



(11) **EP 3 409 287 B9**

(12) **CORRECTED EUROPEAN PATENT SPECIFICATION**

(15) Correction information:

Corrected version no 2 (W2 B1)
Corrections, see
Description Paragraph(s) 1

(51) Int Cl.:

C07K 16/30 ^(2006.01) **A61P 35/00** ^(2006.01)
A61P 43/00 ^(2006.01) **A61K 47/68** ^(2017.01)
A61K 39/00 ^(2006.01) **A61N 5/10** ^(2006.01)

(48) Corrigendum issued on:

13.10.2021 Bulletin 2021/41

(45) Date of publication and mention
of the grant of the patent:

07.04.2021 Bulletin 2021/14

(21) Application number: **18171803.2**

(22) Date of filing: **29.09.2011**

(54) **ANTIBODY DRUG CONJUGATES (ADC) THAT BIND TO 191P4D12 PROTEINS**

AN 191P4D12-PROTEINE BINDENDE ANTIKÖRPER-WIRKSTOFFKONJUGATE

CONJUGUÉS ANTICORPS-MÉDICAMENTS (ADC) SE LIANT AUX PROTÉINES 191P4D12

(84) Designated Contracting States:

AL AT BE BG CH CY CZ DE DK EE ES FI FR GB
GR HR HU IE IS IT LI LT LU LV MC MK MT NL NO
PL PT RO RS SE SI SK SM TR

(30) Priority: **29.09.2010 US 38793310 P**

(43) Date of publication of application:

05.12.2018 Bulletin 2018/49

(60) Divisional application:

21166650.8

(62) Document number(s) of the earlier application(s) in
accordance with Art. 76 EPC:

11831345.1 / 2 621 526

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- **Andrew C.R. Martin: "Protein Sequence and Structure Analysis of Antibody Variable Domains" In: S Kontermann et al.: "Antibody engineering", 2010, Springer Verlag Berlin Heidelberg 2010 vol. 2, pages 33-53, DOI: DOI 10.1007/978-3-642-01147-4_3,,**

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Description

[0001] The detailed technical disclosure set out below may in some respects go beyond the disclosure of the invention per se, and may also provide technical background for related technical developments. It will be appreciated that the additional technical background provided is not intended to define the invention as such (which is defined exclusively by the claims), but rather to place it in a broader technical context. Accordingly, it will be appreciated that the terms "embodiments" and "aspects" - to the extent that they describe subject matter that falls outside the scope of the invention - reflect specific details of the disclosure and insofar as they refer to a part of the additional technical background, are not intended to define as part of the invention subject-matter that does not fall within the scope of the appended claims.

FIELD OF THE INVENTION

[0002] The invention described herein relates to antibodies, binding fragments, and antibody drug conjugates (ADCs) thereof, that bind proteins, termed 191P4D12. The invention further relates to prognostic, prophylactic and therapeutic methods and compositions useful in the treatment of cancers that express 191P4D12.

BACKGROUND OF THE INVENTION

[0003] Cancer is the second leading cause of human death next to coronary disease. Worldwide, millions of people die from cancer every year. In the United States alone, as reported by the American Cancer Society, cancer causes the death of well over a half-million people annually, with over 1.2 million new cases diagnosed per year. While deaths from heart disease have been declining significantly, those resulting from cancer generally are on the rise. In the early part of the next century, cancer is predicted to become the leading cause of death.

[0004] Worldwide, several cancers stand out as the leading killers. In particular, carcinomas of the lung, prostate, breast, colon, pancreas, ovary, and bladder represent the primary causes of cancer death. These and virtually all other carcinomas share a common lethal feature. With very few exceptions, metastatic disease from a carcinoma is fatal. Moreover, even for those cancer patients who initially survive their primary cancers, common experience has shown that their lives are dramatically altered. Many cancer patients experience strong anxieties driven by the awareness of the potential for recurrence or treatment failure. Many cancer patients experience physical debilitations following treatment. Furthermore, many cancer patients experience a recurrence.

[0005] Worldwide, prostate cancer is the fourth most prevalent cancer in men. In North America and Northern Europe, it is by far the most common cancer in males and is the second leading cause of cancer death in men. In the United States alone, well over 30,000 men die annually of this disease - second only to lung cancer. Despite the magnitude of these figures, there is still no effective treatment for metastatic prostate cancer. Surgical prostatectomy, radiation therapy, hormone ablation therapy, surgical castration and chemotherapy continue to be the main treatment modalities. Unfortunately, these treatments are ineffective for many and are often associated with undesirable consequences.

[0006] On the diagnostic front, the lack of a prostate tumor marker that can accurately detect early-stage, localized tumors remains a significant limitation in the diagnosis and management of this disease. Although the serum prostate specific antigen (PSA) assay has been a very useful tool, its specificity and general utility is widely regarded as lacking in several important respects.

[0007] Progress in identifying additional specific markers for prostate cancer has been improved by the generation of prostate cancer xenografts that can recapitulate different stages of the disease in mice. The LAPC (Los Angeles Prostate Cancer) xenografts are prostate cancer xenografts that have survived passage in severe combined immune deficient (SCID) mice and have exhibited the capacity to mimic the transition from androgen dependence to androgen independence (Klein et al., 1997, Nat. Med. 3:402). More recently identified prostate cancer markers include PCTA-1 (Su et al., 1996, Proc. Natl. Acad. Sci. USA 93: 7252), prostate-specific membrane antigen (PSMA) (Pinto et al., Clin Cancer Res 1996 Sep 2 (9): 1445-51), STEAP (Hubert, et al., Proc Natl Acad Sci U S A. 1999 Dec 7; 96(25): 14523-8) and prostate stem cell antigen (PSCA) (Reiter et al., 1998, Proc. Natl. Acad. Sci. USA 95: 1735).

[0008] While previously identified markers such as PSA have facilitated efforts to diagnose and treat prostate cancer, there is need for the identification of additional markers and therapeutic targets for prostate and related cancers in order to further improve diagnosis and therapy. An estimated 130,200 cases of colorectal cancer occurred in 2000 in the United States, including 93,800 cases of colon cancer and 36,400 of rectal cancer.

[0009] Colorectal cancers are the third most common cancers in men and women. Incidence rates declined significantly during 1992-1996 (-2.1% per year). Research suggests that these declines have been due to increased screening and polyp removal, preventing progression of polyps to invasive cancers. There were an estimated 56,300 deaths (47,700 from colon cancer, 8,600 from rectal cancer) in 2000, accounting for about 11% of all U.S. cancer deaths.

[0010] At present, surgery is the most common form of therapy for colorectal cancer, and for cancers that have not spread, it is frequently curative. Chemotherapy, or chemotherapy plus radiation, is given before or after surgery to most

patients whose cancer has deeply perforated the bowel wall or has spread to the lymph nodes. A permanent colostomy (creation of an abdominal opening for elimination of body wastes) is occasionally needed for colon cancer and is infrequently required for rectal cancer. There continues to be a need for effective diagnostic and treatment modalities for colorectal cancer.

[0011] Of all new cases of cancer in the United States, bladder cancer represents approximately 5 percent in men (fifth most common neoplasm) and 3 percent in women (eighth most common neoplasm). The incidence is increasing slowly, concurrent with an increasing older population. In 1998, there were an estimated 54,500 cases, including 39,500 in men and 15,000 in women. The age-adjusted incidence in the United States is 32 per 100,000 for men and eight per 100,000 in women. The historic male/female ratio of 3:1 may be decreasing related to smoking patterns in women. There were an estimated 11,000 deaths from bladder cancer in 1998 (7,800 in men and 3,900 in women). Bladder cancer incidence and mortality strongly increase with age and will be an increasing problem as the population becomes more elderly.

[0012] Most bladder cancers recur in the bladder. Bladder cancer is managed with a combination of transurethral resection of the bladder (TUR) and intravesical chemotherapy or immunotherapy. The multifocal and recurrent nature of bladder cancer points out the limitations of TUR. Most muscle-invasive cancers are not cured by TUR alone. Radical cystectomy and urinary diversion is the most effective means to eliminate the cancer but carry an undeniable impact on urinary and sexual function. There continues to be a significant need for treatment modalities that are beneficial for bladder cancer patients.

[0013] There were an estimated 164,100 new cases of lung and bronchial cancer in 2000, accounting for 14% of all U.S. cancer diagnoses. The incidence rate of lung and bronchial cancer is declining significantly in men, from a high of 86.5 per 100,000 in 1984 to 70.0 in 1996. In the 1990s, the rate of increase among women began to slow. In 1996, the incidence rate in women was 42.3 per 100,000.

[0014] Lung and bronchial cancer caused an estimated 156,900 deaths in 2000, accounting for 28% of all cancer deaths. During 1992-1996, mortality from lung cancer declined significantly among men (-1.7% per year) while rates for women were still significantly increasing (0.9% per year). Since 1987, more women have died each year of lung cancer than breast cancer, which, for over 40 years, was the major cause of cancer death in women. Decreasing lung cancer incidence and mortality rates most likely resulted from decreased smoking rates over the previous 30 years; however, decreasing smoking patterns among women lag behind those of men. Of concern, although the declines in adult tobacco use have slowed, tobacco use in youth is increasing again.

[0015] Treatment options for lung and bronchial cancer are determined by the type and stage of the cancer and include surgery, radiation therapy, and chemotherapy. For many localized cancers, surgery is usually the treatment of choice. Because the disease has usually spread by the time it is discovered, radiation therapy and chemotherapy are often needed in combination with surgery. Chemotherapy alone or combined with radiation is the treatment of choice for small cell lung cancer; on this regimen, a large percentage of patients experience remission, which in some cases is long lasting. There is however, an ongoing need for effective treatment and diagnostic approaches for lung and bronchial cancers.

[0016] An estimated 182,800 new invasive cases of breast cancer were expected to occur among women in the United States during 2000. Additionally, about 1,400 new cases of breast cancer were expected to be diagnosed in men in 2000. After increasing about 4% per year in the 1980s, breast cancer incidence rates in women have leveled off in the 1990s to about 110.6 cases per 100,000.

[0017] In the U.S. alone, there were an estimated 41,200 deaths (40,800 women, 400 men) in 2000 due to breast cancer. Breast cancer ranks second among cancer deaths in women. According to the most recent data, mortality rates declined significantly during 1992-1996 with the largest decreases in younger women, both white and black. These decreases were probably the result of earlier detection and improved treatment.

[0018] Taking into account the medical circumstances and the patient's preferences, treatment of breast cancer may involve lumpectomy (local removal of the tumor) and removal of the lymph nodes under the arm; mastectomy (surgical removal of the breast) and removal of the lymph nodes under the arm; radiation therapy; chemotherapy; or hormone therapy. Often, two or more methods are used in combination. Numerous studies have shown that, for early stage disease, long-term survival rates after lumpectomy plus radiotherapy are similar to survival rates after modified radical mastectomy. Significant advances in reconstruction techniques provide several options for breast reconstruction after mastectomy. Recently, such reconstruction has been done at the same time as the mastectomy.

[0019] Local excision of ductal carcinoma in situ (DCIS) with adequate amounts of surrounding normal breast tissue may prevent the local recurrence of the DCIS. Radiation to the breast and/or tamoxifen may reduce the chance of DCIS occurring in the remaining breast tissue. This is important because DCIS, if left untreated, may develop into invasive breast cancer. Nevertheless, there are serious side effects or sequelae to these treatments. There is, therefore, a need for efficacious breast cancer treatments.

[0020] There were an estimated 23,100 new cases of ovarian cancer in the United States in 2000. It accounts for 4% of all cancers among women and ranks second among gynecologic cancers. During 1992-1996, ovarian cancer incidence

rates were significantly declining. Consequent to ovarian cancer, there were an estimated 14,000 deaths in 2000. Ovarian cancer causes more deaths than any other cancer of the female reproductive system.

[0021] Surgery, radiation therapy, and chemotherapy are treatment options for ovarian cancer. Surgery usually includes the removal of one or both ovaries, the fallopian tubes (salpingo-oophorectomy), and the uterus (hysterectomy). In some very early tumors, only the involved ovary will be removed, especially in young women who wish to have children. In advanced disease, an attempt is made to remove all intra-abdominal disease to enhance the effect of chemotherapy. There continues to be an important need for effective treatment options for ovarian cancer.

[0022] There were an estimated 28,300 new cases of pancreatic cancer in the United States in 2000. Over the past 20 years, rates of pancreatic cancer have declined in men. Rates among women have remained approximately constant but may be beginning to decline. Pancreatic cancer caused an estimated 28,200 deaths in 2000 in the United States. Over the past 20 years, there has been a slight but significant decrease in mortality rates among men (about -0.9% per year) while rates have increased slightly among women.

[0023] Surgery, radiation therapy, and chemotherapy are treatment options for pancreatic cancer. These treatment options can extend survival and/or relieve symptoms in many patients but are not likely to produce a cure for most. There is a significant need for additional therapeutic and diagnostic options for cancers. These include the use of antibodies, vaccines, and small molecules as treatment modalities. Additionally, there is also a need to use these modalities as research tools to diagnose, detect, monitor, and further the state of the art in all areas of cancer treatment and studies.

[0024] The therapeutic utility of monoclonal antibodies (mAbs) (G. Kohler and C. Milstein, *Nature* 256:495-497 (1975)) is being realized. Monoclonal antibodies have now been approved as therapies in transplantation, cancer, infectious disease, cardiovascular disease and inflammation. Different isotypes have different effector functions. Such differences in function are reflected in distinct 3-dimensional structures for the various immunoglobulin isotypes (P.M. Alzari et al., *Annual Rev. Immunol.*, 6:555-580 (1988)).

[0025] Because mice are convenient for immunization and recognize most human antigens as foreign, mAbs against human targets with therapeutic potential have typically been of murine origin. However, murine mAbs have inherent disadvantages as human therapeutics. They require more frequent dosing as mAbs have a shorter circulating half-life in humans than human antibodies. More critically, the repeated administration of murine antibodies to the human immune system causes the human immune system to respond by recognizing the mouse protein as a foreign and generating a human anti-mouse antibody (HAMA) response. Such a HAMA response may result in allergic reaction and the rapid clearing of the murine antibody from the system thereby rendering the treatment by murine antibody useless. To avoid such affects, attempts to create human immune systems within mice have been attempted.

[0026] Initial attempts hoped to create transgenic mice capable of responding to antigens with antibodies having human sequences (See Bruggemann et al., *Proc. Nat'l. Acad. Sci. USA* 86:6709-6713 (1989)), but were limited by the amount of DNA that could be stably maintained by available cloning vehicles. The use of yeast artificial chromosome (YAC) cloning vectors led the way to introducing large germline fragments of human Ig locus into transgenic mammals. Essentially a majority of the human V, D, and J region genes arranged with the same spacing found in the human genome and the human constant regions were introduced into mice using YACs. One such transgenic mouse strain is known as XenoMouse® mice and is commercially available from Amgen Fremont, Inc. (Fremont CA).

[0027] The patent application AU 2008 202 217 A1 (Agensys Inc., 5 June 2008) discloses the gene of 191P4D12(b) and its encoded protein. Antibodies or T-cells reactive with 191P4D12(b) can be used in active or passive immunization. Further recited is that antibodies may also be conjugated to an anti-cancer pro-drug activating enzyme capable of converting the pro-drug to its active form. However, the antibodies are not characterized by their sequences and they are not used in combination with monomethyl auristatins as cytotoxic agent as one of the main compounds.

SUMMARY OF THE INVENTION

[0028] The invention provides antibodies, binding fragments, and antibody drug conjugates (ADCs) thereof that bind to 191P4D12 proteins and polypeptide fragments of 191P4D12 proteins. In some embodiments, the invention comprises fully human antibodies conjugated with a therapeutic agent. In certain embodiments, there is a proviso that the entire nucleic acid sequence of Figure 3 is not encoded and/or the entire amino acid sequence of Figure 2 is not prepared. In certain embodiments, the entire nucleic acid sequence of Figure 3 is encoded and/or the entire amino acid sequence of Figure 2 is prepared, either of which are in respective human unit dose forms.

[0029] The invention further provides various immunogenic or therapeutic compositions, such as antibody drug conjugates, and strategies for treating cancers that express 191P4D12 such as cancers of tissues listed in Table I.

[0030] In a first aspect, the invention provides an anti-191P4D12 antibody or antigen binding fragment thereof comprising a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises a CDRH1 consisting of the amino acid sequence ranging from 45 to 52 of SEQ ID NO:7, a CDRH2 consisting of the amino acid sequence ranging from 70 to 77 of SEQ ID NO:7, and a CDRH3 consisting of the amino acid sequence ranging from 116 to 125 of SEQ ID NO:7, and wherein the light chain variable region comprises a CDRL1 consisting of

the amino acid sequence ranging from 49 to 54 of SEQ ID NO:8, a CDRL2 consisting of the amino acid sequence ranging from 72 to 74 of SEQ ID NO:8, and a CDRL3 consisting of the amino acid sequence ranging from 111 to 119 of SEQ ID NO:8.

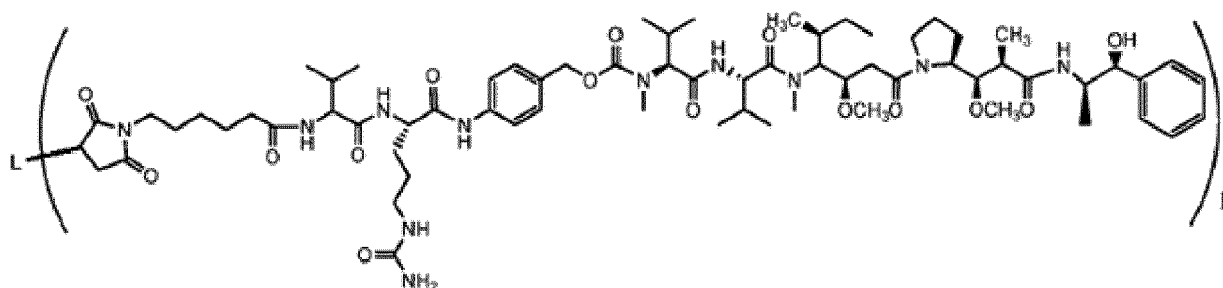
[0031] In one embodiment, the heavy chain variable region comprises amino acid residue 20 to amino acid residue 136 of SEQ ID NO: 7 and the light chain variable region comprises amino acid residue 23 to amino acid residue 130 of SEQ ID NO:8. In another embodiment, the antibody comprises a heavy chain comprising amino acid residue 20 to amino acid residue 466 of SEQ ID NO: 7 and a light chain comprising amino acid residue 23 to amino acid residue 236 of SEQ ID NO:8.

[0032] In a second aspect, the invention provides an antibody or antigen binding fragment thereof comprising a heavy chain variable region comprising the amino acid sequence of the heavy chain variable region of an antibody produced by a hybridoma deposited under American Type Culture Collection (ATCC) Accession No. PTA-11267, and a light chain variable region comprising the amino acid sequence of the light chain variable region of an antibody produced by a hybridoma deposited under ATCC Accession No. PTA-11267.

[0033] In one embodiment, the antibody comprises a heavy chain comprising the amino acid sequence of the heavy chain of an antibody produced by a hybridoma deposited under ATCC. Accession No. PTA-11267, and a light chain comprising the amino acid sequence of the light chain of an antibody produced by a hybridoma deposited under ATCC Accession No. PTA-11267.

[0034] In one embodiment, the antigen binding fragment is an Fab, F(ab')₂, Fv or scFv. In another embodiment, the antibody or antigen binding fragment thereof is a fully human antibody or antigen binding fragment thereof.

[0035] In a third aspect, the invention provides an antibody drug conjugate comprising the antibody or antigen binding fragment thereof conjugated to monomethyl auristatin E (MMAE), wherein the antibody drug conjugate has the following structure:



wherein L is the antibody, and wherein p ranges from about 3 to about 5. In one embodiment, p is about 3.8.

[0036] In a fourth aspect, the invention provides a pharmaceutical composition comprising the antibody or antigen binding fragment thereof, or the antibody drug conjugate of any preceding aspect or embodiment, and a pharmaceutically acceptable excipient.

[0037] In a fifth aspect, the invention provides an antibody or antigen binding fragment thereof, or an antibody drug conjugate as defined in any preceding aspect or embodiment for use in a method of treating cancer.

[0038] In one embodiment the cancer expresses 191P4D12. In another embodiment, the cancer is bladder cancer, breast cancer, pancreatic cancer, lung cancer, ovarian cancer, esophageal cancer, or head and neck cancer. In a particular embodiment, the cancer is bladder cancer. In a further particular embodiment, the bladder cancer is advanced bladder cancer.

BRIEF DESCRIPTION OF THE FIGURES

[0039]

Figure 1. The cDNA and amino acid sequence of 191P4D12 is shown in Figure 1. The start methionine is underlined. The open reading frame extends from nucleic acid 264-1796 including the stop codon.

Figures 2A-B. Nucleic acid and amino acid sequences of 191P4D12 antibodies. **Figure 2A.** The cDNA and amino acid sequence of Ha22-2(2,4)6.1 heavy chain. Double-underlined is the leader sequence, underlined is the heavy chain variable region, and underlined with a dashed line is the human IgG1 constant region. **Figure 2B.** The cDNA and amino acid sequence of Ha22-2(2,4)6.1 light chain. Double-underlined is the leader sequence, underlined is the light chain variable region, and underlined with a dashed line is the human kappa constant region.

Figures 3A-B. Amino acid sequences of 191P4D12 antibodies. **Figure 3A.** The amino acid sequence of Ha22-2(2.4)6.1 heavy chain. Double-underlined is the leader sequence, underlined is the heavy chain variable

region, and underlined with a dashed line is the human IgG1 constant region. **Figure 3B.** The amino acid sequence of Ha22-2(2,4)6.1 light chain. Double-underlined is the leader sequence, underlined is the light chain variable region, and underlined with a dashed line is the human kappa constant region.

Figures 4A-B. Alignment of Ha22-2(2,4)6.1 antibodies to human Ig germline. **Figure 4A.** Alignment of Ha22-2(2,4)6.1 heavy chain to human Ig germline. **Figure 4B.** Alignment of Ha22-2(2,4)6.1 light chain to human Ig germline.

Figures 5A-B. Ha22-2(2,4)6.1 MAb binding assays. **Figure 5A:** RAT-control and RAT-191P4D12 cells were stained with Ha22-2(2,4)6.1 MAb from either hybridoma or CHO cells. Binding was detected by flow cytometry. Results show Ha22-2(2,4)6.1 MAb recombinantly expressed in CHO cells is secreted and binds specifically to cell-surface 191P4D12. **Figure 5B:** Ha22-2(2,4)6.1 MAb from either hybridoma or CHO cells was tested for binding to recombinant 191P4D12 purified extracellular protein by ELISA. The results show that 191P4D12 protein binding to Ha22-2(2,4)6.1 derived from CHO and hybridoma was identical.

Figure 6. Ha22-2(2,4)6.1vcMMAE Affinity Determination by FACS using PC3-Human-191P4D12 cells. The affinity is 0.69 Kd.

Figure 7. Ha22-2(2,4)6.1vcMMAE Affinity Determination by FACS using PC3-Cynomolgus-191P4D12 cells. The affinity is 0.34 Kd.

Figure 8. Ha22-2(2,4)6.1vcMMAE Affinity Determination by FACS using PC3-Rat-191P4D12 cells. The affinity is 1.6 Kd.

Figures 9A-D. Cell cytotoxicity mediated by Ha22-2(2,4)6.1vcMMAE. **Figure 9A:** Cell cytotoxicity assay using PC3-Human-191P4D12 cells. **Figure 9B:** Cell cytotoxicity assay using PC3-Cynomolgus-191P4D12 cells. **Figure 9C:** Cell cytotoxicity assay using PC3-Rat-191P4D12 cells. **Figure 9D:** Cell cytotoxicity assay using PC3-Neo cells.

Figure 10. Domain mapping of Ha22-2(2,4)6.1 MAb by FACS.

Figure 11. Ha22-2(2,4)6.1 MAb domain mapping by Western Blot Analysis.

Figure 12. Evaluation of Ha22-2(2,4)6.1 MAb in the subcutaneous tumor formation model of human lung cancer xenograft AG-L4 in SCID mice. The results show that the 191P4D12 MAbs did not significantly inhibit tumor growth in human lung cancer xenograft AG-L4 in SCID mice.

