficacious in Calu-3 non-small cell lung adenocarcinoma tumor xenograft model.

Example 15
Anti-tumor Activity of anti-ADAM9 Antibody Drug Conjugates in Nude Mice Bearing H1703 Human Non-Small Cell Lung Squamous Cell Carcinoma Xenografts

[00361] The anti-tumor activity of 50 μg/kg of DM payload of hMAB-A(2I.2)-sSPDB-DM4 (3.6 DAR), hMAB-A(2I.2)-sGMBS-LDL-DM (3.3 DAR), hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR), hMAB-A(2I.2)-sGMBS-LDL-DM (1.9 DAR), hMAB-A(2I.2)-S442C-Mal-SPBD-DM4 (1.8 DAR), and hMAB-A(2I.2)-S442C-Mal-LDL-DM (1.8 DAR) conjugates were evaluated in female Nude mice bearing H1703 cells, a human non-small cell lung squamous cell carcinoma xenograft model.

[00362] H1703 cells were harvested for inoculation, with 100% viability determined by trypan blue exclusion. Mice were inoculated with 5 x 106 H1703 cells in 0.2ml 50% Matrigel/ 50% serum free medium by subcutaneous injection in the area on the right hind flank. Sixty-six female athymic Nude-Foxn1nu Mice (6 weeks of age) were obtained. Upon receipt, the animals were observed for 3 days prior to study initiation. Animals showed no sign of disease or illness upon arrival, or prior to treatment.

[00363] Forty-two mice were randomized into 7 groups (6 mice per group) by tumor volume. The tumor volumes ranged from 61.84 to 310.17 (128.05 ± 46.61, Mean ± SD) mm^3. The mice were measured and randomized based on the tumor volume on day 26 post implantation. The mice were dosed on day 27 post implantation (12/28/17). Body weight of the mice ranged from 19.69 to 26.59 (23.54 ± 1.61, Mean ± SD) grams. Mice in each group were identified by punch method. Administration of the test agents and vehicle were carried out intravenously by using a 1.0 ml syringe fitted with a 27 gauge, ½ inch needle. Antibody drug conjugate test agents were dosed qdx1 at 50 μg/kg DM payload, which is ~2.5 mg/kg antibody for the DAR ~3.5 conjugates and ~4.3 mg/kg antibody for the DAR ~2.0 conjugates. The groups included: a control group dosed with vehicle (PBS, 150 μL), hMAB-A(2I.2)-sSPDB-DM4 (3.6 DAR) at 2.6 mg/kg antibody, hMAB-A(2I.2)-sGMBS-LDL-DM (3.3 DAR) at 2.9 mg/kg antibody, hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR) at 4.3 mg/kg antibody, hMAB-A(2I.2)-sGMBS-LDL-DM (1.9 DAR) at 5.1 mg/kg antibody, hMAB-A(2I.2)-S442C-Mal-SPBD-DM4 (1.8 DAR) at 5.3 mg/kg antibody, and hMAB-A(2I.2)-S442C-Mal-LDL-DM (1.8 DAR) at 5.3 mg/kg antibody.

[00364] Tumor size was measured two times per week in three dimensions using a caliper. The tumor volume was expressed in mm^3 using the formula Volume = Length x Width x Height x ½. A mouse was considered to have a partial regression (PR) when tumor volume was reduced by 50% or greater, a complete tumor regression (CR) when no palpable tumor could be detected, and to be a tumor-free survivor (TFS) if no palpable tumor was detected at the end of the study. Tumor volume was determined by StudyLog software.

[00365] Tumor growth inhibition (%T/C) is the ratio of the median tumor volume (TV) of the treatment group (T) to the median TV of the control group (C) at a predetermined time (e.g. the time when the median TV for control tumors reach a maximum tumor volume ~1000mm^3, which is when the mice are euthanized). %T/C was calculated on day 44 post inoculation, when the median TV of the control group reached 1206 mm^3. According to

NCI standards, a T/C $\leq$ 42% is the minimum level of anti-tumor activity and a T/C <10% is considered a high anti-tumor activity level. Tumor growth delay (T-C), is the difference between the median time (in days) for the treatment group (T) and control group tumors (C) to reach a predetermined size of 1000 mm^3 (tumor-free survivors excluded). Tumor doubling time (Td) is estimated from nonlinear exponential curve fit of daily median of control tumor growth and determined by StudyLog software. Td was 7.60 days with an R2=0.994. Log10 cell kill (LCK) is calculated with the formula LCK = (T – C) / Td x 3.32, where 3.32 is the number of cell doublings per log of cell growth. The Southern Research Institute (SRI) activity criteria for LCK are <0.7: - (inactive), 0.7-1.2: +, 1.3-1.9: ++, 2.0-2.8: +++, >2.8: ++++ (highly active).

[00366] Body weight (BW) of all the mice was measured two times per week as a rough index of drug toxicity and was determined by StudyLog software. Body weights of mice were expressed as percent change in body weight from the pre-treatment body weight as follows: % BW change = [(BWpost / BWpre) – 1] x 100, where BWpost is weight after treatment and BWpre is the starting body weight prior to treatment. Percent body weight loss (BWL) was expressed as the mean change in body weight post treatment. Animals were euthanized if the tumor volume became larger than 1000 mm3, the tumors became necrotic, the mice lost >20% of their initial body weight, or the mice become moribund at any time during the study.

[00367] The results of the study are shown in FIG. 13. The LDL-DM ADCs were all more active than their SPDB-DM4 counterparts. The hMAB-A(2I.2)-sSPDB-DM4 (3.6 DAR) conjugate had a tumor growth inhibition (T/C) value of 5% (highly active), tumor growth delay (T-C) value of 32 days, and a log10 cell kill (LCK) value of 1.3 (++), with 3 partial tumor regressions out of 6 mice, 1 complete regression, and 1 tumor-free survivor. The hMAB-A(2I.2)-sGMBS-LDL-DM (3.3 DAR) conjugate had a T/C value of 0% (highly active), T-C value of >85 days, and a LCK value of >3.4 (++++), with 6 partial tumor regressions out of 6 mice, 6 complete regressions, and 5 tumor-free survivors. This demonstrates that hMAB-A(2I.2)-sGMBS-LDL-DM is more active than hMAB-A(2I.2)-sSPDB-DM4 at ~3.5 DAR. The hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR) had a T/C value of 1% (highly active), T-C value of >66 days, and a LCK value of >2.6 (+++), with 6 partial tumor regressions out of 6 mice, 5 complete regressions, and 2 tumor-free survivors. hMAB-A(2I.2)-sGMBS-LDL-DM (1.9 DAR) had a T/C value of 1% (highly active), T-C

value of 64 days, and a LCK value of 2.5 (+++), with 6 partial tumor regressions out of 6 mice, 5 complete regressions, and 1 tumor-free survivor. This demonstrates that hMAB-A(2I.2)-sGMBS-LDL-DM is as active than hMAB-A(2I.2)-sSPDB-DM4 at ~2.0 DAR. hMAB-A(2I.2)-S442C-Mal-SPBD-DM4 (1.8 DAR) had a T/C value of 36% (active), T-C value of 13 days, and a LCK value of 0.5 (-), with 1 partial tumor regressions out of 6 mice and no complete regressions. hMAB-A(2I.2)-S442C-Mal-LDL-DM (1.8 DAR) had a T/C value of 1% (highly active), T-C value of 38 days, and a LCK value of 1.5 (++), with 6 partial tumor regressions out of 6 mice, 5 complete regressions, and 4 tumor-free survivors. This demonstrates that the hMAB-A(2I.2)-S442C-Mal-LDL-DM is more active than the hMAB-A(2I.2)-S442C-Mal-SPBD-DM4 at a DAR ~2.0 with site specific conjugation. No significant body weight loss was observed with any of the ADCs at the indicated doses, and thus all six conjugates were well tolerated in mice in this study.

[00368] In addition, DAR ~2.0 ADCs were comparably active as their DAR ~3.5 counterparts. Specifically, hMAB-A(2I.2)-sGMBS-LDL-DM (3.3 DAR) was about as active as hMAB-A(2I.2)-sGMBS-LDL-DM (1.9 DAR) and hMAB-A(2I.2)-S442C-Mal-LDL-DM (1.8 DAR). Since tolerability and toxicity are determined by the payload concentration, an ADC with DAR 2.0 can be dosed at a higher antibody concentration than an ADC with DAR 3.5. The increased exposure of the DAR 2.0 ADC may improve efficacy by saturating target-mediated drug disposition (TMDD) and/or increasing tumor penetration. The results from this study suggest that the hMAB-A(2I.2)-S442C-Mal-LDL-DM (1.8 DAR) conjugate demonstrated compelling anti-tumor activity and is highly efficacious in the H1703 non-small cell squamous lung cancer tumor xenograft model.

Example 16
Anti-tumor Activity of anti-ADAM9 Antibody Drug Conjugates in Nude Mice Bearing SNU-5 Human Gastric Carcinoma Xenografts

[00369] The anti-tumor activity of 50 μg/kg of DM payload of hMAB-A(2I.2)-sSPDB-DM4 (3.6 DAR), hMAB-A(2I.2)-sGMBS-LDL-DM (3.3 DAR), hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR), hMAB-A(2I.2)-sGMBS-LDL-DM (1.9 DAR), hMAB-A(2I.2)-S442C-Mal-SPBD-DM4 (1.8 DAR), and hMAB-A(2I.2)-S442C-Mal-LDL-DM (1.8 DAR) conjugates were evaluated in female Nude mice bearing SNU-5 cells, a human gastric carcinoma xenograft model.

[00370] SNU-5 cells were harvested for inoculation, with 100% viability determined by trypan blue exclusion. Mice were inoculated with 5 x 10^6 SNU-5 cells in 0.1ml 50% Matrigel/ 50% serum free medium by subcutaneous injection in the area on the right hind flank. Sixty-six female athymic Nude-Foxn1nu Mice (6 weeks of age) were obtained. Upon receipt, the animals were observed for 6 days prior to study initiation. Animals showed no sign of disease or illness upon arrival, or prior to treatment.

[00371] Forty-two mice were randomized into 7 groups (6 mice per group) by tumor volume. The tumor volumes ranged from 61.84 to 310.17 (128.05 ± 46.61, Mean ± SD) mm^3. The mice were measured and randomized based on the tumor volume on day 18 post implantation. The mice were dosed on day 20 post implantation (1/7/18). Body weight of the mice ranged from 19.69 to 26.59 (23.63 ± 1.57, Mean ± SD) grams. Mice in each group were identified by punch method. Administration of the test agents and vehicle were carried out intravenously by using a 1.0 ml syringe fitted with a 27 gauge, ½ inch needle. Antibody drug conjugate test agents were dosed qdx1 at 50 μg/kg DM payload, which is ~2.5 mg/kg antibody for the DAR ~3.5 conjugates and ~4.3 mg/kg antibody for the DAR ~2.0 conjugates. The groups included: a control group dosed with vehicle (PBS, 150 μL), hMAB-A(2I.2)-sSPDB-DM4 (3.6 DAR) at 2.6 mg/kg antibody, hMAB-A(2I.2)-sGMBS-LDL-DM (3.3 DAR) at 2.9 mg/kg antibody, hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR) at 4.3 mg/kg antibody, hMAB-A(2I.2)-sGMBS-LDL-DM (1.9 DAR) at 5.1 mg/kg antibody, hMAB-A(2I.2)-S442C-Mal-SPBD-DM4 (1.8 DAR) at 5.3 mg/kg antibody, and hMAB-A(2I.2)-S442C-Mal-LDL-DM (1.8 DAR) at 5.3 mg/kg antibody.

[00372] Tumor size was measured two times per week in three dimensions using a caliper. The tumor volume was expressed in mm^3 using the formula Volume = Length x Width x Height x ½. A mouse was considered to have a partial regression (PR) when tumor volume was reduced by 50% or greater, a complete tumor regression (CR) when no palpable tumor could be detected, and to be a tumor-free survivor (TFS) if no palpable tumor was detected at the end of the study. Tumor volume was determined by StudyLog software.

[00373] Tumor growth inhibition (%T/C) is the ratio of the median tumor volume (TV) of the treatment group (T) to the median TV of the control group (C) at a predetermined time (e.g. the time when the median TV for control tumors reach a maximum tumor volume ~1000mm^3, which is when the mice are euthanized). %T/C was calculated on day 70 post inoculation, when the median TV of the control group reached 1122 mm^3. According to

NCI standards, a T/C ≤ 42% is the minimum level of anti-tumor activity and a T/C <10% is considered a high anti-tumor activity level. Tumor growth delay (T-C), is the difference between the median time (in days) for the treatment group (T) and control group tumors (C) to reach a predetermined size of 1000 mm^3 (tumor-free survivors excluded). Tumor doubling time (Td) is estimated from nonlinear exponential curve fit of daily median of control tumor growth and determined by StudyLog software. Td was 19.7 days with an R2=0.986. Log10 cell kill (LCK) is calculated with the formula LCK = (T – C) / Td x 3.32, where 3.32 is the number of cell doublings per log of cell growth. The Southern Research Institute (SRI) activity criteria for LCK are <0.7: - (inactive), 0.7-1.2: +, 1.3-1.9: ++, 2.0-2.8: +++, >2.8: ++++ (highly active).

[00374] Body weight (BW) of all the mice was measured two times per week as a rough index of drug toxicity and was determined by StudyLog software. Body weights of mice were expressed as percent change in body weight from the pre-treatment body weight as follows: % BW change = [(BWpost / BWpre) – 1] x 100, where BWpost is weight after treatment and BWpre is the starting body weight prior to treatment. Percent body weight loss (BWL) was expressed as the mean change in body weight post treatment. Animals were euthanized if the tumor volume became larger than 1000 mm^3, the tumors became necrotic, the mice lost >20% of their initial body weight, or the mice become moribund at any time during the study.

[00375] The results of the study are shown in FIG. 14. The LDL-DM ADCs were all more active than their SPDB-DM4 counterparts. The hMAB-A(2I.2)-sSPDB-DM4 (3.6 DAR) conjugate had a tumor growth inhibition (T/C) value of 66% (inactive), tumor growth delay (T-C) value of 0 days, and a log10 cell kill (LCK) value of 0.0 (-), with 2 partial tumor regressions out of 6 mice and no complete regressions. The hMAB-A(2I.2)-sGMBS-LDL-DM (3.3 DAR) conjugate had a T/C value of 14% (active), T-C value of 45 days, and a LCK value of 0.7 (+), with 4 partial tumor regressions out of 6 mice, 1 complete regression, and 1 tumor-free survivor. This demonstrates that hMAB-A(2I.2)-sGMBS-LDL-DM is more active than hMAB-A(2I.2)-sSPDB-DM4 at ~3.5 DAR. The hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR) had a T/C value of 47% (inactive), T-C value of 10 days, and a LCK value of 0.2 (-), with 1 partial tumor regression out of 6 mice, 1 complete regression, and 1 tumor-free survivor. hMAB-A(2I.2)-sGMBS-LDL-DM (1.9 DAR) had a T/C value of 41% (active), T-C value of 10 days, and a LCK value of 0.2 (-), with 2 partial tumor

regressions out of 6 mice, 1 complete regression, and 1 tumor-free survivor. This demonstrates that hMAB-A(2I.2)-sGMBS-LDL-DM is more active than hMAB-A(2I.2)-sSPDB-DM4 at ~2.0 DAR. hMAB-A(2I.2)-S442C-Mal-SPBD-DM4 (1.8 DAR) had a T/C value of 107% (inactive), T-C value of -11 days, and a LCK value of -0.2 (-), with 1 partial tumor regression out of 6 mice, 1 complete regression, and 1 tumor-free survivor. hMAB-A(2I.2)-S442C-Mal-LDL-DM (1.8 DAR) had a T/C value of 22% (active), T-C value of 28 days, and a LCK value of 0.4 (-), with 2 partial tumor regressions out of 6 mice, 1 complete regression, and 1 tumor-free survivor. This demonstrates that the hMAB-A(2I.2)-S442C-Mal-LDL-DM is more active than the hMAB-A(2I.2)-S442C-Mal-SPBD-DM4 at a DAR ~2.0 with site specific conjugation. No significant body weight loss was observed with any of the ADCs at the indicated doses, and thus all six conjugates were well tolerated in mice in this study.

[00376] In addition, DAR ~2.0 ADCs were comparably active as their DAR ~3.5 counterparts. Specifically, hMAB-A(2I.2)-sGMBS-LDL-DM (3.3 DAR) was about as active as hMAB-A(2I.2)-sGMBS-LDL-DM (1.9 DAR) and hMAB-A(2I.2)-S442C-Mal-LDL-DM (1.8 DAR). Since tolerability and toxicity are determined by the payload concentration, an ADC with DAR 2.0 can be dosed at a higher antibody concentration than an ADC with DAR 3.5. The increased exposure of the DAR 2.0 ADC may improve efficacy by saturating target-mediated drug disposition (TMDD) and/or increasing tumor penetration. The results from this study suggest that the hMAB-A(2I.2)-S442C-Mal-LDL-DM (1.8 DAR) conjugate demonstrated anti-tumor activity and is efficacious in SNU-5 gastric carcinoma tumor xenograft model.

Example 17
Anti-tumor Activity of anti-ADAM9 Antibody Drug Conjugates in SCID Mice Bearing EBC-1 Human Non-Small Cell Lung Squamous Cell Carcinoma Xenografts

[00377] The anti-tumor activity of 25, 50, and 100 μg/kg of DM payload of hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR) and hMAB-A(2I.2)-S442C-Mal-LDL-DM (2.1 DAR) conjugates were evaluated in female SCID mice bearing EBC-1 cells, a human non-small cell lung squamous cell carcinoma xenograft model.

[00378] EBC-1 cells were harvested for inoculation, with 100% viability determined by trypan blue exclusion. Mice were inoculated with 5 x 10^6 EBC-1 cells in 0.2ml 50% Matrigel/ 50% serum free medium by subcutaneous injection in the area on the right hind

flank. Sixty-six female CB.17 SCID Mice (6 weeks of age) were obtained. Upon receipt, the animals were observed for 6 days prior to study initiation. Animals showed no sign of disease or illness upon arrival, or prior to treatment.

[00379] Forty-two mice were randomized into 7 groups (6 mice per group) by tumor volume. The tumor volumes ranged from 79.38 to 124.29 (95.81 ± 11.83, Mean ± SD) mm^3. The mice were measured, randomized, and dosed based on the tumor volume on day 7 post implantation (4/16/18). Body weight of the mice ranged from 15.94 to 21.10 (18.55 ± 1.17, Mean ± SD) grams. Mice in each group were identified by punch method. Administration of the test agents and vehicle were carried out intravenously by using a 1.0 ml syringe fitted with a 27 gauge, ½ inch needle. Antibody drug conjugate test agents were dosed qdx1 at 25, 50, or 100 µg/kg DM payload, which is ~2, 4, and 9 mg/kg antibody (Ab) for the DAR ~2.0 conjugates. The groups included: a control group dosed with vehicle (PBS, 200 µL), hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR) at 2.18, 4.36, and 8.76 mg/kg Ab, and hMAB-A(2I.2)-S442C-Mal-LDL-DM (2.1 DAR) at 2.14, 4.28, and 8.57 mg/kg Ab.

[00380] Tumor size was measured two times per week in three dimensions using a caliper. The tumor volume was expressed in mm^3 using the formula Volume = Length x Width x Height x ½. A mouse was considered to have a partial regression (PR) when tumor volume was reduced by 50% or greater, a complete tumor regression (CR) when no palpable tumor could be detected, and to be a tumor-free survivor (TFS) if no palpable tumor was detected at the end of the study. Tumor volume was determined by StudyLog software.

[00381] Tumor growth inhibition (%T/C) is the ratio of the median tumor volume (TV) of the treatment group (T) to the median TV of the control group (C) at a predetermined time (e.g. the time when the median TV for control tumors reach a maximum tumor volume ~1000mm^3, which is when the mice are euthanized). %T/C was calculated on day 28 post inoculation, when the median TV of the control group reached 1279 mm^3. According to NCI standards, a T/C $\leq$ 42% is the minimum level of anti-tumor activity and a T/C <10% is considered a high anti-tumor activity level. Tumor growth delay (T-C), is the difference between the median time (in days) for the treatment group (T) and control group tumors (C) to reach a predetermined size of 1000 mm^3 (tumor-free survivors excluded). Tumor doubling time (Td) is estimated from nonlinear exponential curve fit of daily median of control tumor growth and determined by StudyLog software. Td was 6.04 days with an R2=0.995. Log10 cell kill (LCK) is calculated with the formula LCK = (T – C) / Td x 3.32,

where 3.32 is the number of cell doublings per log of cell growth. The Southern Research Institute (SRI) activity criteria for LCK are <0.7: - (inactive), 0.7-1.2: +, 1.3-1.9: ++, 2.0-2.8: +++, >2.8: ++++ (highly active).

[00382] Body weight (BW) of all the mice was measured two times per week as a rough index of drug toxicity and was determined by StudyLog software. Body weights of mice were expressed as percent change in body weight from the pre-treatment body weight as follows: % BW change = [(BWpost / BWpre) – 1] x 100, where BWpost is weight after treatment and BWpre is the starting body weight prior to treatment. Percent body weight loss (BWL) was expressed as the mean change in body weight post treatment. Animals were euthanized if the tumor volume became larger than 1000 mm^3, the tumors became necrotic, the mice lost >20% of their initial body weight, or the mice become moribund at any time during the study.

[00383] The results of the study are shown in FIG. 15. The LDL-DM ADC was more active than the SPDB-DM4 counterpart. hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR) dosed at 25 µg/kg DM (2.18 mg/kg Ab) had a T/C value of 17% (active), T-C value of 21 days, and a LCK value of 1.06 (+), with no tumor regressions or tumor-free survivors. hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR) dosed at 50 µg/kg DM (4.36 mg/kg Ab) had a T/C value of 2% (highly active), T-C value of 34 days, and a LCK value of 1.68 (++), with 6 partial tumor regressions out of 6 mice, 1 complete regression, and no tumor-free survivors. hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR) dosed at 100 µg/kg DM (8.76 mg/kg Ab) had a T/C value of 2% (highly active), T-C value of >65 days, and a LCK value of >3.26 (++++), with 6 partial tumor regressions out of 6 mice, 6 complete regressions, and 2 tumor-free survivors. hMAB-A(2I.2)-S442C-Mal-LDL-DM (2.1 DAR) dosed at 25 µg/kg DM (2.14 mg/kg Ab) had a T/C value of 2% (highly active), T-C value of 56 days, and a LCK value of 2.79 (+++), with 6 partial tumor regressions out of 6 mice, 3 complete regressions, and no tumor-free survivors. hMAB-A(2I.2)-S442C-Mal-LDL-DM (2.1 DAR) dosed at 50 µg/kg DM (4.28 mg/kg Ab) had a T/C value of 2% (highly active), T-C value of >65 days, and a LCK value of >3.26 (++++), with 6 partial tumor regressions out of 6 mice, 6 complete regressions, and no tumor-free survivors. hMAB-A(2I.2)-S442C-Mal-LDL-DM (2.1 DAR) dosed at 100 µg/kg DM (8.57 mg/kg Ab) had a T/C value of 1% (highly active), T-C value of >65 days, and a LCK value of >3.26 (++++), with 6 partial tumor regressions out of 6 mice, 6 complete regressions, and 6 tumor-free survivors. No significant body weight loss

was observed with any of the ADCs at the indicated doses, and thus all six conjugates were well tolerated in mice in this study. The results from this study suggest that both the hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR) and hMAB-A(2I.2)-S442C-Mal-LDL-DM (2.1 DAR) conjugates demonstrated dose dependent anti-tumor activity and were efficacious in EBC-1 non-small cell lung squamous cell carcinoma tumor xenograft model.

Example 18
Anti-tumor Activity of an anti-ADAM9 Antibody Drug Conjugates in CD1 Nude Mice Bearing SW48 Human Colorectal Adenocarcinoma Xenografts

[00384] The anti-tumor activity of 25, 50, and 100 µg/kg of DM payload of hMAB-A(2I.2)(YTE/C/-K)-Mal-LDL-DM (1.8 DAR) and 100 ug/kg of DM payload for the nonbinding control huKTI-Mal-LDL-DM (2.0 DAR) conjugate were evaluated in female CD1 Nude immunodeficient mice bearing SW48 cells, a human colorectal adenocarcinoma xenograft model.

[00385] SW48 (ATCC CCL-231) cells were harvested for inoculation, with greater than 90% viability determined by trypan blue exclusion. Mice were inoculated with 5 x 10^6 SW48 cells in 0.1ml 50% Matrigel/ 50% serum free medium by subcutaneous injection in the area on the right hind flank. Female CD1 Nude Mice (5-7 weeks of age) were obtained from Charles Rivers Laboratories. Upon receipt, the animals were observed for 3-4 days prior to study initiation. Animals showed no sign of disease or illness upon arrival, or prior to treatment

[00386] Forty mice were randomized into 5 groups (8 mice per group) by tumor volume. The tumor volumes ranged from 121.33 to 186.59 (152.49 ± 18.50, Mean ± SD) mm^3 on day 19 post implantation. The mice were measured and randomized based on tumor volume at day 19 and dosed on day 21 post implantation. Body weight of the mice on day 19 ranged from 18.80 to 29.90 (25.75 ± 2.50, Mean ± SD) grams. Mice in each group were identified by ear tag method. Administration of the test agents and vehicle were carried out intravenously by tail vein injection using a 0.5 ml syringe fitted with a 28 gauge, ½ inch needle. Antibody drug conjugate test agents were dosed qdx1 at 25, 50, or 100 µg/kg DM payload, which is equivalent to ~2, 4, and 9 mg/kg antibody (Ab) for the DAR ~2.0 conjugates. The groups included: a control group dosed with vehicle (1X PBS, 100 µL), hMAB-A(2I.2)(YTE/C/-K)-Mal-LDL-DM (1.8 DAR) at 2.18, 4.36, and 8.57 mg/kg Ab, and huKTI-Mal-LDL-DM (2.0 DAR) at 8.57 mg/kg Ab.