Figure 13. Evaluation of Ha22-2(2,4)6.1 MAb in the subcutaneous tumor formation model of human pancreatic cancer xenograft HPAC in SCID mice. The results show that the 191P4D12 MAbs did not inhibit tumor growth in a human pancreatic xenograft in SCID mice when compared to the control antibody.

Figure 14. Evaluation of Ha22-2(2,4)6.1 MAb in the subcutaneous tumor formation model of human pancreatic cancer xenograft AG-Panc3 in SCID mice. The results show that the 191P4D12 MAbs did not inhibit tumor growth in a human pancreatic xenograft in SCID mice when compared to the control antibody.

Figure 15. Efficacy of Ha22-2(2,4)6.1-vcMMAE in subcutaneous established human lung cancer xenograft AG-L4 in SCID mice. The results show that treatment with Ha22-2(2,4)6.1-vcMMAE significantly inhibited the growth of AG-L4 lung cancer xenografts implanted subcutaneously in nude mice compared to both the treated and untreated control.

Figure 16. Efficacy of Ha22-2(2,4)6.1-vcMMAE in subcutaneous established human breast cancer xenograft BT-483 in SCID mice. The results show that treatment with Ha22-2(2,4)6.1-vcMMAE significantly inhibited the growth of BT-483 breast tumor xenografts implanted subcutaneously in SCID mice compared to the treated and untreated control ADCs.

Figure 17. Efficacy of Ha22-2(2,4)6.1-vcMMAE in subcutaneous established human bladder cancer xenograft AG-B1 in SCID mice. The results show that treatment with Ha22-2(2,4)6.1-vcMMAE significantly inhibited the growth of AG-B1 bladder cancer xenografts as compared to the control ADCs.

Figure 18. Efficacy of Ha22-2(2,4)6.1-vcMMAE in subcutaneous established human pancreatic cancer xenograft AG-Panc2 in SCID mice. The results show that treatment with Ha22-2(2,4)6.1-vcMMAE significantly inhibited the growth of AG-Panc2 pancreatic cancer xenografts as compared to the control ADCs.

Figure 19. Efficacy of Ha22-2(2,4)6.1-vcMMAE in subcutaneous established human lung cancer xenograft AG-Panc4 in SCID mice. The results show that treatment with Ha22-2(2,4)6.1-vcMMAE significantly inhibited the growth of AG-Panc4 pancreatic cancer xenografts as compared to the control ADCs.

Figure 20. Efficacy of Ha22-2(2,4)6.1-vcMMAE at comparative dosage in subcutaneous established human bladder cancer xenograft AG-B8 in SCID mice. The results show that treatment with Ha22-2(2,4)6.1vcMMAE at 10mg/kg significantly inhibited the growth of AG-B8 bladder cancer xenografts as compared to the Ha22-2(2,4)6.1vcMMAE at 5mg/kg.

Figures 21A-N. Detection of 191P4D12 protein in cancer patient specimens by IHC. **Figures 21A-B** show bladder cancer specimens. **Figures 21C-D** show breast cancer specimens. **Figures 21E-F** show pancreatic cancer specimens. **Figures 21G-H** show lung cancer specimens. **Figures 21I-J** show ovarian cancer specimens. **Figures 21K-L** show esophageal cancer specimens. **Figure 21M-N** show esophageal cancer specimens.

Figures 22A-B. Show binding curves used to determine the affinity of Ha22-2(2,4)6.1 Mab and

Ha22-2(2,4)6.1vcMMAE to purified recombinant 191P4D12 (ECD amino acids 1-348).

Figures 23A-D. Show binding of Ha22-2(2,4)6.1 to PC3 cells expressing 191P4D12 (**Figure 23A**) and orthologs from cynomolgus monkey (**Figure 23B**), rat (**Figure 23C**) and mouse (**Figure 23D**).

Figures 24A-D. Show binding of Ha22-2(2,4)6.1 to the double mutant A76I, S91N is similar to murine ortholog binding.

Figure 25. Shows a model of the V-domain of 191P4D12 based on published crystal structure data for family members of 191P4D12 and Ig-domain containing proteins using PyMOL. The positions of Ala-76 (stippled) and Ser-91 (crosshatched) are shown.

Figures 26A-C. Shows binding of Ha22-2(2,4)6.1 binds to V-domain expressing cells (**Figure 26A**) as well as wild-type 191P4D12 (**Figure 26B**), but not to C1C2 domain expressing cells generated earlier (**Figure 26C**).

DETAILED DESCRIPTION OF THE INVENTION

[0040]

Outline of Sections

- I.) Definitions
- II.) 191P4D12 Antibodies
- III.) Antibody Drug Conjugates Generally
 - III(A). Maytansinoids
 - III(B). Auristatins and dolostatins
 - III(C). Calicheamicin
 - III(D). Other Cytotoxic Agents
- IV.) Antibody Drug Conjugates which Bind 191P4D12
- V.) Linker Units
- VI.) The Stretcher Unit
- VII.) The Amino Acid Unit
- VIII.) The Spacer Unit
- IX.) The Drug Unit
- X.) Drug Loading
- XI.) Methods of Determining Cytotoxic effect of ADCs
- XII.) Treatment of Cancer(s) Expressing 191P4D12
- XIII.) 191P4D12 as a Target for Antibody-based Therapy
- XIV.) 191P4D12 ADC Cocktails
- XV.) Combination Therapy
- XVI.) Kits/Articles of Manufacture

I.) Definitions:

[0041] Unless otherwise defined, all terms of art, notations and other scientific terms or terminology used herein are intended to have the meanings commonly understood by those of skill in the art to which this invention pertains. In some cases, terms with commonly understood meanings are defined herein for clarity and/or for ready reference, and the inclusion of such definitions herein should not necessarily be construed to represent a substantial difference over what is generally understood in the art. Many of the techniques and procedures described or referenced herein are well understood and commonly employed using conventional methodology by those skilled in the art, such as, for example, the widely utilized molecular cloning methodologies described in Sambrook et al., Molecular Cloning: A Laboratory Manual 2nd. edition (1989) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. As appropriate, procedures involving the use of commercially available kits and reagents are generally carried out in accordance with manufacturer defined protocols and/or parameters unless otherwise noted.

[0042] When a trade name is used herein, reference to the trade name also refers to the product formulation, the generic drug, and the active pharmaceutical ingredient(s) of the trade name product, unless otherwise indicated by context.

[0043] The terms "advanced cancer", "locally advanced cancer", "advanced disease" and "locally advanced disease" mean cancers that have extended through the relevant tissue capsule, and are meant to include stage C disease under the American Urological Association (AUA) system, stage C1 - C2 disease under the Whitmore-Jewett system, and

stage T3 - T4 and N+ disease under the TNM (tumor, node, metastasis) system. In general, surgery is not recommended for patients with locally advanced disease, and these patients have substantially less favorable outcomes compared to patients having clinically localized (organ-confined) cancer.

[0044] The abbreviation "AFP" refers to dimethylvaline-valine-dolaisoleuine-dolaproine-phenylalanine-p-phenylene-diamine (see Formula XVI *infra*).

[0045] The abbreviation "MMAE" refers to monomethyl auristatin E (see Formula XI *infra*).

[0046] The abbreviation "AEB" refers to an ester produced by reacting auristatin E with paraacetyl benzoic acid (see Formula XX *infra*).

[0047] The abbreviation "AEVB" refers to an ester produced by reacting auristatin E with benzoylvaleric acid (see Formula XXI *infra*).

[0048] The abbreviation "MMAF" refers to dovaline-valine-dolaisoleuine-dolaproine-phenylalanine (see Formula XXIV *infra*).

[0049] Unless otherwise noted, the term "alkyl" refers to a saturated straight or branched hydrocarbon having from about 1 to about 20 carbon atoms (and all combinations and subcombinations of ranges and specific numbers of carbon atoms therein), with from about 1 to about 8 carbon atoms being preferred. Examples of alkyl groups are methyl, ethyl, *n*-propyl, *iso*-propyl, *n*-butyl, *iso*-butyl, *sec*-butyl, *tert*-butyl, *n*-pentyl, 2-pentyl, 3-pentyl, 2-methyl-2-butyl, *n*-hexyl, *n*-heptyl, *n*-octyl, *n*-nonyl, *n*-decyl, 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, and 3,3-dimethyl-2-butyl.

[0050] Alkyl groups, whether alone or as part of another group, can be optionally substituted with one or more groups, preferably 1 to 3 groups (and any additional substituents selected from halogen), including, but not limited to, -halogen, -O-(C₁-C₈ alkyl), -O-(C₂-C₈ alkenyl), -O-(C₂-C₈ alkynyl), -aryl, -C(O)R', -OC(O)R', -C(O)OR', -C(O)NH₂, -C(O)NHR', -C(O)N(R')₂, -NHC(O)R', -SR', -SO₃R', -S(O)₂R', -S(O)R', -OH, =O, -N₃, -NH₂, -NH(R'), -N(R')₂ and -CN, where each R' is independently selected from -H, -C₁-C₈ alkyl, -C₂-C₈ alkenyl, -C₂-C₈ alkynyl, or -aryl, and wherein said -O-(C₁-C₈ alkyl), -O-(C₂-C₈ alkenyl), -O-(C₂-C₈ alkynyl), -aryl, -C₁-C₈ alkyl, -C₂-C₈ alkenyl, and -C₂-C₈ alkynyl groups can be optionally further substituted with one or more groups including, but not limited to, -C₁-C₈ alkyl, -C₂-C₈ alkenyl, -C₂-C₈ alkynyl, -halogen, -O-(C₁-C₈ alkyl), -O-(C₂-C₈ alkenyl), -O-(C₂-C₈ alkynyl), -aryl, -C(O)R", -OC(O)R", -C(O)OR", -C(O)NH₂, -C(O)NHR", -C(O)N(R")₂, -NHC(O)R", -SR", -SO₃R", -S(O)₂R", -S(O)R", -OH, -N₃, -NH₂, -NH(R"), -N(R")₂ and -CN, where each R" is independently selected from -H, -C₁-C₈ alkyl, -C₂-C₈ alkenyl, -C₂-C₈ alkynyl, or -aryl.

[0051] Unless otherwise noted, the terms "alkenyl" and "alkynyl" refer to straight and branched carbon chains having from about 2 to about 20 carbon atoms (and all combinations and subcombinations of ranges and specific numbers of carbon atoms therein), with from about 2 to about 8 carbon atoms being preferred. An alkenyl chain has at least one double bond in the chain and an alkynyl chain has at least one triple bond in the chain. Examples of alkenyl groups include, but are not limited to, ethylene or vinyl, allyl, -1-butenyl, -2-butenyl, -isobutylene, -1-pentenyl, -2-pentenyl, -3-methyl-1-butenyl, -2-methyl-2-butenyl, and -2,3-dimethyl-2-butenyl. Examples of alkynyl groups include, but are not limited to, acetylenic, propargyl, acetylenyl, propynyl, -1-butyne, -2-butyne, -1-pentyne, -2-pentyne, and -3-methyl-1-butyne.

[0052] Alkenyl and alkynyl groups, whether alone or as part of another group, can be optionally substituted with one or more groups, preferably 1 to 3 groups (and any additional substituents selected from halogen), including but not limited to, -halogen, -O-(C₁-C₈ alkyl), -O-(C₂-C₈ alkenyl), -O-(C₂-C₈ alkynyl), -aryl, -C(O)R', -OC(O)R', -C(O)OR', -C(O)NH₂, -C(O)NHR', -C(O)N(R')₂, -NHC(O)R', -SR', -SO₃R', -S(O)₂R', -S(O)R', -OH, =O, -N₃, -NH₂, -NH(R'), -N(R')₂ and -CN, where each R' is independently selected from -H, -C₁-C₈ alkyl, -C₂-C₈ alkenyl, -C₂-C₈ alkynyl, or -aryl and wherein said -O-(C₁-C₈ alkyl), -O-(C₂-C₈ alkenyl), -O-(C₂-C₈ alkynyl), -aryl, -C₁-C₈ alkyl, -C₂-C₈ alkenyl, and -C₂-C₈ alkynyl groups can be optionally further substituted with one or more substituents including, but not limited to, -C₁-C₈ alkyl, -C₂-C₈ alkenyl, -C₂-C₈ alkynyl, -halogen, -O-(C₁-C₈ alkyl), -O-(C₂-C₈ alkenyl), -O-(C₂-C₈ alkynyl), -aryl, -C(O)R", -OC(O)R", -C(O)OR", -C(O)NH₂, -C(O)NHR", -C(O)N(R")₂, -NHC(O)R", -SR", -SO₃R", -S(O)₂R", -S(O)R", -OH, -N₃, -NH₂, -NH(R"), -N(R")₂ and -CN, where each R" is independently selected from -H, -C₁-C₈ alkyl, -C₂-C₈ alkenyl, -C₂-C₈ alkynyl, or -aryl.

[0053] Unless otherwise noted, the term "alkylene" refers to a saturated branched or straight chain hydrocarbon radical having from about 1 to about 20 carbon atoms (and all combinations and subcombinations of ranges and specific numbers of carbon atoms therein), with from about 1 to about 8 carbon atoms being preferred and having two monovalent radical centers derived by the removal of two hydrogen atoms from the same or two different carbon atoms of a parent alkane. Typical alkylenes include, but are not limited to, methylene, ethylene, propylene, butylene, pentylene, hexylene, heptylene, octylene, nonylene, decalene, 1,4-cyclohexylene, and the like. Alkylene groups, whether alone or as part of another group, can be optionally substituted with one or more groups, preferably 1 to 3 groups (and any additional substituents selected from halogen), including, but not limited to, -halogen, -O-(C₁-C₈ alkyl), -O-(C₂-C₈ alkenyl), -O-(C₂-C₈ alkynyl), -aryl, -C(O)R', -OC(O)R', -C(O)OR', -C(O)NH₂, -C(O)NHR', -C(O)N(R')₂, -NHC(O)R', -SR', -SO₃R', -S(O)₂R', -S(O)R', -OH, =O, -N₃, -NH₂, -NH(R'), -N(R')₂ and -CN, where each R' is independently selected from -H, -C₁-C₈ alkyl,

-C₂-C₈ alkenyl, -C₂-C₈ alkynyl, or -aryl and wherein said -O-(C₁-C₈ alkyl), -O-(C₂-C₈ alkenyl), -O-(C₂-C₈ alkynyl), -aryl, -C₁-C₈ alkyl, -C₂-C₈ alkenyl, and -C₂-C₈ alkynyl groups can be further optionally substituted with one or more substituents including, but not limited to, -C₁-C₈ alkyl, -C₂-C₈ alkenyl, -C₂-C₈ alkynyl, -halogen, -O-(C₁-C₈ alkyl), -O-(C₂-C₈ alkenyl), -O-(C₂-C₈ alkynyl), -aryl, -C(O)R", -OC(O)R", -C(O)OR", -C(O)NH₂, -C(O)NHR", -C(O)N(R")₂, -NHC(O)R", -SR", -SO₃R", -S(O)₂R", -S(O)R", -OH, -N₃, -NH₂, -NH(R"), -N(R")₂ and -CN, where each R" is independently selected from -H, -C₁-C₈ alkyl, -C₂-C₈ alkenyl, -C₂-C₈ alkynyl, or -aryl.

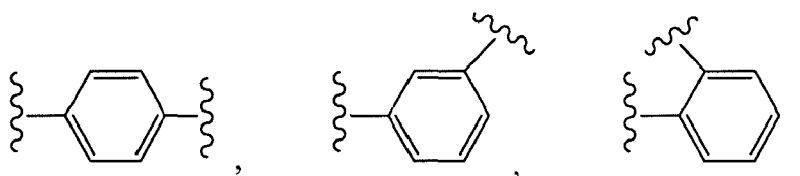
[0054] Unless otherwise noted, the term "alkenylene" refers to an optionally substituted alkylene group containing at least one carbon-carbon double bond. Exemplary alkenylene groups include, for example, ethenylene (-CH=CH-) and propenylene (-CH=CHCH₂-).

[0055] Unless otherwise noted, the term "alkynylene" refers to an optionally substituted alkylene group containing at least one carbon-carbon triple bond. Exemplary alkynylene groups include, for example, acetylene (-C≡C-), propargyl (-CH₂C≡C-), and 4-pentynyl (-CH₂CH₂CH₂C≡CH-).

[0056] Unless otherwise noted, the term "aryl" refers to a monovalent aromatic hydrocarbon radical of 6-20 carbon atoms (and all combinations and subcombinations of ranges and specific numbers of carbon atoms therein) derived by the removal of one hydrogen atom from a single carbon atom of a parent aromatic ring system. Some aryl groups are represented in the exemplary structures as "Ar". Typical aryl groups include, but are not limited to, radicals derived from benzene, substituted benzene, phenyl, naphthalene, anthracene, biphenyl, and the like.

[0057] An aryl group, whether alone or as part of another group, can be optionally substituted with one or more, preferably 1 to 5, or even 1 to 2 groups including, but not limited to, -halogen, -C₁-C₈ alkyl, -C₂-C₈ alkenyl, -C₂-C₈ alkynyl, -O-(C₁-C₈ alkyl), -O-(C₂-C₈ alkenyl), -O-(C₂-C₈ alkynyl), -aryl, -C(O)R', -OC(O)R', -C(O)OR', -C(O)NH₂, -C(O)NHR', -C(O)N(R')₂, -NHC(O)R', -SR', -SO₃R', -S(O)₂R', -S(O)R', -OH, -NO₂, -N₃, -NH₂, -NH(R'), -N(R')₂ and -CN, where each R' is independently selected from -H, -C₁-C₈ alkyl, -C₂-C₈ alkenyl, -C₂-C₈ alkynyl, or -aryl and wherein said -C₁-C₈ alkyl, -C₂-C₈ alkenyl, -C₂-C₈ alkynyl, O-(C₁-C₈ alkyl), -O-(C₂-C₈ alkenyl), -O-(C₂-C₈ alkynyl), and -aryl groups can be further optionally substituted with one or more substituents including, but not limited to, -C₁-C₈ alkyl, -C₂-C₈ alkenyl, -C₂-C₈ alkynyl, -halogen, -O-(C₁-C₈ alkyl), -O-(C₂-C₈ alkenyl), -O-(C₂-C₈ alkynyl), -aryl, -C(O)R", -OC(O)R", -C(O)OR", -C(O)NH₂, -C(O)NHR", -C(O)N(R")₂, -NHC(O)R", -SR", -SO₃R", -S(O)₂R", -S(O)R", -OH, -N₃, -NH₂, -NH(R"), -N(R")₂ and -CN, where each R" is independently selected from -H, -C₁-C₈ alkyl, -C₂-C₈ alkenyl, -C₂-C₈ alkynyl, or -aryl.

[0058] Unless otherwise noted, the term "arylene" refers to an optionally substituted aryl group which is divalent (i.e., derived by the removal of two hydrogen atoms from the same or two different carbon atoms of a parent aromatic ring system) and can be in the ortho, meta, or para configurations as shown in the following structures with phenyl as the exemplary aryl group.



Typical "-(C₁-C₈ alkylene)aryl", "-(C₂-C₈ alkenylene)aryl", and "-(C₂-C₈ alkynylene)aryl" groups include, but are not limited to, benzyl, 2-phenylethan-1-yl, 2-phenylethen-1-yl, naphthylmethyl, 2-naphthylethan-1-yl, 2-naphthylethen-1-yl, naphthobenzyl, 2-naphthophenylethan-1-yl and the like.

[0059] Unless otherwise noted, the term "heterocycle," refers to a monocyclic, bicyclic, or polycyclic ring system having from 3 to 14 ring atoms (also referred to as ring members) wherein at least one ring atom in at least one ring is a heteroatom selected from N, O, P, or S (and all combinations and subcombinations of ranges and specific numbers of carbon atoms and heteroatoms therein). The heterocycle can have from 1 to 4 ring heteroatoms independently selected from N, O, P, or S. One or more N, C, or S atoms in a heterocycle can be oxidized. A monocyclic heterocycle preferably has 3 to 7 ring members (e.g., 2 to 6 carbon atoms and 1 to 3 heteroatoms independently selected from N, O, P, or S), and a bicyclic heterocycle preferably has 5 to 10 ring members (e.g., 4 to 9 carbon atoms and 1 to 3 heteroatoms independently selected from N, O, P, or S). The ring that includes the heteroatom can be aromatic or non-aromatic. Unless otherwise noted, the heterocycle is attached to its pendant group at any heteroatom or carbon atom that results in a stable structure.

[0060] Heterocycles are described in Paquette, "Principles of Modern Heterocyclic Chemistry" (W.A. Benjamin, New York, 1968), particularly Chapters 1, 3, 4, 6, 7, and 9; "The Chemistry of Heterocyclic Compounds, A series of Monographs" (John Wiley & Sons, New York, 1950 to present), in particular Volumes 13, 14, 16, 19, and 28; and J. Am. Chem. Soc. 82:5566 (1960).

[0061] Examples of "heterocycle" groups include by way of example and not limitation pyridyl, dihydropyridyl, tetrahydropyridyl (piperidyl), thiazolyl, pyrimidinyl, furanyl, thienyl, pyrrolyl, pyrazolyl, imidazolyl, tetrazolyl, benzofuranyl, thian-

aphthalenyl, indolyl, indolenyl, quinolinyl, isoquinolinyl, benzimidazolyl, piperidinyl, 4-piperidonyl, pyrrolidinyl, 2-pyrrolidonyl, pyrrolinyl, tetrahydrofuranyl, bis-tetrahydrofuranyl, tetrahydropyranyl, bis-tetrahydropyranyl, tetrahydroquinolinyl, tetrahydroisoquinolinyl, decahydroquinolinyl, octahydroisoquinolinyl, azocinyl, triazinyl, 6H-1,2,5-thiadiazinyl, 2H,6H-1,5,2-dithiazinyl, thienyl, thianthrenyl, pyranyl, isobenzofuranyl, chromenyl, xanthenyl, phenoxathinyl, 2H-pyrrolyl, isothiazolyl, isoxazolyl, pyrazinyl, pyridazinyl, indolizynyl, isoindolyl, 3H-indolyl, 1H-indazolyl, purinyl, 4H-quinolizynyl, phthalazinyl, naphthyridinyl, quinoxalyl, quinazolinyl, cinnolinyl, pteridinyl, 4H-carbazolyl, carbazolyl, β -carbolinyl, phenanthridinyl, acridinyl, pyrimidinyl, phenanthrolinyl, phenazinyl, phenothiazinyl, furazanyl, phenoxazinyl, isochromanlyl, chromanlyl, imidazolidinyl, imidazolynyl, pyrazolidinyl, pyrazolynyl, piperazinyl, indolynyl, isoindolynyl, quinuclidinyl, morpholinyl, oxazolidinyl, benzotriazolyl, benzisoxazolyl, oxindolyl, benzoxazolynyl, and isatinoyl. Preferred "heterocycle" groups include, but are not limited to, benzofuranyl, benzothiophenyl, indolyl, benzopyrazolyl, coumarinyl, isoquinolinyl, pyrrolyl, thiophenyl, furanyl, thiazolyl, imidazolyl, pyrazolyl, triazolyl, quinolinyl, pyrimidinyl, pyridinyl, pyridonyl, pyrazinyl, pyridazinyl, isothiazolyl, isoxazolyl and tetrazolyl.

[0062] A heterocycle group, whether alone or as part of another group, can be optionally substituted with one or more groups, preferably 1 to 2 groups, including but not limited to, $-C_1-C_8$ alkyl, $-C_2-C_8$ alkenyl, $-C_2-C_8$ alkynyl, -halogen, $-O-(C_1-C_8 \text{ alkyl})$, $-O-(C_2-C_8 \text{ alkenyl})$, $-O-(C_2-C_8 \text{ alkynyl})$, -aryl, $-C(O)R'$, $-OC(O)R'$, $-C(O)OR'$, $-C(O)NH_2$, $-C(O)NHR'$, $-C(O)N(R')_2$, $-NHC(O)R'$, $-SR'$, $-SO_3R'$, $-S(O)_2R'$, $-S(O)R'$, $-OH$, $-N_3$, $-NH_2$, $-NH(R')$, $-N(R')_2$ and $-CN$, where each R' is independently selected from $-H$, $-C_1-C_8$ alkyl, $-C_2-C_8$ alkenyl, $-C_2-C_8$ alkynyl, or -aryl and wherein said $-O-(C_1-C_8 \text{ alkyl})$, $-O-(C_2-C_8 \text{ alkenyl})$, $-O-(C_2-C_8 \text{ alkynyl})$, $-C_1-C_8$ alkyl, $-C_2-C_8$ alkenyl, $-C_2-C_8$ alkynyl, and -aryl groups can be further optionally substituted with one or more substituents including, but not limited to, $-C_1-C_8$ alkyl, $-C_2-C_8$ alkenyl, $-C_2-C_8$ alkynyl, -halogen, $-O-(C_1-C_8 \text{ alkyl})$, $-O-(C_2-C_8 \text{ alkenyl})$, $-O-(C_2-C_8 \text{ alkynyl})$, -aryl, $-C(O)R''$, $-OC(O)R''$, $-C(O)OR''$, $-C(O)NH_2$, $-C(O)NHR''$, $-C(O)N(R'')_2$, $-NHC(O)R''$, $-SR''$, $-SO_3R''$, $-S(O)_2R''$, $-S(O)R''$, $-OH$, $-N_3$, $-NH_2$, $-NH(R'')$, $-N(R'')_2$ and $-CN$, where each R'' is independently selected from $-H$, $-C_1-C_8$ alkyl, $-C_2-C_8$ alkenyl, $-C_2-C_8$ alkynyl, or aryl.

[0063] By way of example and not limitation, carbon-bonded heterocycles can be bonded at the following positions: position 2, 3, 4, 5, or 6 of a pyridine; position 3, 4, 5, or 6 of a pyridazine; position 2, 4, 5, or 6 of a pyrimidine; position 2, 3, 5, or 6 of a pyrazine; position 2, 3, 4, or 5 of a furan, tetrahydrofuran, thiofuran, thiophene, pyrrole or tetrahydropyrrole; position 2, 4, or 5 of an oxazole, imidazole or thiazole; position 3, 4, or 5 of an isoxazole, pyrazole, or isothiazole; position 2 or 3 of an aziridine; position 2, 3, or 4 of an azetidine; position 2, 3, 4, 5, 6, 7, or 8 of a quinoline; or position 1, 3, 4, 5, 6, 7, or 8 of an isoquinoline. Still more typically, carbon bonded heterocycles include 2-pyridyl, 3-pyridyl, 4-pyridyl, 5-pyridyl, 6-pyridyl, 3-pyridazinyl, 4-pyridazinyl, 5-pyridazinyl, 6-pyridazinyl, 2-pyrimidinyl, 4-pyrimidinyl, 5-pyrimidinyl, 6-pyrimidinyl, 2-pyrazinyl, 3-pyrazinyl, 5-pyrazinyl, 6-pyrazinyl, 2-thiazolyl, 4-thiazolyl, or 5-thiazolyl.

[0064] By way of example and not limitation, nitrogen bonded heterocycles can be bonded at position 1 of an aziridine, azetidine, pyrrole, pyrrolidine, 2-pyrroline, 3-pyrroline, imidazole, imidazolidine, 2-imidazoline, 3-imidazoline, pyrazole, pyrazoline, 2-pyrazoline, 3-pyrazoline, piperidine, piperazine, indole, indoline, or 1H-indazole; position 2 of a isoindole, or isoindoline; position 4 of a morpholine; and position 9 of a carbazole, or β -carboline. Still more typically, nitrogen bonded heterocycles include 1-aziridyl, 1-azetetyl, 1-pyrrolyl, 1-imidazolyl, 1-pyrazolyl, and 1-piperidinyl.

[0065] Unless otherwise noted, the term "carbocycle," refers to a saturated or unsaturated non-aromatic monocyclic, bicyclic, or polycyclic ring system having from 3 to 14 ring atoms (and all combinations and subcombinations of ranges and specific numbers of carbon atoms therein) wherein all of the ring atoms are carbon atoms. Monocyclic carbocycles preferably have 3 to 6 ring atoms, still more preferably 5 or 6 ring atoms. Bicyclic carbocycles preferably have 7 to 12 ring atoms, e.g., arranged as a bicyclo [4,5], [5,5], [5,6] or [6,6] system, or 9 or 10 ring atoms arranged as a bicyclo [5,6] or [6,6] system. The term "carbocycle" includes, for example, a monocyclic carbocycle ring fused to an aryl ring (e.g., a monocyclic carbocycle ring fused to a benzene ring). Carbocycles preferably have 3 to 8 carbon ring atoms.

[0066] Carbocycle groups, whether alone or as part of another group, can be optionally substituted with, for example, one or more groups, preferably 1 or 2 groups (and any additional substituents selected from halogen), including, but not limited to, -halogen, $-C_1-C_8$ alkyl, $-C_2-C_8$ alkenyl, $-C_2-C_8$ alkynyl, $-O-(C_1-C_8 \text{ alkyl})$, $-O-(C_2-C_8 \text{ alkenyl})$, $-O-(C_2-C_8 \text{ alkynyl})$, -aryl, $-C(O)R'$, $-OC(O)R'$, $-C(O)OR'$, $-C(O)NH_2$, $-C(O)NHR'$, $-C(O)N(R')_2$, $-NHC(O)R'$, $-SR'$, $-SO_3R'$, $-S(O)_2R'$, $-S(O)R'$, $-OH$, $=O$, $-N_3$, $-NH_2$, $-NH(R')$, $-N(R')_2$ and $-CN$, where each R' is independently selected from $-H$, $-C_1-C_8$ alkyl, $-C_2-C_8$ alkenyl, $-C_2-C_8$ alkynyl, or -aryl and wherein said $-C_1-C_8$ alkyl, $-C_2-C_8$ alkenyl, $-C_2-C_8$ alkynyl, $-O-(C_1-C_8 \text{ alkyl})$, $-O-(C_2-C_8 \text{ alkenyl})$, $-O-(C_2-C_8 \text{ alkynyl})$, and -aryl groups can be further optionally substituted with one or more substituents including, but not limited to, $-C_1-C_8$ alkyl, $-C_2-C_8$ alkenyl, $-C_2-C_8$ alkynyl, -halogen, $-O-(C_1-C_8 \text{ alkyl})$, $-O-(C_2-C_8 \text{ alkenyl})$, $-O-(C_2-C_8 \text{ alkynyl})$, -aryl, $-C(O)R''$, $-OC(O)R''$, $-C(O)OR''$, $-C(O)NH_2$, $-C(O)NHR''$, $-C(O)N(R'')_2$, $-NHC(O)R''$, $-SR''$, $-SO_3R''$, $-S(O)_2R''$, $-S(O)R''$, $-OH$, $-N_3$, $-NH_2$, $-NH(R'')$, $-N(R'')_2$ and $-CN$, where each R'' is independently selected from $-H$, $-C_1-C_8$ alkyl, $-C_2-C_8$ alkenyl, $-C_2-C_8$ alkynyl, or -aryl.

[0067] Examples of monocyclic carbocyclic substituents include -cyclopropyl, -cyclobutyl, -cyclopentyl, -1-cyclopent-1-enyl, -1-cyclopent-2-enyl, -1-cyclopent-3-enyl, cyclohexyl, -1-cyclohex-1-enyl, -1-cyclohex-2-enyl, -1-cyclohex-3-enyl, -cycloheptyl, -cyclooctyl, -1,3-cyclohexadienyl, -1,4-cyclohexadienyl, -1,3-cycloheptadienyl, -1,3,5-cycloheptatrienyl, and -cyclooctadienyl.

[0068] A "carbocyclo," whether used alone or as part of another group, refers to an optionally substituted carbocycle

group as defined above that is divalent (*i.e.*, derived by the removal of two hydrogen atoms from the same or two different carbon atoms of a parent carbocyclic ring system).

[0069] Unless otherwise indicated by context, a hyphen (-) designates the point of attachment to the pendant molecule. Accordingly, the term " $-(C_1-C_8 \text{ alkylene})\text{aryl}$ " or " $-C_1-C_8 \text{ alkylene(aryl)}$ " refers to a C_1-C_8 alkylene radical as defined herein wherein the alkylene radical is attached to the pendant molecule at any of the carbon atoms of the alkylene radical and one of the hydrogen atoms bonded to a carbon atom of the alkylene radical is replaced with an aryl radical as defined herein.

[0070] When a particular group is "substituted", that group may have one or more substituents, preferably from one to five substituents, more preferably from one to three substituents, most preferably from one to two substituents, independently selected from the list of substituents. The group can, however, generally have any number of substituents selected from halogen. Groups that are substituted are so indicated.

[0071] It is intended that the definition of any substituent or variable at a particular location in a molecule be independent of its definitions elsewhere in that molecule. It is understood that substituents and substitution patterns on the compounds of this invention can be selected by one of ordinary skill in the art to provide compounds that are chemically stable and that can be readily synthesized by techniques known in the art as well as those methods set forth herein.

[0072] Protective groups as used herein refer to groups which selectively block, either temporarily or permanently, one reactive site in a multifunctional compound. Suitable hydroxy-protecting groups for use in the present invention are pharmaceutically acceptable and may or may not need to be cleaved from the parent compound after administration to a subject in order for the compound to be active. Cleavage is through normal metabolic processes within the body. Hydroxy protecting groups are well known in the art, see, Protective Groups in Organic Synthesis by T. W. Greene and P. G. M. Wuts (John Wiley & sons, 3rd Edition) incorporated herein by reference in its entirety and for all purposes and include, for example, ether (*e.g.*, alkyl ethers and silyl ethers including, for example, dialkylsilyl ether, trialkylsilyl ether, dialkylalkoxysilyl ether), ester, carbonate, carbamates, sulfonate, and phosphate protecting groups. Examples of hydroxy protecting groups include, but are not limited to, methyl ether; methoxymethyl ether, methylthiomethyl ether, (phenyldimethylsilyl)methoxymethyl ether, benzyloxymethyl ether, p-methoxybenzyloxymethyl ether, p-nitrobenzyloxymethyl ether, o-nitrobenzyloxymethyl ether, (4-methoxyphenoxy)methyl ether, guaiacolmethyl ether, t-butoxymethyl ether, 4-pentenylloxymethyl ether, siloxymethyl ether, 2-methoxyethoxymethyl ether, 2,2,2-trichloroethoxymethyl ether, bis(2-chloroethoxy)methyl ether, 2-(trimethylsilyl)ethoxymethyl ether, menthoxymethyl ether, tetrahydropyranyl ether, 1-methoxycyclohexyl ether, 4-methoxytetrahydrothiopyranyl ether, 4-methoxytetrahydrothiopyranyl ether S,S-Dioxide, 1-[(2-chloro-4-methyl)phenyl]-4-methoxypiperidin-4-yl ether, 1-(2-fluorophenyl)-4-methoxypiperidin-4-yl ether, 1,4-dioxan-2-yl ether, tetrahydrofuranyl ether, tetrahydrothiofuranyl ether; substituted ethyl ethers such as 1-ethoxyethyl ether, 1-(2-chloroethoxy)ethyl ether, 1-[2-(trimethylsilyl)ethoxy]ethyl ether, 1-methyl-1-methoxyethyl ether, 1-methyl-1-benzyloxyethyl ether, 1-methyl-1-benzyloxy-2-fluoroethyl ether, 1-methyl-1-phenoxyethyl ether, 2-trimethylsilyl ether, t-butyl ether, allyl ether, propargyl ethers, p-chlorophenyl ether, p-methoxyphenyl ether, benzyl ether, p-methoxybenzyl ether 3,4-dimethoxybenzyl ether, trimethylsilyl ether, triethylsilyl ether, tripropylsilyl ether, dimethylisopropylsilyl ether, diethylisopropylsilyl ether, dimethylhexylsilyl ether, t-butyl dimethylsilyl ether, diphenylmethylsilyl ether, benzoylformate ester, acetate ester, chloroacetate ester, dichloroacetate ester, trichloroacetate ester, trifluoroacetate ester, methoxyacetate ester, triphenylmethoxyacetate ester, phenylacetate ester, benzoate ester, alkyl methyl carbonate, alkyl 9-fluorenylmethyl carbonate, alkyl ethyl carbonate, alkyl 2,2,2-trichloroethyl carbonate, 1,1-dimethyl-2,2,2-trichloroethyl carbonate, alkyl-sulfonate, methanesulfonate, benzylsulfonate, tosylate, methylene acetal, ethylidene acetal, and t-butylmethylidene ketal. Preferred protecting groups are represented by the formulas $-R^a$, $-\text{Si}(R^a)(R^a)(R^a)$, $-\text{C}(\text{O})R^a$, $-\text{C}(\text{O})\text{OR}^a$, $-\text{C}(\text{O})\text{NH}(R^a)$, $-\text{S}(\text{O})_2R^a$, $-\text{S}(\text{O})_2\text{OH}$, $\text{P}(\text{O})(\text{OH})_2$, and $-\text{P}(\text{O})(\text{OH})\text{OR}^a$, wherein R^a is C_1-C_{20} alkyl, C_2-C_{20} alkenyl, C_2-C_{20} alkynyl, $-C_1-C_{20}$ alkylene(carbocycle), $-C_2-C_{20}$ alkenylene(carbocycle), $-C_2-C_{20}$ alkynylene(carbocycle), $-C_6-C_{10}$ aryl, $-C_1-C_{20}$ alkylene(aryl), $-C_2-C_{20}$ alkenylene(aryl), $-C_2-C_{20}$ alkynylene(aryl), $-C_1-C_{20}$ alkylene(heterocycle), $-C_2-C_{20}$ alkenylene(heterocycle), or $-C_2-C_{20}$ alkynylene(heterocycle) wherein said alkyl, alkenyl, alkynyl, alkylene, alkenylene, alkynylene, aryl, carbocycle, and heterocycle radicals whether alone or as part of another group are optionally substituted.

[0073] "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence 191P4D12 (either by removing the underlying glycosylation site or by deleting the glycosylation by chemical and/or enzymatic means), and/or adding one or more glycosylation sites that are not present in the native sequence 191P4D12. In addition, the phrase includes qualitative changes in the glycosylation of the native proteins, involving a change in the nature and proportions of the various carbohydrate moieties present.

[0074] The term "analog" refers to a molecule which is structurally similar or shares similar or corresponding attributes with another molecule (*e.g.* a 191P4D12-related protein). For example, an analog of a 191P4D12 protein can be specifically bound by an antibody or T cell that specifically binds to 191P4D12.

[0075] The term "antibody" is used in the broadest sense unless clearly indicated otherwise. Therefore, an "antibody" can be naturally occurring or man-made such as monoclonal antibodies produced by conventional hybridoma technology. 191P4D12 antibodies comprise monoclonal and polyclonal antibodies as well as fragments containing the antigen-binding domain and/or one or more complementarity determining regions of these antibodies. As used herein, the term

"antibody" refers to any form of antibody or fragment thereof that specifically binds 191P4D12 and/or exhibits the desired biological activity and specifically covers monoclonal antibodies (including full length monoclonal antibodies), polyclonal antibodies, multispecific antibodies (e.g., bispecific antibodies), and antibody fragments so long as they specifically bind 191P4D12 and/or exhibit the desired biological activity. Any specific antibody can be used in the methods and compositions provided herein. Thus, in one embodiment the term "antibody" encompasses a molecule comprising at least one variable region from a light chain immunoglobulin molecule and at least one variable region from a heavy chain molecule that in combination form a specific binding site for the target antigen. In one embodiment, the antibody is an IgG antibody. For example, the antibody is a IgG1, IgG2, IgG3, or IgG4 antibody. The antibodies useful in the present methods and compositions can be generated in cell culture, in phage, or in various animals, including but not limited to cows, rabbits, goats, mice, rats, hamsters, guinea pigs, sheep, dogs, cats, monkeys, chimpanzees, and apes. Therefore, in one embodiment, an antibody of the present invention is a mammalian antibody. Phage techniques can be used to isolate an initial antibody or to generate variants with altered specificity or avidity characteristics. Such techniques are routine and well known in the art. In one embodiment, the antibody is produced by recombinant means known in the art. For example, a recombinant antibody can be produced by transfecting a host cell with a vector comprising a DNA sequence encoding the antibody. One or more vectors can be used to transfect the DNA sequence expressing at least one VL and one VH region in the host cell. Exemplary descriptions of recombinant means of antibody generation and production include Delves, ANTIBODY PRODUCTION: ESSENTIAL TECHNIQUES (Wiley, 1997); Shephard, et al., MONOCLONAL ANTIBODIES (Oxford University Press, 2000); Goding, MONOCLONAL ANTIBODIES: PRINCIPLES AND PRACTICE (Academic Press, 1993); and CURRENT PROTOCOLS IN IMMUNOLOGY (John Wiley & Sons, most recent edition). An antibody of the present invention can be modified by recombinant means to increase efficacy of the antibody in mediating the desired function. Thus, it is within the scope of the invention that antibodies can be modified by substitutions using recombinant means. Typically, the substitutions will be conservative substitutions. For example, at least one amino acid in the constant region of the antibody can be replaced with a different residue. See, e.g., U.S. Patent No. 5,624,821, U.S. Patent No. 6,194,551, Application No. WO 9958572; and Angal, et al., Mol. Immunol. 30: 105-08 (1993). The modification in amino acids includes deletions, additions, and substitutions of amino acids. In some cases, such changes are made to reduce undesired activities, e.g., complement-dependent cytotoxicity. Frequently, the antibodies are labeled by joining, either covalently or non-covalently, a substance which provides for a detectable signal. A wide variety of labels and conjugation techniques are known and are reported extensively in both the scientific and patent literature. These antibodies can be screened for binding to normal or defective 191P4D12. See e.g., Antibody Engineering: A Practical Approach (Oxford University Press, 1996). Suitable antibodies with the desired biologic activities can be identified using the following *in vitro* assays including but not limited to: proliferation, migration, adhesion, soft agar growth, angiogenesis, cell-cell communication, apoptosis, transport, signal transduction, and the following *in vivo* assays such as the inhibition of tumor growth. The antibodies provided herein can also be useful in diagnostic applications. As capture or non-neutralizing antibodies, they can be screened for the ability to bind to the specific antigen without inhibiting the receptor-binding or biological activity of the antigen. As neutralizing antibodies, the antibodies can be useful in competitive binding assays. They can also be used to quantify the 191P4D12 or its receptor.

[0076] The term "antigen-binding portion" or "antibody fragment" of an antibody (or simply "antibody portion"), as used herein, refers to one or more fragments of a 191P4D12 antibody that retain the ability to specifically bind to an antigen (e.g., 191P4D12 and variants; Figure 1). It has been shown that the antigen-binding function of an antibody can be performed by fragments of a full-length antibody. Examples of binding fragments encompassed within the term "antigen-binding portion" of an antibody include (i) a Fab fragment, a monovalent fragment consisting of the V_L , V_H , C_L and C_{H1} domains; (ii) a $F(ab')_2$ fragment, a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region; (iii) a Fd fragment consisting of the V_H and C_{H1} domains; (iv) a Fv fragment consisting of the V_L and V_H domains of a single arm of an antibody, (v) a dAb fragment (Ward et al., (1989) Nature 341:544-546), which consists of a V_H domain; and (vi) an isolated complementarily determining region (CDR). Furthermore, although the two domains of the Fv fragment, V_L and V_H , are coded for by separate genes, they can be joined, using recombinant methods, by a synthetic linker that enables them to be made as a single protein chain in which the V_L and V_H regions pair to form monovalent molecules (known as single chain Fv (scFv); see e.g., Bird et al. (1988) Science 242:423-426; and Huston et al. (1988) Proc. Natl. Acad. Sci. USA 85:5879-5883). Such single chain antibodies are also intended to be encompassed within the term "antigen-binding portion" of an antibody. These antibody fragments are obtained using conventional techniques known to those with skill in the art, and the fragments are screened for utility in the same manner as are intact antibodies.

[0077] As used herein, any form of the "antigen" can be used to generate an antibody that is specific for 191P4D12. Thus, the eliciting antigen may be a single epitope, multiple epitopes, or the entire protein alone or in combination with one or more immunogenicity enhancing agents known in the art. The eliciting antigen may be an isolated full-length protein, a cell surface protein (e.g., immunizing with cells transfected with at least a portion of the antigen), or a soluble protein (e.g., immunizing with only the extracellular domain portion of the protein). The antigen may be produced in a genetically modified cell. The DNA encoding the antigen may be genomic or non-genomic (e.g., cDNA) and encodes at

least a portion of the extracellular domain. As used herein, the term "portion" refers to the minimal number of amino acids or nucleic acids, as appropriate, to constitute an immunogenic epitope of the antigen of interest. Any genetic vectors suitable for transformation of the cells of interest may be employed, including but not limited to adenoviral vectors, plasmids, and non-viral vectors, such as cationic lipids. In one embodiment, the antibody of the methods and compositions

herein specifically bind at least a portion of the extracellular domain of the 191P4D12 of interest.

[0078] The antibodies or antigen binding fragments thereof provided herein may be conjugated to a "bioactive agent." As used herein, the term "bioactive agent" refers to any synthetic or naturally occurring compound that binds the antigen and/or enhances or mediates a desired biological effect to enhance cell-killing toxins. In one embodiment, the binding fragments useful in the present invention are biologically active fragments. As used herein, the term "biologically active" refers to an antibody or antibody fragment that is capable of binding the desired antigenic epitope and directly or indirectly exerting a biologic effect. Direct effects include, but are not limited to the modulation, stimulation, and/or inhibition of a growth signal, the modulation, stimulation, and/or inhibition of an anti-apoptotic signal, the modulation, stimulation, and/or inhibition of an apoptotic or necrotic signal, modulation, stimulation, and/or inhibition the ADCC cascade, and modulation, stimulation, and/or inhibition the CDC cascade.

[0079] "Bispecific" antibodies are also useful in the present methods and compositions. As used herein, the term "bispecific antibody" refers to an antibody, typically a monoclonal antibody, having binding specificities for at least two different antigenic epitopes. In one embodiment, the epitopes are from the same antigen. In another embodiment, the epitopes are from two different antigens. Methods for making bispecific antibodies are known in the art. For example, bispecific antibodies can be produced recombinantly using the co-expression of two immunoglobulin heavy chain/light chain pairs. See, e.g., Milstein et al., *Nature* 305:537-39 (1983). Alternatively, bispecific antibodies can be prepared using chemical linkage. See, e.g., Brennan, et al., *Science* 229:81 (1985). Bispecific antibodies include bispecific antibody fragments. See, e.g., Hollinger, et al., *Proc. Natl. Acad. Sci. U.S.A.* 90:6444-48 (1993), Gruber, et al., *J. Immunol.* 152:5368 (1994).

[0080] The monoclonal antibodies described herein specifically include "chimeric" antibodies in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, so long as they specifically bind the target antigen and/or exhibit the desired biological activity (U.S. Pat. No. 4,816,567; and Morrison et al., *Proc. Natl. Acad. Sci. USA* 81: 6851-6855 (1984)).

[0081] The term "Chemotherapeutic Agent" refers to all chemical compounds that are effective in inhibiting tumor growth. Non-limiting examples of chemotherapeutic agents include alkylating agents; for example, nitrogen mustards, ethyleneimine compounds and alkyl sulphonates; antimetabolites, for example, folic acid, purine or pyrimidine antagonists; mitotic inhibitors, for example, anti-tubulin agents such as vinca alkaloids, auristatins and derivatives of podophyllotoxin; cytotoxic antibiotics; compounds that damage or interfere with DNA expression or replication, for example, DNA minor groove binders; and growth factor receptor antagonists. In addition, chemotherapeutic agents include cytotoxic agents (as defined herein), antibodies, biological molecules and small molecules.

[0082] The term "compound" refers to and encompasses the chemical compound itself as well as, whether explicitly stated or not, and unless the context makes clear that the following are to be excluded: amorphous and crystalline forms of the compound, including polymorphic forms, where these forms may be part of a mixture or in isolation; free acid and free base forms of the compound, which are typically the forms shown in the structures provided herein; isomers of the compound, which refers to optical isomers, and tautomeric isomers, where optical isomers include enantiomers and diastereomers, chiral isomers and non-chiral isomers, and the optical isomers include isolated optical isomers as well as mixtures of optical isomers including racemic and non-racemic mixtures; where an isomer may be in isolated form or in a mixture with one or more other isomers; isotopes of the compound, including deuterium- and tritium-containing compounds, and including compounds containing radioisotopes, including therapeutically- and diagnostically-effective radioisotopes; multimeric forms of the compound, including dimeric, trimeric, etc. forms; salts of the compound, preferably pharmaceutically acceptable salts, including acid addition salts and base addition salts, including salts having organic counterions and inorganic counterions, and including zwitterionic forms, where if a compound is associated with two or more counterions, the two or more counterions may be the same or different; and solvates of the compound, including hemisolvates, monosolvates, disolvates, etc., including organic solvates and inorganic solvates, said inorganic solvates including hydrates; where if a compound is associated with two or more solvent molecules, the two or more solvent molecules may be the same or different. In some instances, reference made herein to a compound of the invention will include an explicit reference to one or of the above forms, e.g., salts and/or solvates; however, this reference is for emphasis only, and is not to be construed as excluding other of the above forms as identified above.