[00387] Tumor size was measured once per week by orthogonal measurements using electronic calipers and measured twice per week once groups were dosed. The tumor volume was expressed in mm^3 using the formula Volume = Length x Width x Height x ½. A mouse was considered to have a partial regression (PR) when tumor volume was reduced by 50% or greater from day of dosing, a complete tumor regression (CR) when no palpable tumor could be detected (≤14.08 mm^3) for three to four consecutive measurements, and to be tumor-free survivors (TFS) if no palpable tumor was detected (≤14.08 mm^3) at the end of the study. Tumor volume was recorded within the Study Director software.

[00388] Tumor growth inhibition (%T/C) is the ratio of the median tumor volume (TV) of the treatment group (T) to the median TV of the control group (C) at a predetermined time (e.g. the time point when all vehicle control animals remain on study). %T/C was calculated on day 56 post inoculation, when the median TV of the control group reached 663.04 mm^3. According to NCI standards, a T/C ≤ 42% is the minimum level of anti-tumor activity and a T/C <10% is considered a high level of anti-tumor activity.

[00389] Body weight (BW) of all the mice was measured once per week prior to dosing and measured twice per week after dosing as a rough index of drug toxicity and was recorded within the Study Director software. Body weights of mice were expressed as percent change in body weight from the pre-treatment body weight as follows: % BW change = [(BWpost / BWpre) – 1] x 100, where BWpost is weight after treatment and BWpre is the starting body weight prior to treatment. Percent body weight loss (BWL) was expressed as the mean change in body weight post treatment. Animals were euthanized if the tumor volume became larger than 2000 mm^3, the tumors showed signs of significant ulceration or necrosis, the mice lost >20% of their initial body weight, or the mice became moribund at any time during the study.

[00390] The results of the study are shown in FIG. 16. hMAB-A(2I.2)(YTE/C/-K)-Mal-LDL-DM (1.8 DAR) was highly active at a dose of 100 µg/kg DM (8.57 mg/kg Ab) with partial regression 8/8 mice, complete regression 7/8 mice, tumor-free survivors 7/8 mice, and a % T/C of 1%. At a dose level of 50 µg/kg DM (4.36 mg/kg Ab), hMAB-A(2I.2)(YTE/C/-K)-Mal-LDL-DM (1.8 DAR) was active with partial regression of 5/8 mice, complete regression 2/8 mice, tumor-free survivors 2/8 mice, and a %T/C of 15%. hMAB-A(2I.2)(YTE/C/-K)-Mal-LDL-DM (1.8 DAR) was considered inactive by NCI standards at 25 µg/kg DM (2.18 mg/kg Ab) with partial regression 1/8 mice, complete

regression 0/8 mice, tumor-free survivors 0/8 mice, and %T/C at 51%. Results demonstrated that hMAB-A(2I.2)(YTE/C/-K)-Mal-LDL-DM (1.8 DAR) was ADAM9-targeted as the nonbinding control huKTI-Mal-LDL-DM (2.0 DAR) conjugate was inactive at a dose of 100 μg/kg DM (8.57 mg/kg Ab) with 0/8 partial regression, 0/8 complete regression, 0/8 tumor-free survivors, and a %T/C of 93%. No significant body weight loss was observed with any of the ADCs at the indicated doses, and thus all conjugates were well tolerated in mice in this study. The results from this study suggested that the hMAB-A(2I.2)(YTE/C/-K)-Mal-LDL-DM (1.8 DAR) conjugate demonstrated dose dependent targeted anti-tumor activity and was efficacious in an SW48 colorectal adenocarcinoma xenograft model.

Example 19
Anti-tumor Activity of an anti-ADAM9 Antibody Drug Conjugates in CD1 Nude Mice Bearing HPAF-II Human Pancreatic Adenocarcinoma Xenografts

[00391] The anti-tumor activity of 25, 50, and 100 μg/kg of DM payload of hMAB-A(2I.2)(YTE/C/-K)-Mal-LDL-DM (1.8 DAR) and 100 ug/kg of DM payload for the nonbinding control huKTI-Mal-LDL-DM (2.0 DAR) conjugate were evaluated in female CD1 Nude immunodeficient mice bearing HPAF-II cells, a human pancreatic adenocarcinoma xenograft model.

[00392] HPAF-II (ATCC CRL-1997) cells were harvested for inoculation, with greater than 90% viability determined by trypan blue exclusion. Mice were inoculated with 5 x 10^6 HPAF-II cells in 0.1ml 50% Matrigel/ 50% serum free medium by subcutaneous injection in the area on the right hind flank. Female CD1 Nude Mice (5-7 weeks of age) were obtained from Charles Rivers Laboratories. Upon receipt, the animals were observed for 3-4 days prior to study initiation. Animals showed no sign of disease or illness upon arrival, or prior to treatment.

[00393] Thirty-five mice were randomized into 5 groups (7 mice per group) by tumor volume. The tumor volumes ranged from 81.64 to 136.77 (104.94 ± 13.89, Mean ± SD) mm^3 on day 15 post implantation. The mice were measured and randomized based on tumor volume at day 15 and dosed on day 16 post implantation. Body weight of the mice on day 15 ranged from 21.00 to 28.60 (25.21 ± 1.70, Mean ± SD) grams. Mice in each group were identified by ear tag method. Administration of the test agents and vehicle were carried out intravenously by tail vein injection using a 0.5 ml syringe fitted with a 28 gauge, ½ inch

needle. Antibody drug conjugate test agents were dosed qdx1 at 25, 50, or 100 μg/kg DM payload, which is equivalent to ~2, 4, and 9 mg/kg antibody (Ab) for the DAR ~2.0 conjugates. The groups included: a control group dosed with vehicle (1X PBS, 100 μL), hMAB-A(2I.2)(YTE/C/-K)-Mal-LDL-DM (1.8 DAR) at 2.18, 4.36, and 8.57 mg/kg Ab, and huKTI-Mal-LDL-DM (2.0 DAR) at 8.57 mg/kg Ab.

[00394] Tumor size was measured once per week by orthogonal measurements using electronic calipers and measured twice per week once groups were dosed. The tumor volume was expressed in mm^3 using the formula Volume = Length x Width x Height x ½. A mouse was considered to have a partial regression (PR) when tumor volume was reduced by 50% or greater from day of dosing, a complete tumor regression (CR) when no palpable tumor could be detected ($\leq$14.08 mm^3) for three to four consecutive measurements, and to be tumor-free survivors (TFS) if no palpable tumor was detected ($\leq$14.08 mm^3) at the end of the study. Tumor volume was recorded within the Study Director software.

[00395] Tumor growth inhibition (%T/C) is the ratio of the median tumor volume (TV) of the treatment group (T) to the median TV of the control group (C) at a predetermined time (e.g. the time when all vehicle control animals remain on study). %T/C was calculated on day 47 post inoculation, when the median TV of the control group reached 882.83 mm^3. According to NCI standards, a T/C $\leq$ 42% is the minimum level of anti-tumor activity and a T/C <10% is considered a high level of anti-tumor activity.

[00396] Body weight (BW) of all the mice was measured once per week prior to dosing and measured twice per week after dosing as a rough index of drug toxicity and was recorded within the Study Director software. Body weights of mice were expressed as percent change in body weight from the pre-treatment body weight as follows: % BW change = [(BWpost / BWpre) – 1] x 100, where BWpost is weight after treatment and BWpre is the starting body weight prior to treatment. Percent body weight loss (BWL) was expressed as the mean change in body weight post treatment. Animals were euthanized if the tumor volume became larger than 2000 mm^3, the tumors showed signs of significant ulceration or necrosis, the mice lost >20% of their initial body weight, or the mice became moribund at any time during the study.

[00397] The results of the study are shown in FIG. 17. hMAB-A(2I.2)(YTE/C/-K)-Mal-LDL-DM (1.8 DAR) was highly active at a dose of 100 µg/kg DM (8.57 mg/kg Ab) with partial regression 7/7 mice, complete regression 3/7 mice, tumor-free survivors 3/7 mice, and a % T/C of 3%. At a dose level of 50 µg/kg DM (4.36 mg/kg Ab), hMAB-A(2I.2)(YTE/C/-K)-Mal-LDL-DM (1.8 DAR) was active with partial regression of 5/7 mice, complete regression 1/7 mice, tumor-free survivors 1/7 mice, and a %T/C of 11%. hMAB-A(2I.2)(YTE/C/-K)-Mal-LDL-DM (1.8 DAR) was considered inactive by NCI standards at 25 µg/kg DM (2.18 mg/kg Ab) with partial regression 0/7 mice, complete regression 0/7 mice, tumor-free survivors 0/7 mice, and %T/C at 56%. Results demonstrated that hMAB-A(2I.2)(YTE/C/-K)-Mal-LDL-DM (1.8 DAR) was ADAM9-targeted as the nonbinding control huKTI-Mal-LDL-DM (2.0 DAR) conjugate was considered inactive by NCI standards at a dose of 100 µg/kg DM (8.57 mg/kg Ab) with 0/7 partial regression, 0/7 complete regression, 0/7 tumor-free survivors, and a %T/C of 48%. No significant body weight loss was observed with any of the ADCs at the indicated doses, and thus all conjugates were well tolerated in mice in this study. The results from this study suggested that the hMAB-A(2I.2)(YTE/C/-K)-Mal-LDL-DM (1.8 DAR) conjugate demonstrated dose dependent targeted anti-tumor activity and was efficacious in an HPAF-II pancreatic adenocarcinoma xenograft model.

Example 20
Anti-tumor Activity of anti-ADAM9 Antibody Drug Conjugates in Nude Mice Bearing H1975 Human Non-Small Cell Lung Adenocarcinoma Xenografts

[00398] The anti-tumor activity of 25, 50, and 100 µg/kg of DM payload of hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR) and hMAB-A(2I.2)-S442C-Mal-LDL-DM (2.1 DAR) conjugates were evaluated in female Nude mice bearing H1975 cells, a human non-small cell lung adenocarcinoma xenograft model.

[00399] H1975 cells were harvested for inoculation, with 100% viability determined by trypan blue exclusion. Mice were inoculated with 3 x 10^6 H1975 cells in 0.2ml 50% Matrigel/ 50% serum free medium by subcutaneous injection in the area on the right hind flank. Sixty-six female athymic Foxn1^{nu} Mice (6 weeks of age) were obtained. Upon receipt, the animals were observed for 7 days prior to study initiation. Animals showed no sign of disease or illness upon arrival, or prior to treatment.

[00400] Forty-two mice were randomized into 7 groups (6 mice per group) by tumor volume. The tumor volumes ranged from 79.43 to 119.61 (92.44 ± 10.36, Mean ± SD) mm^3. The mice were measured, randomized, and dosed based on the tumor volume on day 7 post implantation (4/10/18). Body weight of the mice ranged from 18.87 to 26.30 (22.92 ± 1.50, Mean ± SD) grams. Mice in each group were identified by punch method. Administration of the test agents and vehicle were carried out intravenously by using a 1.0 ml syringe fitted with a 27 gauge, ½ inch needle. Antibody drug conjugate test agents were dosed qdx1 at 25, 50, or 100 µg/kg DM payload, which is ~2, 4, and 9 mg/kg antibody (Ab) for the DAR ~2.0 conjugates. The groups included: a control group dosed with vehicle (PBS, 200 µL), hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR) at 2.18, 4.36, and 8.76 mg/kg Ab, and hMAB-A(2I.2)-S442C-Mal-LDL-DM (2.1 DAR) at 2.14, 4.28, and 8.57 mg/kg Ab.

[00401] Tumor size was measured two times per week in three dimensions using a caliper. The tumor volume was expressed in mm^3 using the formula Volume = Length x Width x Height x ½. A mouse was considered to have a partial regression (PR) when tumor volume was reduced by 50% or greater, a complete tumor regression (CR) when no palpable tumor could be detected, and to be a tumor-free survivor (TFS) if no palpable tumor was detected at the end of the study. Tumor volume was determined by StudyLog software.

[00402] Tumor growth inhibition (%T/C) is the ratio of the median tumor volume (TV) of the treatment group (T) to the median TV of the control group (C) at a predetermined time (e.g. the time when the median TV for control tumors reach a maximum tumor volume ~1000mm^3, which is when the mice are euthanized). %T/C was calculated on day 20 post inoculation, when the median TV of the control group reached 729 mm^3. According to NCI standards, a T/C $\leq$ 42% is the minimum level of anti-tumor activity and a T/C <10% is considered a high anti-tumor activity level. Tumor growth delay (T-C), is the difference between the median time (in days) for the treatment group (T) and control group tumors (C) to reach a predetermined size of 1000 mm^3 (tumor-free survivors excluded). Tumor doubling time (Td) is estimated from nonlinear exponential curve fit of daily median of control tumor growth and determined by StudyLog software. Td was 3.84 days with an R2=0.998. Log10 cell kill (LCK) is calculated with the formula LCK = (T – C) / Td x 3.32, where 3.32 is the number of cell doublings per log of cell growth. The Southern Research Institute (SRI) activity criteria for LCK are <0.7: - (inactive), 0.7-1.2: +, 1.3-1.9: ++, 2.0-2.8: +++, >2.8: ++++ (highly active).

[00403] Body weight (BW) of all the mice was measured two times per week as a rough index of drug toxicity and was determined by StudyLog software. Body weights of mice were expressed as percent change in body weight from the pre-treatment body weight as follows: % BW change = [(BWpost / BWpre) – 1] x 100, where BWpost is weight after treatment and BWpre is the starting body weight prior to treatment. Percent body weight loss (BWL) was expressed as the mean change in body weight post treatment. Animals were euthanized if the tumor volume became larger than 1000 mm^3, the tumors became necrotic, the mice lost >20% of their initial body weight, or the mice become moribund at any time during the study.

[00404] The results of the study are shown in FIG. 18. The LDL-DM ADC was more active than the SPDB-DM4 ADC counterpart. hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR) dosed at 25 µg/kg DM (2.18 mg/kg Ab) had a T/C value of 26% (active), T-C value of 10 days, and a LCK value of 0.79 (+), with no tumor regressions or tumor-free survivors. hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR) dosed at 50 µg/kg DM (4.36 mg/kg Ab) had a T/C value of 8% (highly active), T-C value of 35 days, and a LCK value of 2.72 (+++), with 5 partial tumor regressions out of 6 mice, 1 complete regression, and no tumor-free survivors. hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR) dosed at 100 µg/kg DM (8.76 mg/kg Ab) had a T/C value of 7% (highly active), T-C value of >38 days, and a LCK value of >2.98 (++++), with 6 partial tumor regressions out of 6 mice, no complete regressions, and no tumor-free survivors. hMAB-A(2I.2)-S442C-Mal-LDL-DM (2.1 DAR) dosed at 25 µg/kg DM (2.14 mg/kg Ab) had a T/C value of 6% (highly active) with 4 partial tumor regressions out of 6 mice, 1 complete regression, and no tumor-free survivors. The T-C and LCK values could not be calculated because of loss of animals in this group due to tumor necrosis or body weight loss at nadir of 7% (10 days post injection 1 animal in the group had to be euthanized due to body weight loss >20%). hMAB-A(2I.2)-S442C-Mal-LDL-DM (2.1 DAR) dosed at 50 µg/kg DM (4.28 mg/kg Ab) had a T/C value of 4% (highly active) with 5 partial tumor regressions out of 6 mice, no complete regressions, and no tumor-free survivors. The T-C and LCK values could not be calculated because of loss of animals in this group due to body weight loss at nadir of 35% (20 days post injection all the animals in this group had to be euthanized due to body weight loss >20% due to a water bottle clog). hMAB-A(2I.2)-S442C-Mal-LDL-DM (2.1 DAR) dosed at 100 µg/kg DM (8.57 mg/kg Ab) had a T/C value of 6% (highly active), T-C value of >38 days, and a LCK value of >2.98 (++++), with 6 partial tumor regressions out of 6 mice, 2 complete regressions, and 2 tumor-

free survivors. No significant body weight loss was observed with hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR) at any of the indicated doses or with hMAB-A(2I.2)-S442C-Mal-LDL-DM (2.1 DAR) at the highest dose of 100 μg/kg and thus both conjugates were well tolerated in mice in this study. The results from this study suggest that both the hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR) and hMAB-A(2I.2)-S442C-Mal-LDL-DM (2.1 DAR) conjugates demonstrated dose dependent anti-tumor activity and were efficacious in H1975 non-small cell lung adenocarcinoma tumor xenograft model.

Example 21
Anti-tumor Activity of anti-ADAM9 Antibody Drug Conjugates in SCID Mice Bearing Hs 746T Human Gastric Carcinoma Xenografts

[00405] The anti-tumor activity of 25, 50, and 100 μg/kg of DM payload of hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR) and hMAB-A(2I.2)-S442C-Mal-LDL-DM (2.1 DAR) conjugates were evaluated in female SCID mice bearing Hs 746T cells, a human gastric carcinoma xenograft model.

[00406] Hs 746T cells were harvested for inoculation, with 100% viability determined by trypan blue exclusion. Mice were inoculated with 5 x 10^6 Hs 746T cells in 0.1ml serum free medium by subcutaneous injection in the area on the right hind flank. Sixty female CB.17 SCID Mice (6 weeks of age) were obtained. Upon receipt, the animals were observed for 7 days prior to study initiation. Animals showed no sign of disease or illness upon arrival, or prior to treatment.

[00407] Forty-two mice were randomized into 7 groups (6 mice per group) by tumor volume. The tumor volumes ranged from 69.09 to 136.75 (101.40 ± 19.16, Mean ± SD) mm^3. The mice were measured, randomized, and dosed based on the tumor volume on day 13 post implantation (7/11/18). Body weight of the mice ranged from 18.03 to 23.21 (19.66 ± 1.21, Mean ± SD) grams. Mice in each group were identified by punch method. Administration of the test agents and vehicle were carried out intravenously by using a 1.0 ml syringe fitted with a 27 gauge, ½ inch needle. Antibody drug conjugate test agents were dosed qdx1 at 25, 50, or 100 μg/kg DM payload, which is ~2, 4, and 9 mg/kg antibody (Ab) for the DAR ~2.0 conjugates. The groups included: a control group dosed with vehicle (PBS, 200 μL), hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR) at 2.18, 4.36, and 8.76 mg/kg Ab, and hMAB-A(2I.2)-S442C-Mal-LDL-DM (2.1 DAR) at 2.14, 4.28, and 8.57 mg/kg Ab.

[00408] Tumor size was measured two times per week in three dimensions using a caliper. The tumor volume was expressed in mm^3 using the formula Volume = Length x Width x Height x ½. A mouse was considered to have a partial regression (PR) when tumor volume was reduced by 50% or greater, a complete tumor regression (CR) when no palpable tumor could be detected, and to be a tumor-free survivor (TFS) if no palpable tumor was detected at the end of the study. Tumor volume was determined by StudyLog software.

[00409] Tumor growth inhibition (%T/C) is the ratio of the median tumor volume (TV) of the treatment group (T) to the median TV of the control group (C) at a predetermined time (e.g. the time when the median TV for control tumors reach a maximum tumor volume ~1000mm^3, which is when the mice are euthanized). %T/C was calculated on day 25 post inoculation, when the median TV of the control group reached 1536 mm^3. According to NCI standards, a T/C $\leq$ 42% is the minimum level of anti-tumor activity and a T/C <10% is considered a high anti-tumor activity level. Tumor growth delay (T-C), is the difference between the median time (in days) for the treatment group (T) and control group tumors (C) to reach a predetermined size of 1000 mm^3 (tumor-free survivors excluded). Tumor doubling time (Td) is estimated from nonlinear exponential curve fit of daily median of control tumor growth and determined by StudyLog software. Td was 3.38 days with an R2=0.991. Log10 cell kill (LCK) is calculated with the formula LCK = (T – C) / Td x 3.32, where 3.32 is the number of cell doublings per log of cell growth. The Southern Research Institute (SRI) activity criteria for LCK are <0.7: - (inactive), 0.7-1.2: +, 1.3-1.9: ++, 2.0-2.8: +++, >2.8: ++++ (highly active).

[00410] Body weight (BW) of all the mice was measured two times per week as a rough index of drug toxicity and was determined by StudyLog software. Body weights of mice were expressed as percent change in body weight from the pre-treatment body weight as follows: % BW change = [(BWpost / BWpre) – 1] x 100, where BWpost is weight after treatment and BWpre is the starting body weight prior to treatment. Percent body weight loss (BWL) was expressed as the mean change in body weight post treatment. Animals were euthanized if the tumor volume became larger than 1000 mm^3, the tumors became necrotic, the mice lost >20% of their initial body weight, or the mice become moribund at any time during the study.

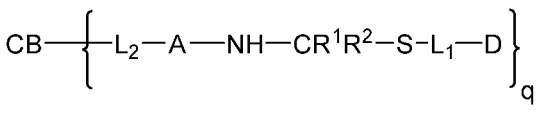
[00411] The results of the study are shown in FIG. 19. The LDL-DM ADC was more active than the SPDB-DM4 ADC counterpart. hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR) dosed at 25 μg/kg DM (2.18 mg/kg Ab) had a T/C value of 77% (inactive), T-C value of 1 day, and a LCK value of 0.12 (-), with no tumor regressions or tumor-free survivors. hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR) dosed at 50 μg/kg DM (4.36 mg/kg Ab) had a T/C value of 67% (inactive), T-C value of 3 days, and a LCK value of 0.24 (-), with no tumor regressions or tumor-free survivors. hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR) dosed at 100 μg/kg DM (8.76 mg/kg Ab) had a T/C value of 12% (active), T-C value of 15 days, and a LCK value of 1.35 (++), with 1 partial tumor regression out of 6 mice, no complete regressions, and no tumor-free survivors. hMAB-A(2I.2)-S442C-Mal-LDL-DM (2.1 DAR) dosed at 25 μg/kg DM (2.14 mg/kg Ab) had a T/C value of 58% (inactive), T-C value of 4 days, and a LCK value of 0.33 (-), with no tumor regressions or tumor-free survivors. hMAB-A(2I.2)-S442C-Mal-LDL-DM (2.1 DAR) dosed at 50 μg/kg DM (4.28 mg/kg Ab) had a T/C value of 26% (active), T-C value of 12 days, and a LCK value of 1.09 (+), with no tumor regressions or tumor-free survivors. hMAB-A(2I.2)-S442C-Mal-LDL-DM (2.1 DAR) dosed at 100 μg/kg DM (8.57 mg/kg Ab) had a T/C value of 6% (highly active), T-C value of 29 days, and a LCK value of 2.59 (+++), with 4 partial tumor regressions out of 6 mice, no complete regressions, and no tumor-free survivors. No significant body weight loss was observed with any of the ADCs at the indicated doses, and thus all six conjugates were well tolerated in mice in this study. The results from this study suggest that both the hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR) and hMAB-A(2I.2)-S442C-Mal-LDL-DM (2.1 DAR) conjugates demonstrated dose dependent anti-tumor activity and were efficacious in Hs 746T gastric carcinoma tumor xenograft model.

[00412] All publications and patents mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference in its entirety. While the invention has been described in connection with specific embodiments thereof, it will be understood that it is capable of further modifications and this application is intended to cover any variations, uses, or adaptations of the invention following, in general, the principles of the invention and including such departures from the present disclosure as come within known or customary practice within the art to which the invention pertains and as may be applied to the essential features hereinbefore set forth.

CLAIMS

WHAT IS CLAIMED IS:

1. An immunoconjugate represented by the following formula:

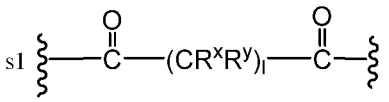


(I)

or a pharmaceutically acceptable salt thereof, wherein:

CB is an anti-ADAM9 antibody or ADAM9-binding fragment thereof;

L_2 is represented by one of the following formula:



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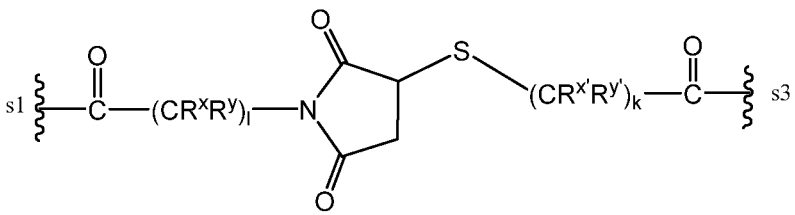
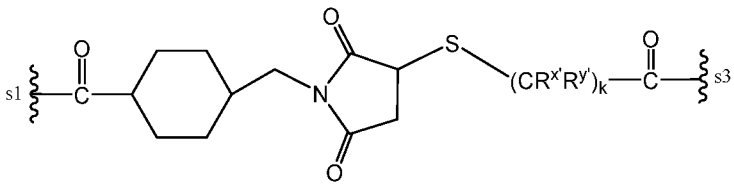
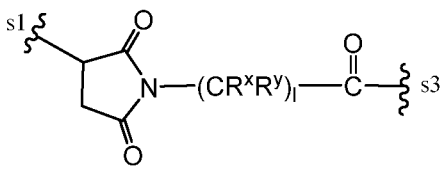


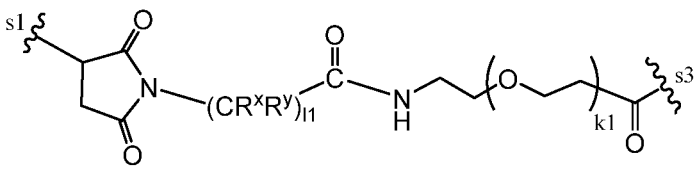
(L2b),



(L2c),



(L2d), or



(L2e);

wherein:

R^x, R^y, $R^{x'}$ and $R^{y'}$, for each occurrence, are independently H, -OH, halogen, -O-(C_{1-4} alkyl), -SO_3H, -$NR_{40}R_{41}R_{42}^+$, or a C_{1-4} alkyl optionally substituted with -OH, halogen, SO_3H or $NR_{40}R_{41}R_{42}^+$, wherein R_{40}, R_{41} and R_{42} are each independently H

or a C_{1-4} alkyl;

l and k are each independently an integer from 1 to 10;

l1 is an integer from 2 to 5;

k1 is an integer from 1 to 5; and

s1 indicates the site connected to the cell-binding agent CB and s3 indicates the site connected to the A group;

A is an amino acid residue or a peptide comprising 2 to 20 amino acid residues;

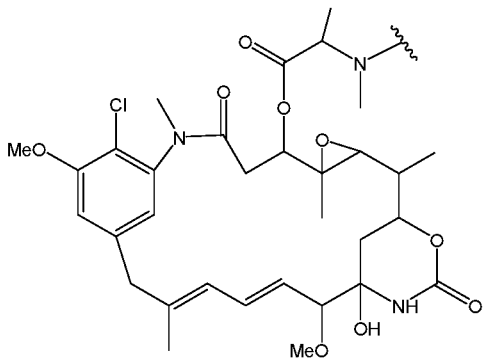
R^1 and R^2 are each independently H or a C_{1-3}alkyl;

L_1 is represented by the following formula:

$$-CR^3R^4-(CH_2)_{1-8}-C(=O)-$$

wherein R^3 and R^4 are each independently H or Me, and the –C(=O)- moiety in L_1 is connected to D;

D is represented by the following formula:



; and

q is an integer from 1 to 20.