[0083] As used herein, the term "conservative substitution" refers to substitutions of amino acids are known to those of skill in this art and may be made generally without altering the biological activity of the resulting molecule. Those of skill in this art recognize that, in general, single amino acid substitutions in non-essential regions of a polypeptide do not

substantially alter biological activity (see, e.g., Watson, et al., MOLECULAR BIOLOGY OF THE GENE, The Benjamin/Cummings Pub. Co., p. 224 (4th Edition 1987)). Such exemplary substitutions are preferably made in accordance with those set forth in Table II and Table(s) III(a-b). For example, such changes include substituting any of isoleucine (I), valine (V), and leucine (L) for any other of these hydrophobic amino acids; aspartic acid (D) for glutamic acid (E) and vice versa; glutamine (Q) for asparagine (N) and vice versa; and serine (S) for threonine (T) and vice versa. Other substitutions can also be considered conservative, depending on the environment of the particular amino acid and its role in the three-dimensional structure of the protein. For example, glycine (G) and alanine (A) can frequently be interchangeable, as can alanine (A) and valine (V). Methionine (M), which is relatively hydrophobic, can frequently be interchanged with leucine and isoleucine, and sometimes with valine. Lysine (K) and arginine (R) are frequently interchangeable in locations in which the significant feature of the amino acid residue is its charge and the differing pK's of these two amino acid residues are not significant. Still other changes can be considered "conservative" in particular environments (see, e.g. Table III(a) herein; pages 13-15 "Biochemistry" 2nd ED. Lubert Stryer ed (Stanford University); Henikoff et al., PNAS 1992 Vol 89 10915-10919; Lei et al., J Biol Chem 1995 May 19; 270(20):11882-11886). Other substitutions are also permissible and may be determined empirically or in accord with known conservative substitutions.

[0084] The term "cytotoxic agent" refers to a substance that inhibits or prevents the expression activity of cells, function of cells and/or causes destruction of cells. The term is intended to include radioactive isotopes, chemotherapeutic agents, and toxins such as small molecule toxins or enzymatically active toxins of bacterial, fungal, plant or animal origin, including fragments and/or variants thereof. Examples of cytotoxic agents include, but are not limited to auristatins (e.g., auristatin E, auristatin F, MMAE and MMAF), auromycins, maytansinoids, ricin, ricin A-chain, combrestatin, duocarmycins, dolastatins, doxorubicin, daunorubicin, taxols, cisplatin, cc1065, ethidium bromide, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicine, dihydroxy anthracin dione, actinomycin, diphtheria toxin, Pseudomonas exotoxin (PE) A, PE40, abrin, abrin A chain, modeccin A chain, alpha-sarcin, gelonin, mitogellin, retstrictocin, phenomycin, enomycin, curicin, crotin, calicheamicin, Sapaonaria officinalis inhibitor, and glucocorticoid and other chemotherapeutic agents, as well as radioisotopes such as At^{211} , I^{131} , I^{125} , Y^{90} , Re^{186} , Re^{188} , Sm^{153} , Bi^{212} or 213 , P^{32} and radioactive isotopes of Lu including Lu^{177} . Antibodies may also be conjugated to an anti-cancer pro-drug activating enzyme capable of converting the pro-drug to its active form.

[0085] As used herein, the term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy chain variable domain (V_H) connected to a light chain variable domain (V_L) in the same polypeptide chain (V_H - V_L). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies are described more fully in, e.g., EP 404,097; WO 93/11161; and Hollinger et al., Proc. Natl. Acad. Sci. USA 90:6444-48 (1993).

[0086] The term "deplete," in the context of the effect of a 191P4D12 binding agent on 191P4D12-expressing cells, refers to a reduction in the number of or elimination of the 191P4D12-expressing cells.

[0087] The term "gene product" is used herein to indicate a peptide/protein or mRNA. For example, a "gene product of the invention" is sometimes referred to herein as a "cancer amino acid sequence", "cancer protein", "protein of a cancer listed in Table I", a "cancer mRNA", "mRNA of a cancer listed in Table I", etc. In one embodiment, the cancer protein is encoded by a nucleic acid of Figure 1. The cancer protein can be a fragment, or alternatively, be the full-length protein encoded by nucleic acids of Figure 1. In one embodiment, a cancer amino acid sequence is used to determine sequence identity or similarity. In another embodiment, the sequences are naturally occurring allelic variants of a protein encoded by a nucleic acid of Figure 1. In another embodiment, the sequences are sequence variants as further described herein.

[0088] "Heteroconjugate" antibodies are useful in the present methods and compositions. As used herein, the term "heteroconjugate antibody" refers to two covalently joined antibodies. Such antibodies can be prepared using known methods in synthetic protein chemistry, including using crosslinking agents. See, e.g., U.S. Patent No. 4,676,980.

[0089] The term "homolog" refers to a molecule which exhibits homology to another molecule, by for example, having sequences of chemical residues that are the same or similar at corresponding positions.

[0090] In one embodiment, the antibody provided herein is a "human antibody." As used herein, the term "human antibody" refers to an antibody in which essentially the entire sequences of the light chain and heavy chain sequences, including the complementary determining regions (CDRs), are from human genes. In one embodiment, human monoclonal antibodies are prepared by the trioma technique, the human B-cell technique (see, e.g., Kozbor, et al., Immunol. Today 4: 72 (1983), EBV transformation technique (see, e.g., Cole et al. Monoclonal Antibodies And Cancer Therapy 77-96 (1985)), or using phage display (see, e.g., Marks et al., J. Mol. Biol. 222:581 (1991)). In a specific embodiment, the human antibody is generated in a transgenic mouse. Techniques for making such partially to fully human antibodies are known in the art and any such techniques can be used. According to one particularly preferred embodiment, fully human antibody sequences are made in a transgenic mouse engineered to express human heavy and light chain antibody genes. An exemplary description of preparing transgenic mice that produce human antibodies found in Application No. WO 02/43478 and United States Patent 6,657,103 (Abgenix) and its progeny. B cells from transgenic mice that produce

the desired antibody can then be fused to make hybridoma cell lines for continuous production of the antibody. See, e.g., U.S. Patent Nos. 5,569,825; 5,625,126; 5,633,425; 5,661,016; and 5,545,806; and Jakobovits, Adv. Drug Del. Rev. 31:33-42 (1998); Green, et al., J. Exp. Med. 188:483-95 (1998).

[0091] As used herein, the term "humanized antibody" refers to forms of antibodies that contain sequences from non-human (e.g., murine) antibodies as well as human antibodies. Such antibodies are chimeric antibodies which contain minimal sequence derived from non-human immunoglobulin. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the hypervariable loops correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin sequence. The humanized antibody optionally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. See e.g., Cabilly U.S. Patent No. 4,816,567; Queen et al. (1989) Proc. Nat'l Acad. Sci. USA 86:10029-10033; and Antibody Engineering: A Practical Approach (Oxford University Press 1996).

[0092] The terms "inhibit" or "inhibition of" as used herein means to reduce by a measurable amount, or to prevent entirely.

[0093] The phrases "isolated" or "biologically pure" refer to material which is substantially or essentially free from components which normally accompany the material as it is found in its native state. Thus, isolated peptides in accordance with the invention preferably do not contain materials normally associated with the peptides in their *in situ* environment. For example, a polynucleotide is said to be "isolated" when it is substantially separated from contaminant polynucleotides that correspond or are complementary to genes other than the 191P4D12 genes or that encode polypeptides other than 191P4D12 gene product or fragments thereof. A skilled artisan can readily employ nucleic acid isolation procedures to obtain an isolated 191P4D12 polynucleotide. A protein is said to be "isolated," for example, when physical, mechanical or chemical methods are employed to remove the 191P4D12 proteins from cellular constituents that are normally associated with the protein. A skilled artisan can readily employ standard purification methods to obtain an isolated 191P4D12 protein. Alternatively, an isolated protein can be prepared by chemical means.

[0094] Suitable "labels" include radionuclides, enzymes, substrates, cofactors, inhibitors, fluorescent moieties, chemiluminescent moieties, magnetic particles, and the like. Patents teaching the use of such labels include U.S. Patent Nos. 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149; and 4,366,241. In addition, the antibodies provided herein can be useful as the antigen-binding component of fluorobodies. See e.g., Zeytun et al., Nat. Biotechnol. 21:1473-79 (2003).

[0095] The term "mammal" refers to any organism classified as a mammal, including mice, rats, rabbits, dogs, cats, cows, horses and humans. In one embodiment of the invention, the mammal is a mouse. In another embodiment of the invention, the mammal is a human.

[0096] The terms "metastatic cancer" and "metastatic disease" mean cancers that have spread to regional lymph nodes or to distant sites, and are meant to include stage D disease under the AUA system and stage TxNxM+ under the TNM system.

[0097] The term "modulator" or "test compound" or "drug candidate" or grammatical equivalents as used herein describe any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the cancer phenotype or the expression of a cancer sequence, e.g., a nucleic acid or protein sequences, or effects of cancer sequences (e.g., signaling, gene expression, protein interaction, etc.) In one aspect, a modulator will neutralize the effect of a cancer protein of the invention. By "neutralize" is meant that an activity of a protein is inhibited or blocked, along with the consequent effect on the cell. In another aspect, a modulator will neutralize the effect of a gene, and its corresponding protein, of the invention by normalizing levels of said protein. In preferred embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein, or downstream effector pathways. In one embodiment, the modulator suppresses a cancer phenotype, e.g. to a normal tissue fingerprint. In another embodiment, a modulator induced a cancer phenotype. Generally, a plurality of assay mixtures is run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

[0098] Modulators, drug candidates, or test compounds encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 Daltons. Preferred small molecules are less than 2000, or less than 1500 or less than 1000 or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Modulators also comprise biomolecules such as peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof. Particularly preferred are peptides. One class of modulators are peptides, for example of from about five to about 35 amino acids, with from about five to about 20 amino acids being preferred, and from about 7 to

about 15 being particularly preferred. Preferably, the cancer modulatory protein is soluble, includes a non-transmembrane region, and/or, has an N-terminal Cys to aid in solubility. In one embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, *i.e.*, to cysteine. In one embodiment, a cancer protein of the invention is conjugated to an immunogenic agent as discussed herein. In one embodiment, the cancer protein is conjugated to BSA. The peptides of the invention, *e.g.*, of preferred lengths, can be linked to each other or to other amino acids to create a longer peptide/protein. The modulatory peptides can be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. In a preferred embodiment, peptide/protein-based modulators are antibodies, and fragments thereof, as defined herein.

[0099] The term "monoclonal antibody", as used herein, refers to an antibody obtained from a population of substantially homogeneous antibodies, *i.e.*, the individual antibodies comprising the population are identical except for possible naturally occurring mutations that may be present in minor amounts. Monoclonal antibodies are highly specific, being directed against a single antigenic epitope. In contrast, conventional (polyclonal) antibody preparations typically include a multitude of antibodies directed against (or specific for) different epitopes. In one embodiment, the polyclonal antibody contains a plurality of monoclonal antibodies with different epitope specificities, affinities, or avidities within a single antigen that contains multiple antigenic epitopes. The modifier "monoclonal" indicates the character of the antibody as being obtained from a substantially homogeneous population of antibodies, and is not to be construed as requiring production of the antibody by any particular method. For example, the monoclonal antibodies to be used in accordance with the present invention may be made by the hybridoma method first described by Kohler et al., Nature 256: 495 (1975), or may be made by recombinant DNA methods (see, *e.g.*, U.S. Pat. No. 4,816,567). The "monoclonal antibodies" may also be isolated from phage antibody libraries using the techniques described in Clackson et al., Nature 352: 624-628 (1991) and Marks et al., J. Mol. Biol. 222: 581-597 (1991), for example. These monoclonal antibodies will usually bind with at least a K_d of about 1 μM, more usually at least about 300 nM, typically at least about 30 nM, preferably at least about 10 nM, more preferably at least about 3 nM or better, usually determined by ELISA.

[0100] A "pharmaceutical excipient" comprises a material such as an adjuvant, a carrier, pH-adjusting and buffering agents, tonicity adjusting agents, wetting agents, preservative, and the like.

[0101] "Pharmaceutically acceptable" refers to a non-toxic, inert, and/or composition that is physiologically compatible with humans or other mammals.

[0102] The term "polynucleotide" means a polymeric form of nucleotides of at least 10 bases or base pairs in length, either ribonucleotides or deoxynucleotides or a modified form of either type of nucleotide, and is meant to include single and double stranded forms of DNA and/or RNA. In the art, this term is often used interchangeably with "oligonucleotide". A polynucleotide can comprise a nucleotide sequence disclosed herein wherein thymidine (T), as shown for example in Figure 1, can also be uracil (U); this definition pertains to the differences between the chemical structures of DNA and RNA, in particular the observation that one of the four major bases in RNA is uracil (U) instead of thymidine (T).

[0103] The term "polypeptide" means a polymer of at least about 4, 5, 6, 7, or 8 amino acids. Throughout the specification, standard three letter or single letter designations for amino acids are used. In the art, this term is often used interchangeably with "peptide" or "protein".

[0104] A "recombinant" DNA or RNA molecule is a DNA or RNA molecule that has been subjected to molecular manipulation *in vitro*.

[0105] As used herein, the term "single-chain Fv" or "scFv" or "single chain" antibody refers to antibody fragments comprising the V_H and V_L domains of antibody, wherein these domains are present in a single polypeptide chain. Generally, the Fv polypeptide further comprises a polypeptide linker between the V_H and V_L domains which enables the scFv to form the desired structure for antigen binding. For a review of scFv, see Pluckthun, The Pharmacology Of Monoclonal Antibodies, vol. 113, Rosenberg and Moore eds. Springer-Verlag, New York, pp. 269-315 (1994).

[0106] As used herein, the terms "specific", "specifically binds" and "binds specifically" refer to the selective binding of the antibody to the target antigen epitope. Antibodies can be tested for specificity of binding by comparing binding to appropriate antigen to binding to irrelevant antigen or antigen mixture under a given set of conditions. If the antibody binds to the appropriate antigen at least 2, 5, 7, and preferably 10 times more than to irrelevant antigen or antigen mixture then it is considered to be specific. In one embodiment, a specific antibody is one that only binds the 191P4D12 antigen, but does not bind to the irrelevant antigen. In another embodiment, a specific antibody is one that binds human 191P4D12 antigen but does not bind a non-human 191P4D12 antigen with 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or greater amino acid homology with the 191P4D12 antigen. In another embodiment, a specific antibody is one that binds human 191P4D12 antigen and binds murine 191P4D12 antigen, but with a higher degree of binding the human antigen. In another embodiment, a specific antibody is one that binds human 191P4D12 antigen and binds primate 191P4D12 antigen, but with a higher degree of binding the human antigen. In another embodiment, the specific antibody binds to human 191P4D12 antigen and any non-human 191P4D12 antigen, but with a higher degree of binding the human antigen or any combination thereof.

[0107] As used herein "to treat" or "therapeutic" and grammatically related terms, refer to any improvement of any consequence of disease, such as prolonged survival, less morbidity, and/or a lessening of side effects which are the

byproducts of an alternative therapeutic modality; as is readily appreciated in the art, full eradication of disease is a preferred but albeit not a requirement for a treatment act.

[0108] The term "variant" refers to a molecule that exhibits a variation from a described type or norm, such as a protein that has one or more different amino acid residues in the corresponding position(s) of a specifically described protein (e.g. the 191P4D12 protein shown in Figure 1.) An analog is an example of a variant protein. Splice isoforms and single nucleotides polymorphisms (SNPs) are further examples of variants.

[0109] The "191P4D12 proteins" and/or "191P4D12 related proteins" of the invention include those specifically identified herein (see, Figure 1), as well as allelic variants, conservative substitution variants, analogs and homologs that can be isolated/generated and characterized without undue experimentation following the methods outlined herein or readily available in the art. Fusion proteins that combine parts of different 191P4D12 proteins or fragments thereof, as well as fusion proteins of a 191P4D12 protein and a heterologous polypeptide are also included. Such 191P4D12 proteins are collectively referred to as the 191P4D12-related proteins, the proteins of the invention, or 191P4D12. The term "191P4D12-related protein" refers to a polypeptide fragment or a 191P4D12 protein sequence of 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, or more than 25 amino acids; or, at least 30, 35, 40, 45, 50, 55, 60, 65, 70, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 225, 250, 275, 300, 325, 330, 335, 339 or more amino acids.

II.) 191P4D12 Antibodies

[0110] Another aspect of the invention provides antibodies that bind to 191P4D12-related proteins (See Figure 1). In one embodiment, the antibody that binds to 191P4D12-related proteins is an antibody that specifically binds to 191P4D12 protein comprising amino acid sequence of SEQ ID NO.: 2. The antibody that specifically binds to 191P4D12 protein comprising amino acid sequence of SEQ ID NO.: 2 includes antibodies that can bind to other 191P4D12-related proteins. For example, antibodies that bind 191P4D12 protein comprising amino acid sequence of SEQ ID NO.:2 can bind 191P4D12-related proteins such as 191P4D12 variants and the homologs or analogs thereof.

[0111] 191P4D12 antibodies of the invention are particularly useful in cancer (see, e.g., Table I) prognostic assays, imaging, and therapeutic methodologies. Similarly, such antibodies are useful in the treatment, and/or prognosis of colon and other cancers, to the extent 191P4D12 is also expressed or overexpressed in these other cancers. Moreover, intracellularly expressed antibodies (e.g., single chain antibodies) are therapeutically useful in treating cancers in which the expression of 191P4D12 is involved, such as advanced or metastatic colon cancers or other advanced or metastatic cancers.

[0112] Various methods for the preparation of antibodies, specifically monoclonal antibodies, are well known in the art. For example, antibodies can be prepared by immunizing a suitable mammalian host using a 191P4D12-related protein, peptide, or fragment, in isolated or immunoconjugated form (Antibodies: A Laboratory Manual, CSH Press, Eds., Harlow, and Lane (1988); Harlow, Antibodies, Cold Spring Harbor Press, NY (1989)). In addition, fusion proteins of 191P4D12 can also be used, such as a 191P4D12 GST-fusion protein. In a particular embodiment, a GST fusion protein comprising all or most of the amino acid sequence of Figure 1 is produced, and then used as an immunogen to generate appropriate antibodies. In another embodiment, a 191P4D12-related protein is synthesized and used as an immunogen.

[0113] In addition, naked DNA immunization techniques known in the art are used (with or without purified 191P4D12-related protein or 191P4D12 expressing cells) to generate an immune response to the encoded immunogen (for review, see Donnelly et al., 1997, Ann. Rev. Immunol. 15: 617-648).

[0114] The amino acid sequence of a 191P4D12 protein as shown in Figure 1 can be analyzed to select specific regions of the 191P4D12 protein for generating antibodies. For example, hydrophobicity and hydrophilicity analyses of a 191P4D12 amino acid sequence are used to identify hydrophilic regions in the 191P4D12 structure. Regions of a 191P4D12 protein that show immunogenic structure, as well as other regions and domains, can readily be identified using various other methods known in the art, such as Chou-Fasman, Garnier-Robson, Kyte-Doolittle, Eisenberg, Karplus-Schultz or Jameson-Wolf analysis. Hydrophilicity profiles can be generated using the method of Hopp, T.P. and Woods, K.R., 1981, Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828. Hydropathicity profiles can be generated using the method of Kyte, J. and Doolittle, R.F., 1982, J. Mol. Biol. 157:105-132. Percent (%) Accessible Residues profiles can be generated using the method of Janin J., 1979, Nature 277:491-492. Average Flexibility profiles can be generated using the method of Bhaskaran R., Ponnuswamy P.K., 1988, Int. J. Pept. Protein Res. 32:242-255. Beta-turn profiles can be generated using the method of Deleage, G., Roux B., 1987, Protein Engineering 1:289-294. Thus, each region identified by any of these programs or methods is within the scope of the present invention. Preferred methods for the generation of 191P4D12 antibodies are further illustrated by way of the examples provided herein. Methods for preparing a protein or polypeptide for use as an immunogen are well known in the art. Also well known in the art are methods for preparing immunogenic conjugates of a protein with a carrier, such as BSA, KLH or other carrier protein. In some circumstances, direct conjugation using, for example, carbodiimide reagents are used; in other instances linking reagents such as those supplied by Pierce Chemical Co., Rockford, IL, are effective. Administration of a 191P4D12 immunogen

is often conducted by injection over a suitable time period and with use of a suitable adjuvant, as is understood in the art. During the immunization schedule, titers of antibodies can be taken to determine adequacy of antibody formation.

[0115] 191P4D12 monoclonal antibodies can be produced by various means well known in the art. For example, immortalized cell lines that secrete a desired monoclonal antibody are prepared using the standard hybridoma technology of Kohler and Milstein or modifications that immortalize antibody-producing B cells, as is generally known. Immortalized cell lines that secrete the desired antibodies are screened by immunoassay in which the antigen is a 191P4D12-related protein. When the appropriate immortalized cell culture is identified, the cells can be expanded and antibodies produced either from *in vitro* cultures or from ascites fluid.

[0116] The antibodies or fragments of the invention can also be produced by recombinant means. Regions that bind specifically to the desired regions of a 191P4D12 protein can also be produced in the context of chimeric or complementarity-determining region (CDR) grafted antibodies of multiple species origin. Humanized or human 191P4D12 antibodies can also be produced, and are preferred for use in therapeutic contexts. Methods for humanizing murine and other non-human antibodies, by substituting one or more of the non-human antibody CDRs for corresponding human antibody sequences, are well known (see for example, Jones et al., 1986, Nature 321: 522-525; Riechmann et al., 1988, Nature 332: 323-327; Verhoeyen et al., 1988, Science 239: 1534-1536). See also, Carter et al., 1993, Proc. Natl. Acad. Sci. USA 89: 4285 and Sims et al., 1993, J. Immunol. 151: 2296.

[0117] In a preferred embodiment, the antibodies of the present invention comprise fully human 191P4D12 antibodies (191P4D12 MAbs). Various methods in the art provide means for producing fully human 191P4D12 MAbs. For example, a preferred embodiment provides for techniques using transgenic mice, inactivated for antibody production, engineered with human heavy and light chains loci referred to as Xenomouse (Amgen Fremont, Inc.). An exemplary description of preparing transgenic mice that produce human antibodies can be found in U.S. 6,657,103. See, also, U.S. Patent Nos. 5,569,825; 5,625,126; 5,633,425; 5,661,016; and 5,545,806; and Mendez, et. al. Nature Genetics, 15: 146-156 (1998); Kellerman, S.A. & Green, L.L., Curr. Opin. Biotechnol 13, 593-597 (2002).

[0118] In addition, human antibodies of the invention can be generated using the HuMAb mouse (Medarex, Inc.) which contains human immunoglobulin gene miniloci that encode unrearranged human heavy (μ and γ) and kappa light chain immunoglobulin sequences, together with targeted mutations that inactivate the endogenous μ and kappa chain loci (see e.g., Lonberg, et al. (1994) Nature 368(6474): 856-859).

[0119] In another embodiment, fully human antibodies of the invention can be raised using a mouse that carries human immunoglobulin sequences on transgenes and transchromosomes, such as a mouse that carries a human heavy chain transgene and a human light chain transchromosome. Such mice, referred to herein as "KM mice", such mice are described in Tomizuka et al. (2000) Proc. Natl. Acad. Sci. USA 97:722-727 and PCT Publication WO 02/43478 to Tomizuka, et al.

[0120] Human monoclonal antibodies of the invention can also be prepared using phage display methods for screening libraries of human immunoglobulin genes. Such phage display methods for isolating human antibodies are established in the art. See for example: U.S. Pat. Nos. 5,223,409; 5,403,484; and 5,571,698 to Ladner et al.; U.S. Pat. Nos. 5,427,908 and 5,580,717 to Dower et al.; U.S. Pat. Nos. 5,969,108 and 6,172,197 to McCafferty et al.; and U.S. Pat. Nos. 5,885,793; 6,521,404; 6,544,731; 6,555,313; 6,582,915 and 6,593,081 to Griffiths et al.

[0121] Human monoclonal antibodies of the invention can also be prepared using SCID mice into which human immune cells have been reconstituted such that a human antibody response can be generated upon immunization. Such mice are described in, for example, U.S. Pat. Nos. 5,476,996 and 5,698,767 to Wilson et al.

[0122] In a preferred embodiment, an 191P4D12 MAbs of the invention comprises heavy and light chain variable regions of an antibody designated Ha22-2(2,4)6.1 produced by a hybridoma deposited under the American Type Culture Collection (ATCC) Accession No.: PTA-11267 (See, Figure 3), or heavy and light variable regions comprising amino acid sequences that are homologous to the amino acid sequences of the heavy and light chain variable regions of Ha22-2(2,4)6.1, and wherein the antibodies retain the desired functional properties of the 191P4D12 MAbs of the invention. The heavy chain variable region of Ha22-2(2,4)6.1 consists of the amino acid sequence ranging from 20th E residue to the 136th S residue of SEQ ID NO:7, and the light chain variable region of Ha22-2(2,4)6.1 consists of the amino acid sequence ranging from 23rd D residue to the 130th R residue of SEQ ID NO:8. As the constant region of the antibody of the invention, any subclass of constant region can be chosen. In one embodiment, human IgG1 constant region as the heavy chain constant region and human Ig kappa constant region as the light chain constant region can be used.

[0123] For example, the invention provides an isolated monoclonal antibody, or antigen binding portion thereof, comprising a heavy chain variable region and a light chain variable region, wherein:

- (a) the heavy chain variable region comprises an amino acid sequence that is at least 80% homologous to heavy chain variable region amino acid sequence set forth in Figure 3; and
- (b) the light chain variable region comprises an amino acid sequence that is at least 80% homologous to the light chain variable region amino acid sequence set forth in Figure 3.

[0124] In other embodiments, the V_H and/or V_L amino acid sequences may be 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% homologous to the V_H and V_L sequences set forth in Figure 3.

[0125] In another embodiment, the invention provides an isolated monoclonal antibody, or antigen binding portion thereof, comprising a humanized heavy chain variable region and a humanized light chain variable region, wherein:

(a) the heavy chain variable region comprises complementarity determining regions (CDRs) having the amino acid sequences of the heavy chain variable region CDRs set forth in Figure 3;

(b) the light chain variable region comprises CDRs having the amino acid sequences of the light chain variable region CDRs set forth in Figure 3.

[0126] Engineered antibodies of the invention include those in which modifications have been made to framework residues within V_H and/or V_L (e.g. to improve the properties of the antibody). Typically such framework modifications are made to decrease the immunogenicity of the antibody. For example, one approach is to "backmutate" one or more framework residues to the corresponding germline sequence. More specifically, an antibody that has undergone somatic mutation may contain framework residues that differ from the germline sequence from which the antibody is derived. Such residues can be identified by comparing the antibody framework sequences to the germline sequences from which the antibody is derived. To return the framework region sequences to their germline configuration, the somatic mutations can be "backmutated" to the germline sequence by, for example, site-directed mutagenesis or PCR-mediated mutagenesis (e.g., "backmutated" from leucine to methionine). Such "backmutated" antibodies are also intended to be encompassed by the invention.

[0127] Another type of framework modification involves mutating one or more residues within the framework region, or even within one or more CDR regions, to remove T-cell epitopes to thereby reduce the potential immunogenicity of the antibody. This approach is also referred to as "deimmunization" and is described in further detail in U.S. Patent Publication No. 2003/0153043 by Carr et al.

[0128] In addition or alternative to modifications made within the framework or CDR regions, antibodies of the invention may be engineered to include modifications within the Fc region, typically to alter one or more functional properties of the antibody, such as serum half-life, complement fixation, Fc receptor binding, and/or antigen-dependent cellular cytotoxicity. Furthermore, a 191P4D12 MAb of the invention may be chemically modified (e.g., one or more chemical moieties can be attached to the antibody) or be modified to alter its glycosylation, again to alter one or more functional properties of the MAb. Each of these embodiments is described in further detail below.

[0129] In one embodiment, the hinge region of CH1 is modified such that the number of cysteine residues in the hinge region is altered, e.g., increased or decreased. This approach is described further in U.S. Pat. No. 5,677,425 by Bodmer et al. The number of cysteine residues in the hinge region of CH1 is altered to, for example, facilitate assembly of the light and heavy chains or to increase or decrease the stability of the 191P4D12 MAb.

[0130] In another embodiment, the Fc hinge region of an antibody is mutated to decrease the biological half life of the 191P4D12 MAb. More specifically, one or more amino acid mutations are introduced into the CH2-CH3 domain interface region of the Fc-hinge fragment such that the antibody has impaired Staphylococcal protein A (SpA) binding relative to native Fc-hinge domain SpA binding. This approach is described in further detail in U.S. Pat. No. 6,165,745 by Ward et al.

[0131] In another embodiment, the 191P4D12 MAb is modified to increase its biological half life. Various approaches are possible. For example, mutations can be introduced as described in U.S. Pat. No. 6,277,375 to Ward. Alternatively, to increase the biological half life, the antibody can be altered within the CH1 or CL region to contain a salvage receptor binding epitope taken from two loops of a CH2 domain of an Fc region of an IgG, as described in U.S. Pat. Nos. 5,869,046 and 6,121,022 by Presta et al.

[0132] In yet other embodiments, the Fc region is altered by replacing at least one amino acid residue with a different amino acid residue to alter the effector function(s) of the 191P4D12 MAb. For example, one or more amino acids selected from amino acid specific residues can be replaced with a different amino acid residue such that the antibody has an altered affinity for an effector ligand but retains the antigen-binding ability of the parent antibody. The effector ligand to which affinity is altered can be, for example, an Fc receptor or the C1 component of complement. This approach is described in further detail in U.S. Pat. Nos. 5,624,821 and 5,648,260, both by Winter et al.

[0133] Reactivity of 191P4D12 antibodies with a 191P4D12-related protein can be established by a number of well known means, including Western blot, immunoprecipitation, ELISA, and FACS analyses using, as appropriate, 191P4D12-related proteins, 191P4D12-expressing cells or extracts thereof. A 191P4D12 antibody or fragment thereof can be labeled with a detectable marker or conjugated to a second molecule. Suitable detectable markers include, but are not limited to, a radioisotope, a fluorescent compound, a bioluminescent compound, chemiluminescent compound, a metal chelator or an enzyme. Further, bi-specific antibodies specific for two or more 191P4D12 epitopes are generated using methods generally known in the art. Homodimeric antibodies can also be generated by cross-linking techniques known in the art (e.g., Wolff et al., Cancer Res. 53: 2560-2565).

[0134] In yet another preferred embodiment, the 191P4D12 MAb of the invention is an antibody comprising heavy

and light chain of an antibody designated Ha22-2(2,4)6.1. The heavy chain of Ha22-2(2,4)6.1 consists of the amino acid sequence ranging from 20th E residue to the 466th K residue of SEQ ID NO:7 and the light chain of Ha22-2(2,4)6.1 consists of amino acid sequence ranging from 23rd D residue to the 236th C residue of SEQ ID NO:8 sequence. The sequence of which is set forth in Figure 2 and Figure 3. In a preferred embodiment, Ha22-2(2,4)6.1 is conjugated to a cytotoxic agent.

[0135] The hybridoma producing the antibody designated Ha22-2(2,4)6.1 was sent (via Federal Express) to the American Type Culture Collection (ATCC), P.O. Box 1549, Manassas, VA 20108 on 18-August-2010 and assigned Accession number PTA-11267.

III.) Antibody-Drug Conjugates Generally

[0136] In another aspect, the invention provides antibody-drug conjugates (ADCs), comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, a drug, a growth inhibitory agent, a toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate). In another aspect, the invention further provides methods of using the ADCs. In one aspect, an ADC comprises any of the herein 191P4D12 MAbs covalently attached to a cytotoxic agent or a detectable agent.

[0137] The use of antibody-drug conjugates for the local delivery of cytotoxic or cytostatic agents, i.e. drugs to kill or inhibit tumor cells in the treatment of cancer (Syrigos and Epenetos (1999) *Anticancer Research* 19:605-614; Niculescu-Duvaz and Springer (1997) *Adv. Drg Del. Rev.* 26:151-172; U.S. patent 4,975,278) allows targeted delivery of the drug moiety to tumors, and intracellular accumulation therein, where systemic administration of these unconjugated drug agents may result in unacceptable levels of toxicity to normal cells as well as the tumor cells sought to be eliminated (Baldwin et al., (1986) *Lancet* pp. (Mar. 15, 1986):603-05; Thorpe, (1985) "Antibody Carriers Of Cytotoxic Agents In Cancer Therapy: A Review," in *Monoclonal Antibodies '84: Biological And Clinical Applications*, A. Pinchera et al. (ed.s), pp. 475-506). Maximal efficacy with minimal toxicity is sought thereby. Both polyclonal antibodies and monoclonal antibodies have been reported as useful in these strategies (Rowland et al., (1986) *Cancer Immunol. Immunother.*, 21:183-87). Drugs used in these methods include daunomycin, doxorubicin, methotrexate, and vindesine (Rowland et al., (1986) *supra*). Toxins used in antibody-toxin conjugates include bacterial toxins such as diphtheria toxin, plant toxins such as ricin, small molecule toxins such as geldanamycin (Mandler et al (2000) *Jour. of the Nat. Cancer Inst.* 92(19):1573-1581; Mandler et al (2000) *Bioorganic & Med. Chem. Letters* 10:1025-1028; Mandler et al (2002) *Bioconjugate Chem.* 13:786-791), maytansinoids (EP 1391213; Liu et al., (1996) *Proc. Natl. Acad. Sci. USA* 93:8618-8623), and calicheamicin (Lode et al (1998) *Cancer Res.* 58:2928; Hinman et al (1993) *Cancer Res.* 53:3336-3342). The toxins may assert their cytotoxic and cytostatic effects by mechanisms including tubulin binding, DNA binding, or topoisomerase inhibition. Some cytotoxic drugs tend to be inactive or less active when conjugated to large antibodies or protein receptor ligands.

[0138] Examples of antibody drug conjugates are, ZEVALIN® (ibrutinomab tiuxetan, Biogen/Idec) which is an antibody-radioisotope conjugate composed of a murine IgG1 kappa monoclonal antibody directed against the CD20 antigen found on the surface of normal and malignant B lymphocytes and ¹¹¹In or ⁹⁰Y radioisotope bound by a thiourea linker-chelator (Wiseman et al (2000) *Eur. Jour. Nucl. Med.* 27(7):766-77; Wiseman et al (2002) *Blood* 99(12):4336-42; Witzig et al (2002) *J. Clin. Oncol.* 20(10):2453-63; Witzig et al (2002) *J. Clin. Oncol.* 20(15):3262-69).

[0139] Additionally, MYLOTARG™ (gemtuzumab ozogamicin, Wyeth Pharmaceuticals), an antibody drug conjugate composed of a hu CD33 antibody linked to calicheamicin, was approved in 2000 for the treatment of acute myeloid leukemia by injection (Drugs of the Future (2000) 25(7):686; US Patent Nos. 4970198; 5079233; 5585089; 5606040; 5693762; 5739116; 5767285; 5773001).

[0140] In addition, Cantuzumab mertansine (Immunogen, Inc.), an antibody drug conjugate composed of the huC242 antibody linked via the disulfide linker SPP to the maytansinoid drug moiety, DM1, is advancing into Phase II trials for the treatment of cancers that express CanAg, such as colon, pancreatic, gastric, and others.

[0141] Additionally, MLN-2704 (Millennium Pharm., BZL Biologics, Immunogen Inc.), an antibody drug conjugate composed of the anti-prostate specific membrane antigen (PSMA) monoclonal antibody linked to the maytansinoid drug moiety, DM1, is under development for the potential treatment of prostate tumors.

[0142] Finally, the auristatin peptides, auristatin E (AE) and monomethylauristatin (MMAE), synthetic analogs of dolastatin, were conjugated to chimeric monoclonal antibodies cBR96 (specific to Lewis Y on carcinomas) and cAC10 (specific to CD30 on hematological malignancies) (Doronina et al (2003) *Nature Biotechnology* 21(7):778-784) and are under therapeutic development.

[0143] Further, chemotherapeutic agents useful in the generation of ADCs are described herein. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolaca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the

tricothecenes. See, e.g., WO 93/21232 published October 28, 1993. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi , ^{131}I , ^{131}In , ^{90}Y , and ^{186}Re . Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCl), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis-(p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as toluene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta et al (1987) Science, 238:1098. Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody (WO94/11026).

[0144] Conjugates of an antibody and one or more small molecule toxins, such as a calicheamicin, maytansinoids, dolastatins, auristatins, a tricothecene, and CC1065, and the derivatives of these toxins that have toxin activity, are also contemplated herein.

III(A). Maytansinoids

[0145] Maytansine compounds suitable for use as maytansinoid drug moieties are well known in the art, and can be isolated from natural sources according to known methods, produced using genetic engineering techniques (see Yu et al (2002) PNAS 99:7968-7973), or maytansinol and maytansinol analogues prepared synthetically according to known methods.

[0146] Exemplary maytansinoid drug moieties include those having a modified aromatic ring, such as: C-19-dechloro (US 4256746) (prepared by lithium aluminum hydride reduction of ansamycin P2); C-20-hydroxy (or C-20-demethyl) +/-C-19-dechloro (US Pat. Nos. 4,361,650 and 4,307,016) (prepared by demethylation using Streptomyces or Actinomyces or dechlorination using LAH); and C-20-demethoxy, C-20-acyloxy (-OCOR), +/-dechloro (U.S. Pat. No. 4,294,757) (prepared by acylation using acyl chlorides). and those having modifications at other positions

[0147] Exemplary maytansinoid drug moieties also include those having modifications such as: C-9-SH (US 4,424,219) (prepared by the reaction of maytansinol with H_2S or P_2S_5); C-14-alkoxymethyl(demethoxy/ CH_2OR)(US 4331598); C-14-hydroxymethyl or acyloxymethyl (CH_2OH or CH_2OAc) (US 4450254) (prepared from Nocardia); C-15-hydroxy/acyloxy (US 4,364,866) (prepared by the conversion of maytansinol by Streptomyces); C-15-methoxy (US Pat. Nos. 4,313,946 and 4,315,929) (isolated from Trewia nudiflora); C-18-N-demethyl (US Pat. Nos. 4,362,663 and 4,322,348) (prepared by the demethylation of maytansinol by Streptomyces); and 4,5-deoxy (US 4,371,533) (prepared by the titanium trichloride/LAH reduction of maytansinol).

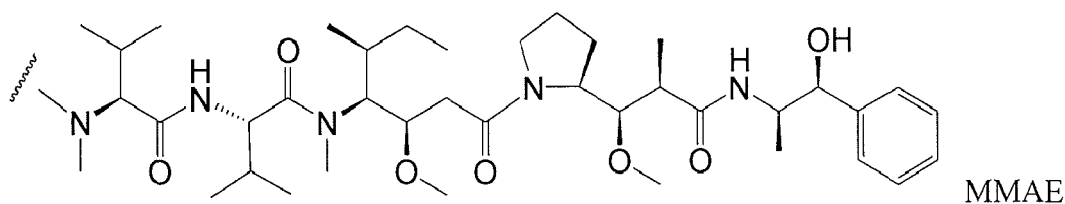
[0148] ADCs containing maytansinoids, methods of making same, and their therapeutic use are disclosed, for example, in U.S. Patent Nos. 5,208,020; 5,416,064; 6,441,163 and European Patent EP 0 425 235 B1, the disclosures of which are hereby expressly incorporated by reference. Liu et al., Proc. Natl. Acad. Sci. USA 93:8618-8623 (1996) described ADCs comprising a maytansinoid designated DM1 linked to the monoclonal antibody C242 directed against human colorectal cancer. The conjugate was found to be highly cytotoxic towards cultured colon cancer cells, and showed antitumor activity in an in vivo tumor growth assay. Chari et al., Cancer Research 52:127-131 (1992) describe ADCs in which a maytansinoid was conjugated via a disulfide linker to the murine antibody A7 binding to an antigen on human colon cancer cell lines, or to another murine monoclonal antibody TA.1 that binds the HER-2/neu oncogene. The cytotoxicity of the TA.1-maytansinoid conjugate was tested in vitro on the human breast cancer cell line SK-BR-3, which expresses 3×10^5 HER-2 surface antigens per cell. The drug conjugate achieved a degree of cytotoxicity similar to the free maytansinoid drug, which could be increased by increasing the number of maytansinoid molecules per antibody molecule. The A7-maytansinoid conjugate showed low systemic cytotoxicity in mice.

III(B). Auristatins and dolastatins

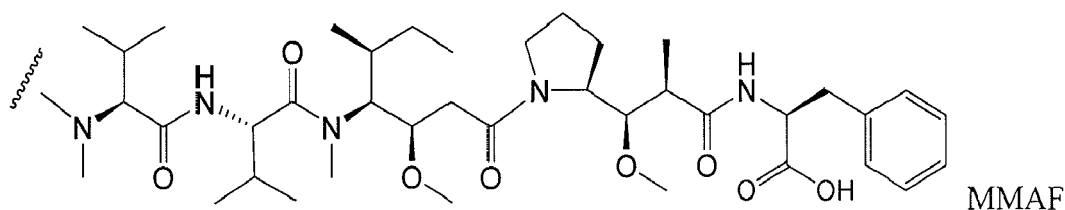
[0149] In some embodiments, the ADC comprises an antibody of the invention conjugated to dolastatins or dolostatin peptidic analogs and derivatives, the auristatins (US Patent Nos. 5,635,483; 5,780,588). Dolastatins and auristatins have been shown to interfere with microtubule dynamics, GTP hydrolysis, and nuclear and cellular division (Woyke et al (2001) Antimicrob. Agents and Chemother. 45(12):3580-3584) and have anticancer (US 5,663,149) and antifungal activity (Pettit et al (1998) Antimicrob. Agents Chemother. 42:2961-2965). The dolastatin or auristatin drug moiety may be attached to the antibody through the N (amino) terminus or the C (carboxyl) terminus of the peptidic drug moiety (WO 02/088172).

[0150] Exemplary auristatin embodiments include the N-terminus linked monomethylauristatin drug moieties DE and DF, disclosed in "Senter et al, Proceedings of the American Association for Cancer Research, Volume 45, Abstract Number 623, presented March 28, 2004 and described in United States Patent Publication No. 2005/0238649, the disclosure of which is expressly incorporated by reference in its entirety.

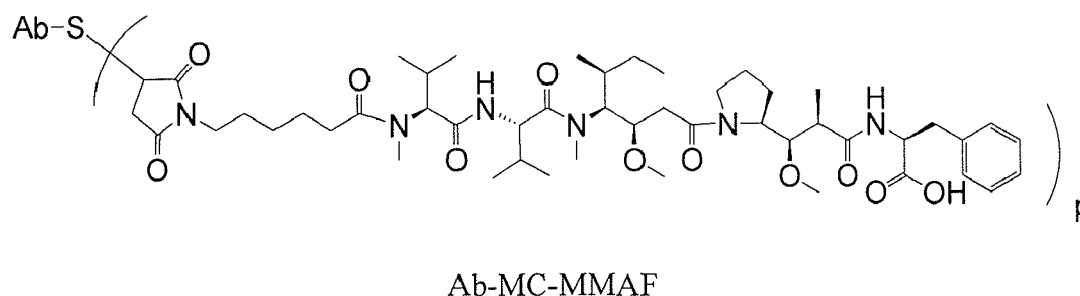
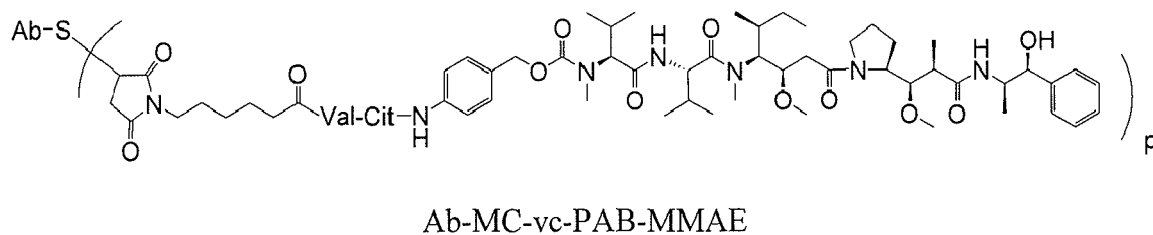
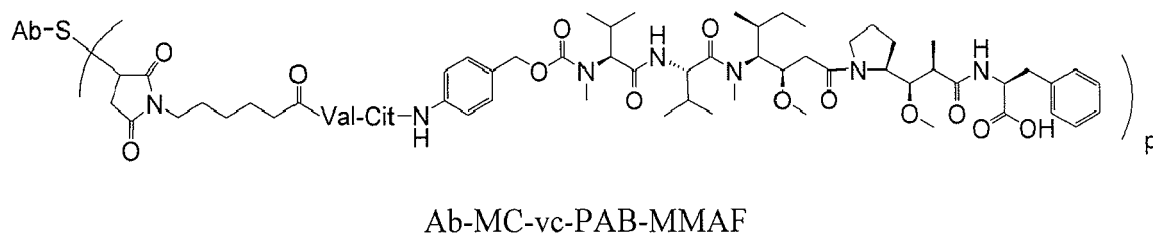
[0151] An exemplary auristatin embodiment is MMAE (wherein the wavy line indicates the covalent attachment to a linker (L) of an antibody drug conjugate).



[0152] Another exemplary auristatin embodiment is MMAF, wherein the wavy line indicates the covalent attachment to a linker (L) of an antibody drug conjugate (US 2005/0238649):



[0153] Additional exemplary embodiments comprising MMAE or MMAF and various linker components (described further herein) have the following structures and abbreviations (wherein Ab means antibody, S is a sulfur of the antibody, and p is 1 to about 8):



[0154] Typically, peptide-based drug moieties can be prepared by forming a peptide bond between two or more amino acids and/or peptide fragments. Such peptide bonds can be prepared, for example, according to the liquid phase synthesis method (see E. Schroder and K. Lübke, "The Peptides", volume 1, pp 76-136, 1965, Academic Press) that is well known

in the field of peptide chemistry. The auristatin/dolastatin drug moieties may be prepared according to the methods of: US 5635483; US 5780588; Pettit et al (1989) J. Am. Chem. Soc. 111:5463-5465; Pettit et al (1998) Anti-Cancer Drug Design 13:243-277; Pettit, G.R., et al. Synthesis, 1996, 719-725; Pettit et al (1996) J. Chem. Soc. Perkin Trans. 1 5:859-863; and Doronina (2003) Nat Biotechnol 21(7):778-784.

III(C). Calicheamicin

[0155] In other embodiments, the ADC comprises an antibody of the invention conjugated to one or more calicheamicin molecules. The calicheamicin family of antibiotics are capable of producing double-stranded DNA breaks at sub-picomolar concentrations. For the preparation of conjugates of the calicheamicin family, see U.S. patents 5,712,374, 5,714,586, 5,739,116, 5,767,285, 5,770,701, 5,770,710, 5,773,001, 5,877,296 (all to American Cyanamid Company). Structural analogues of calicheamicin which may be used include, but are not limited to, γ_1^I , α_2^I , α_3^I , N-acetyl- γ_1^I , PSAG and θ^I_1 (Hinman et al., Cancer Research 53:3336-3342 (1993), Lode et al., Cancer Research 58:2925-2928 (1998) and the aforementioned U.S. patents to American Cyanamid). Another anti-tumor drug that the antibody can be conjugated is QFA which is an antifolate. Both calicheamicin and QFA have intracellular sites of action and do not readily cross the plasma membrane. Therefore, cellular uptake of these agents through antibody mediated internalization greatly enhances their cytotoxic effects.