2. The immunoconjugate of claim 1, wherein R^x, R^y, $R^{x'}$ and $R^{y'}$ are all H; and l and k are each independently an integer an integer from 2 to 6.

3. The immunoconjugate of claim 1 or 2, wherein A is a peptide containing 2 to 5 amino acid residues.

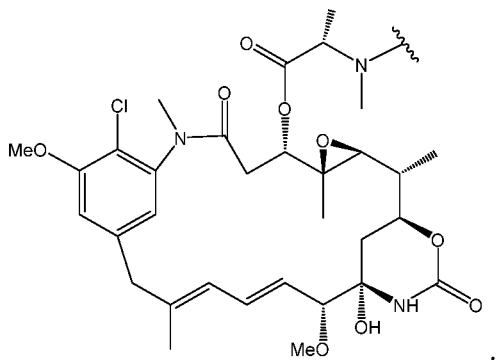
4. The immunoconjugate of claim 3, wherein A is selected from the group consisting of Gly-Gly-Gly, Ala-Val, Val-Ala, D-Val-Ala, Val-Cit, D-Val-Cit, Val-Lys, Phe-Lys, Lys-Lys, Ala-Lys, Phe-Cit, Leu-Cit, Ile-Cit, Phe-Ala, Phe-N^9-tosyl-Arg, Phe-N^9-nitro-Arg, Phe-Phe-Lys, D-Phe-Phe-Lys, Gly-Phe-Lys, Leu-Ala-Leu, Ile-Ala-Leu, Val-Ala-Val, Ala-Ala-Ala, D-Ala-Ala-Ala, Ala-D-Ala-Ala, Ala-Ala-D-Ala, Ala-

Leu-Ala-Leu (SEQ ID NO: 144), β-Ala-Leu-Ala-Leu (SEQ ID NO: 145), Gly-Phe-Leu-Gly (SEQ ID NO: 146), Val-Arg, Arg-Arg, Val-D-Cit, Val-D-Lys, Val-D-Arg, D-Val-Cit, D-Val-Lys, D-Val-Arg, D-Val-D-Cit, D-Val-D-Lys, D-Val-D-Arg, D-Arg-D-Arg, Ala-Ala, Ala-D-Ala, D-Ala-Ala, D-Ala-D-Ala, Ala-Met, Gln-Val, Asn-Ala, Gln-Phe, Gln-Ala, D-Ala-Pro, and D-Ala-tBu-Gly, wherein the first amino acid in each peptide is connected to L_2 group and the last amino acid in each peptide is connected to –NH-CR^1R^2-S-L_1-D.

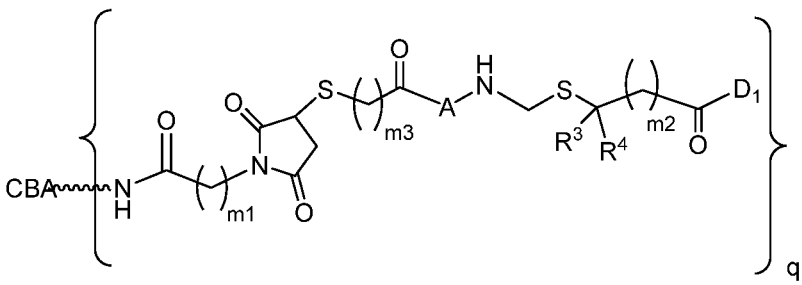
5. The immunoconjugate of any one of claims 1-4, wherein R^1 and R^2 are both H.

6. The immunoconjugate of any one of claims 1-5, wherein L_1 is $–(CH_2)_{4-6}$-C(=O)-.

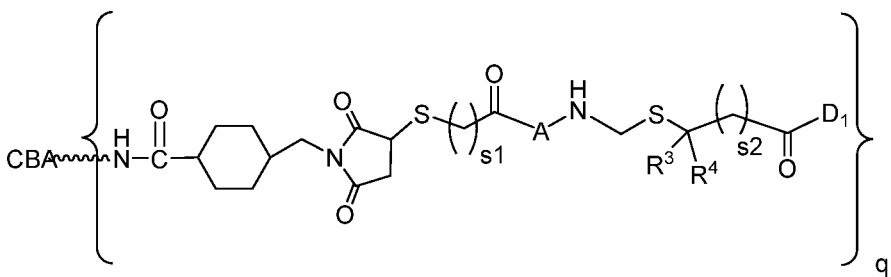
7. The immunoconjugate of any one of claims 1-6, wherein D is represented by the following formula:



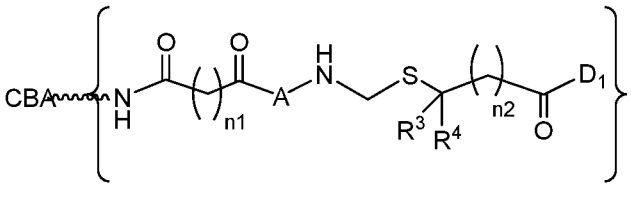
8. The immunoconjugate of any one of claims 1-7, wherein the immunoconjugate is represented by the following formula:

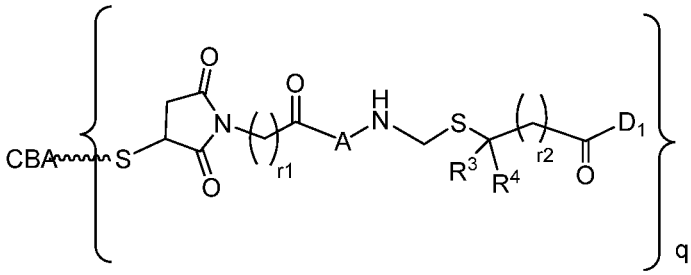


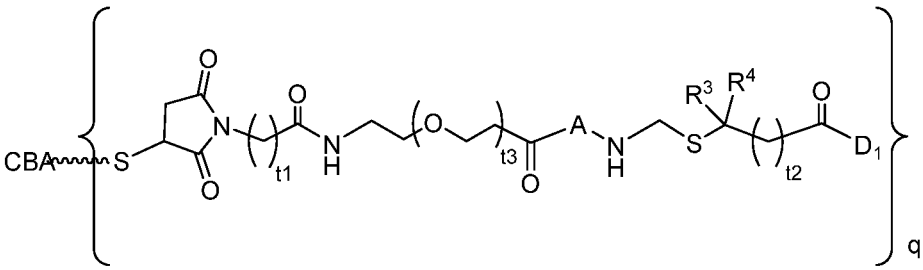
q (Ia);



q (Ib);

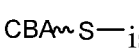

(Ic);


(Id); or


(Ie);

or a pharmaceutically acceptable salt thereof, wherein:

 is the anti-ADAM9 antibody or ADAM9-binding fragment thereof connected to the L_2 group through a Lys amine group;

 is the anti-ADAM9 antibody or ADAM9-binding fragment thereof connected to the L_2 group through a Cys thiol group;

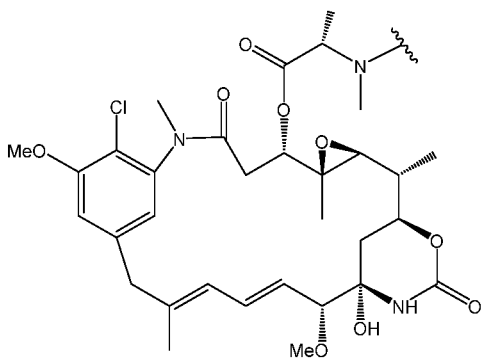
R^3 and R^4 are each independently H or Me;

m1, m3, n1, r1, s1 and t1 are each independently an integer from 1 to 6;

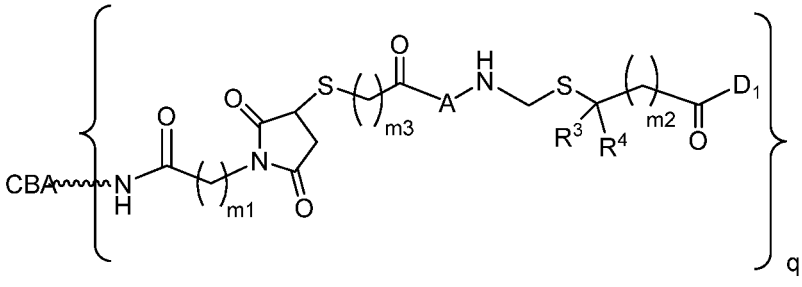
m2, n2, r2, s2 and t2 are each independently an integer from 1 to 7;

t3 is an integer from 1 to 12;

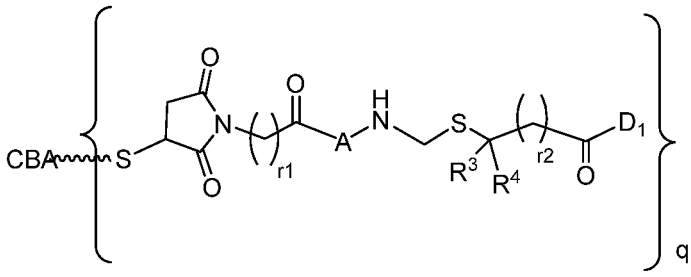
D_1 is represented by the following formula:



9. The immunoconjugate of claim 8, wherein the immunoconjugate is represented by the following formula:



(Ia), or



(Id);

wherein:

m1 and m3 are each independently an integer from 2 to 4;

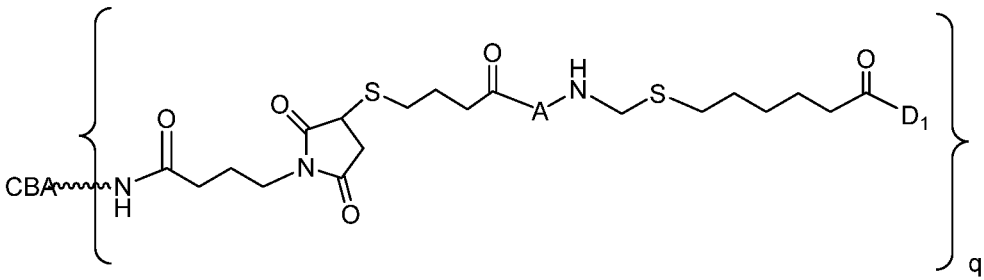
m2 is an integer from 2 to 5;

r1 is an integer from 2 to 6; and

r2 is an integer from 2 to 5.

10. The immunoconjugate of claim 8 or 9, wherein A is Ala-Ala-Ala, Ala-D-Ala-Ala, Ala-Ala, D-Ala-Ala, Val-Ala, D-Val-Ala, D-Ala-Pro, or D-Ala-tBu-Gly.

11. The immunoconjugate of claim 8, wherein the immununoconjugate is represented by the following formula:



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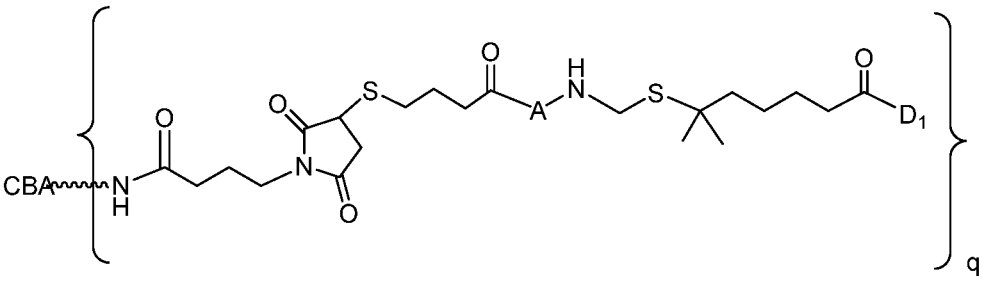

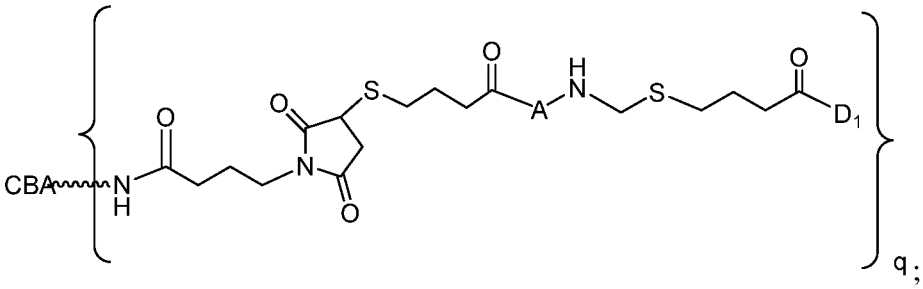

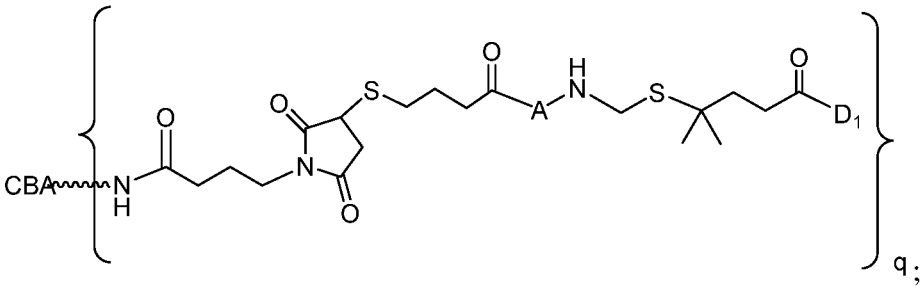

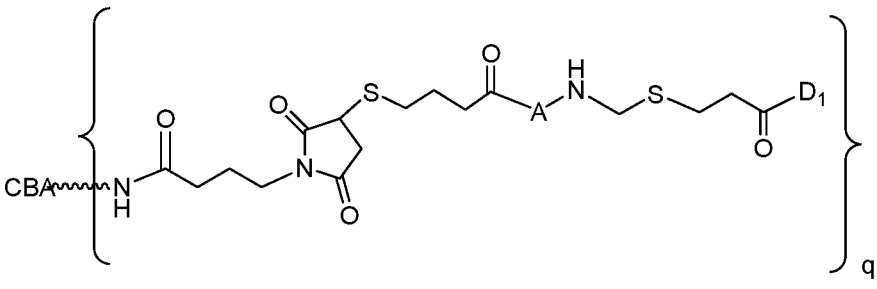

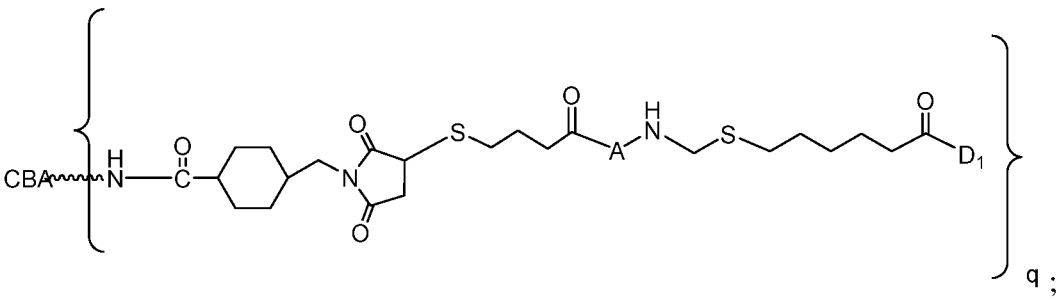

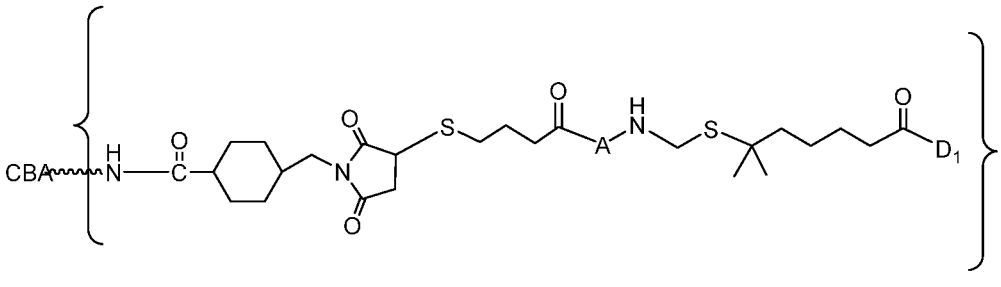

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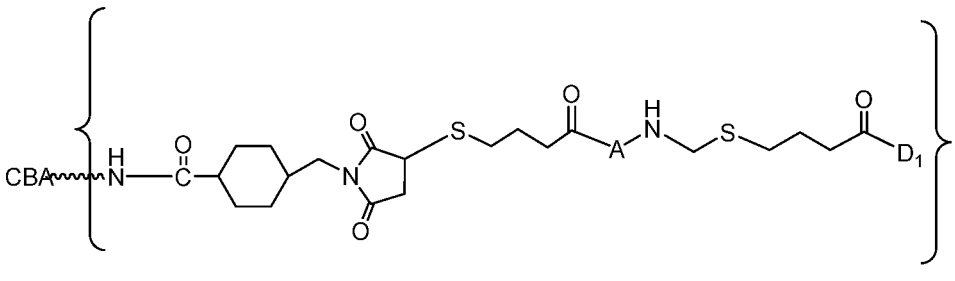

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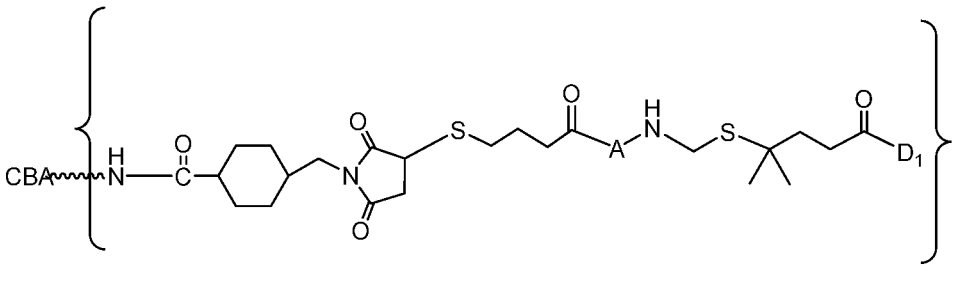

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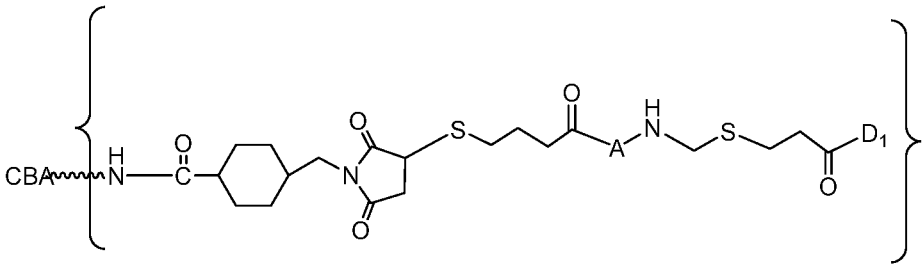

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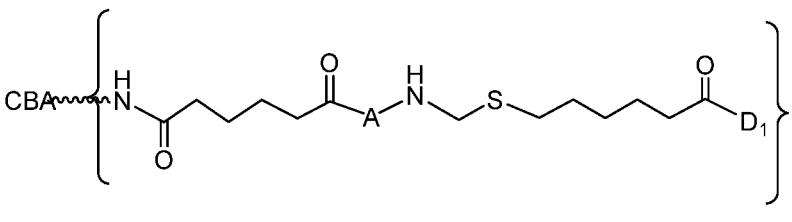

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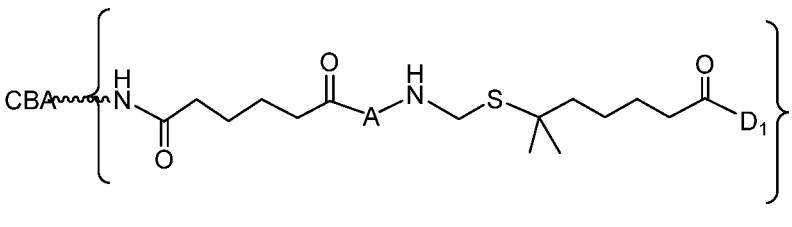

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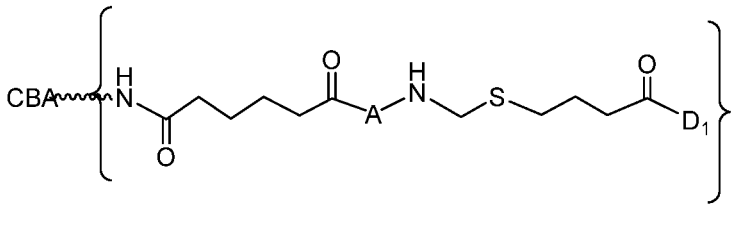

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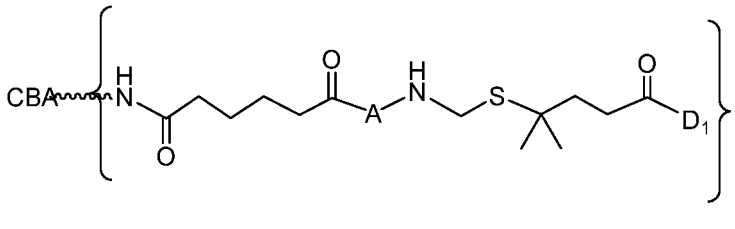

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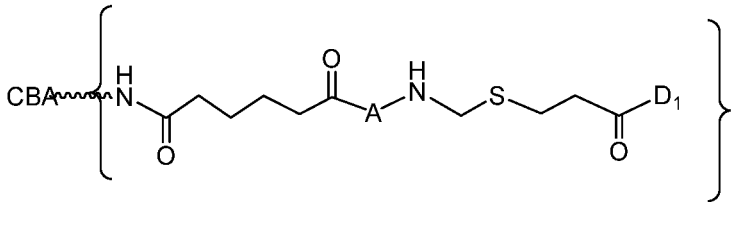

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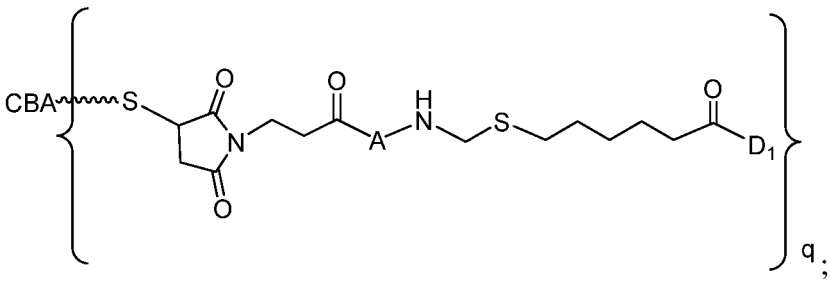

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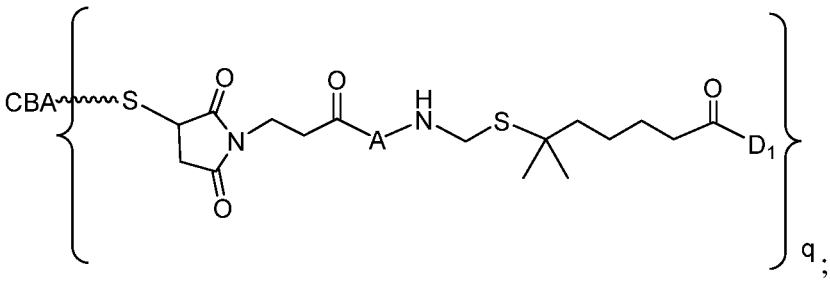

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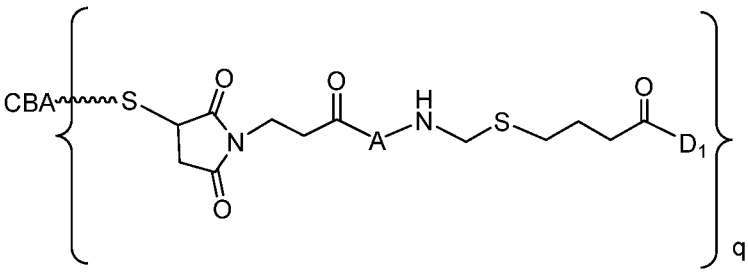

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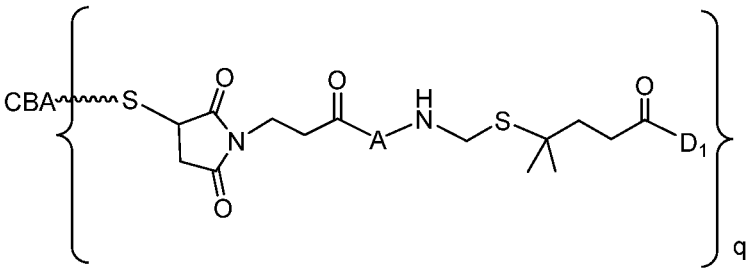
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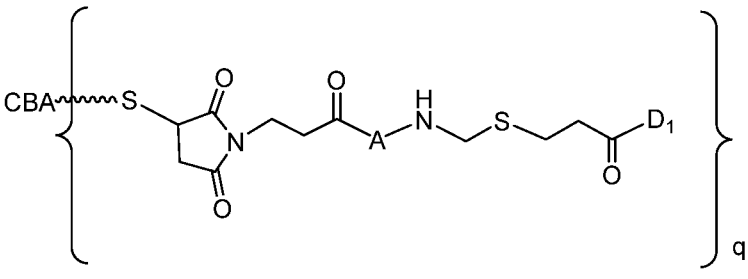
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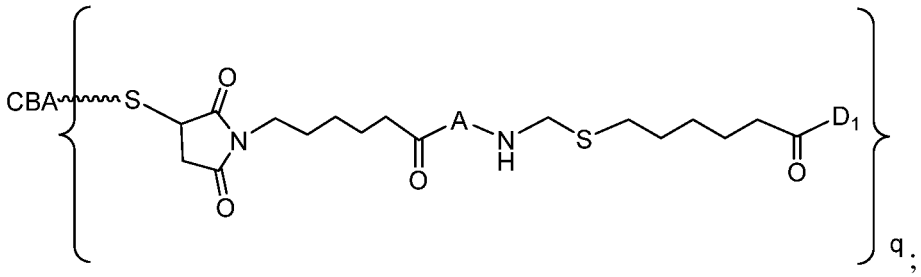
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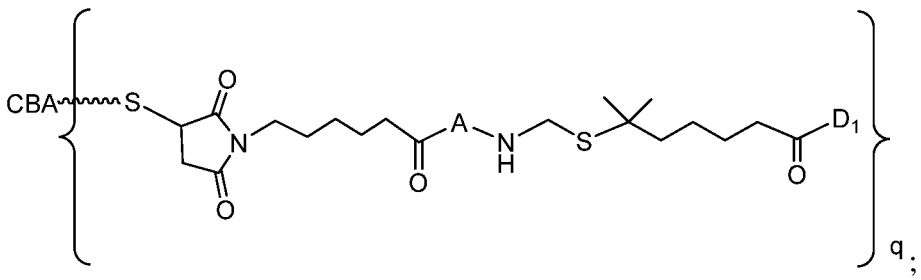
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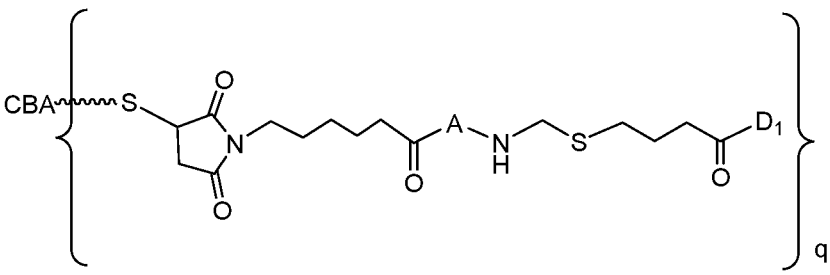
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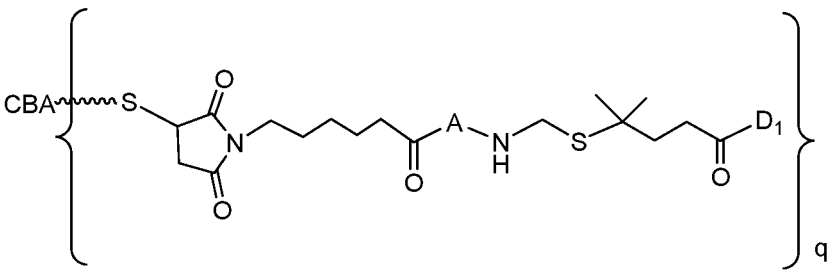
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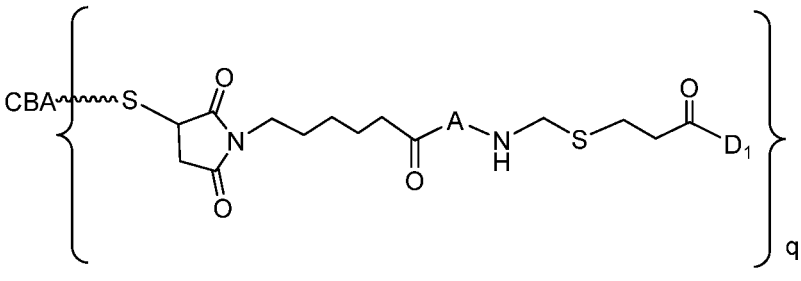

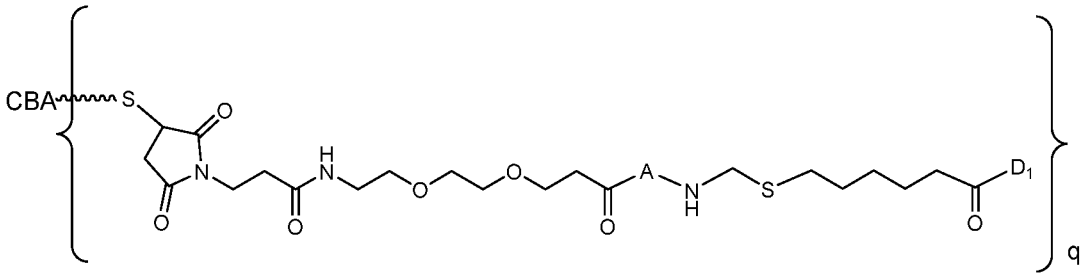

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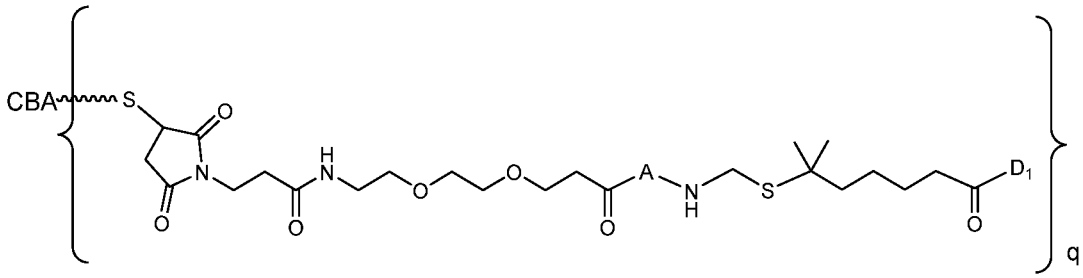

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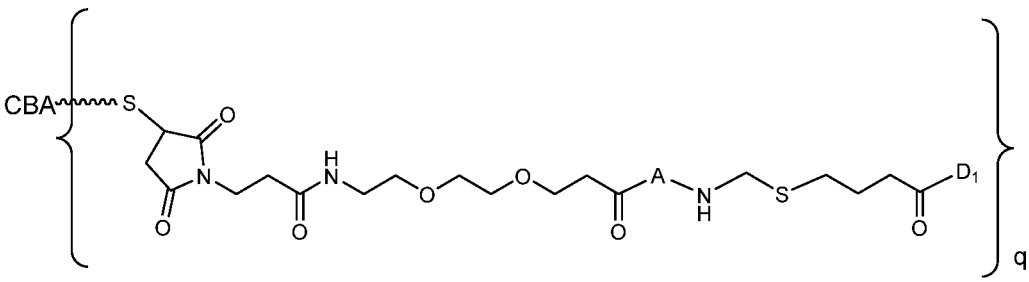

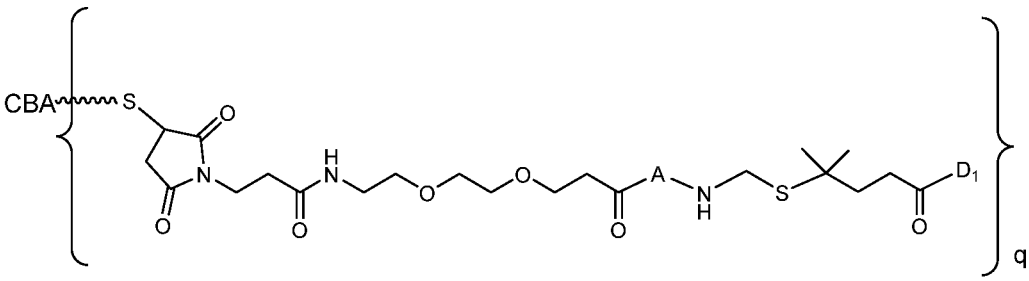

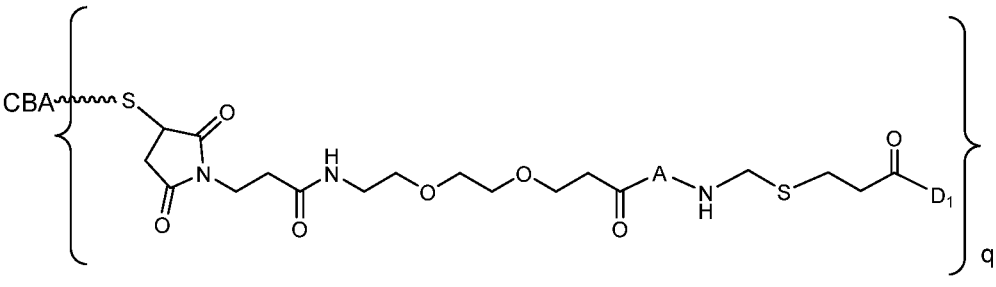

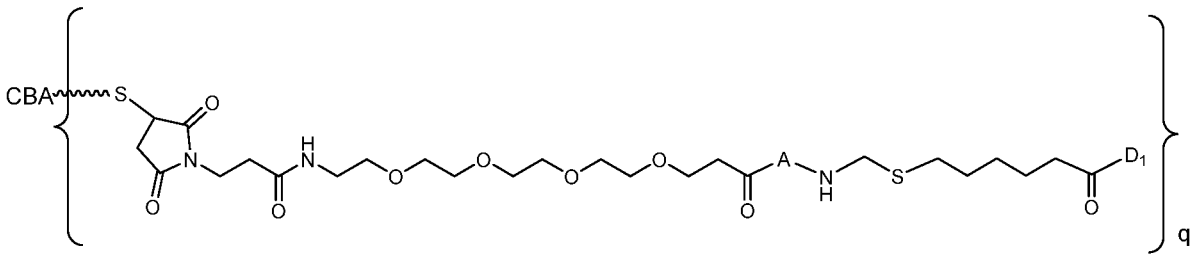

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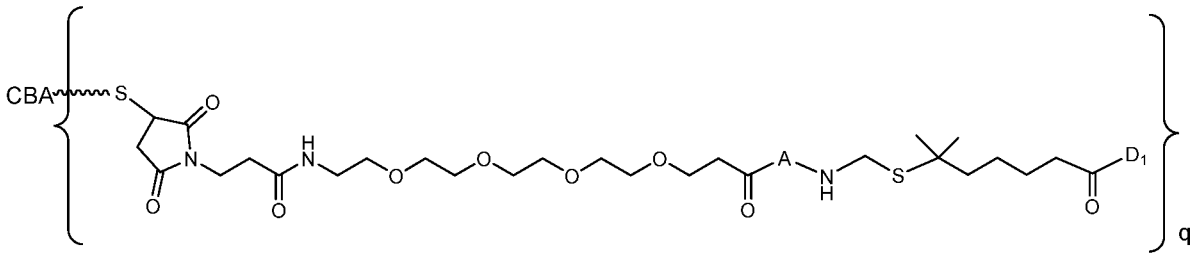

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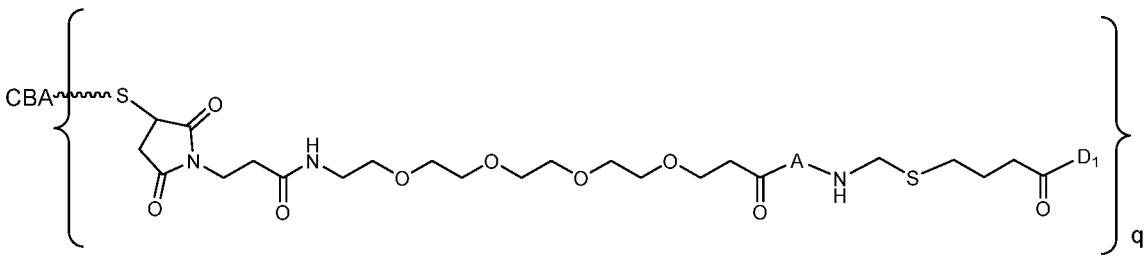
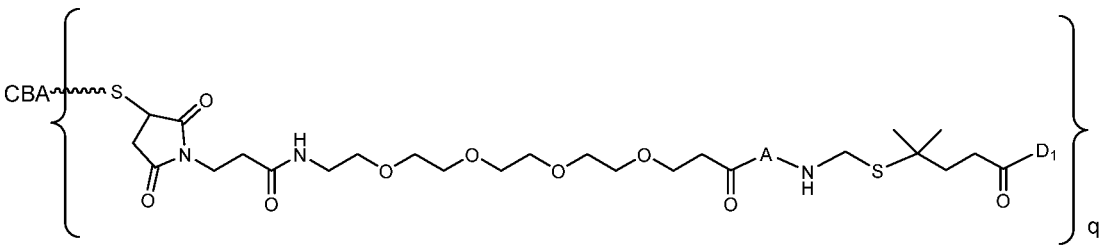
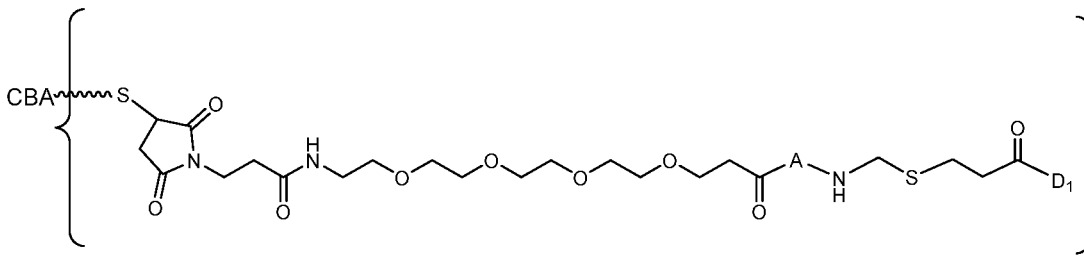




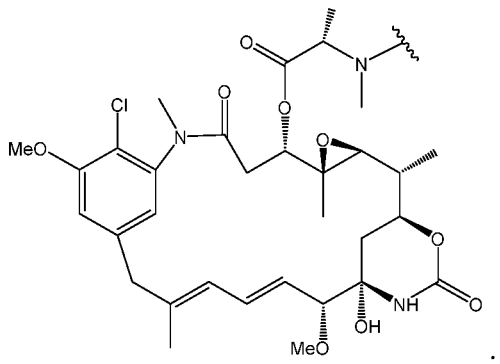
; or



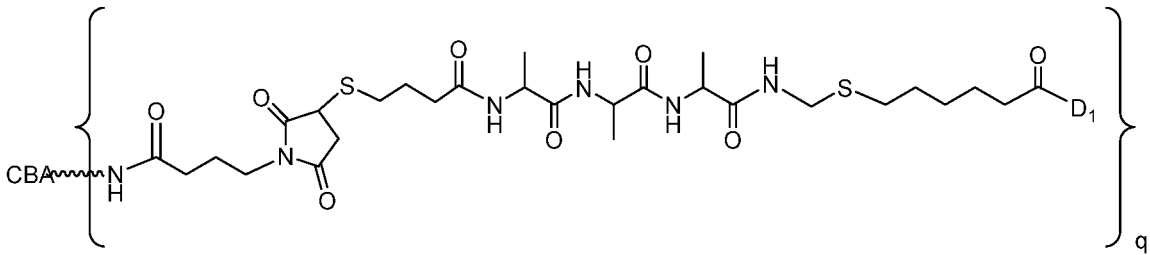
or a pharmaceutically acceptable salt thereof, wherein:

A is Ala-Ala-Ala, Ala-D-Ala-Ala, Ala-Ala, D-Ala-Ala, Val-Ala, D-Val-Ala, D-Ala-Pro, or D-Ala-tBu-Gly, and

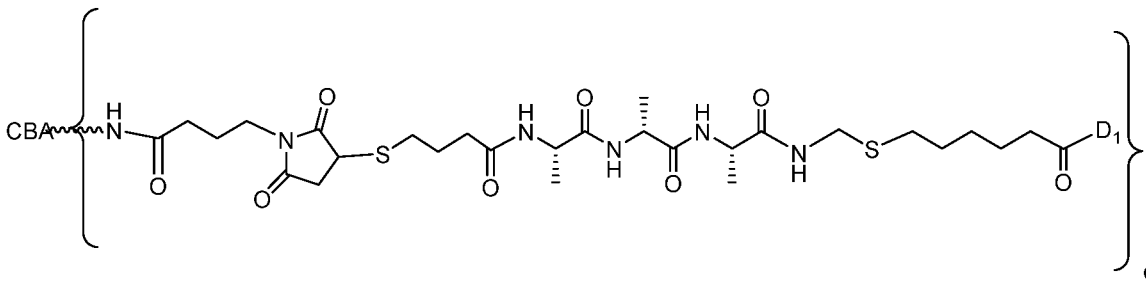
D_1 is represented by the following formula:



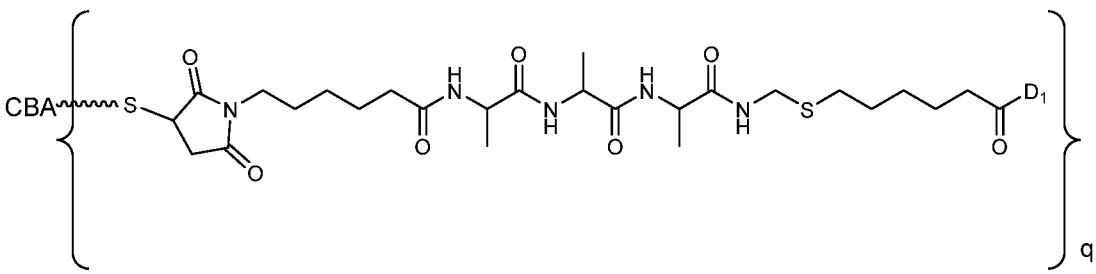
12. The immunoconjugate of claim 11, wherein the immunoconjugate is represented by the following formula:



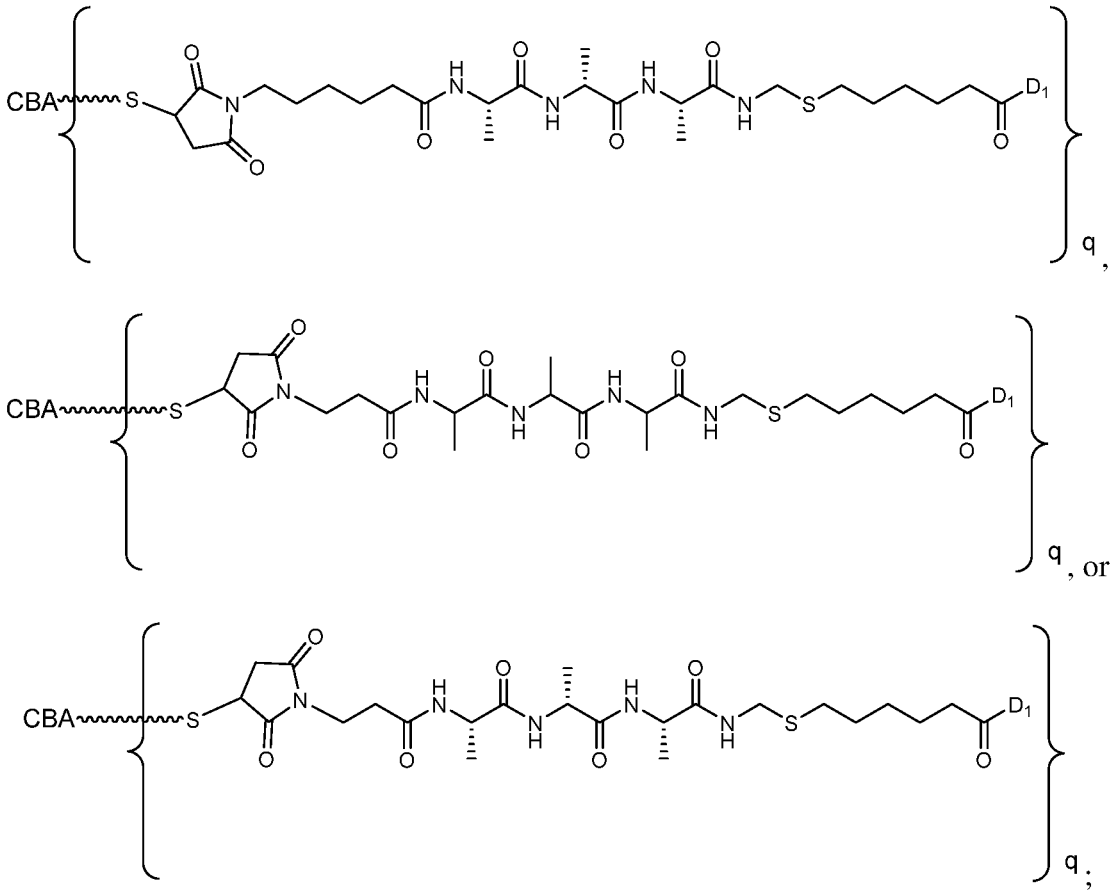
q;



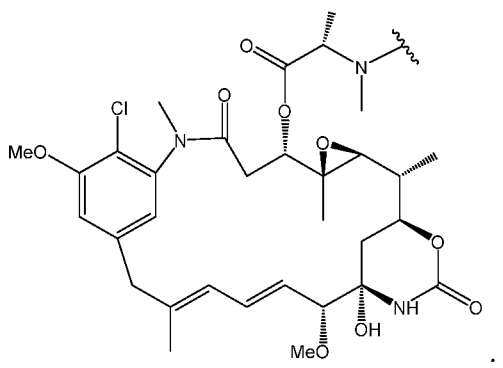
q;



q; or



wherein D_1 is represented by the following formula:



13. The immunoconjugate of any one of claims 1-12, wherein the immunoconjugate comprises a humanized anti-ADAM9 antibody or ADAM9-binding fragment thereof that specifically binds to human ADAM9 and cyno ADAM9 wherein said humanized anti-ADAM9 antibody or ADAM9-binding fragment thereof is conjugated to the pharmacological agent.

14. The immunoconjugate of claim 13, wherein said humanized anti-ADAM9 antibody or ADAM9-binding fragment thereof comprises a CDR_H1 domain, a CDR_H2 domain, and a CDR_H3 domain and a CDR_L1 domain, a CDR_L2 domain, and a CDR_L3 domain having the sequences selected from the group consisting of:
(a) SEQ ID NOs: 8, 35, and 10 and SEQ ID NOs: 62, 13, 14, respectively;
(b) SEQ ID NOs: 8, 35, and 10 and SEQ ID NOs: 63, 13, 14, respectively;
(c) SEQ ID NOs: 8, 36, and 10 and SEQ ID NOs: 63, 13, 14, respectively; and
(d) SEQ ID NOs: 34, 36, and 10 and SEQ ID NO:64, 13, 65, respectively.

15. The immunoconjugate of claims 13 or 14, wherein said humanized anti-ADAM9 antibody or ADAM9-binding fragment thereof comprises a heavy chain variable domain (VH) and a light chain variable domain (VL) having sequences that are at least 90%, at least 95%, or at least 99% identical to sequences selected from the group consisting of:
(a) SEQ ID NO:17 and SEQ ID NO:55, respectively;
(b) SEQ ID NO:17 and SEQ ID NO:56, respectively;
(c) SEQ ID NO:18 and SEQ ID NO:56, respectively; and
(d) SEQ ID NO:19 and SEQ ID NO:57, respectively.

16. The immunoconjugate of claim 15, wherein said humanized anti-ADAM9 antibody or ADAM9-binding fragment thereof comprises a heavy chain variable domain (VH) and a light chain variable domain (VL) having the sequences selected from the group consisting of:
(a) SEQ ID NO:17 and SEQ ID NO:55, respectively;
(b) SEQ ID NO:17 and SEQ ID NO:56, respectively;
(c) SEQ ID NO:18 and SEQ ID NO:56, respectively; and
(d) SEQ ID NO:19 and SEQ ID NO:57, respectively.

17. The immunoconjugate of claim 13, wherein said humanized anti-ADAM9 antibody or ADAM9-binding fragment thereof is optimized to have at least a 100-fold enhancement in binding affinity to cyno ADAM9 and retains high affinity binding to human ADAM9 as compared to the chimeric or murine parental antibody.

18. The immunoconjugate of claim 17, wherein said anti-ADAM9 antibody or ADAM9-binding fragment thereof comprises a CDR_H1 domain, a CDR_H2 domain, and a CDR_H3 domain and a CDR_L1 domain, a CDR_L2 domain, and a CDR_L3 domain having the sequences selected from the group consisting of:
(a) SEQ ID NOs: 8, 35, and 37 and SEQ ID NOs: 62, 13, 14, respectively;
(b) SEQ ID NOs: 8, 35, and 38 and SEQ ID NOs: 62, 13, 14, respectively;
(c) SEQ ID NOs: 8, 35, and 39 and SEQ ID NOs: 62, 13, 14, respectively;
(d) SEQ ID NOs: 8, 35, and 40 and SEQ ID NOs: 62, 13, 14, respectively;
(e) SEQ ID NOs: 8, 35, and 41 and SEQ ID NOs: 62, 13, 14, respectively;
(f) SEQ ID NOs: 8, 35, and 42 and SEQ ID NOs: 62, 13, 14, respectively;
(g) SEQ ID NOs: 8, 35, and 43 and SEQ ID NOs: 62, 13, 14, respectively;
(h) SEQ ID NOs: 8, 35, and 44 and SEQ ID NOs: 62, 13, 14, respectively;
(i) SEQ ID NOs: 8, 35, and 45 and SEQ ID NOs: 62, 13, 14, respectively; and
(j) SEQ ID NOs: 8, 35, and 46 and SEQ ID NOs: 62, 13, 14, respectively.

19. The immunoconjugate of claim 18, wherein said humanized anti-ADAM9 antibody or ADAM9-binding fragment thereof comprises a heavy chain variable domain (VH) and a light chain variable domain (VL) having sequences that are at least 90%, at least 95%, or at least 99% identical to sequences selected from the group consisting of:
(a) SEQ ID NO:20 and SEQ ID NO:55, respectively;
(b) SEQ ID NO:21 and SEQ ID NO:55, respectively;
(c) SEQ ID NO:22 and SEQ ID NO:55, respectively;
(d) SEQ ID NO:23 and SEQ ID NO:55, respectively;
(e) SEQ ID NO:24 and SEQ ID NO:55, respectively;
(f) SEQ ID NO:25 and SEQ ID NO:55, respectively;
(g) SEQ ID NO:26 and SEQ ID NO:55, respectively;
(h) SEQ ID NO:27 and SEQ ID NO:55, respectively;
(i) SEQ ID NO:28 and SEQ ID NO:55, respectively; and
(j) SEQ ID NO:29 and SEQ ID NO:55, respectively.