III(D). Other Cytotoxic Agents

[0156] Other antitumor agents that can be conjugated to the antibodies of the invention include BCNU, streptozocin, vincristine and 5-fluorouracil, the family of agents known collectively LL-E33288 complex described in U.S. patents 5,053,394, 5,770,710, as well as esperamicins (U.S. patent 5,877,296).

[0157] Enzymatically active toxins and fragments thereof which can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, Aleurites fordii proteins, dianthin proteins, Phytolacca americana proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin and the tricothecenes. See, for example, WO 93/21232 published October 28, 1993.

[0158] The present invention further contemplates an ADC formed between an antibody and a compound with nucleolytic activity (e.g., a ribonuclease or a DNA endonuclease such as a deoxyribonuclease; DNase).

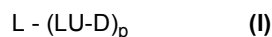
[0159] For selective destruction of the tumor, the antibody may comprise a highly radioactive atom. A variety of radioactive isotopes are available for the production of radioconjugated antibodies. Examples include At^{211} , I^{131} , I^{125} , Y^{90} , Re^{186} , Re^{188} , Sm^{153} , Bi^{212} , P^{32} , Pb^{212} and radioactive isotopes of Lu. When the conjugate is used for detection, it may comprise a radioactive atom for scintigraphic studies, for example Tc^{99m} or I^{123} , or a spin label for nuclear magnetic resonance (NMR) imaging (also known as magnetic resonance imaging, mri), such as iodine-123 again, iodine-131, indium-111, fluorine-19, carbon-13, nitrogen-15, oxygen-17, gadolinium, manganese or iron.

[0160] The radio- or other labels may be incorporated in the conjugate in known ways. For example, the peptide may be biosynthesized or may be synthesized by chemical amino acid synthesis using suitable amino acid precursors involving, for example, fluorine-19 in place of hydrogen. Labels such as Tc^{99m} or I^{123} , Re^{186} , Re^{188} and In^{111} can be attached via a cysteine residue in the peptide. Yttrium-90 can be attached via a lysine residue. The IODOGEN method (Fraker et al (1978) Biochem. Biophys. Res. Commun. 80: 49-57 can be used to incorporate iodine-123. "Monoclonal Antibodies in Immunoscintigraphy" (Chatal, CRC Press 1989) describes other methods in detail.

IV.) Antibody-Drug Conjugate Compounds which bind 191P4D12

[0161] The present invention provides, *inter alia*, antibody-drug conjugate compounds for targeted delivery of drugs. The inventors have made the discovery that the antibody-drug conjugate compounds have potent cytotoxic and/or cytostatic activity against cells expressing 191P4D12. The antibody-drug conjugate compounds comprise an Antibody unit covalently linked to at least one Drug unit. The Drug units can be covalently linked directly or via a Linker unit (LU).

[0162] In some embodiments, the antibody drug conjugate compound has the following formula:



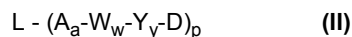
or a pharmaceutically acceptable salt or solvate thereof; wherein:

L is the Antibody unit, e.g., 191P4D12 MAb of the present invention, and
(LU-D) is a Linker unit-Drug unit moiety, wherein:
LU- is a Linker unit, and

-D is a drug unit having cytostatic or cytotoxic activity against a target cell; and
p is an integer from 1 to 20.

[0163] In some embodiments, p ranges from 1 to 10, 1 to 9, 1 to 8, 1 to 7, 1 to 6, 1 to 5, 1 to 4, 1 to 3, or 1 to 2. In some embodiments, p ranges from 2 to 10, 2 to 9, 2 to 8, 2 to 7, 2 to 6, 2 to 5, 2 to 4 or 2 to 3. In other embodiments, p is 1, 2, 3, 4, 5 or 6. In some embodiments, p is 2 or 4.

[0164] In some embodiments, the antibody drug conjugate compound has the following formula:



or a pharmaceutically acceptable salt or solvate thereof, wherein:

L is the Antibody unit, e.g., 191P4D12 MAb; and

-A_a-W_w-Y_y- is a Linker unit (LU), wherein:

-A- is a Stretcher unit,

a is 0 or 1,

each -W- is independently an Amino Acid unit,

w is an integer ranging from 0 to 12,

-Y- is a self-immolative spacer unit,

y is 0, 1 or 2;

-D is a drug units having cytostatic or cytotoxic activity against the target cell; and

p is an integer from 1 to 20.

[0165] In some embodiments, a is 0 or 1, w is 0 or 1, and y is 0, 1 or 2. In some embodiments, a is 0 or 1, w is 0 or 1, and y is 0 or 1. In some embodiments, p ranges from 1 to 10, 1 to 9, 1 to 8, 1 to 7, 1 to 6, 1 to 5, 1 to 4, 1 to 3, or 1 to 2. In some embodiments, p ranges from 2 to 8, 2 to 7, 2 to 6, 2 to 5, 2 to 4 or 2 to 3. In other embodiments, p is 1, 2, 3, 4, 5 or 6. In some embodiments, p is 2 or 4. In some embodiments, when w is not zero, y is 1 or 2. In some embodiments, when w is 1 to 12, y is 1 or 2. In some embodiments, w is 2 to 12 and y is 1 or 2. In some embodiments, a is 1 and w and y are 0.

[0166] For compositions comprising a plurality antibodies, the drug loading is represented by p, the average number of drug molecules per Antibody. Drug loading may range from 1 to 20 drugs (D) per Antibody. The average number of drugs per antibody in preparation of conjugation reactions may be characterized by conventional means such as mass spectroscopy, ELISA assay, and HPLC. The quantitative distribution of Antibody-Drug-Conjugates in terms of p may also be determined. In some instances, separation, purification, and characterization of homogeneous Antibody-Drug-conjugates where p is a certain value from Antibody-Drug-Conjugates with other drug loadings may be achieved by means such as reverse phase HPLC or electrophoresis. In exemplary embodiments, p is from 2 to 8.

[0167] The generation of Antibody-drug conjugate compounds can be accomplished by any technique known to the skilled artisan. Briefly, the Antibody-drug conjugate compounds comprise 191P4D12 MAb as the Antibody unit, a drug, and optionally a linker that joins the drug and the binding agent. In a preferred embodiment, the Antibody is 191P4D12 MAb comprising heavy and light chain variable regions of an antibody designated Ha22-2(2,4)6.1 described above. In more preferred embodiment, the Antibody is 191P4D12 MAb comprising heavy and light chain of an antibody designated Ha22-2(2,4)6.1 described above. A number of different reactions are available for covalent attachment of drugs and/or linkers to binding agents. This is often accomplished by reaction of the amino acid residues of the binding agent, e.g., antibody molecule, including the amine groups of lysine, the free carboxylic acid groups of glutamic and aspartic acid, the sulfhydryl groups of cysteine and the various moieties of the aromatic amino acids. One of the most commonly used non-specific methods of covalent attachment is the carbodiimide reaction to link a carboxy (or amino) group of a compound to amino (or carboxy) groups of the antibody. Additionally, bifunctional agents such as dialdehydes or imidoesters have been used to link the amino group of a compound to amino groups of an antibody molecule. Also available for attachment of drugs to binding agents is the Schiff base aldehyde. This method involves the periodate oxidation of a drug that contains glycol or hydroxy groups, thus forming an aldehyde which is then reacted with the binding agent. Attachment occurs via formation of a Schiff base with amino groups of the binding agent. Isothiocyanates can also be used as coupling agents for covalently attaching drugs to binding agents. Other techniques are known to the skilled artisan and within the scope of the present invention.

[0168] In certain embodiments, an intermediate, which is the precursor of the linker, is reacted with the drug under appropriate conditions. In certain embodiments, reactive groups are used on the drug and/or the intermediate. The product of the reaction between the drug and the intermediate, or the derivatized drug, is subsequently reacted with the 191P4D12 MAb under appropriate conditions.

[0169] Each of the particular units of the Antibody-drug conjugate compounds is described in more detail herein. The synthesis and structure of exemplary Linker units, Stretcher units, Amino Acid units, self-immolative Spacer unit, and

Drug units are also described in U.S. Patent Application Publication Nos. 2003-0083263, 2005-0238649 and 2005-0009751, each of which is incorporated herein by reference in its entirety and for all purposes.

V.) Linker Units

[0170] Typically, the antibody-drug conjugate compounds comprise a Linker unit between the drug unit and the antibody unit. In some embodiments, the linker is cleavable under intracellular conditions, such that cleavage of the linker releases the drug unit from the antibody in the intracellular environment. In yet other embodiments, the linker unit is not cleavable and the drug is released, for example, by antibody degradation.

[0171] In some embodiments, the linker is cleavable by a cleaving agent that is present in the intracellular environment (e.g., within a lysosome or endosome or caveolea). The linker can be, e.g., a peptidyl linker that is cleaved by an intracellular peptidase or protease enzyme, including, but not limited to, a lysosomal or endosomal protease. In some embodiments, the peptidyl linker is at least two amino acids long or at least three amino acids long. Cleaving agents can include cathepsins B and D and plasmin, all of which are known to hydrolyze dipeptide drug derivatives resulting in the release of active drug inside target cells (see, e.g., Dubowchik and Walker, 1999, Pharm. Therapeutics 83:67-123). Most typical are peptidyl linkers that are cleavable by enzymes that are present in 191P4D12-expressing cells. For example, a peptidyl linker that is cleavable by the thiol-dependent protease cathepsin-B, which is highly expressed in cancerous tissue, can be used (e.g., a Phe-Leu or a Gly-Phe-Leu-Gly linker (SEQ ID NO:9)). Other examples of such linkers are described, e.g., in U.S. Patent No. 6,214,345. In a specific embodiment, the peptidyl linker cleavable by an intracellular protease is a Val-Cit linker or a Phe-Lys linker (see, e.g., U.S. Patent 6,214,345, which describes the synthesis of doxorubicin with the Val-Cit linker). One advantage of using intracellular proteolytic release of the therapeutic agent is that the agent is typically attenuated when conjugated and the serum stabilities of the conjugates are typically high.

[0172] In other embodiments, the cleavable linker is pH-sensitive, i.e., sensitive to hydrolysis at certain pH values. Typically, the pH-sensitive linker hydrolyzable under acidic conditions. For example, an acid-labile linker that is hydrolyzable in the lysosome (e.g., a hydrazone, semicarbazone, thiosemicarbazone, cis-aconitic amide, orthoester, acetal, ketal, or the like) can be used. (See, e.g., U.S. Patent Nos. 5,122,368; 5,824,805; 5,622,929; Dubowchik and Walker, 1999, Pharm. Therapeutics 83:67-123; Neville et al., 1989, Biol. Chem. 264:14653-14661.) Such linkers are relatively stable under neutral pH conditions, such as those in the blood, but are unstable at below pH 5.5 or 5.0, the approximate pH of the lysosome. In certain embodiments, the hydrolyzable linker is a thioether linker (such as, e.g., a thioether attached to the therapeutic agent via an acylhydrazone bond (see, e.g., U.S. Patent No. 5,622,929).

[0173] In yet other embodiments, the linker is cleavable under reducing conditions (e.g., a disulfide linker). A variety of disulfide linkers are known in the art, including, for example, those that can be formed using SATA (N-succinimidyl-S-acetylthioacetate), SPDP (N-succinimidyl-3-(2-pyridyldithio)propionate), SPDB (N-succinimidyl-3-(2-pyridyldithio)butyrate) and SMPT (N-succinimidyl-oxycarbonyl-alpha-methyl-alpha-(2-pyridyl-dithio)toluene), SPDB and SMPT. (See, e.g., Thorpe et al., 1987, Cancer Res. 47:5924-5931; Wawrzynczak et al., In Immunoconjugates: Antibody Conjugates in Radioimaging and Therapy of Cancer (C. W. Vogel ed., Oxford U. Press, 1987. See also U.S. Patent No. 4,880,935.)

[0174] In yet other specific embodiments, the linker is a malonate linker (Johnson et al., 1995, Anticancer Res. 15:1387-93), a maleimidobenzoyl linker (Lau et al., 1995, Bioorg-Med-Chem. 3(10):1299-1304), or a 3'-N-amide analog (Lau et al., 1995, Bioorg-Med-Chem. 3(10):1305-12).

[0175] In yet other embodiments, the linker unit is not cleavable and the drug is released by antibody degradation. (See U.S. Publication No. 2005/0238649).

[0176] Typically, the linker is not substantially sensitive to the extracellular environment. As used herein, "not substantially sensitive to the extracellular environment," in the context of a linker, means that no more than about 20%, typically no more than about 15%, more typically no more than about 10%, and even more typically no more than about 5%, no more than about 3%, or no more than about 1% of the linkers, in a sample of antibody-drug conjugate compound, are cleaved when the antibody-drug conjugate compound presents in an extracellular environment (e.g., in plasma). Whether a linker is not substantially sensitive to the extracellular environment can be determined, for example, by incubating with plasma the antibody-drug conjugate compound for a predetermined time period (e.g., 2, 4, 8, 16, or 24 hours) and then quantitating the amount of free drug present in the plasma.

[0177] In other, non-mutually exclusive embodiments, the linker promotes cellular internalization. In certain embodiments, the linker promotes cellular internalization when conjugated to the therapeutic agent (i.e., in the milieu of the linker-therapeutic agent moiety of the antibody-drug conjugate compound as described herein). In yet other embodiments, the linker promotes cellular internalization when conjugated to both the auristatin compound and the 191P4D12 Mab.

[0178] A variety of exemplary linkers that can be used with the present compositions and methods are described in WO 2004-010957, U.S. Publication No. 2006/0074008, U.S. Publication No. 20050238649, and U.S. Publication No. 2006/0024317

[0179] A "Linker unit" (LU) is a bifunctional compound that can be used to link a Drug unit and an Antibody unit to form an antibody-drug conjugate compound. In some embodiments, the Linker unit has the formula:



wherein: -A- is a Stretcher unit,
a is 0 or 1,
each -W- is independently an Amino Acid unit,
w is an integer ranging from 0 to 12,
-Y- is a self-immolative Spacer unit, and
y is 0, 1 or 2.

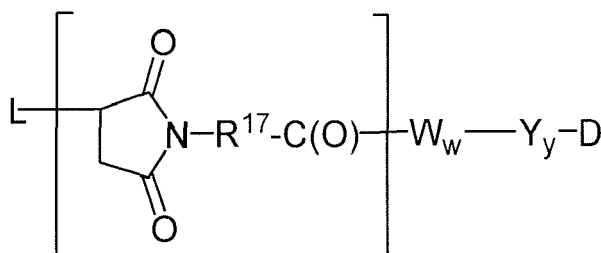
[0180] In some embodiments, a is 0 or 1, w is 0 or 1, and y is 0, 1 or 2. In some embodiments, a is 0 or 1, w is 0 or 1, and y is 0 or 1. In some embodiments, when w is 1 to 12, y is 1 or 2. In some embodiments, w is 2 to 12 and y is 1 or 2. In some embodiments, a is 1 and w and y are 0.

VI.) The Stretcher Unit

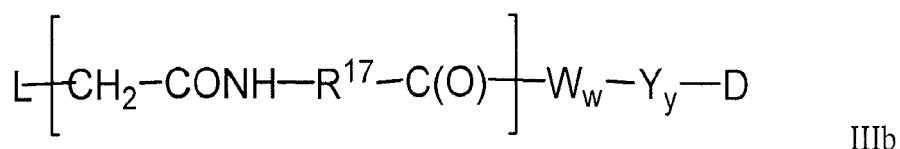
[0181] The Stretcher unit (A), when present, is capable of linking an Antibody unit to an Amino Acid unit (-W-), if present, to a Spacer unit (-Y-), if present; or to a Drug unit (-D). Useful functional groups that can be present on a 191P4D12 MAb (e.g. Ha22-2(2,4)6.1), either naturally or via chemical manipulation include, but are not limited to, sulfhydryl, amino, hydroxyl, the anomeric hydroxyl group of a carbohydrate, and carboxyl. Suitable functional groups are sulfhydryl and amino. In one example, sulfhydryl groups can be generated by reduction of the intramolecular disulfide bonds of a 191P4D12 MAb. In another embodiment, sulfhydryl groups can be generated by reaction of an amino group of a lysine moiety of a 191P4D12 MAb with 2-iminothiolane (Traut's reagent) or other sulfhydryl generating reagents. In certain embodiments, the 191P4D12 MAb is a recombinant antibody and is engineered to carry one or more lysines. In certain other embodiments, the recombinant 191P4D12 MAb is engineered to carry additional sulfhydryl groups, e.g., additional cysteines.

[0182] In one embodiment, the Stretcher unit forms a bond with a sulfur atom of the Antibody unit. The sulfur atom can be derived from a sulfhydryl group of an antibody. Representative Stretcher units of this embodiment are depicted within the square brackets of Formulas IIIa and IIIb, wherein L-, -W-, -Y-, -D, w and y are as defined above, and R¹⁷ is selected from -C₁-C₁₀ alkylene-, -C₁-C₁₀ alkenylene-, -C₁-C₁₀ alkynylene-, carbocyclo-, -O-(C₁-C₈ alkylene)-, O-(C₁-C₈ alkenylene)-, -O-(C₁-C₈ alkynylene)-, -arylene-, -C₁-C₁₀ alkylene-arylene-, -C₂-C₁₀ alkenylene-arylene-, -C₂-C₁₀ alkynylene-arylene-, -arylene-C₁-C₁₀ alkylene-, -arylene-C₂-C₁₀ alkenylene-, -arylene-C₂-C₁₀ alkynylene-, -C₁-C₁₀ alkylene-(carbocyclo)-, -C₂-C₁₀ alkenylene-(carbocyclo)-, -C₂-C₁₀ alkynylene-(carbocyclo)-, -(carbocyclo)-C₁-C₁₀ alkylene-, -(carbocyclo)-C₂-C₁₀ alkenylene-, -(carbocyclo)-C₂-C₁₀ alkynylene-, -heterocyclo-, -C₁-C₁₀ alkylene-(heterocyclo)-, -C₂-C₁₀ alkenylene-(heterocyclo)-, -C₂-C₁₀ alkynylene-(heterocyclo)-, -(heterocyclo)-C₁-C₁₀ alkylene-, -(heterocyclo)-C₂-C₁₀ alkenylene-, -(heterocyclo)-C₁-C₁₀ alkynylene-, -(CH₂CH₂O)_r, or -(CH₂CH₂O)_r-CH₂-, and r is an integer ranging from 1-10, wherein said alkyl, alkenyl, alkynyl, alkylene, alkenylene, alkynylene, aryl, carbocycle, carbocyclo, heterocyclo, and arylene radicals, whether alone or as part of another group, are optionally substituted. In some embodiments, said alkyl, alkenyl, alkynyl, alkylene, alkenylene, alkynylene, aryl, carbocycle, carbocyclo, heterocyclo, and arylene radicals, whether alone or as part of another group, are unsubstituted. In some embodiments, R¹⁷ is selected from -C₁-C₁₀ alkylene-, -carbocyclo-, -O-(C₁-C₈ alkylene)-, -arylene-, -C₁₀-C₁₀ alkylene-arylene-, -arylene-C₁-C₁₀ alkylene-, -C₁-C₁₀ alkylene-(carbocyclo)-, -(carbocyclo)-C₁-C₁₀ alkylene-, -C₃-C₈ heterocyclo-, -C₁-C₁₀ alkylene-(heterocyclo)-, -(heterocyclo)-C₁-C₁₀ alkylene-, -(CH₂CH₂O)_r, and -(CH₂CH₂O)_r-CH₂-; and r is an integer ranging from 1-10, wherein said alkylene groups are unsubstituted and the remainder of the groups are optionally substituted.

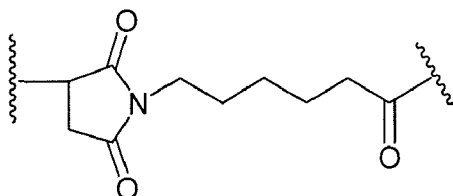
[0183] It is to be understood from all the exemplary embodiments that even where not denoted expressly, from 1 to 20 drug moieties can be linked to an Antibody (p = 1-20).



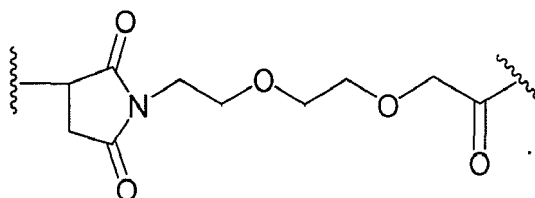
IIIa



[0184] An illustrative Stretcher unit is that of Formula IIIa wherein R^{17} is $-(\text{CH}_2)_5-$:

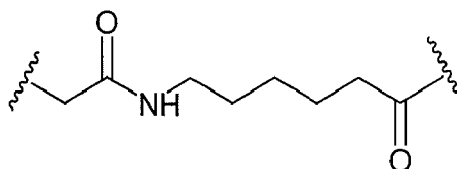


[0185] Another illustrative Stretcher unit is that of Formula IIIa wherein R^{17} is $-(\text{CH}_2\text{CH}_2\text{O})_r-\text{CH}_2-$; and r is 2:

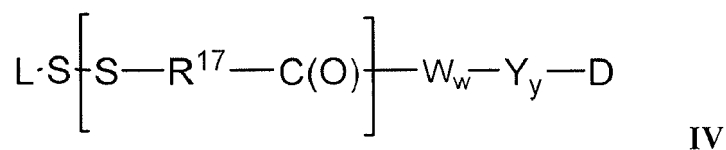


[0186] An illustrative Stretcher unit is that of Formula IIIa wherein R^{17} is arylene- or arylene- C_1 - C_{10} alkylene-. In some embodiments, the aryl group is an unsubstituted phenyl group.

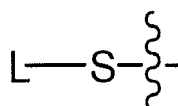
[0187] Still another illustrative Stretcher unit is that of Formula IIIb wherein R^{17} is $-(\text{CH}_2)_5-$:



[0188] In certain embodiments, the Stretcher unit is linked to the Antibody unit via a disulfide bond between a sulfur atom of the Antibody unit and a sulfur atom of the Stretcher unit. A representative Stretcher unit of this embodiment is depicted within the square brackets of Formula IV, wherein R^{17} , L-, -W-, -Y-, -D, w and y are as defined above.

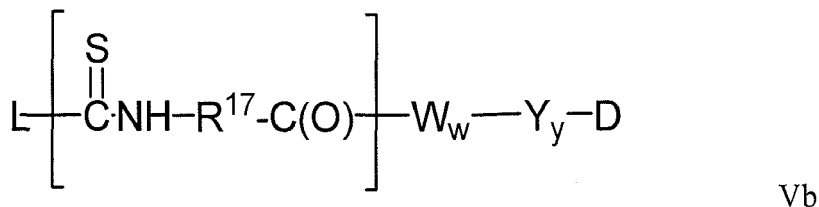
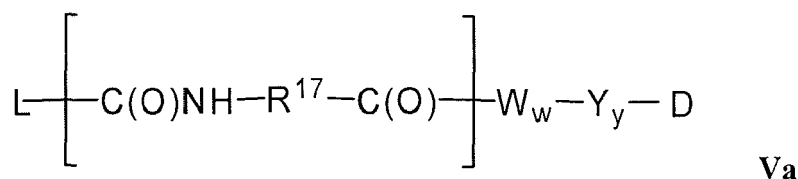


[0189] It should be noted that throughout this application, the S moiety in the formula below refers to a sulfur atom of the Antibody unit, unless otherwise indicated by context.