20. The immunoconjugate of claim 19, wherein said humanized anti-ADAM9 antibody or ADAM9-binding fragment thereof comprises a heavy chain variable domain (VH) and a light chain variable domain (VL) having the sequences selected from the group consisting of:
(a) SEQ ID NO:20 and SEQ ID NO:55, respectively;
(b) SEQ ID NO:21 and SEQ ID NO:55, respectively;
(c) SEQ ID NO:22 and SEQ ID NO:55, respectively;
(d) SEQ ID NO:23 and SEQ ID NO:55, respectively;
(e) SEQ ID NO:24 and SEQ ID NO:55, respectively;
(f) SEQ ID NO:25 and SEQ ID NO:55, respectively;
(g) SEQ ID NO:26 and SEQ ID NO:55, respectively;
(h) SEQ ID NO:27 and SEQ ID NO:55, respectively;
(i) SEQ ID NO:28 and SEQ ID NO:55, respectively; and
(j) SEQ ID NO:29 and SEQ ID NO:55, respectively.

21. The immunoconjugate of any one of claims 13-20, wherein said humanized anti-ADAM9 antibody is a full length antibody comprising an Fc region.

22. The immunoconjugate of claim 21, wherein said humanized anti-ADAM9 antibody comprises a heavy chain and a light chain having the sequences selected from the group consisting of:
(a) SEQ ID NO:50 and SEQ ID NO:68, respectively;
(b) SEQ ID NO:51 and SEQ ID NO:68, respectively; and
(c) SEQ ID NO:52 and SEQ ID NO:68, respectively.

23. The immunoconjugate of any one of claims 13-22, wherein said Fc region is a variant Fc region that comprises:
(a) one or more amino acid modification(s) that reduces(s) the affinity of the variant Fc region for an FcγR selected from the group consisting of: L234A, L235A, and L234A and L235A; and/or
(b) an amino acid modification that introduces a cysteine residue at S442, wherein said numbering is that of the EU index as in Kabat; and/or
(c) one or more amino acid substitution(s) that extend(s) the half-life of the variant Fc region for FcRn selected from the group consisting of: M252Y, S254T, and T256E .

24. The immunoconjugate of claim 18, wherein said humanized anti-ADAM9 antibody comprises a heavy chain and a light chain having the sequences selected from the group consisting of:

(a) SEQ ID NO:141 and SEQ ID NO:68, respectively;

(b) SEQ ID NO:142 and SEQ ID NO:68, respectively;

(c) SEQ ID NO:143 and SEQ ID NO:68, respectively;

(d) SEQ ID NO:151 and SEQ ID NO:68, respectively;

(e) SEQ ID NO:152 and SEQ ID NO:68, respectively;

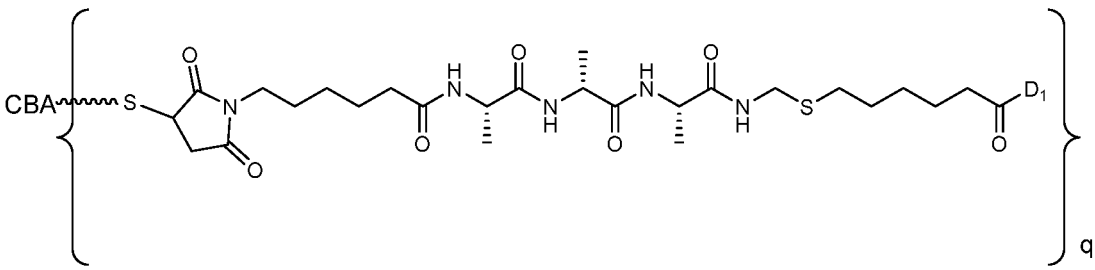
(f) SEQ ID NO:153 and SEQ ID NO:68, respectively; and

(g) SEQ ID NO:154 and SEQ ID NO:68, respectively.

25. The immunoconjugate of claim 24, wherein X in SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153 or SEQ ID NO:154 is lysine.

26. The immunoconjugate of claim 24, wherein X in SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153 or SEQ ID NO:154 is absent.

27. The immunoconjugate of claim 1, wherein the immunoconjugate is represented by the following formula:

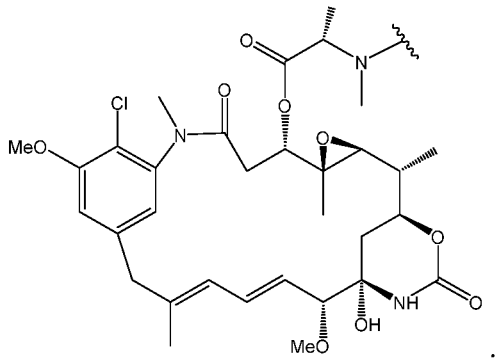


wherein:

CBA is a humanized anti-ADAM9 antibody or ADAM9-binding fragment thereof comprising a CDR_H1 domain, a CDR_H2 domain, and a CDR_H3 domain and a CDR_L1 domain, a CDR_L2 domain, and a CDR_L3 domain having the sequences of SEQ ID NOs: 8, 35, and 45 and SEQ ID NOs: 62, 13, 14, respectively;

q is 1 or 2;

D_1 is represented by the following formula:



28. The immunoconjugate of claim 27, wherein said humanized anti-ADAM9 antibody or ADAM9-binding fragment thereof comprises a heavy chain variable domain (VH) and a light chain variable domain (VL) having sequences of SEQ ID NO:28 and SEQ ID NO:55, respectively.

29. The immunoconjugate of claim 27, wherein said humanized anti-ADAM9 antibody comprises a heavy chain and a light chain having the sequences of SEQ ID NO:142 and SEQ ID NO:68, respectively.

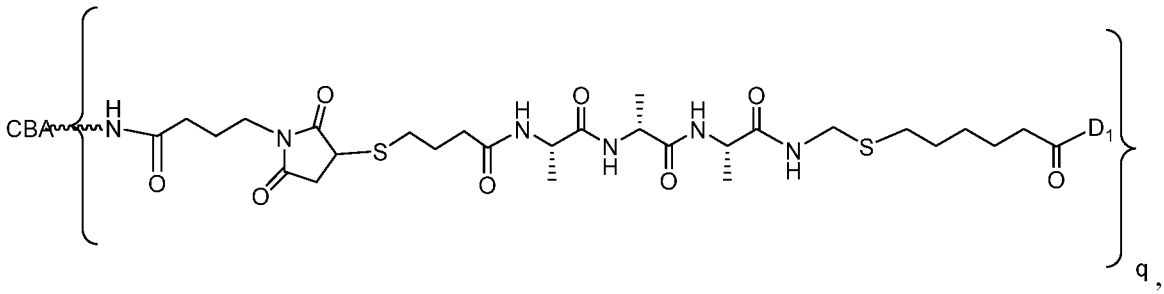
30. The immunoconjugate of claim 27, wherein said humanized anti-ADAM9 antibody comprises a heavy chain and a light chain having the sequences of SEQ ID NO:152 and SEQ ID NO:68, respectively.

31. The immunoconjugate of claim 29 or 30, wherein X in SEQ ID NO:142 or SEQ ID NO:152 is lysine.

32. The immunoconjugate of claim 29, wherein X in SEQ ID NO:142 is absent.

33. The immunoconjugate of claim 27, wherein said humanized anti-ADAM9 antibody comprises a heavy chain and a light chain having the sequences of SEQ ID NO:156 and SEQ ID NO:68, respectively.

34. The immunoconjugate of claim 1, wherein the immunoconjugate is represented by the following formula:

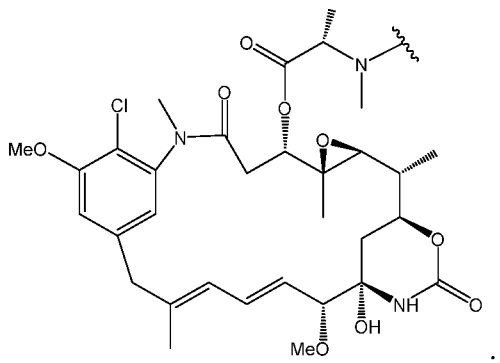


wherein:

CBA is an humanized anti-ADAM9 antibody or ADAM9-binding fragment thereof comprising a CDR_H1 domain, a CDR_H2 domain, and a CDR_H3 domain and a CDR_L1 domain, a CDR_L2 domain, and a CDR_L3 domain having the sequences of SEQ ID NOs: 8, 35, and 45 and SEQ ID NOs: 62, 13, 14, respectively;

q is an integer from 1 or 10;

D_1 is represented by the following formula:



35. The immunoconjugate of claim 33, wherein said humanized anti-ADAM9 antibody or ADAM9-binding fragment thereof comprises a heavy chain variable domain (VH) and a light chain variable domain (VL) having sequences of SEQ ID NO:28 and SEQ ID NO:55, respectively.

36. The immunoconjugate of claim 35, wherein said humanized anti-ADAM9 antibody comprises a heavy chain and a light chain having the sequences of SEQ ID NO:52 and SEQ ID NO:68, respectively.

37. The immunoconjugate of claim 34, wherein said humanized anti-ADAM9 antibody comprises a heavy chain and a light chain having the sequences of SEQ ID NO:151 and SEQ ID NO:68, respectively.

38. The immunoconjugate of claim 36 or 37, wherein X in SEQ ID NO:52 or SEQ ID NO:151 is lysine.

39. The immunoconjugate of claim 36, wherein X in SEQ ID NO:52 is absent.

40. The immunoconjugate of claim 34, wherein said humanized anti-ADAM9 antibody comprises a heavy chain and a light chain having the sequences of SEQ ID NO:155 and SEQ ID NO:68, respectively.

41. A pharmaceutical composition comprising an effective amount of the immunoconjugate of any of claims 1-40 and a pharmaceutically acceptable carrier, excipient or diluent.

42. A method for treating a disease or condition associated with, or characterized by, the expression of ADAM9 in a subject comprising administering to said subject an effective amount of the immunoconjugate of any one of claims 1-40 or the pharmaceutical composition of claim 41.

43. The method of claim 42, wherein said disease or condition associated with, or characterized by, the expression of ADAM9 is cancer.

44. The method of claims 43, wherein said cancer is selected from the group consisting of non-small-cell lung cancer, colorectal cancer, bladder cancer, gastric cancer, pancreatic cancer, renal cell carcinoma, prostate cancer, esophageal cancer, breast cancer, head and neck cancer, uterine cancer, ovarian cancer, liver cancer, cervical cancer, thyroid cancer, testicular cancer, myeloid cancer, melanoma, and lymphoid cancer.

45. The method of claim 44, wherein said non-small-cell lung cancer is squamous cell carcinoma, nonsquamous cell carcinoma, adenocarcinoma, or large-cell undifferentiated carcinoma.

46. The method of claim 44, wherein said colorectal cancer is adenocarcinoma, gastrointestinal carcinoid tumors, gastrointestinal stromal tumors, primary colorectal lymphoma, leiomyosarcoma, or squamous cell carcinoma.

47. The method of claim 42, wherein the method is for treating non-small-cell lung cancer, gastric cancer, pancreatic cancer, triple negative breast cancer (TNBC) or colorectal cancer.

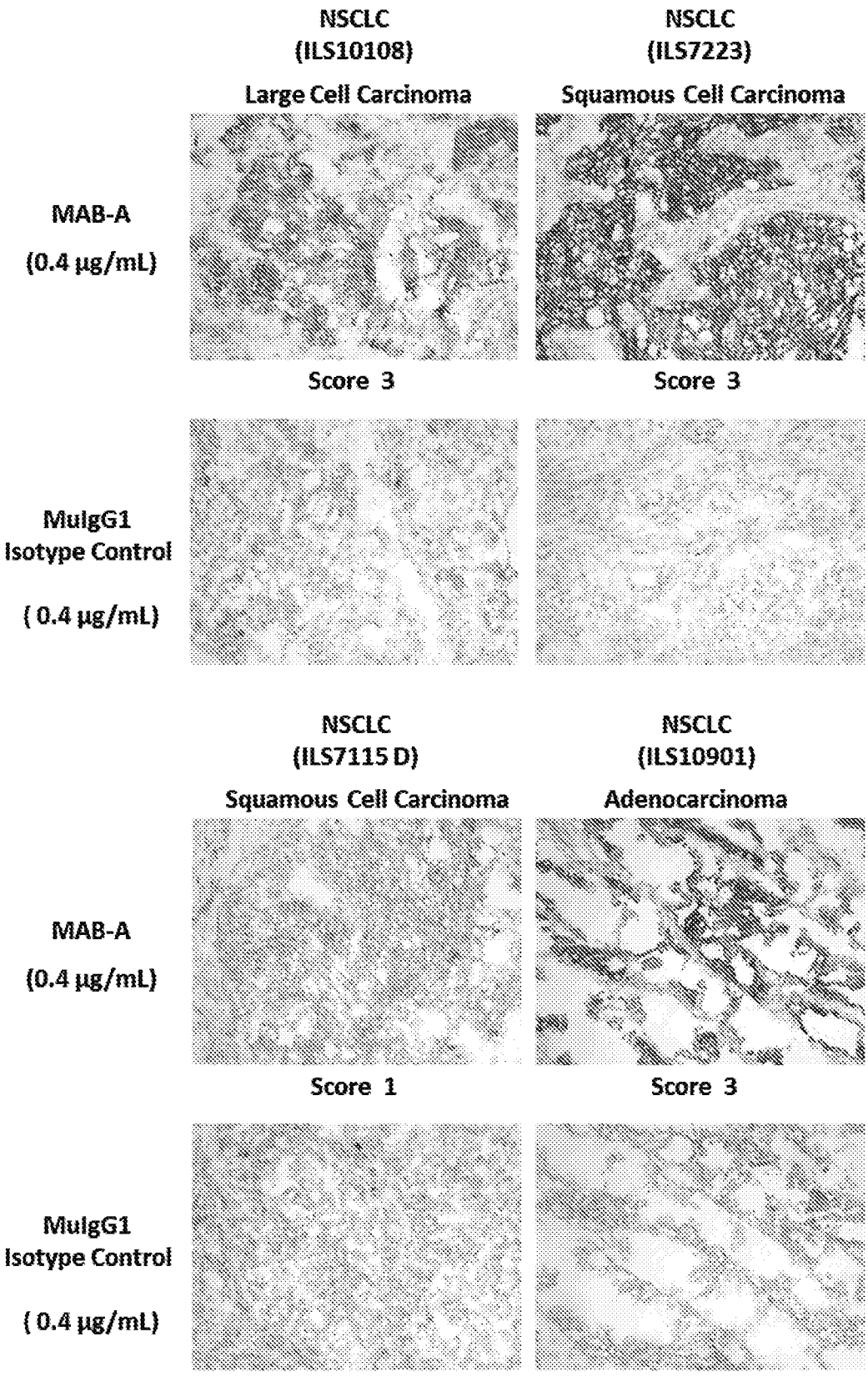

NSCLC
(ILS10108)
Large Cell Carcinoma
NSCLC
(ILS7223)
Squamous Cell Carcinoma
MAB-A
(0.4 µg/mL)
Score 3
Score 3
MuIgG1
Isotype Control
(0.4 µg/mL)
NSCLC
(ILS7115 D)
Squamous Cell Carcinoma
NSCLC
(ILS10901)
Adenocarcinoma
MAB-A
(0.4 µg/mL)
Score 1
Score 3
MuIgG1
Isotype Control
(0.4 µg/mL)

FIG. 1A

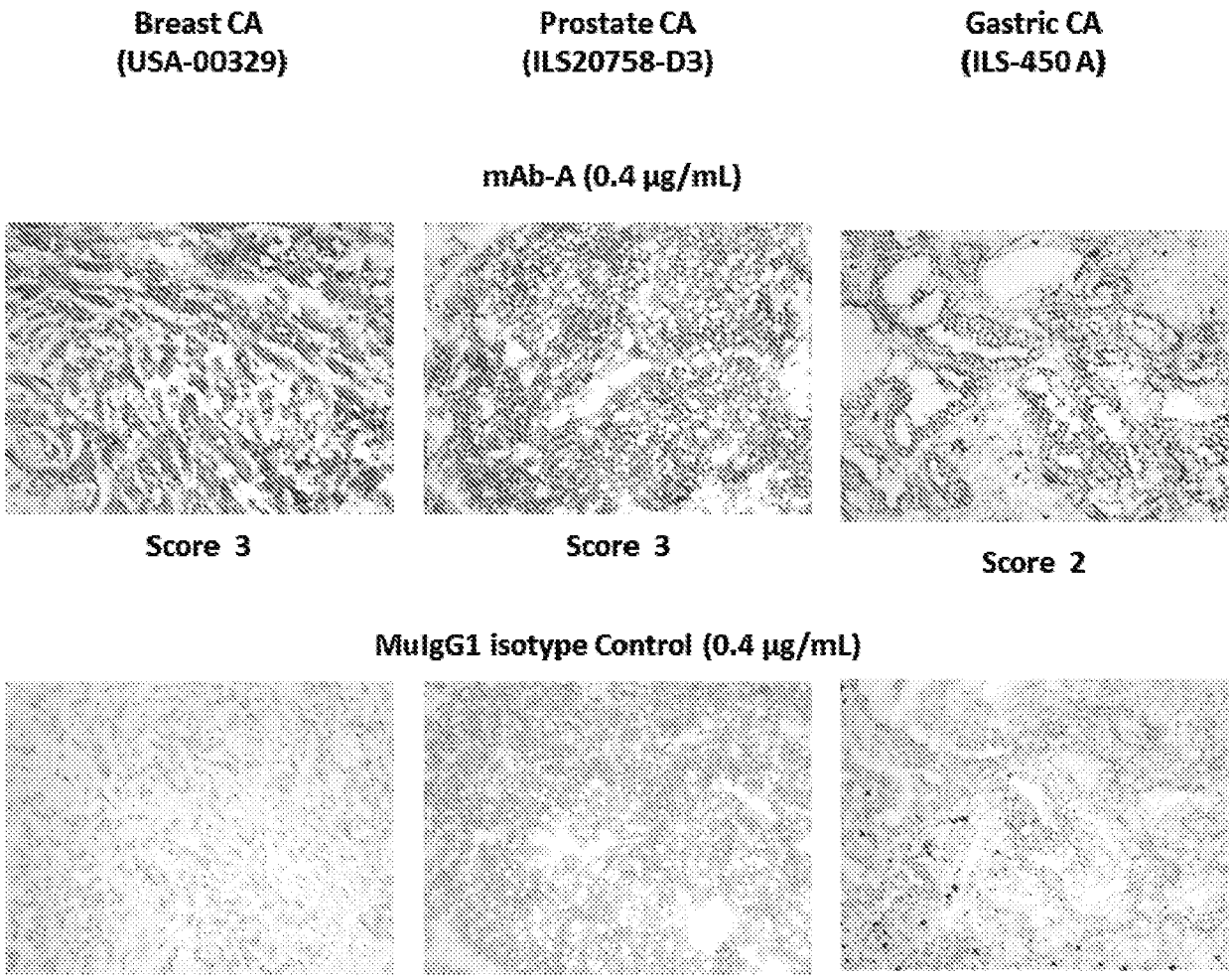

Breast CA
(USA-00329)
Prostate CA
(ILS20758-D3)
Gastric CA
(ILS-450 A)
mAb-A (0.4 µg/mL)
Score 3
Score 3
Score 2
MuIgG1 isotype Control (0.4 µg/mL)

FIG. 1B

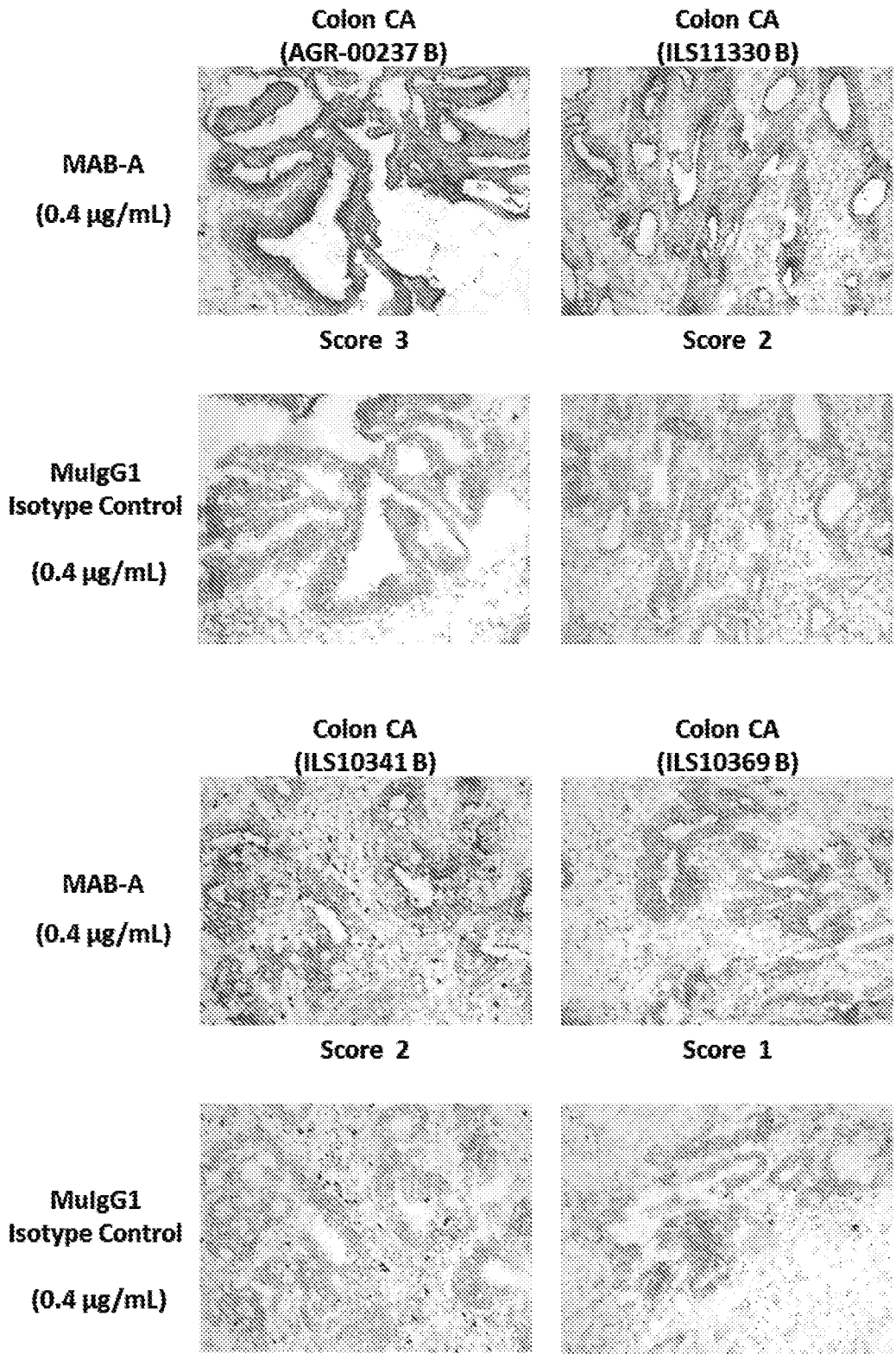

Colon CA
(AGR-00237 B)
Colon CA
(ILS11330 B)
MAB-A
(0.4 µg/mL)
Score 3
Score 2
MuIgG1
Isotype Control
(0.4 µg/mL)
Colon CA
(ILS10341 B)
Colon CA
(ILS10369 B)
MAB-A
(0.4 µg/mL)
Score 2
Score 1
MuIgG1
Isotype Control
(0.4 µg/mL)

FIG. 1C

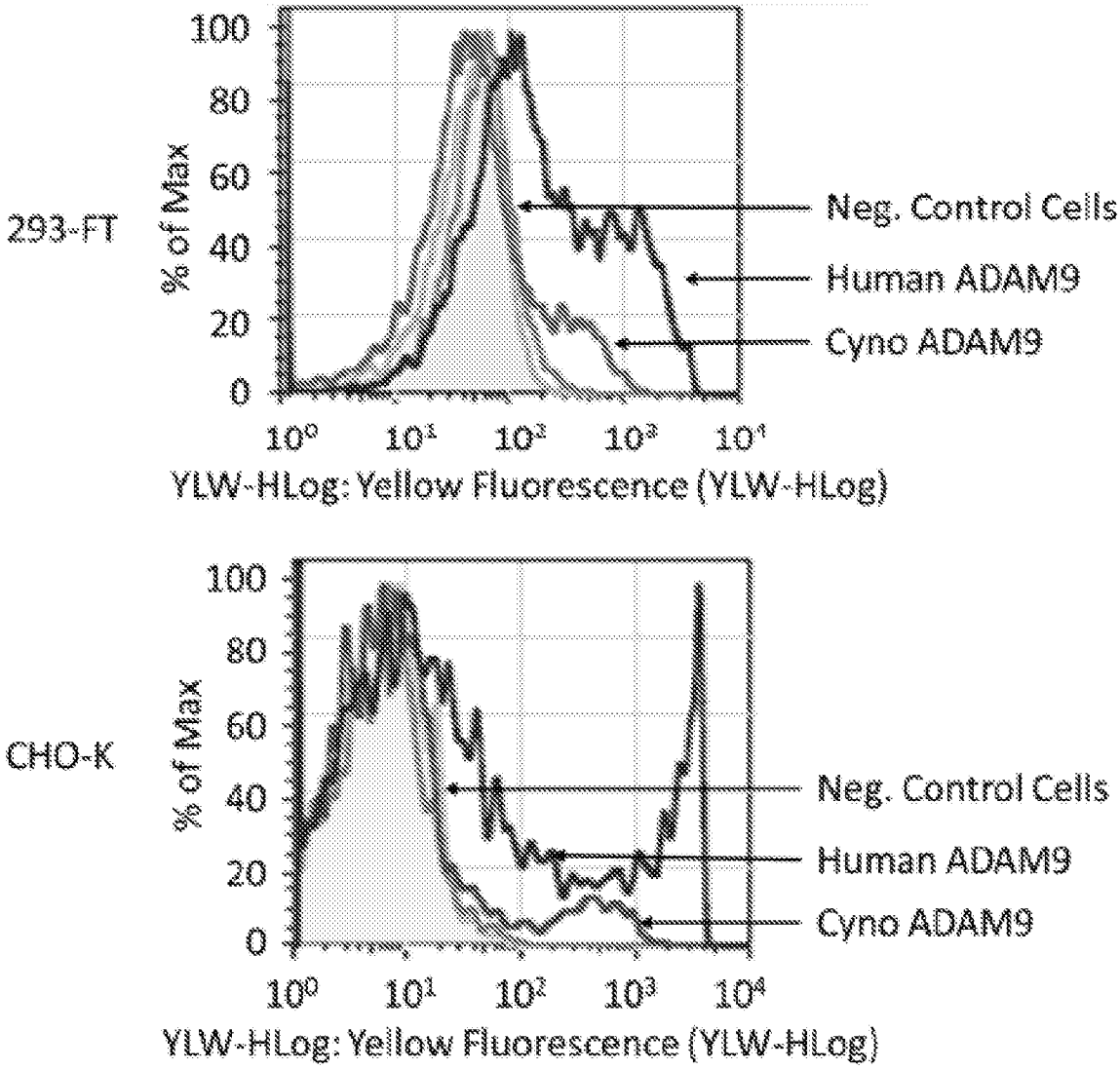

293-FT
100
80
60
40
20
0
% of Max
Neg. Control Cells
Human ADAM9
Cyno ADAM9
10⁰ 10¹ 10² 10³ 10⁴
YLW-HLog: Yellow Fluorescence (YLW-HLog)
CHO-K
100
80
60
40
20
0
% of Max
Neg. Control Cells
Human ADAM9
Cyno ADAM9
10⁰ 10¹ 10² 10³ 10⁴
YLW-HLog: Yellow Fluorescence (YLW-HLog)

FIG. 2

		FR1	CDR1
murine MAB-A VH	**SEQ ID NO:7**	QVQLQQPGAELVKPGASVKLSCKASGYTFT	SYWMH
hMAB-A VH(1)	**SEQ ID NO:16**	E...VES.GG.....G.LR...A...F..S	.....
hMAB-A VH(2)	**SEQ ID NO:17**	E...VES.GG.....G.LR...A...F..S	.....
hMAB-A VH(3)	**SEQ ID NO:18**	E...VES.GG.....G.LR...A...F..S	.....
hMAB-A VH(4)	**SEQ ID NO:19**	E...VES.GG.....G.LR...A...F..S	...I.
hMAB-A VH(2B)	**SEQ ID NO:21**	E...VES.GG.....G.LR...A...F..S	.....
hMAB-A VH(2C)	**SEQ ID NO:22**	E...VES.GG.....G.LR...A...F..S	.....
hMAB-A VH(2D)	**SEQ ID NO:23**	E...VES.GG.....G.LR...A...F..S	.....
hMAB-A VH(2I)	**SEQ ID NO:28**	E...VES.GG.....G.LR...A...F..S	.....