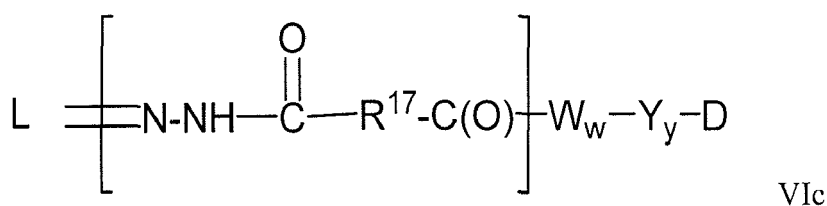
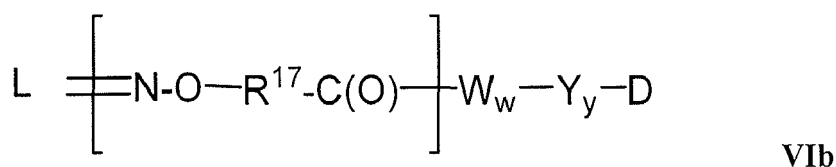
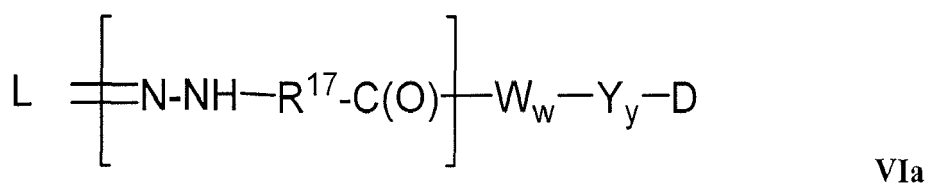


[0190] In yet other embodiments, the Stretcher contains a reactive site that can form a bond with a primary or secondary amino group of an Antibody. Examples of these reactive sites include, but are not limited to, activated esters such as succinimide esters, 4 nitrophenyl esters, pentafluorophenyl esters, tetrafluorophenyl esters, anhydrides, acid chlorides,

sulfonyl chlorides, isocyanates and isothiocyanates. Representative Stretcher units of this embodiment are depicted within the square brackets of Formulas Va and Vb, wherein $-R^{17}$ -, L -, $-W$ -, $-Y$ -, $-D$, w and y are as defined above;



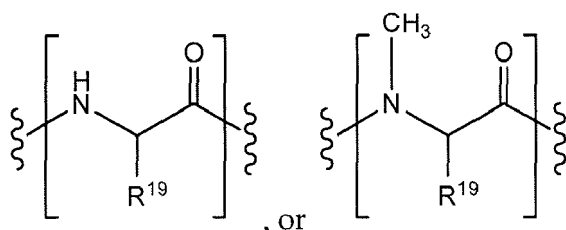
[0191] In some embodiments, the Stretcher contains a reactive site that is reactive to a modified carbohydrate's ($-CHO$) group that can be present on an Antibody. For example, a carbohydrate can be mildly oxidized using a reagent such as sodium periodate and the resulting ($-CHO$) unit of the oxidized carbohydrate can be condensed with a Stretcher that contains a functionality such as a hydrazide, an oxime, a primary or secondary amine, a hydrazine, a thiosemicarbazone, a hydrazine carboxylate, and an arylhydrazide such as those described by Kaneko et al., 1991, Bioconjugate Chem. 2:133-41. Representative Stretcher units of this embodiment are depicted within the square brackets of Formulas VIa, VIb, and VIc, wherein $-R^{17}$ -, L -, $-W$ -, $-Y$ -, $-D$, w and y are as defined as above.



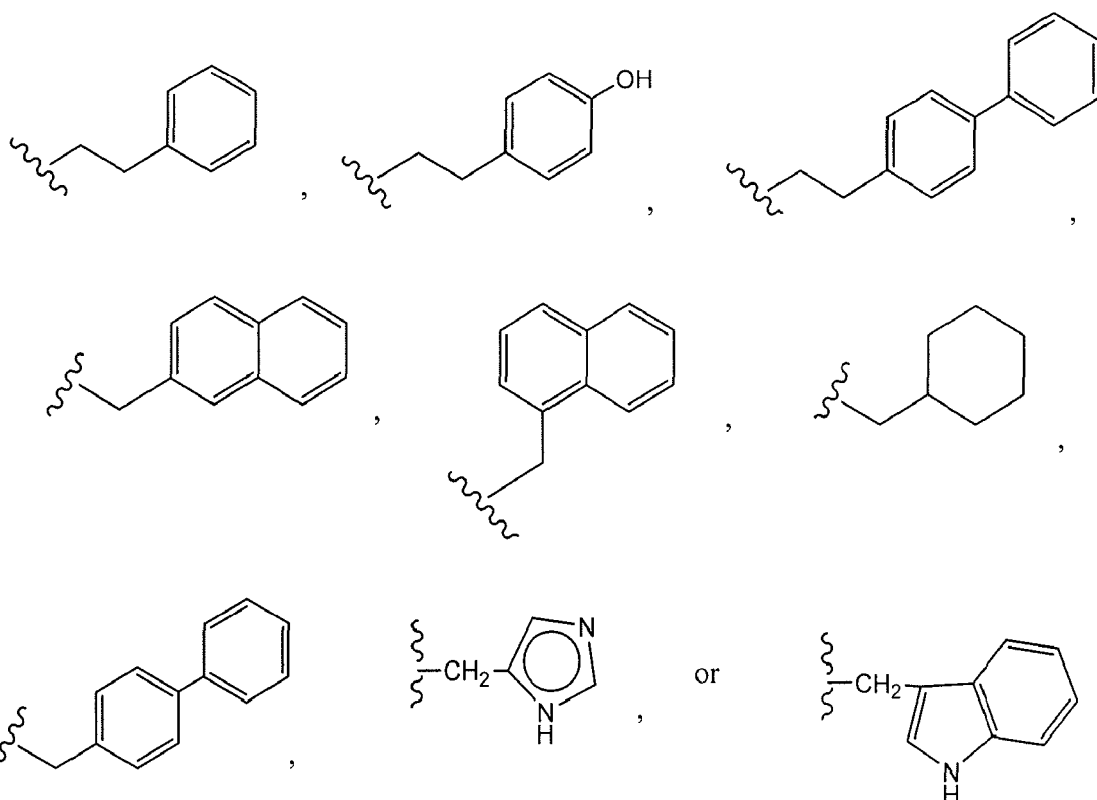
VII.) The Amino Acid Unit

[0192] The Amino Acid unit ($-W$ -), when present, links the Stretcher unit to the Spacer unit if the Spacer unit is present, links the Stretcher unit to the Drug moiety if the Spacer unit is absent, and links the Antibody unit to the Drug unit if the Stretcher unit and Spacer unit are absent.

[0193] W_w - can be, for example, a monopeptide, dipeptide, tripeptide, tetrapeptide, pentapeptide, hexapeptide, heptapeptide, octapeptide, nonapeptide, decapeptide, undecapeptide or dodecapeptide unit. Each $-W$ - unit independently has the formula denoted below in the square brackets, and w is an integer ranging from 0 to 12:

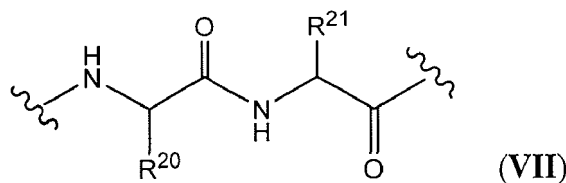


wherein R^{19} is hydrogen, methyl, isopropyl, isobutyl, sec-butyl, benzyl, *p*-hydroxybenzyl, $-\text{CH}_2\text{OH}$, $-\text{CH}(\text{OH})\text{CH}_3$, $-\text{CH}_2\text{CH}_2\text{SCH}_3$, $-\text{CH}_2\text{CONH}_2$, $-\text{CH}_2\text{COOH}$, $-\text{CH}_2\text{CH}_2\text{CONH}_2$, $-\text{CH}_2\text{CH}_2\text{COOH}$, $-(\text{CH}_2)_3\text{NHC}(=\text{NH})\text{NH}_2$, $-(\text{CH}_2)_3\text{NH}_2$, $-(\text{CH}_2)_3\text{NHCOCH}_3$, $-(\text{CH}_2)_3\text{NHCHO}$, $-(\text{CH}_2)_4\text{NHC}(=\text{NH})\text{NH}_2$, $-(\text{CH}_2)_4\text{NH}_2$, $-(\text{CH}_2)_4\text{NHCOCH}_3$, $-(\text{CH}_2)_4\text{NHCHO}$, $-(\text{CH}_2)_3\text{NHCONH}_2$, $-(\text{CH}_2)_4\text{NHCONH}_2$, $-\text{CH}_2\text{CH}_2\text{CH}(\text{OH})\text{CH}_2\text{NH}_2$, 2-pyridylmethyl-, 3-pyridylmethyl-, 4-pyridylmethyl-, phenyl, cyclohexyl,

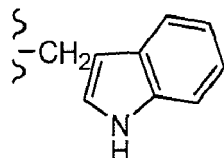


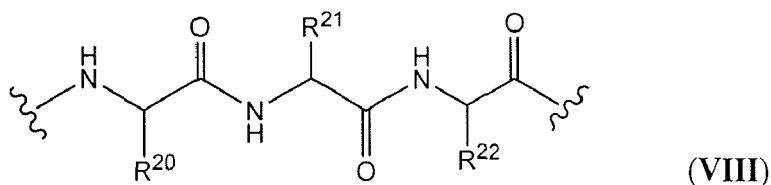
[0194] In some embodiments, the Amino Acid unit can be enzymatically cleaved by one or more enzymes, including a cancer or tumor-associated protease, to liberate the Drug unit ($-\text{D}$), which in one embodiment is protonated *in vivo* upon release to provide a Drug (D).

[0195] In certain embodiments, the Amino Acid unit can comprise natural amino acids. In other embodiments, the Amino Acid unit can comprise non-natural amino acids. Illustrative Ww units are represented by formulas (VII)-(IX):



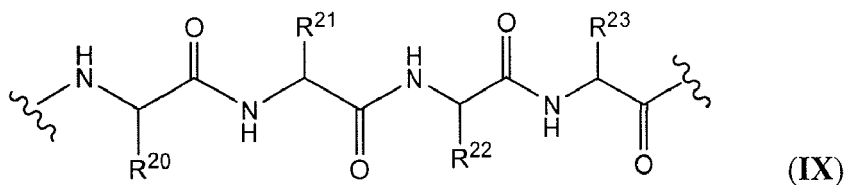
wherein R^{20} and R^{21} are as follows:

R ²⁰	R ²¹
Benzyl	(CH ₂) ₄ NH ₂ ;
methyl	(CH ₂) ₄ NH ₂ ;
isopropyl	(CH ₂) ₄ NH ₂ ;
isopropyl	(CH ₂) ₃ NHCONH ₂ ;
benzyl	(CH ₂) ₃ NHCONH ₂ ;
isobutyl	(CH ₂) ₃ NHCONH ₂ ;
sec-butyl	(CH ₂) ₃ NHCONH ₂ ;
	(CH ₂) ₃ NHCONH ₂ ;
	
benzyl	methyl;
benzyl	(CH ₂) ₃ NHC(=NH)NH ₂ ;



wherein R²⁰, R²¹ and R²² are as follows:

R ²⁰	R ²¹	R ²²
benzyl	benzyl	(CH ₂) ₄ NH ₂ ;
isopropyl	benzyl	(CH ₂) ₄ NH ₂ ; and
H	benzyl	(CH ₂) ₄ NH ₂ ;



wherein R²⁰, R²¹, R²² and R²³ are as follows:

R ²⁰	R ²¹	R ²²	R ²³
H	benzyl	isobutyl	H; and
methyl	isobutyl	methyl	isobutyl.

[0196] Exemplary Amino Acid units include, but are not limited to, units of formula VII where: R²⁰ is benzyl and R²¹ is -(CH₂)₄NH₂; R²⁰ is isopropyl and R²¹ is -(CH₂)₄NH₂; or R²⁰ is isopropyl and R²¹ is -(CH₂)₃NHCONH₂. Another exemplary Amino Acid unit is a unit of formula VIII wherein R²⁰ is benzyl, R²¹ is benzyl, and R²² is -(CH₂)₄NH₂.

[0197] Useful -W_w- units can be designed and optimized in their selectivity for enzymatic cleavage by a particular enzyme, for example, a tumor-associated protease. In one embodiment, a -W_w- unit is that whose cleavage is catalyzed by cathepsin B, C and D, or a plasmin protease.

[0198] In one embodiment, -W_w- is a dipeptide, tripeptide, tetrapeptide or pentapeptide. When R¹⁹, R²⁰, R²¹, R²² or R²³ is other than hydrogen, the carbon atom to which R¹⁹, R²⁰, R²¹, R²² or R²³ is attached is chiral.

[0199] Each carbon atom to which R¹⁹, R²⁰, R²¹, R²² or R²³ is attached is independently in the (S) or (R) configuration.

[0200] In one aspect of the Amino Acid unit, the Amino Acid unit is valine-citrulline (vc or Val-Cit). In another aspect,

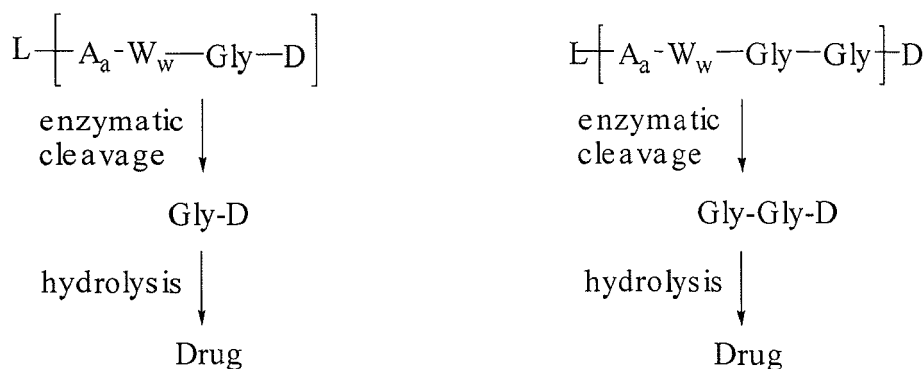
the Amino Acid unit is phenylalanine-lysine (i.e., fk). In yet another aspect of the Amino Acid unit, the Amino Acid unit is N-methylvaline-citrulline. In yet another aspect, the Amino Acid unit is 5-aminovaleric acid, homo phenylalanine lysine, tetraisoquinolinecarboxylate lysine, cyclohexylalanine lysine, isonepecotic acid lysine, beta-alanine lysine, glycine serine valine glutamine and isonepecotic acid.

VIII.) The Spacer Unit

[0201] The Spacer unit (-Y-), when present, links an Amino Acid unit to the Drug unit when an Amino Acid unit is present. Alternately, the Spacer unit links the Stretcher unit to the Drug unit when the Amino Acid unit is absent. The Spacer unit also links the Drug unit to the Antibody unit when both the Amino Acid unit and Stretcher unit are absent.

[0202] Spacer units are of two general types: non self-immolative or self-immolative. A non self-immolative Spacer unit is one in which part or all of the Spacer unit remains bound to the Drug moiety after cleavage, particularly enzymatic, of an Amino Acid unit from the antibody-drug conjugate. Examples of a non self-immolative Spacer unit include, but are not limited to a (glycine-glycine) Spacer unit and a glycine Spacer unit (both depicted in Scheme 1) (infra). When a conjugate containing a glycine-glycine Spacer unit or a glycine Spacer unit undergoes enzymatic cleavage via an enzyme (e.g., a tumor-cell associated-protease, a cancer-cell-associated protease or a lymphocyte-associated protease), a glycine-glycine-Drug moiety or a glycine-Drug moiety is cleaved from L-Aa-Ww-. In one embodiment, an independent hydrolysis reaction takes place within the target cell, cleaving the glycine-Drug moiety bond and liberating the Drug.

Scheme 1



[0203] In some embodiments, a non self-immolative Spacer unit (-Y-) is -Gly-. In some embodiments, a non self-immolative Spacer unit (-Y-) is -Gly-Gly-.

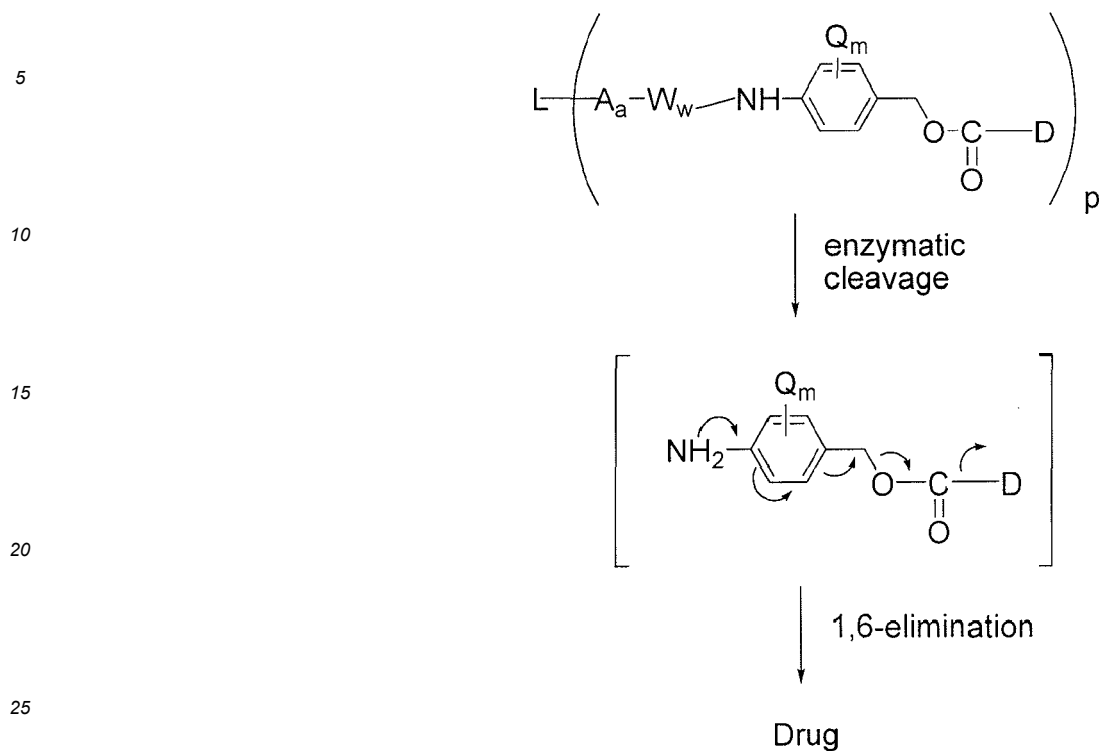
[0204] In one embodiment, a Drug-Linker conjugate is provided in which the Spacer unit is absent (-Y_y - where y=0), or a pharmaceutically acceptable salt or solvate thereof.

[0205] Alternatively, a conjugate containing a self-immolative Spacer unit can release -D. As used herein, the term "self-immolative Spacer" refers to a bifunctional chemical moiety that is capable of covalently linking together two spaced chemical moieties into a stable tripartite molecule. It will spontaneously separate from the second chemical moiety if its bond to the first moiety is cleaved.

[0206] In some embodiments, -Y_y- is a p-aminobenzyl alcohol (PAB) unit (see Schemes 2 and 3) whose phenylene portion is substituted with Q_m wherein Q is -C₁-C₈ alkyl, -C₁-C₈ alkenyl, -C₁-C₈ alkynyl, -O-(C₁-C₈ alkyl), -O-(C₁-C₈ alkenyl), -O-(C₁-C₈ alkynyl), -halogen, -nitro or -cyano; and m is an integer ranging from 0-4. The alkyl, alkenyl and alkynyl groups, whether alone or as part of another group, can be optionally substituted.

[0207] In some embodiments, -Y- is a PAB group that is linked to -W_w- via the amino nitrogen atom of the PAB group, and connected directly to -D via a carbonate, carbamate or ether group. Without being bound by any particular theory or mechanism, Scheme 2 depicts a possible mechanism of Drug release of a PAB group which is attached directly to -D via a carbamate or carbonate group as described by Toki et al., 2002, J. Org. Chem. 67:1866-1872.

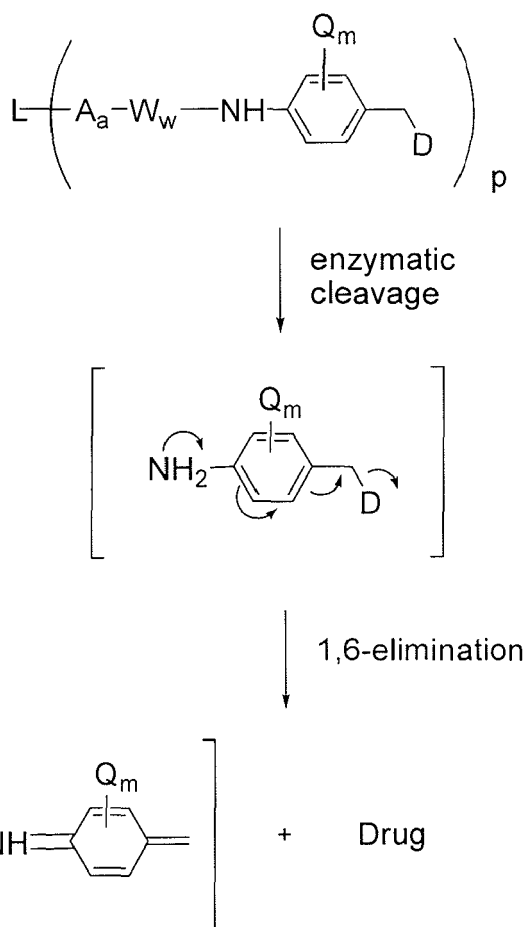
Scheme 2



[0208] In Scheme 2, Q is -C₁-C₈ alkyl, -C₁-C₈ alkenyl, -C₁-C₈ alkynyl, -O-(C₁-C₈ alkyl), -O-(C₁-C₈ alkenyl), -O-(C₁-C₈ alkynyl), -halogen, -nitro or -cyano; m is an integer ranging from 0-4; and p ranges from 1 to about 20. The alkyl, alkenyl and alkynyl groups, whether alone or as part of another group, can be optionally substituted.

[0209] Without being bound by any particular theory or mechanism, Scheme 3 depicts a possible mechanism of Drug release of a PAB group which is attached directly to -D via an ether or amine linkage, wherein D includes the oxygen or nitrogen group that is part of the Drug unit.

Scheme 3

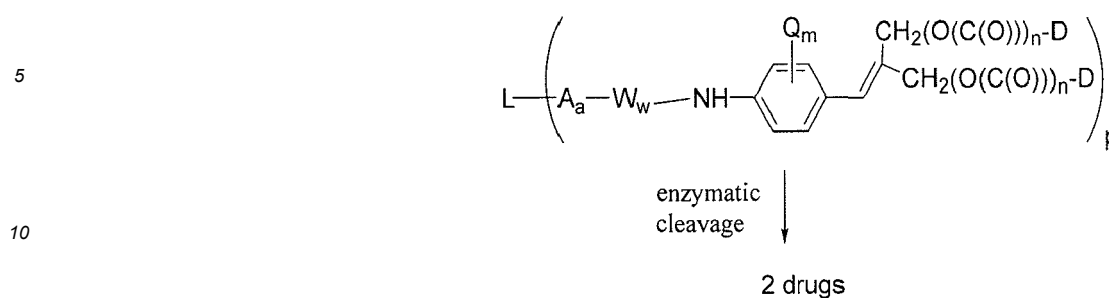


35 **[0210]** In Scheme 3, Q is -C₁-C₈ alkyl, -C₁-C₈ alkenyl, -C₁-C₈ alkynyl, -O-(C₁-C₈ alkyl), -O-(C₁-C₈ alkenyl), -O-(C₁-C₈ alkynyl), -halogen, -nitro or -cyano; m is an integer ranging from 0-4; and p ranges from 1 to about 20. The alkyl, alkenyl and alkynyl groups, whether alone or as part of another group, can be optionally substituted.

40 **[0211]** Other examples of self-immolative spacers include, but are not limited to, aromatic compounds that are electronically similar to the PAB group such as 2-aminoimidazol-5-methanol derivatives (Hay et al., 1999, Bioorg. Med. Chem. Lett. 9:2237) and ortho or para-aminobenzylacetals. Spacers can be used that undergo cyclization upon amide bond hydrolysis, such as substituted and unsubstituted 4-aminobutyric acid amides (Rodrigues et al., 1995, Chemistry Biology 2:223), appropriately substituted bicyclo[2.2.1] and bicyclo[2.2.2] ring systems (Storm et al., 1972, J. Amer. Chem. Soc. 94:5815) and 2-aminophenylpropionic acid amides (Amsberry et al., 1990, J. Org. Chem. 55:5867). Elimination of amine-containing drugs that are substituted at the α-position of glycine (Kingsbury et al., 1984, J. Med. Chem. 27:1447) are also examples of self-immolative spacers.

45 **[0212]** In one embodiment, the Spacer unit is a branched bis(hydroxymethyl)-styrene (BHMS) unit as depicted in Scheme 4, which can be used to incorporate and release multiple drugs.