FR2	CDR2	FR3
WVKQRPGQGLEWIG	EIIPINGHTNYNEKFKS	KATLTLDKSSSTAYMQLSSLASEDSAVYYCAR
..R.A..K....V.	.....	RF.IS..N.KN.L.L.MG..RA..T.....
..R.A..K....V.	.....F.....	RF.IS..N.KN.L.L.MG..RA..T.....
..R.A..K....V.	.....F.....R.QG	RF.IS..N.KN.L.L.MG..RA..T.....
..R.A..K....V.	.....F.....R.QG	RF.IS..N.KN.L.L.MG..RA..T.....
..R.A..K....V.	.....F.....	RF.IS..N.KN.L.L.MG..RA..T.....
..R.A..K....V.	.....F.....	RF.IS..N.KN.L.L.MG..RA..T.....
..R.A..K....V.	.....F.....	RF.IS..N.KN.L.L.MG..RA..T.....
..R.A..K....V.	.....F.....	RF.IS..N.KN.L.L.MG..RA..T.....

CDR3	FR4
GGYYYYGSRDYFDY	WGQGTTLTVSS
.....	......V....
.....	......V....
.....	......V....
.....	......V....
......IGKGVL..	......V....
......PRFGWL..	......V....
......TGKGVL..	......V....
......PRQGFL..	......V....

FIG. 3A

		FR1	CDR1
murine MAB-A VL	**SEQ ID NO:11**	DIVLTQSPASLAVSLGQRATISC	KASQSVDYDGDSYMN
hMAB-A VL(1)	**SEQ ID NO:54**	...M....D.......E.....	....
hMAB-A VL(2)	**SEQ ID NO:55**	...M....D.......E.....	........S......
hMAB-A VL(3)	**SEQ ID NO:56**	...M....D.......E.....	R.......S......
hMAB-A VL(4)	**SEQ ID NO:57**	...M....D.......E.....	R.......S....L.

FR2	CDR2	FR3	CDR3	FR4
WYQQIPGQPPKLLIY	AASDLES	GIPARFSGSGSGTDFTLNIHPVEEEDAATYYC	QQSHEDPFT	FGGGTKLEIK
....K..........	....	..................T.SSL.P..F.....	....	....
....K..........	....	..................T.SSL.P..F.....	....	....
....K..........	....	..................T.SSL.P..F.....	....	....
....K..........	....	..................T.SSL.P..F.....	...YST...	....

FIG. 3B

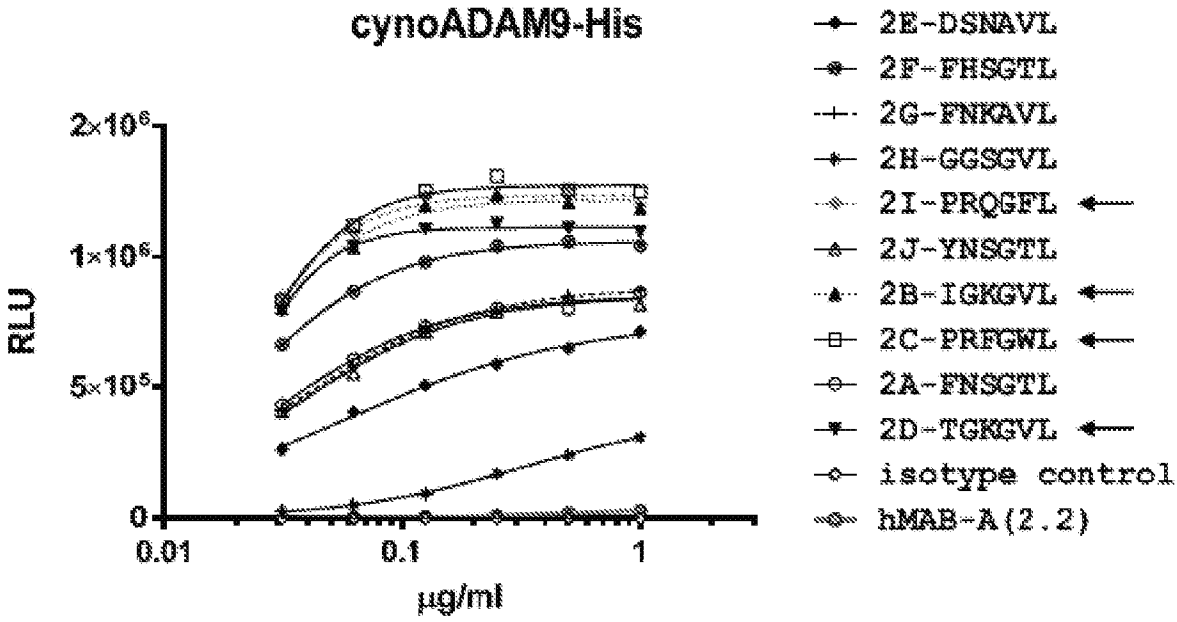

cynoADAM9-His
RLU
2×10⁶
1×10⁶
5×10⁵
0
0.01
0.1
1
µg/ml
2E-DSNAVL
2F-FHSGTL
2G-FNKAVL
2H-GGSGVL
2I-PRQGFL
2J-YNSGTL
2B-IGKGVL
2C-PRFGWL
2A-FNSGTL
2D-TGKGVL
isotype control
hMAB-A(2.2)

FIG. 4A

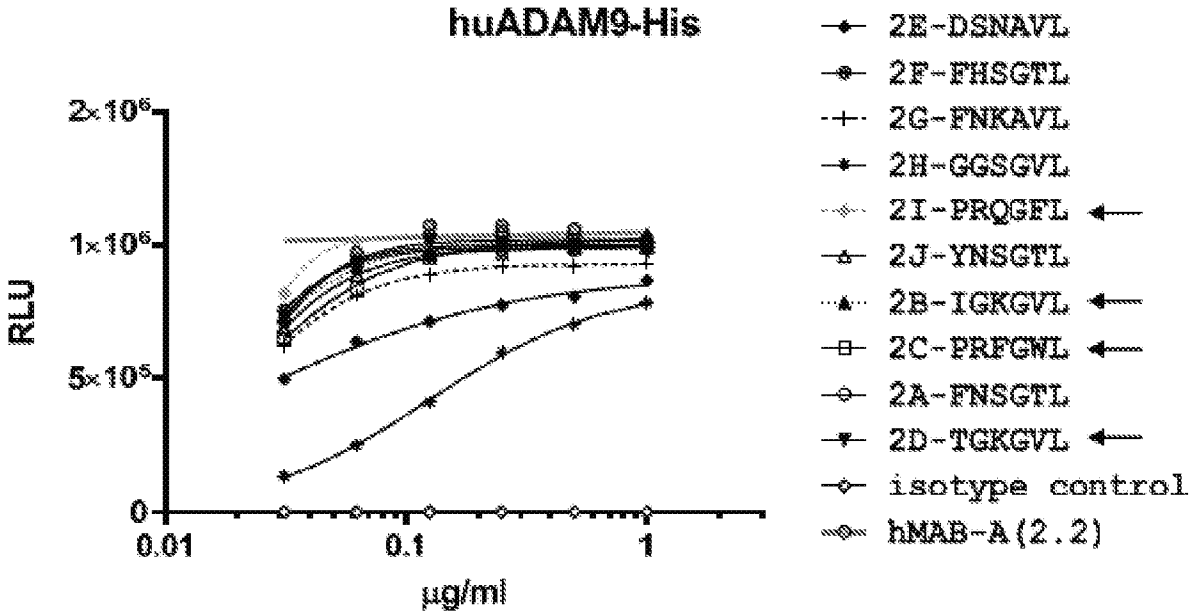

huADAM9-His
RLU
2×10⁶
1×10⁶
5×10⁵
0
0.01
0.1
1
µg/ml
2E-DSNAVL
2F-FHSGTL
2G-FNKAVL
2H-GGSGVL
2I-PRQGFL
2J-YNSGTL
2B-IGKGVL
2C-PRFGWL
2A-FNSGTL
2D-TGKGVL
isotype control
hMAB-A(2.2)

FIG. 4B

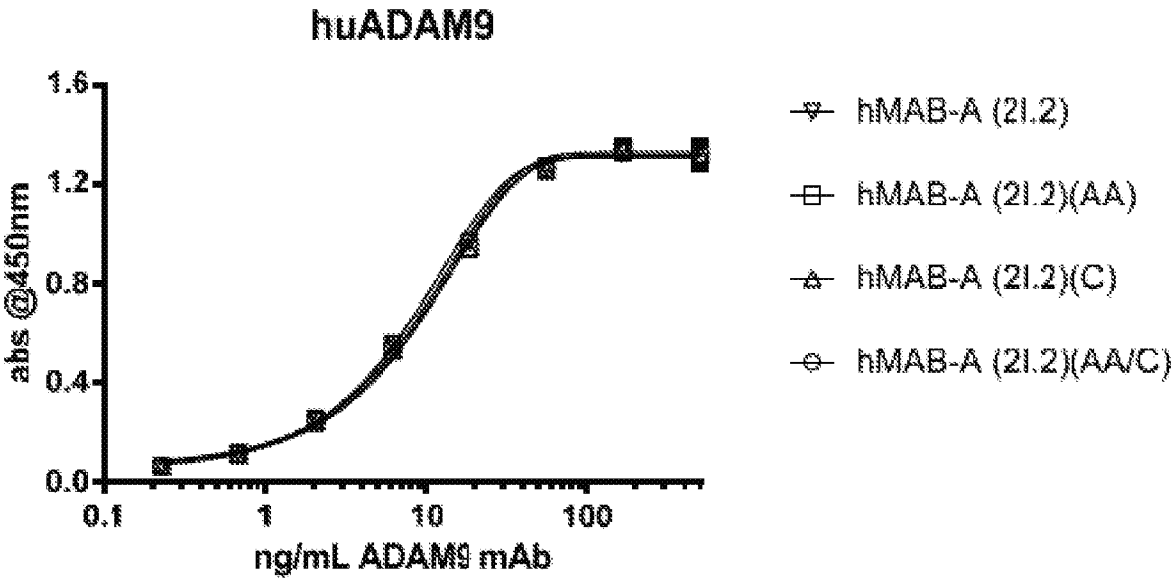

huADAM9
abs @450nm
1.6
1.2
0.8
0.4
0.0
0.1
1
10
100
ng/mL ADAM9 mAb
hMAB-A (2I.2)
hMAB-A (2I.2)(AA)
hMAB-A (2I.2)(C)
hMAB-A (2I.2)(AA/C)

FIG. 5A

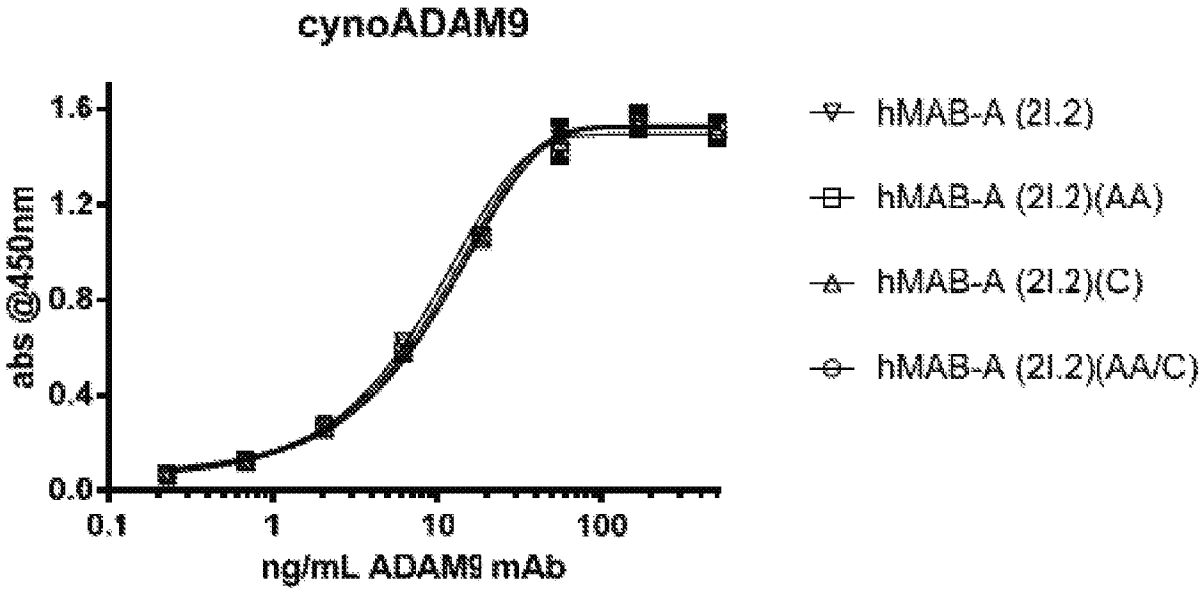

cynoADAM9
abs @450nm
1.6
1.2
0.8
0.4
0.0
0.1
1
10
100
ng/mL ADAM9 mAb
hMAB-A (2I.2)
hMAB-A (2I.2)(AA)
hMAB-A (2I.2)(C)
hMAB-A (2I.2)(AA/C)

FIG. 5B

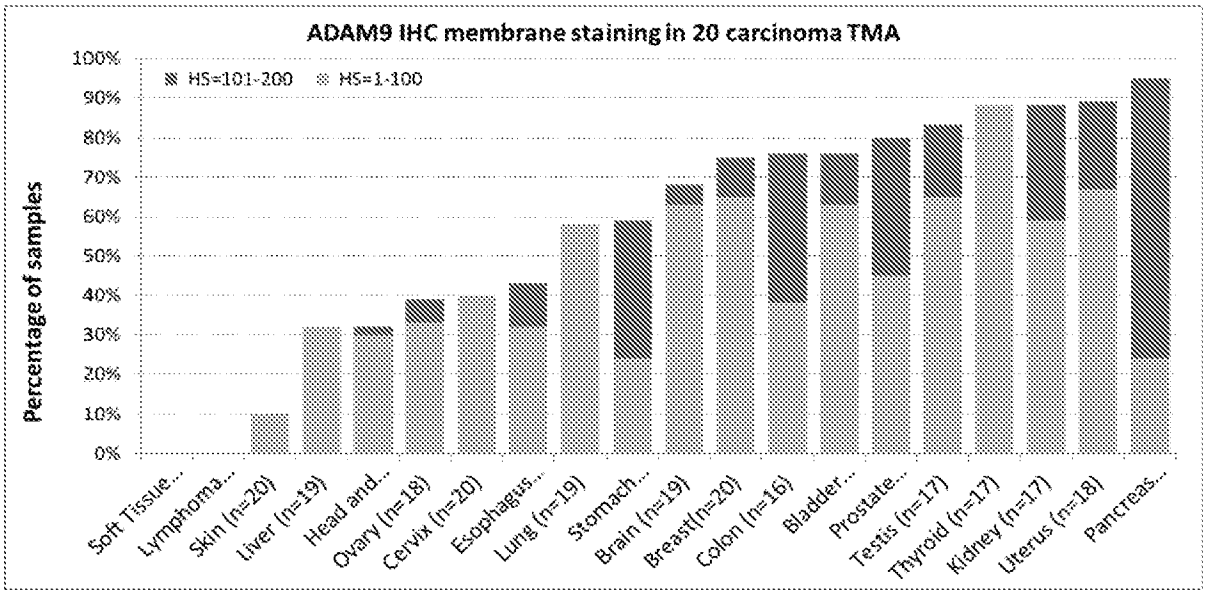

ADAM9 IHC membrane staining in 20 carcinoma TMA
HS=101-300
HS=1-100
Percentage of samples
100%
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
Soft Tissue...
Lymphoma...
Skin (n=20)
Liver (n=19)
Head and...
Ovary (n=18)
Cervix (n=20)
Esophagus...
Lung (n=19)
Stomach...
Brain (n=19)
Breast(n=20)
Colon (n=16)
Bladder...
Prostate...
Testis (n=17)
Thyroid (n=17)
Kidney (n=17)
Uterus (n=18)
Pancreas...

FIG. 6A

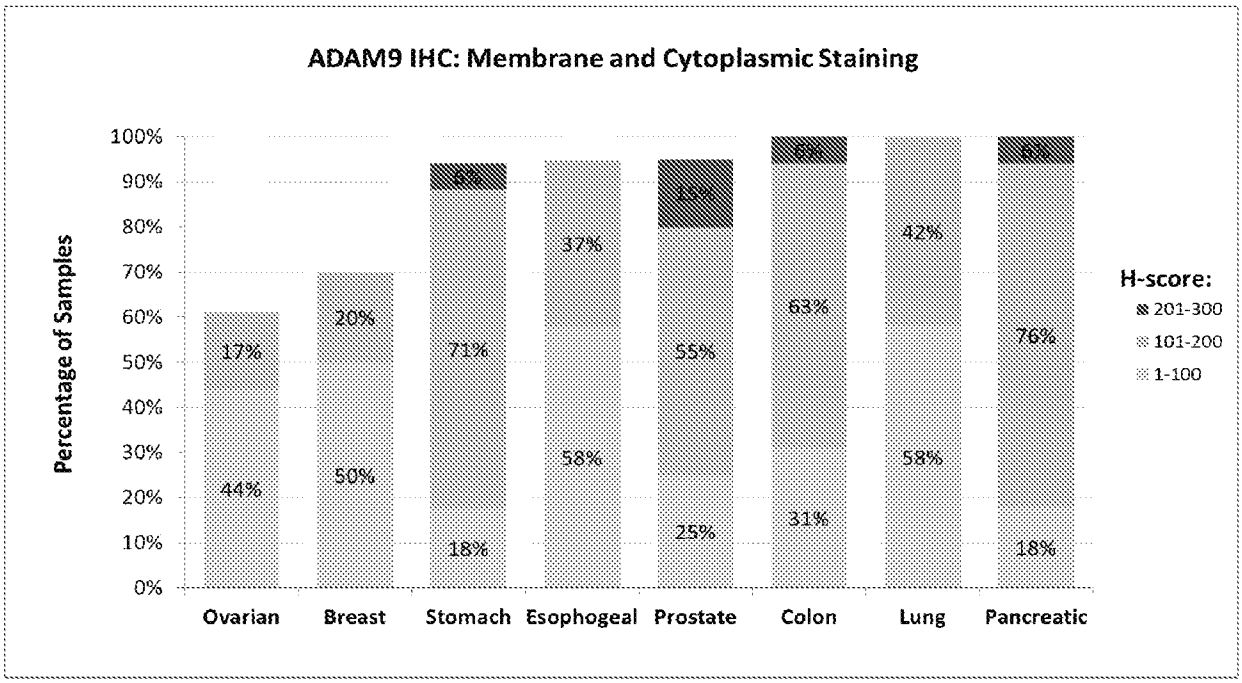

ADAM9 IHC: Membrane and Cytoplasmic Staining
Percentage of Samples
100%
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
17%
44%
20%
50%
6%
71%
18%
37%
58%
14%
55%
25%
6%
63%
31%
42%
58%
6%
76%
18%
Ovarian
Breast
Stomach
Esophogeal
Prostate
Colon
Lung
Pancreatic
H-score:
201-300
101-200
1-100

FIG. 6B

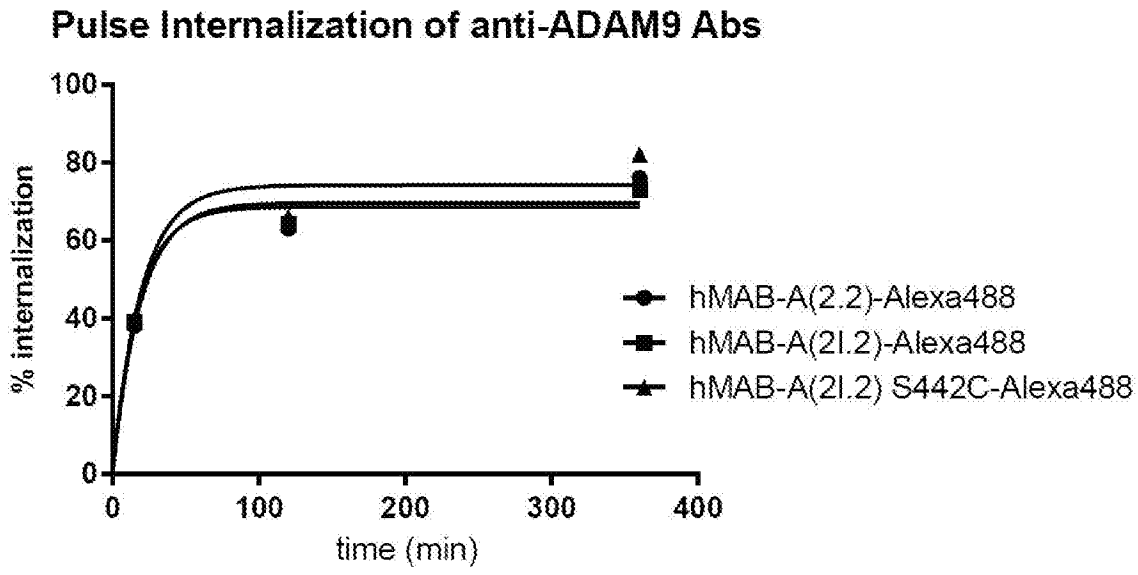

Pulse Internalization of anti-ADAM9 Abs
% internalization
100
80
60
40
20
0
0
100
200
300
400
time (min)
hMAB-A(2.2)-Alexa488
hMAB-A(2I.2)-Alexa488
hMAB-A(2I.2) S442C-Alexa488

FIG. 7A

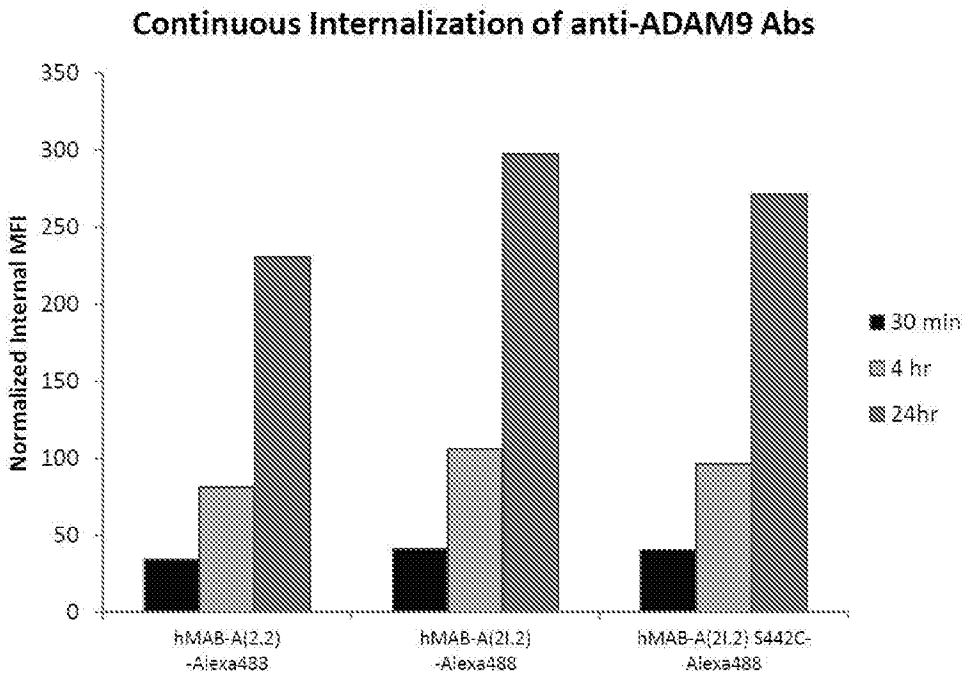

Continuous Internalization of anti-ADAM9 Abs
Normalized Internal MFI
350
300
250
200
150
100
50
0
hMAB-A(2.2) -Alexa488
hMAB-A(2I.2) -Alexa488
hMAB-A(2I.2) S442C-Alexa488
30 min
4 hr
24hr

FIG. 7B

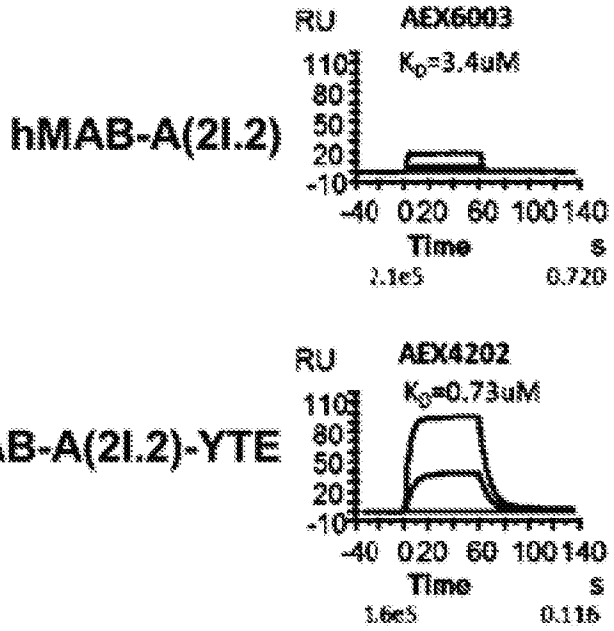

hMAB-A(2I.2)
RU
AEX6003
K_D=3.4uM
110
80
50
20
-10
-40 020 60 100 140
Time
s
2.1e5
0.720
hMAB-A(2I.2)-YTE
RU
AEX4202
K_D=0.73uM
110
80
50
20
-10
-40 020 60 100 140
Time
s
1.6e5
0.116

FIG. 8A

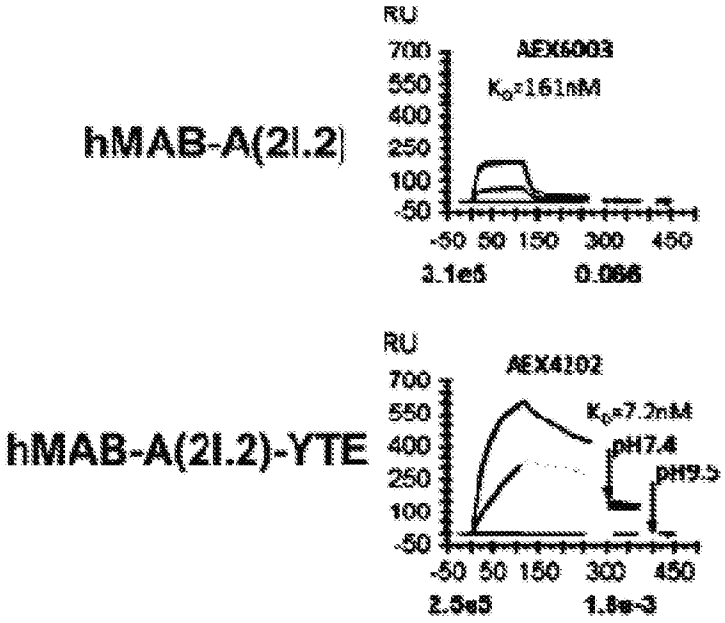
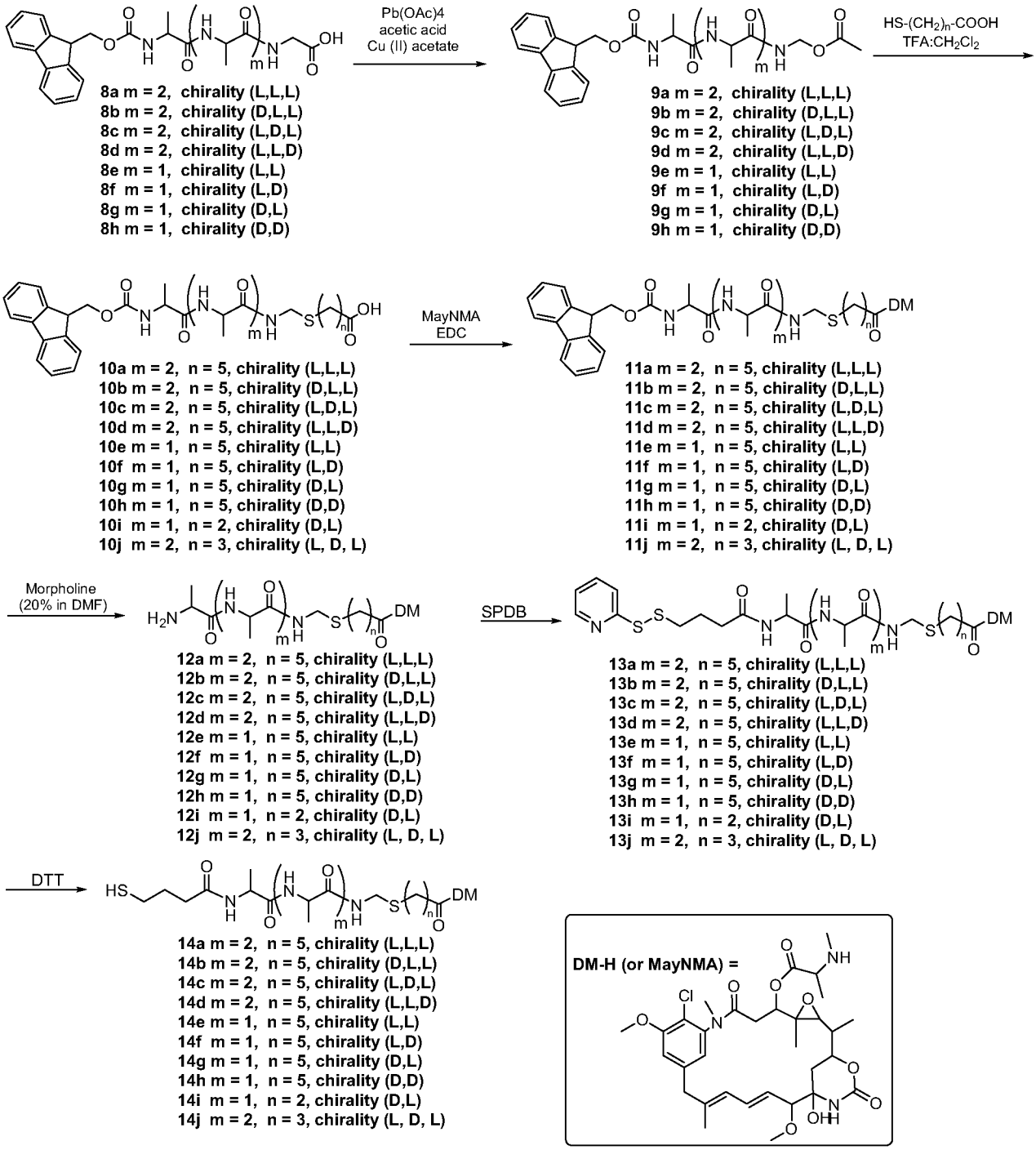

hMAB-A(2I.2)
RU
700
550
400
250
100
-50
AEX6003
K_D=161nM
-50 50 150 300 450
3.1e5
0.066
hMAB-A(2I.2)-YTE
RU
700
550
400
250
100
-50
AEX4102
K_D=7.2nM
pH7.4
pH9.5
-50 50 150 300 450
2.5e3
1.8e-3

FIG. 8B



8a m = 2, chirality (L,L,L)
8b m = 2, chirality (D,L,L)
8c m = 2, chirality (L,D,L)
8d m = 2, chirality (L,L,D)
8e m = 1, chirality (L,L)
8f m = 1, chirality (L,D)
8g m = 1, chirality (D,L)
8h m = 1, chirality (D,D)

9a m = 2, chirality (L,L,L)
9b m = 2, chirality (D,L,L)
9c m = 2, chirality (L,D,L)
9d m = 2, chirality (L,L,D)
9e m = 1, chirality (L,L)
9f m = 1, chirality (L,D)
9g m = 1, chirality (D,L)
9h m = 1, chirality (D,D)

10a m = 2, n = 5, chirality (L,L,L)
10b m = 2, n = 5, chirality (D,L,L)
10c m = 2, n = 5, chirality (L,D,L)
10d m = 2, n = 5, chirality (L,L,D)
10e m = 1, n = 5, chirality (L,L)
10f m = 1, n = 5, chirality (L,D)
10g m = 1, n = 5, chirality (D,L)
10h m = 1, n = 5, chirality (D,D)
10i m = 1, n = 2, chirality (D,L)
10j m = 2, n = 3, chirality (L, D, L)

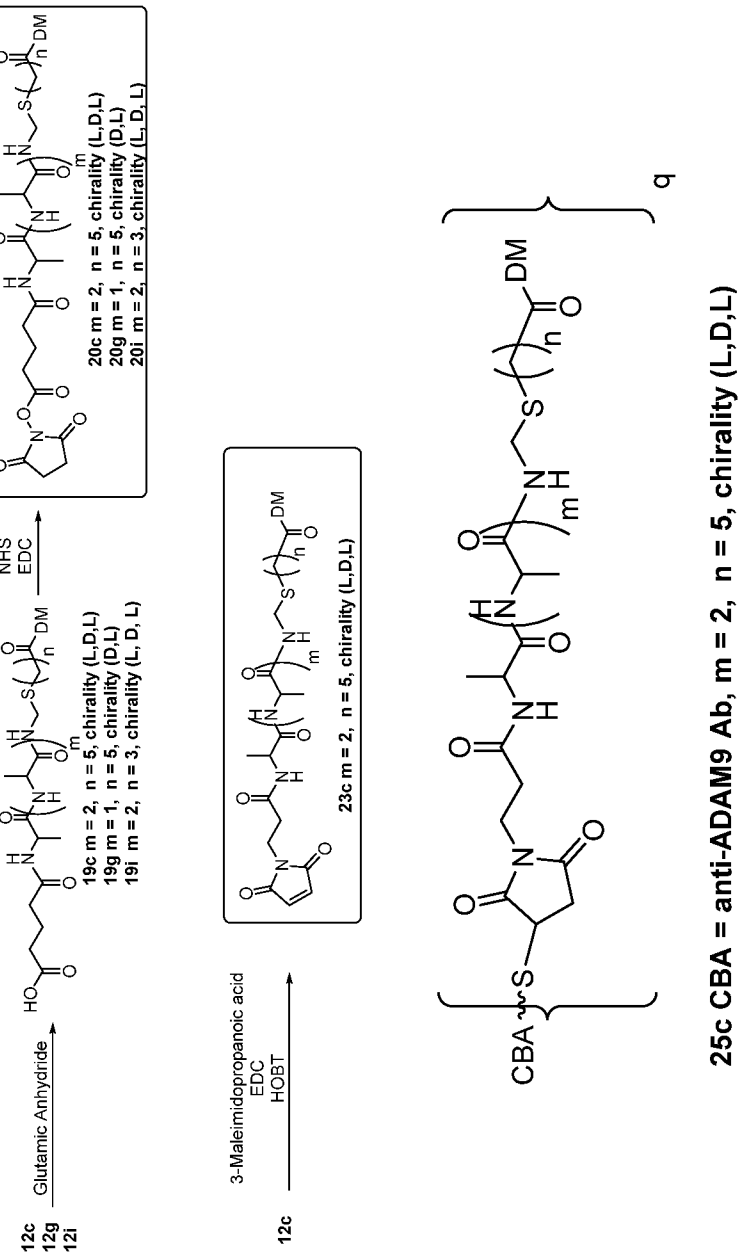
11a m = 2, n = 5, chirality (L,L,L)
11b m = 2, n = 5, chirality (D,L,L)
11c m = 2, n = 5, chirality (L,D,L)
11d m = 2, n = 5, chirality (L,L,D)
11e m = 1, n = 5, chirality (L,L)
11f m = 1, n = 5, chirality (L,D)
11g m = 1, n = 5, chirality (D,L)
11h m = 1, n = 5, chirality (D,D)
11i m = 1, n = 2, chirality (D,L)
11j m = 2, n = 3, chirality (L, D, L)

12a m = 2, n = 5, chirality (L,L,L)
12b m = 2, n = 5, chirality (D,L,L)
12c m = 2, n = 5, chirality (L,D,L)
12d m = 2, n = 5, chirality (L,L,D)
12e m = 1, n = 5, chirality (L,L)
12f m = 1, n = 5, chirality (L,D)
12g m = 1, n = 5, chirality (D,L)
12h m = 1, n = 5, chirality (D,D)
12i m = 1, n = 2, chirality (D,L)
12j m = 2, n = 3, chirality (L, D, L)

13a m = 2, n = 5, chirality (L,L,L)
13b m = 2, n = 5, chirality (D,L,L)
13c m = 2, n = 5, chirality (L,D,L)
13d m = 2, n = 5, chirality (L,L,D)
13e m = 1, n = 5, chirality (L,L)
13f m = 1, n = 5, chirality (L,D)
13g m = 1, n = 5, chirality (D,L)
13h m = 1, n = 5, chirality (D,D)
13i m = 1, n = 2, chirality (D,L)
13j m = 2, n = 3, chirality (L, D, L)

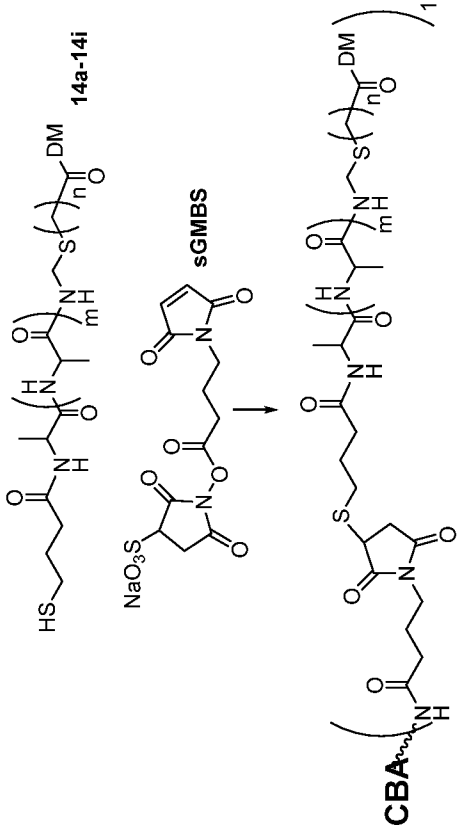
14a m = 2, n = 5, chirality (L,L,L)
14b m = 2, n = 5, chirality (D,L,L)
14c m = 2, n = 5, chirality (L,D,L)
14d m = 2, n = 5, chirality (L,L,D)
14e m = 1, n = 5, chirality (L,L)
14f m = 1, n = 5, chirality (L,D)
14g m = 1, n = 5, chirality (D,L)
14h m = 1, n = 5, chirality (D,D)
14i m = 1, n = 2, chirality (D,L)
14j m = 2, n = 3, chirality (L, D, L)

FIG. 9A



25c CBA = anti-ADAM9 Ab, m = 2, n = 5, chirality (L,D,L)

FIG. 9B



24a m = 2, n = 5, chirality (L,L,L)
24b m = 2, n = 5, chirality (D,L,L)
24c m = 2, n = 5, chirality (L,D,L)
24d m = 2, n = 5, chirality (L,L,D)
24e m = 1, n = 5, chirality (L,L)
24f m = 1, n = 5, chirality (L,D)
24g m = 1, n = 5, chirality (D,L)
24h m = 1, n = 2, chirality (D,L)
24i m = 2, n = 3, chirality (L, D, L)

CBA = anti-ADAM9 antibody

FIG. 9C

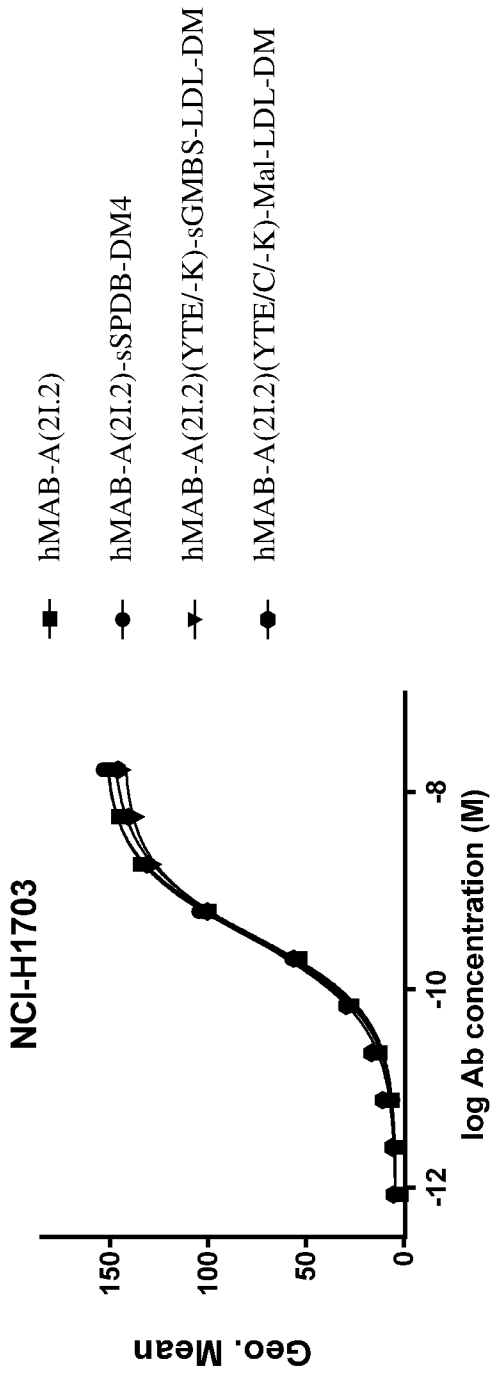

hMAB-A(2I.2)
hMAB-A(2I.2)-sSPDB-DM4
hMAB-A(2I.2)(YTE/-K)-sGMBS-LDL-DM
hMAB-A(2I.2)(YTE/C/-K)-Mal-LDL-DM
NCI-H1703
Geo. Mean
150
100
50
0
-12
-10
-8
log Ab concentration (M)

FIG. 10

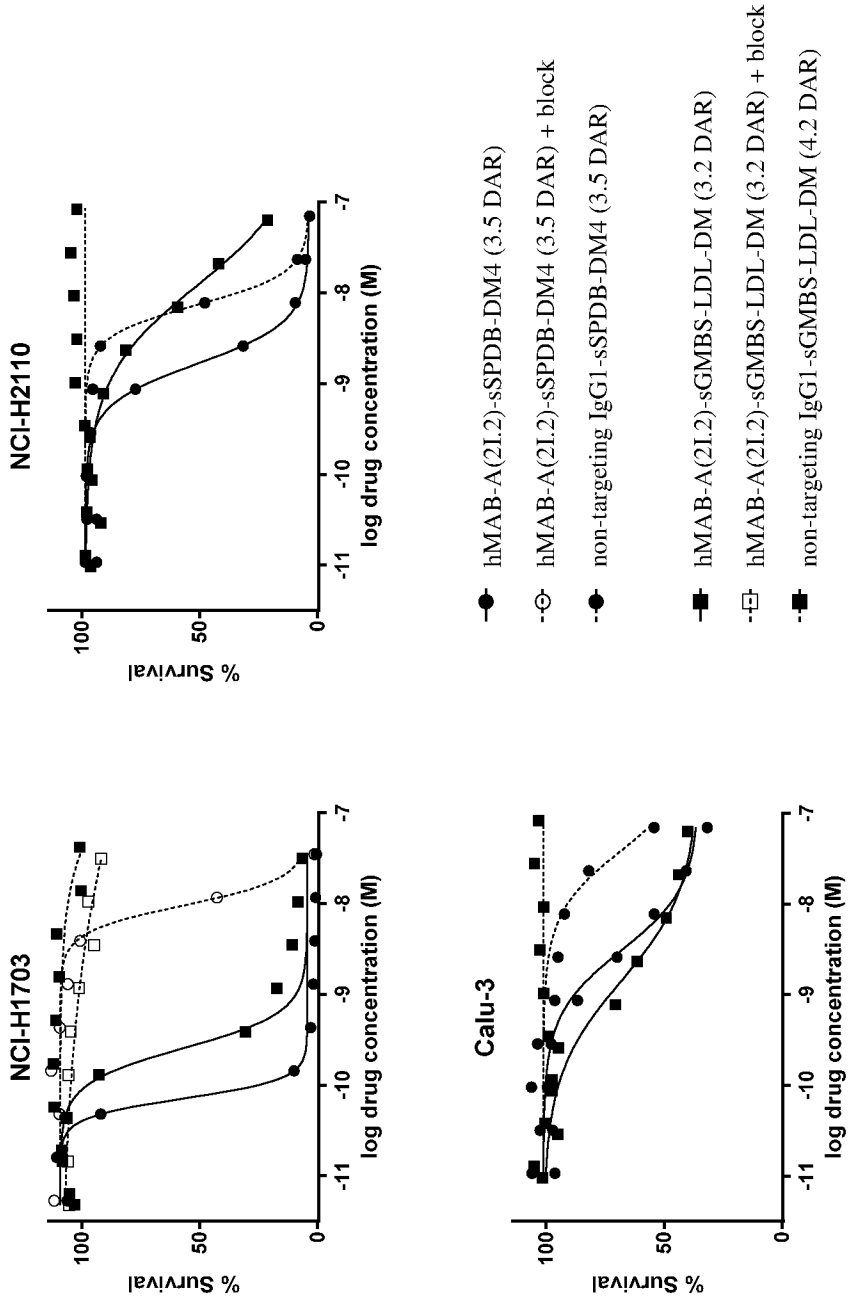

NCI-H2110
NCI-H1703
Calu-3
% Survival
log drug concentration (M)
100
50
0
-7
-8
-9
-10
-11
hMAB-A(2I.2)-sSPDB-DM4 (3.5 DAR)
hMAB-A(2I.2)-sSPDB-DM4 (3.5 DAR) + block
non-targeting IgG1-sSPDB-DM4 (3.5 DAR)
hMAB-A(2I.2)-sGMBS-LDL-DM (3.2 DAR)
hMAB-A(2I.2)-sGMBS-LDL-DM (3.2 DAR) + block
non-targeting IgG1-sGMBS-LDL-DM (4.2 DAR)

FIG. 11A

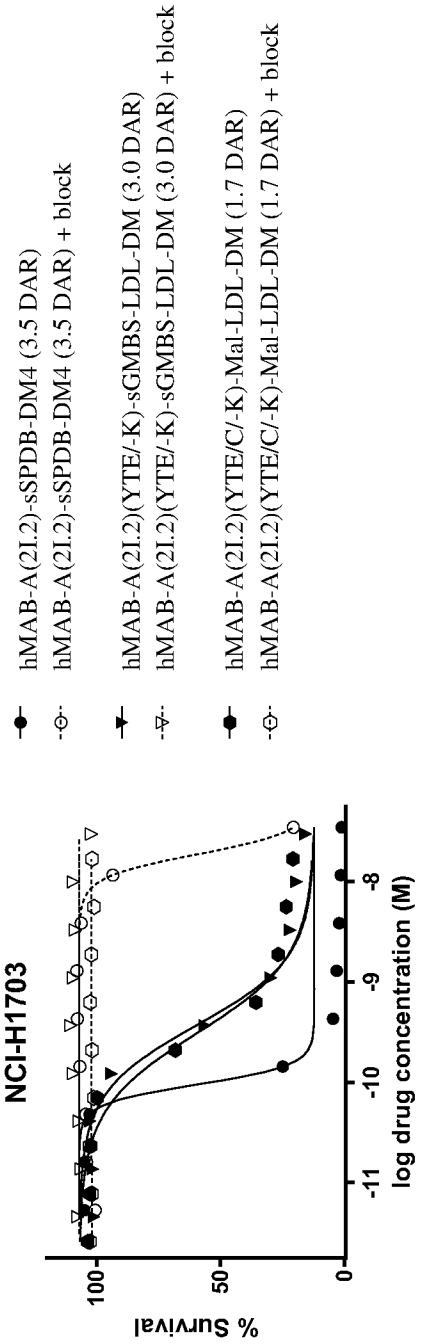
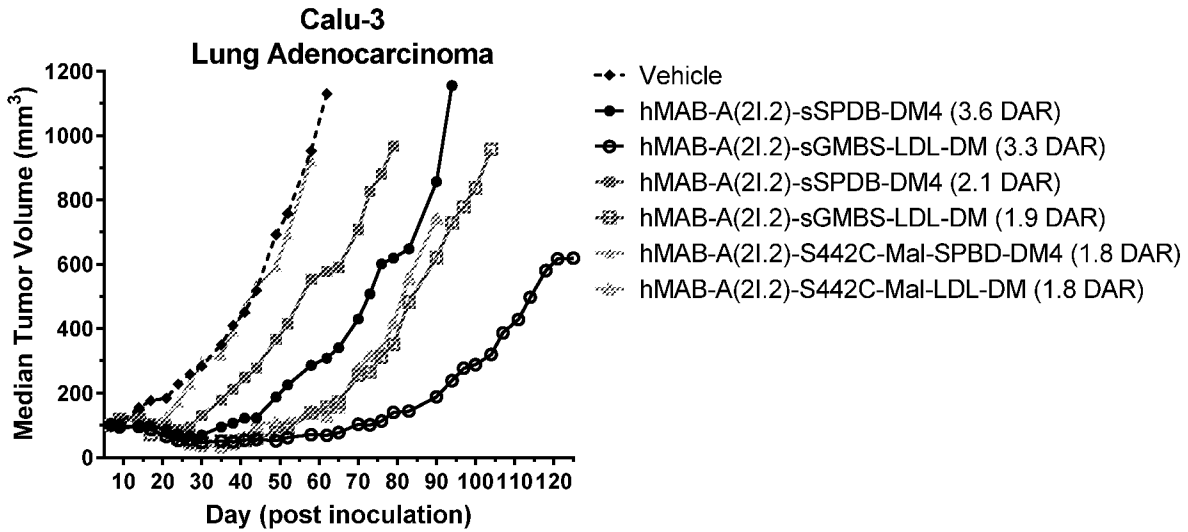
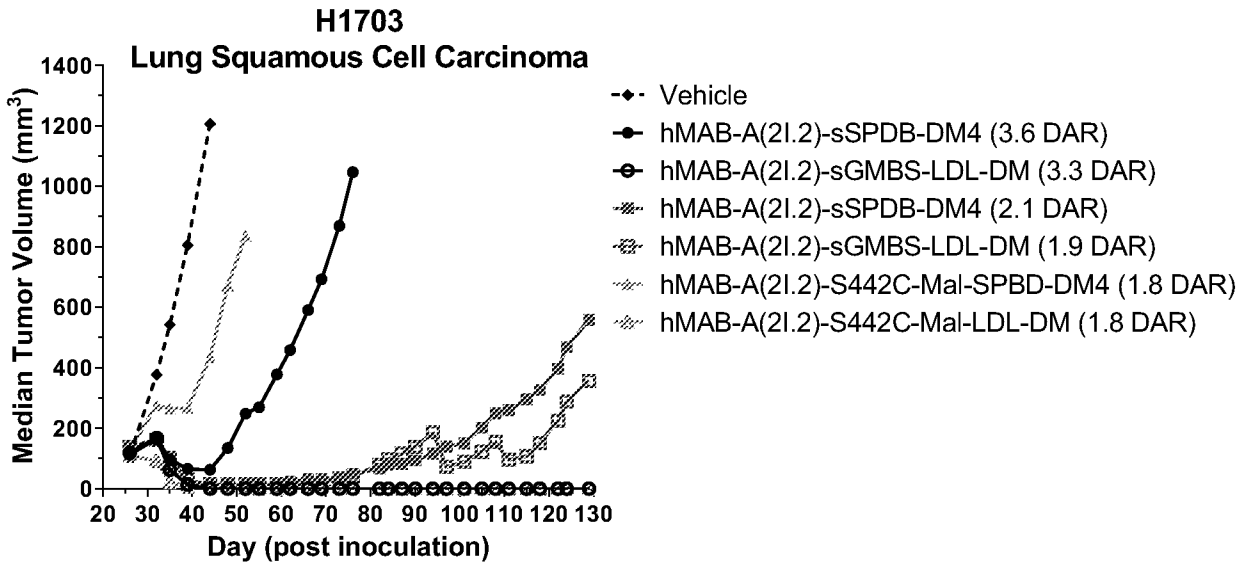

NCI-H1703
% Survival
100
50
0
-11
-10
-9
-8
log drug concentration (M)
hMAB-A(2l.2)-sSPDB-DM4 (3.5 DAR)
hMAB-A(2l.2)-sSPDB-DM4 (3.5 DAR) + block
hMAB-A(2l.2)(YTE/-K)-sGMBS-LDL-DM (3.0 DAR)
hMAB-A(2l.2)(YTE/-K)-sGMBS-LDL-DM (3.0 DAR) + block
hMAB-A(2l.2)(YTE/C/-K)-Mal-LDL-DM (1.7 DAR)
hMAB-A(2l.2)(YTE/C/-K)-Mal-LDL-DM (1.7 DAR) + block

FIG. 11B



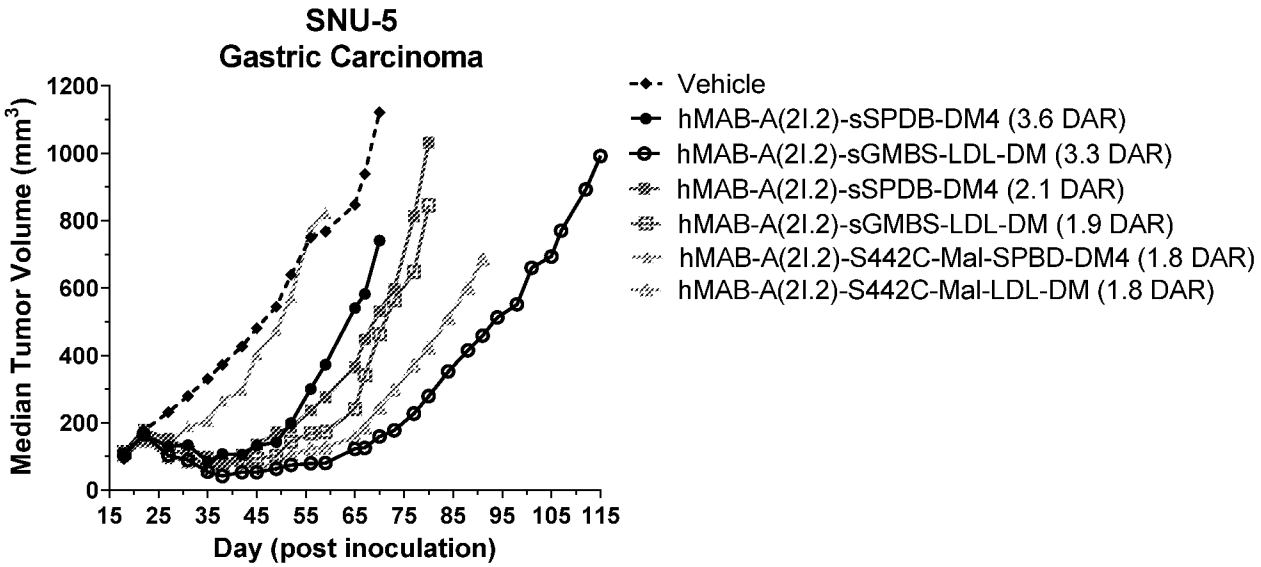
Treatment (50 µg/kg DM on day 7)	%T/C (Day 58)	% T/C Result	T-C (days)	LCK	LCK Result	Regressions		TFS
						PR	CR	
hMAB-A(2l.2)-sSPDB-DM4 (3.6 DAR)	30%	Active	34	6.7	++++	1/8	0/8	0/8
hMAB-A(2l.2)-sGMBS-LDL-DM (3.3 DAR)	7%	Highly Active	>66	>13.0	++++	6/8	0/8	0/8
hMAB-A(2l.2)-sSPDB-DM4 (2.1 DAR)	58%	Inactive	20	4.0	++++	0/8	0/8	0/8
hMAB-A(2l.2)-sGMBS-LDL-DM (1.9 DAR)	15%	Active	47	9.2	++++	6/8	1/8	0/8
hMAB-A(2l.2)-S442C-Mal-SPBD-DM4 (1.8 DAR)	97%	Inactive	3	0.6	-	0/8	0/8	0/8
hMAB-A(2l.2)-S442C-Mal-LDL-DM (1.8 DAR)	15%	Active	39	7.7	++++	6/8	2/8	0/8

FIG. 12



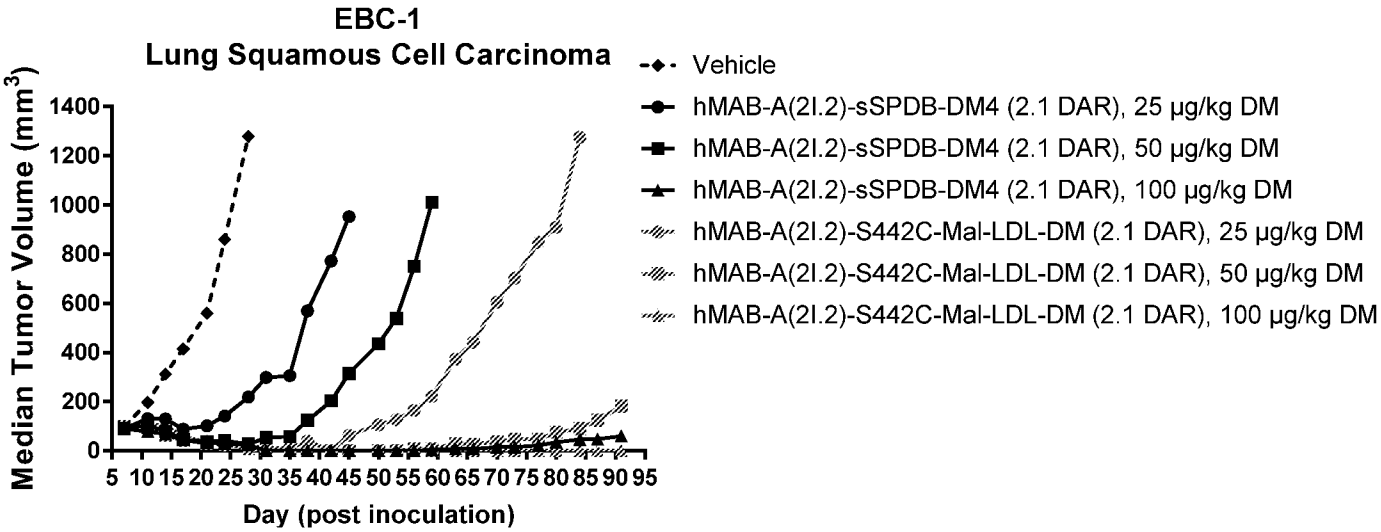
Treatment (50 µg/kg DM on day 7)	%T/C (Day 44)	% T/C Result	T-C (days)	LCK	LCK Result	Regressions		TFS
						PR	CR	
hMAB-A(2I.2)-sSPDB-DM4 (3.6 DAR)	5%	Highly Active	32	1.3	++	3/6	1/6	1/6
hMAB-A(2I.2)-sGMBS-LDL-DM (3.3 DAR)	0%	Highly Active	>85	>3.4	++++	6/6	6/6	5/6
hMAB-A(2I.2)-sSPDB-DM4 (2.1 DAR)	1%	Highly Active	>66	>2.6	+++	6/6	5/6	2/6
hMAB-A(2I.2)-sGMBS-LDL-DM (1.9 DAR)	1%	Highly Active	64	2.5	+++	6/6	5/6	1/6
hMAB-A(2I.2)-S442C-Mal-SPBD-DM4 (1.8 DAR)	36%	Active	13	0.5	-	1/6	0/6	0/6
hMAB-A(2I.2)-S442C-Mal-LDL-DM (1.8 DAR)	1%	Highly Active	38	1.5	++	6/6	5/6	4/6

FIG. 13



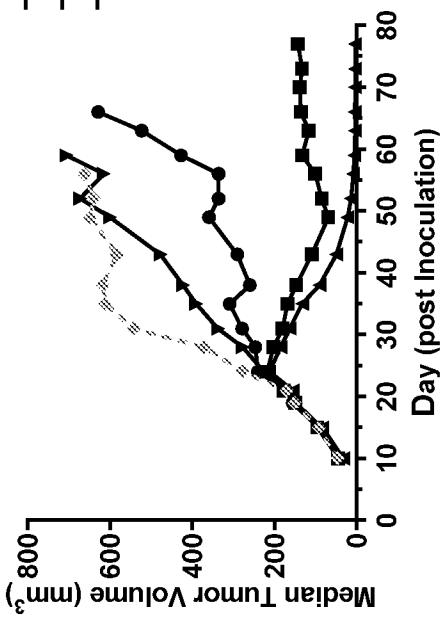
Treatment (50 µg/kg DM on day 7)	%T/C (Day 70)	% T/C Result	T-C (days)	LCK	LCK Result	Regressions		TFS
						PR	CR	
hMAB-A(2l.2)-sSPDB-DM4 (3.6 DAR)	66%	Inactive	0	0.0	-	2/6	0/6	0/6
hMAB-A(2l.2)-sGMBS-LDL-DM (3.3 DAR)	14%	Active	45	0.7	+	4/6	1/6	1/6
hMAB-A(2l.2)-sSPDB-DM4 (2.1 DAR)	47%	Inactive	10	0.2	-	1/6	1/6	1/6
hMAB-A(2l.2)-sGMBS-LDL-DM (1.9 DAR)	41%	Active	10	0.2	-	2/6	1/6	1/6
hMAB-A(2l.2)-S442C-Mal-SPBD-DM4 (1.8 DAR)	107%	Inactive	-11	-0.2	-	1/6	1/6	1/6
hMAB-A(2l.2)-S442C-Mal-LDL-DM (1.8 DAR)	22%	Active	28	0.4	-	2/6	1/6	1/6

FIG. 14



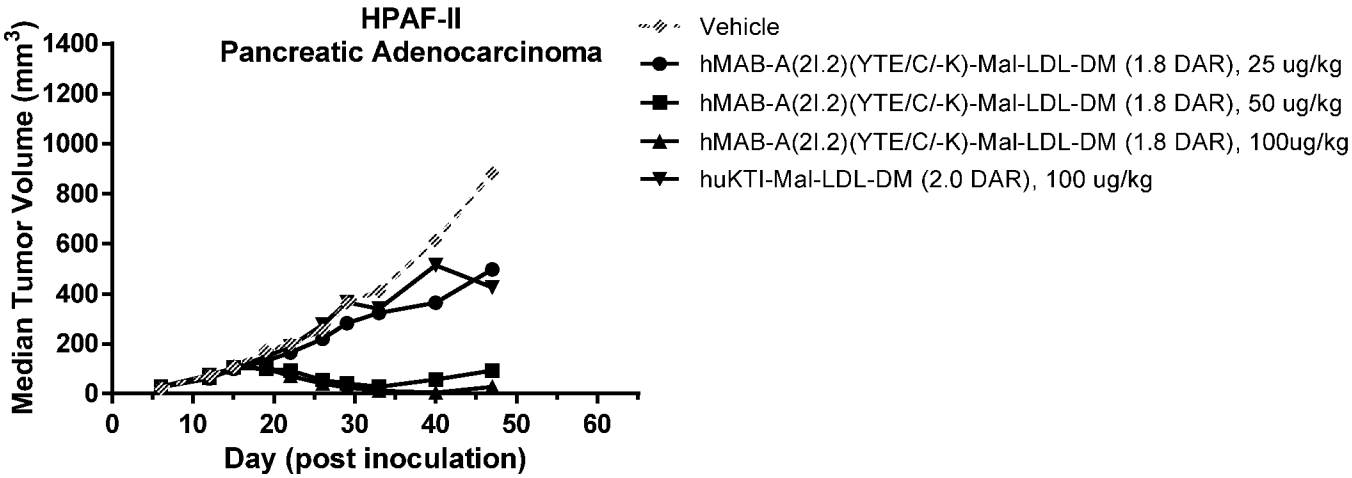
Treatment	Dose (µg/kg DM)	Dose (mg/kg Ab)	%T/C (Day 28)	% T/C Result	T-C (days)	LCK	LCK Result	Regressions		TFS
								PR	CR	
huMAB-A(2I.1)-sSPDB-DM4 (2.1 DAR)	25	2.18	17%	Active	21	1.06	+	0/6	0/6	0/6
huMAB-A(2I.1)-sSPDB-DM4 (2.1 DAR)	50	4.36	2%	Highly active	34	1.68	++	6/6	1/6	0/6
huMAB-A(2I.1)-sSPDB-DM4 (2.1 DAR)	100	8.76	2%	Highly active	>65	>3.26	++++	6/6	6/6	2/6
huMAB-A(2I.1)-S442C-Mal-LDL-DM (2.1 DAR)	25	2.14	2%	Highly active	56	2.79	+++	6/6	3/6	0/6
huMAB-A(2I.1)-S442C-Mal-LDL-DM (2.1 DAR)	50	4.28	2%	Highly active	>65	>3.26	++++	6/6	6/6	0/6
huMAB-A(2I.1)-S442C-Mal-LDL-DM (2.1 DAR)	100	8.57	1%	Highly active	>65	>3.26	++++	6/6	6/6	6/6

FIG. 15



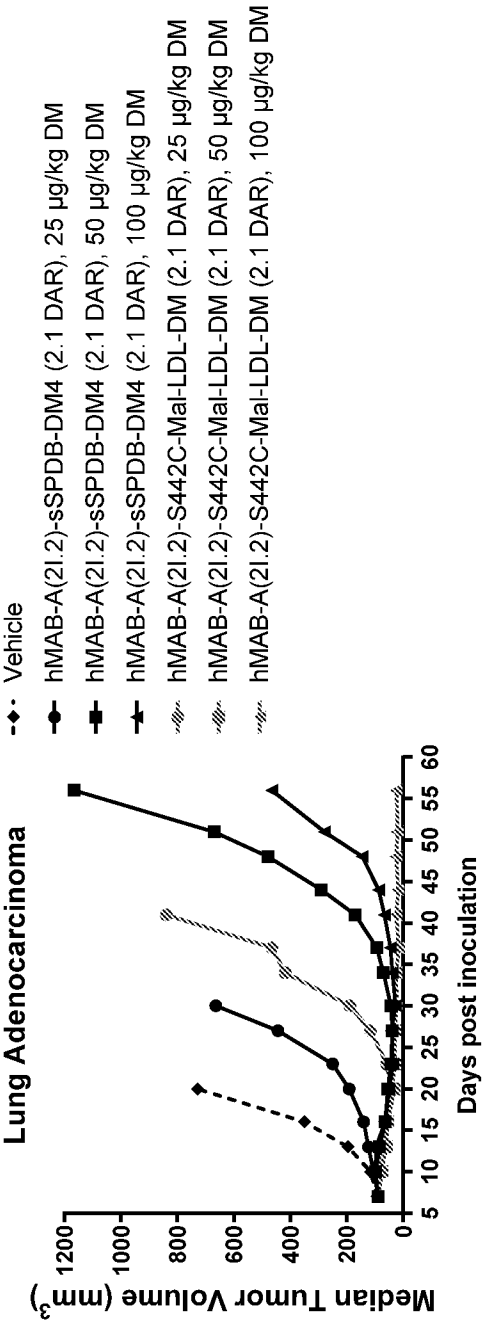
Treatment	Dose (µg/kg DM)	Dose (mg/kg Ab)	%T/C (Day 56)	% T/C Result	Regressions		TFS
					PR	CR	
hMAB-A(2I.2)(YTE/C/-K)-Mal-LDL-DM (1.8 DAR)	25	2.18	51	Inactive	1/8	0/8	0/8
hMAB-A(2I.2)(YTE/C/-K)-Mal-LDL-DM (1.8 DAR)	50	4.36	15	Active	5/8	2/8	2/8
hMAB-A(2I.2)(YTE/C/-K)-Mal-LDL-DM (1.8 DAR)	100	8.57	1	Highly active	8/8	7/8	7/8
huKTI-Mal-LDL-DM (2.0 DAR)	100	8.57	93	Inactive	0/8	0/8	0/8

FIG. 16



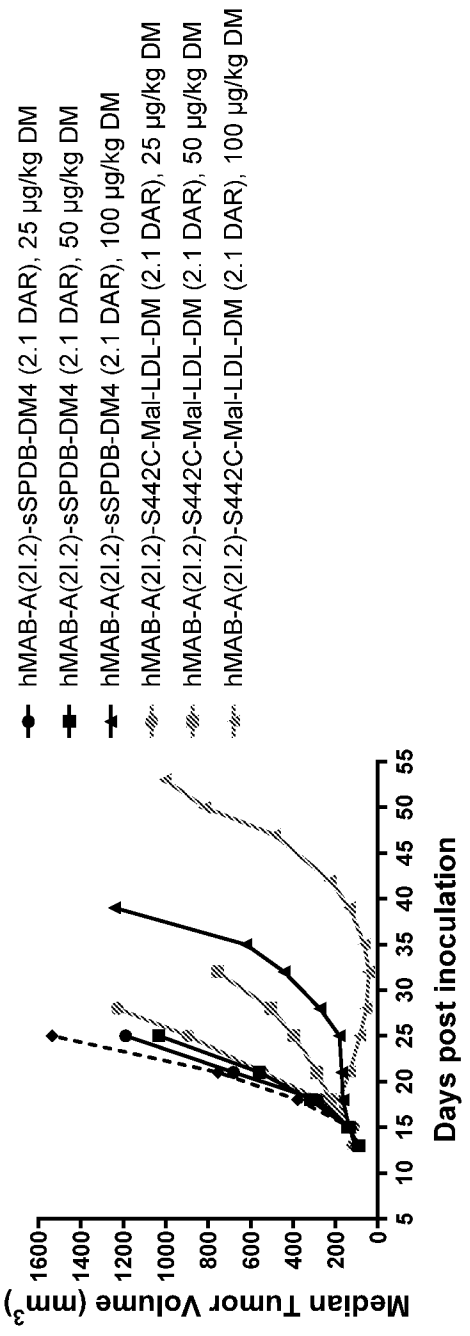
Treatment	Dose (µg/kg DM)	Dose (mg/kg Ab)	%T/C (Day 47)	% T/C Result	Regressions		TFS
					PR	CR	
hMAB-A(2l.2)(YTE/C/-K)-Mal-LDL-DM (1.8 DAR)	25	2.18	56	Inactive	0/7	0/7	0/7
hMAB-A(2l.2)(YTE/C/-K)-Mal-LDL-DM (1.8 DAR)	50	4.36	11	Active	5/7	1/7	1/7
hMAB-A(2l.2)(YTE/C/-K)-Mal-LDL-DM (1.8 DAR)	100	8.57	3	Highly Active	7/7	3/7	3/7
huKTI-Mal-LDL-DM (2.0 DAR)	100	8.57	48	Inactive	0/7	0/7	0/7

FIG. 17



Treatment	Dose (µg/kg DM)	Dose (mg/Kg Ab)	%T/C (Day 20)	% T/C Result	T-C (days)	LCK	LCK Result	Regressions		TFS
								PR	CR	
huMAB-A(2l.1)-sSPDB-DM4 (2.1 DAR)	25	2.18	28%	Active	10	0.79	+	0/6	0/6	0/6
huMAB-A(2l.1)-sSPDB-DM4 (2.1 DAR)	50	4.38	8%	Highly Active	35	2.72	+++	5/6	1/6	0/6
huMAB-A(2l.1)-sSPDB-DM4 (2.1 DAR)	100	8.78	7%	Highly Active	>38	>2.98	++++	6/6	0/6	0/6
huMAB-A(2l.1)-S442C-Mal-LDL-DM (2.1 DAR)	25	2.14	8%	Highly Active	ND	ND	ND	4/6	1/6	0/6
huMAB-A(2l.1)-S442C-Mal-LDL-DM (2.1 DAR)	50	4.28	4%	Highly Active	ND	ND	ND	5/6	0/6	0/6
huMAB-A(2l.1)-S442C-Mal-LDL-DM (2.1 DAR)	100	8.57	6%	Highly Active	>38	>2.98	++++	6/6	2/6	2/6

FIG. 18



Treatment	Dose (µg/kg DM)	Dose (mg/kg Ab)	%T/C (Day 25)	% T/C Result	T-C (days)	LCK	LCK Result	Regressions		TFS
								PR	CR	
huMAB-A(2l.1)-sSPDB-DM4 (2.1 DAR)	25	2.18	77%	Inactive	1	0.12	-	0/6	0/6	0/6
huMAB-A(2l.1)-sSPDB-DM4 (2.1 DAR)	50	4.36	67%	Inactive	3	0.24	-	0/6	0/6	0/6
huMAB-A(2l.1)-sSPDB-DM4 (2.1 DAR)	100	8.76	12%	Active	15	1.35	++	1/6	0/6	0/6
huMAB-A(2l.1)-S442C-Mal-LDL-DM (2.1 DAR)	25	2.14	58%	Inactive	4	0.33	-	0/6	0/6	0/6
huMAB-A(2l.1)-S442C-Mal-LDL-DM (2.1 DAR)	50	4.28	28%	Active	12	1.09	+	0/6	0/6	0/6
huMAB-A(2l.1)-S442C-Mal-LDL-DM (2.1 DAR)	100	8.57	6%	Highly Active	29	2.59	+++	4/6	0/6	0/6

FIG. 19

From the INTERNATIONAL BUREAU

PCT

NOTIFICATION OF THE RECORDING OF A CHANGE

(PCT Rule 92*bis*.1 and Administrative Instructions, Section 422)

To:

BEIJING SANYOU INTELLECTUAL PROPERTY AGENCY LTD.
16th Fl., Block A, Corporate Square
No. 35 Jinrong Street
Beijing 100033
CHINE

Date of mailing *(day/month/year)*
06 October 2020 (06.10.2020)

Applicant's or agent's file reference
GAI18CN2534P

IMPORTANT NOTIFICATION

International application No.
PCT/CN2019/089773

International filing date *(day/month/year)*
03 June 2019 (03.06.2019)

1. The following indications appeared on record concerning:

☒ the applicant ☐ the inventor ☐ the agent ☐ the common representative

Name and Address
INXMED (BEIJING) CO., LTD.
Room 206, No. 2 Building, Courtyard 1, No.8 Life Rd. Zhongguancun Life Science Park, Changping District
Beijing 102206
China

State of Nationality: CN
State of Residence: CN
Telephone No.:
Facsimile No.:
E-mail address:

2. The International Bureau hereby notifies the applicant that the following change has been recorded concerning:

☒ the person ☐ the name ☐ the address ☐ the nationality ☐ the residence

Name and Address
INXMED (NANJING) CO., LTD.
3/F, Building D-2, Building 16, Shuwu, No. 73, Tanmi Road, Jiangbei New District
Nanjing, Jiangsu 210061
China

State of Nationality: CN
State of Residence: CN
Telephone No.:
Facsimile No.:
E-mail address:
☐ Notifications by e-mail authorized

3. Further observations, if necessary:

4. A copy of this notification has been sent to:

☒ the receiving Office
☐ the International Searching Authority
☐ the Authority(ies) specified for supplementary search
☐ the International Preliminary Examining Authority
☒ the designated Offices concerned
☐ the elected Offices concerned
☐ other:

The International Bureau of WIPO
34, chemin des Colombettes
1211 Geneva 20, Switzerland

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