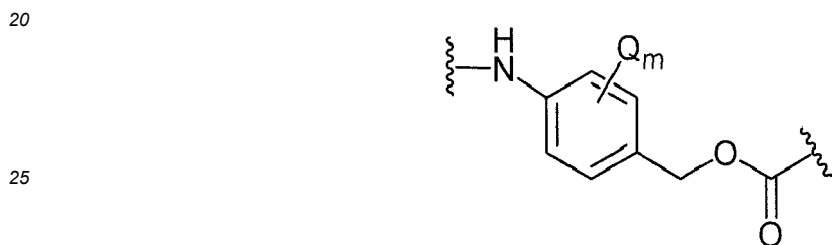
Scheme 4



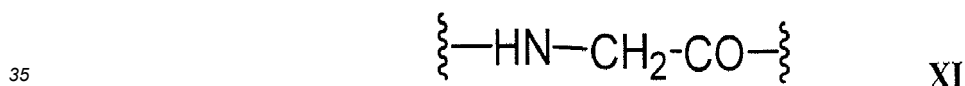
15 **[0213]** In Scheme 4, Q is -C₁-C₈ alkyl, -C₁-C₈ alkenyl, -C₁-C₈ alkynyl, -O-(C₁-C₈ alkyl), -O-(C₁-C₈ alkenyl), -O-(C₁-C₈ alkynyl), -halogen, -nitro or -cyano; m is an integer ranging from 0-4; n is 0 or 1; and p ranges ranging from 1 to about 20. The alkyl, alkenyl and alkynyl groups, whether alone or as part of another group, can be optionally substituted.

[0214] In some embodiments, the -D moieties are the same. In yet another embodiment, the -D moieties are different.

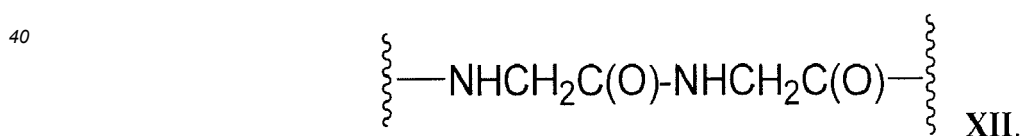
[0215] In one aspect, Spacer units (-Y_y-) are represented by Formulas (X)-(XII):



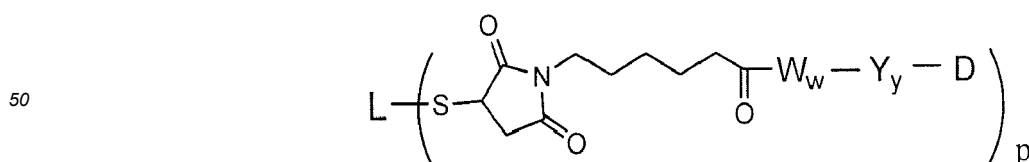
30 wherein Q is -C₁-C₈ alkyl, -C₁-C₈ alkenyl, -C₁-C₈ alkynyl, -O-(C₁-C₈ alkyl), -O-(C₁-C₈ alkenyl), -O-(C₁-C₈ alkynyl), -halogen, -nitro or -cyano; and m is an integer ranging from 0-4. The alkyl, alkenyl and alkynyl groups, whether alone or as part of another group, can be optionally substituted.



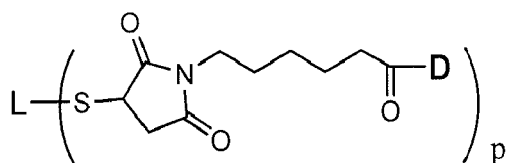
and



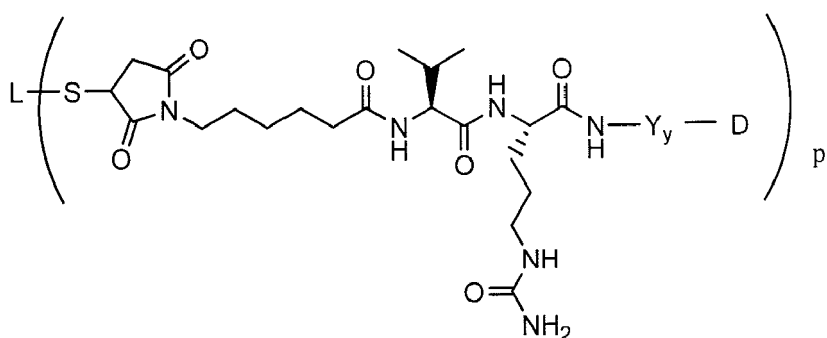
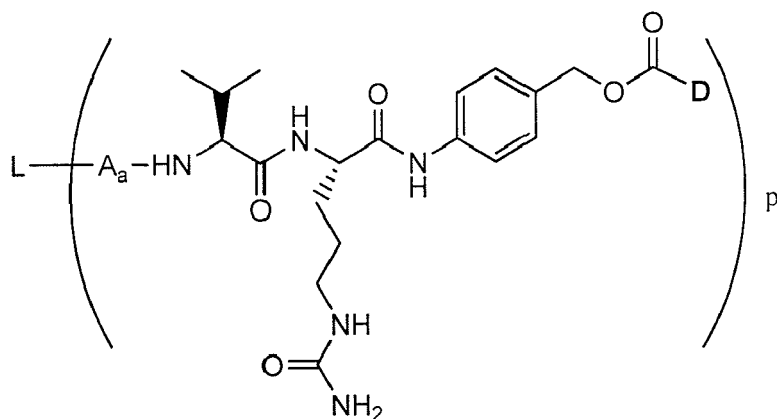
45 **[0216]** Embodiments of the Formula I and II comprising antibody-drug conjugate compounds can include:



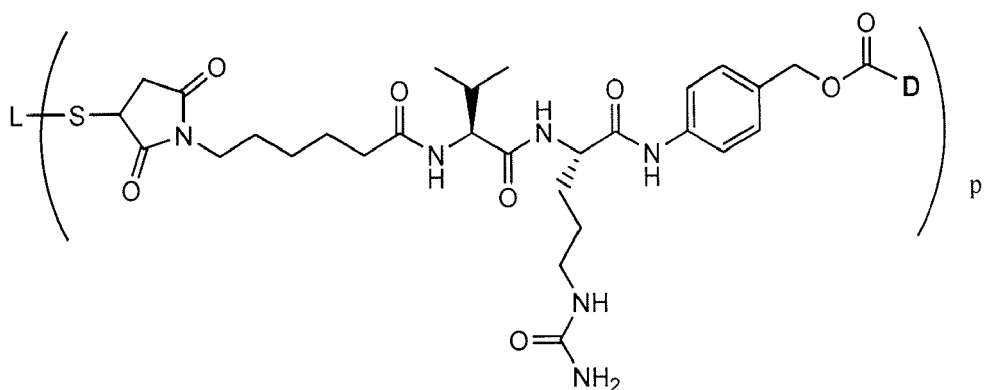
55 wherein w and y are each 0, 1 or 2, and,



wherein w and y are each 0,



and



IX.) The Drug Unit

[0217] The Drug moiety (D) can be any cytotoxic, cytostatic or immunomodulatory (e.g., immunosuppressive) drug. D is a Drug unit (moiety) having an atom that can form a bond with the Spacer unit, with the Amino Acid unit, with the Stretcher unit or with the Antibody unit. In some embodiments, the Drug unit D has a nitrogen atom that can form a bond

with the Spacer unit. As used herein, the terms "Drug unit" and "Drug moiety" are synonymous and used interchangeably.

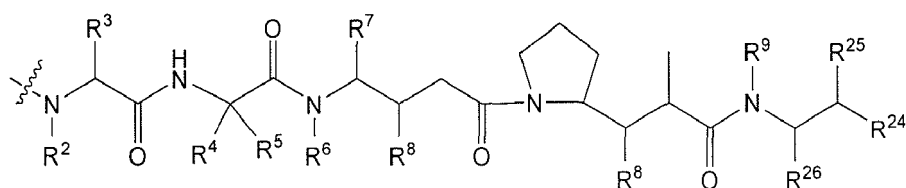
[0218] Useful classes of cytotoxic, cytostatic, or immunomodulatory agents include, for example, antitubulin agents, DNA minor groove binders, DNA replication inhibitors, and alkylating agents.

[0219] In some embodiments, the Drug is an auristatin, such as auristatin E (also known in the art as a derivative of dolastatin-10) or a derivative thereof. The auristatin can be, for example, an ester formed between auristatin E and a keto acid. For example, auristatin E can be reacted with paraacetyl benzoic acid or benzoylvaleric acid to produce AEB and AEVB, respectively. Other typical auristatins include AFP, MMAF, and MMAE. The synthesis and structure of exemplary auristatins are described in U.S. Patent Application Publication No. 2003-0083263; International Patent Publication No. WO 04/010957, International Patent Publication No. WO 02/088172, and U.S. Patent Nos. 7, 498,298, 6,884,869, 6,323,315; 6,239,104; 6,034,065; 5,780,588; 5,665,860; 5,663,149; 5,635,483; 5,599,902; 5,554,725; 5,530,097; 5,521,284; 5,504,191; 5,410,024; 5,138,036; 5,076,973; 4,986,988; 4,978,744; 4,879,278; 4,816,444; and 4,486,414, each of which is incorporated by reference herein in its entirety and for all purposes.

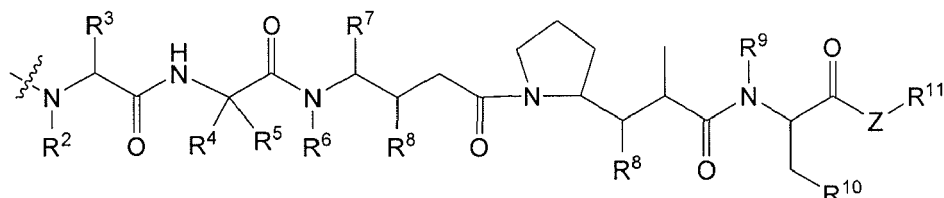
[0220] Auristatins have been shown to interfere with microtubule dynamics and nuclear and cellular division and have anticancer activity. Auristatins bind tubulin and can exert a cytotoxic or cytostatic effect on a 191P4D12-expressing cell. There are a number of different assays, known in the art, which can be used for determining whether an auristatin or resultant antibody-drug conjugate exerts a cytostatic or cytotoxic effect on a desired cell line.

[0221] Methods for determining whether a compound binds tubulin are known in the art. See, for example, Muller et al., Anal. Chem 2006, 78, 4390-4397; Hamel et al., Molecular Pharmacology, 1995 47: 965-976; and Hamel et al., The Journal of Biological Chemistry, 1990 265:28, 17141-17149. For purposes of the present invention, the relative affinity of a compound to tubulin can be determined. Some preferred auristatins of the present invention bind tubulin with an affinity ranging from 10 fold lower (weaker affinity) than the binding affinity of MMAE to tubulin to 10 fold, 20 fold or even 100 fold higher (higher affinity) than the binding affinity of MMAE to tubulin.

[0222] In some embodiments, -D is an auristatin of the formula **D_E** or **D_F**:



D_E



D_F

or a pharmaceutically acceptable salt or solvate form thereof; wherein, independently at each location:

the wavy line indicates a bond;

R² is -C₁-C₂₀ alkyl, -C₂-C₂₀ alkenyl, or -C₂-C₂₀ alkynyl;

R³ is -H, -C₁-C₂₀ alkyl, -C₂-C₂₀ alkenyl, -C₂-C₂₀ alkynyl, -carbocycle, -C₁-C₂₀ alkylene (carbocycle), -C₂-C₂₀ alkenylene(carbocycle), -C₂-C₂₀ alkynylene(carbocycle), -aryl, -C₁-C₂₀ alkylene(aryl), -C₂-C₂₀ alkenylene(aryl), -C₂-C₂₀ alkynylene(aryl), heterocycle, -C₁-C₂₀ alkylene(heterocycle), -C₂-C₂₀ alkenylene(heterocycle), or -C₂-C₂₀ alkynylene(heterocycle);

R⁴ is -H, -C₁-C₂₀ alkyl, -C₂-C₂₀ alkenyl, -C₂-C₂₀ alkynyl, carbocycle, -C₁-C₂₀ alkylene (carbocycle), -C₂-C₂₀ alkenylene(carbocycle), -C₂-C₂₀ alkynylene(carbocycle), aryl, -C₁-C₂₀ alkylene(aryl), -C₂-C₂₀ alkenylene(aryl), -C₂-C₂₀ alkynylene(aryl), -heterocycle, -C₁-C₂₀ alkylene(heterocycle), -C₂-C₂₀ alkenylene(heterocycle), or -C₂-C₂₀ alkynylene(heterocycle);

R⁵ is -H or -C₁-C₈ alkyl;

or **R⁴** and **R⁵** jointly form a carbocyclic ring and have the formula -(C(R^a)R^b)₅- wherein R^a and R^b are independently

-H, -C₁-C₂₀ alkyl, -C₂-C₂₀ alkenyl, -C₂-C₂₀ alkynyl, or -carbocycle and s is 2, 3, 4, 5 or 6,

R⁶ is -H, -C₁-C₂₀ alkyl, -C₂-C₂₀ alkenyl, or -C₂-C₂₀ alkynyl;

R⁷ is -H, -C₁-C₂₀ alkyl, -C₂-C₂₀ alkenyl, -C₂-C₂₀ alkynyl, carbocycle, -C₁-C₂₀ alkylene (carbocycle), -C₂-C₂₀ alkenylene(carbocycle), -C₂-C₂₀ alkynylene(carbocycle), -aryl, -C₁-C₂₀ alkylene(aryl), -C₂-C₂₀ alkenylene(aryl), -C₂-C₂₀ alkynylene(aryl), heterocycle, -C₁-C₂₆ alkylene(heterocycle), -C₂-C₂₀ alkenylene(heterocycle), or -C₂-C₂₀ alkynylene(heterocycle);

each **R⁸** is independently -H, -OH, -C₁-C₂₀ alkyl, -C₂-C₂₀ alkenyl, -C₂-C₂₀ alkynyl, -O-(C₁-C₂₀ alkyl), -O-(C₂-C₂₀ alkenyl), -O-(C₁-C₂₀ alkynyl), or -carbocycle;

R⁹ is -H, -C₁-C₂₀ alkyl, -C₂-C₂₀ alkenyl, or -C₂-C₂₀ alkynyl;

R²⁴ is -aryl, -heterocycle, or -carbocycle;

R²⁵ is -H, -C₁-C₂₀ alkyl, -C₂-C₂₀ alkenyl, -C₂-C₂₀ alkynyl, -carbocycle, -O-(C₁-C₂₀ alkyl), -O-(C₂-C₂₀ alkenyl), -O-(C₂-C₂₀ alkynyl), or **OR¹⁸** wherein **R¹⁸** is -H, a hydroxyl protecting group, or a direct bond where **OR¹⁸** represents =O;

R²⁶ is -H, -C₁-C₂₀ alkyl, -C₂-C₂₀ alkenyl, or -C₂-C₂₀ alkynyl, -aryl, -heterocycle, or -carbocycle;

R¹⁰ is -aryl or -heterocycle;

Z is -O, -S, -NH, or -NR¹², wherein **R¹²** is -C₁-C₂₀ alkyl, -C₂-C₂₀ alkenyl, or -C₂-C₂₀ alkynyl;

R¹¹ is -H, -C₁-C₂₀ alkyl, -C₂-C₂₀ alkenyl, -C₂-C₂₀ alkynyl, -aryl, -heterocycle, -(R¹³O)_m-R¹⁴, or -(R¹³O)_m-CH(R¹⁵)₂;

m is an integer ranging from 1-1000 or m=0-1000;

R¹³ is -C₂-C₂₀ alkylene, -C₂-C₂₀ alkenylene, or -C₂-C₂₀ alkynylene;

R¹⁴ is -H, -C₁-C₂₀ alkyl, -C₂-C₂₀ alkenyl, or -C₂-C₂₀ alkynyl;

each occurrence of **R¹⁵** is independently -H, -COOH, -(CH₂)_n-N(R¹⁶)₂, -(CH₂)_n-SO₃H, -(CH₂)_n-SO₃-C₁-C₂₀ alkyl, -(CH₂)_n-SO₃-C₂-C₂₀ alkenyl, or -(CH₂)_n-SO₃-C₂-C₂₀ alkynyl;

each occurrence of **R¹⁶** is independently -H, -C₁-C₂₀ alkyl, -C₂-C₂₀ alkenyl, -C₂-C₂₀ alkynyl or -(CH₂)_n-COOH; and **n** is an integer ranging from 0 to 6;

wherein said alkyl, alkenyl, alkynyl, alkylene, alkenylene, alkynylene, aryl, carbocycle, and heterocycle radicals, whether alone or as part of another group, are optionally substituted.

[0223] Auristatins of the formula **D_E** include those wherein said alkyl, alkenyl, alkynyl, alkylene, alkenylene, alkynylene, aryl, carbocycle, and heterocycle radicals are unsubstituted.

[0224] Auristatins of the formula **D_E** include those wherein the groups of R², R³, R⁴, R⁵, R⁶, R⁷, R⁸, and R⁹ are unsubstituted and the groups of R¹⁹, R²⁰ and R²¹ are optionally substituted as described herein.

[0225] Auristatins of the formula **D_E** include those wherein

R² is C₁-C₈ alkyl;

R³, R⁴ and R⁷ are independently selected from -H, -C₁-C₂₀ alkyl, -C₂-C₂₀ alkenyl, -C₂-C₂₀ alkynyl, monocyclic C₃-C₆ carbocycle, -C₁-C₂₀ alkylene(monocyclic C₃-C₆ carbocycle), -C₂-C₂₀ alkenylene(monocyclic C₃-C₆ carbocycle), -C₂-C₂₀ alkynylene(monocyclic C₃-C₆ carbocycle), C₆-C₁₀ aryl, -C₁-C₂₆ alkylene(C₆-C₁₀ aryl), -C₂-C₂₀ alkenylene(C₆-C₁₀ aryl), -C₂-C₂₀ alkynylene(C₆-C₁₀ aryl), heterocycle, -C₁-C₂₆ alkylene(heterocycle), -C₂-C₂₀ alkenylene(heterocycle), or -C₂-C₂₀ alkynylene(heterocycle); wherein said alkyl, alkenyl, alkynyl, alkylene, alkenylene, alkynylene, carbocycle, aryl and heterocycle radicals are optionally substituted;

R⁵ is -H;

R⁶ is -C₁-C₈ alkyl;

each **R⁸** is independently selected from -OH, -O-(C₁-C₂₀ alkyl), -O-(C₂-C₂₀ alkenyl), or -O-(C₂-C₂₀ alkynyl) wherein said alkyl, alkenyl, and alkynyl radicals are optionally substituted;

R⁹ is -H or -C₁-C₈ alkyl;

R²⁴ is optionally substituted -phenyl;

R²⁵ is -**OR¹⁸**; wherein **R¹⁸** is H, a hydroxyl protecting group, or a direct bond where **OR¹⁸** represents =O;

R²⁶ is selected from -H, -C₁-C₂₀ alkyl, -C₂-C₂₀ alkenyl, -C₂-C₂₀ alkynyl, or -carbocycle; wherein said alkyl, alkenyl, alkynyl and carbocycle radicals are optionally substituted; or a pharmaceutically acceptable salt or solvate form thereof.

[0226] Auristatins of the formula **D_E** include those wherein

R² is methyl;

R³ is -H, -C₁-C₈ alkyl, -C₂-C₈ alkenyl, or -C₂-C₈ alkynyl, wherein said alkyl, alkenyl and alkynyl radicals are optionally substituted;

R⁴ is -H, -C₁-C₈ alkyl, -C₂-C₈ alkenyl, -C₂-C₈ alkynyl, monocyclic C₃-C₆ carbocycle, -C₆-C₁₀ aryl, -C₁-C₈ alkylene(C₆-C₁₀ aryl), -C₂-C₈ alkenylene(C₆-C₁₀ aryl), -C₂-C₈ alkynylene(C₆-C₁₀ aryl), -C₁-C₈ alkylene (monocyclic

C₃-C₆ carbocycle), -C₂-C₈ alkenylene (monocyclic C₃-C₆ carbocycle), -C₂-C₈ alkynylene (monocyclic C₃-C₆ carbocycle); wherein said alkyl, alkenyl, alkynyl, alkylene, alkenylene, alkynylene, aryl and carbocycle radicals whether alone or as part of another group are optionally substituted;

R⁵ is -H;

R⁶ is methyl;

R⁷ is -C₁-C₈ alkyl, -C₂-C₈ alkenyl or -C₂-C₈ alkynyl;

each **R**⁸ is methoxy;

R⁹ is -H or -C₁-C₈ alkyl;

R²⁴ is -phenyl;

R²⁵ is -**OR**¹⁸; wherein **R**¹⁸ is H, a hydroxyl protecting group, or a direct bond where **OR**¹⁸ represents =O;

R²⁶ is methyl;

or a pharmaceutically acceptable salt form thereof.

[0227] Auristatins of the formula **D_E** include those wherein:

R² is methyl; **R**³ is -H or -C₁-C₃ alkyl; **R**⁴ is -C₁-C₅ alkyl; **R**⁵ is -H; **R**⁶ is methyl; **R**⁷ is isopropyl or sec-butyl; **R**⁸ is methoxy; **R**⁹ is -H or -C₁-C₈ alkyl; **R**²⁴ is phenyl; **R**²⁵ is -**OR**¹⁸; wherein **R**¹⁸ is -H, a hydroxyl protecting group, or a direct bond where **OR**¹⁸ represents =O; and **R**²⁶ is methyl; or a pharmaceutically acceptable salt or solvate form thereof.

[0228] Auristatins of the formula **D_E** include those wherein:

R² is methyl or C₁-C₃ alkyl;

R³ is -H or -C₁-C₃ alkyl;

R⁴ is -C₁-C₅ alkyl;

R⁵ is H;

R⁶ is C₁-C₃ alkyl;

R⁷ is -C₁-C₅ alkyl;

R⁸ is -C₁-C₃ alkoxy;

R⁹ is -H or -C₁-C₈ alkyl;

R²⁴ is phenyl;

R²⁵ is -**OR**¹⁸; wherein **R**¹⁸ is -H, a hydroxyl protecting group, or a direct bond where **OR**¹⁸ represents =O; and

R²⁶ is -C₁-C₃ alkyl;

or a pharmaceutically acceptable salt form thereof.

[0229] Auristatins of the formula **D_F** include those wherein

R² is methyl;

R³, **R**⁴, and **R**⁷ are independently selected from -H, -C₁-C₂₀ alkyl, -C₂-C₂₀ alkenyl, -C₂-C₂₀ alkynyl, monocyclic C₃-C₆ carbocycle, -C₁-C₂₀ alkylene (monocyclic C₃-C₆ carbocycle), -C₂-C₂₀ alkenylene (monocyclic C₃-C₆ carbocycle), -C₂-C₂₀ alkynylene (monocyclic C₃-C₆ carbocycle), -C₆-C₁₀ aryl, -C₁-C₂₀ alkylene (C₆-C₁₀ aryl), -C₂-C₂₀ alkenylene (C₆-C₁₀ aryl), -C₂-C₂₀ alkynylene (C₆-C₁₀ aryl), heterocycle, -C₁-C₂₀ alkylene (heterocycle), -C₂-C₂₀ alkenylene (heterocycle), or -C₂-C₂₀ alkynylene (heterocycle); wherein said alkyl, alkenyl, alkynyl, alkylene, alkenylene, alkynylene, carbocycle, aryl and heterocycle radicals whether alone or as part of another group are optionally substituted;

R⁵ is -H;

R⁶ is methyl;

each **R**⁸ is methoxy;

R⁹ is -H, -C₁-C₂₀ alkyl, -C₂-C₂₀ alkenyl, or -C₂-C₂₀ alkynyl; wherein said alkyl, alkenyl and alkynyl radical are optionally substituted;

R¹⁰ is optionally substituted aryl or optionally substituted heterocycle;

Z is -O-, -S-, -NH-, or -NR¹², wherein **R**¹² is -C₁-C₂₀ alkyl, -C₂-C₂₀ alkenyl, or -C₂-C₂₀ alkynyl, each of which is optionally substituted;

R¹¹ is -H, -C₁-C₂₀ alkyl, -C₂-C₂₀ alkenyl, -C₂-C₂₀ alkynyl, -aryl, -heterocycle, -(R¹³O)_m-R¹⁴, or -(R¹³O)_m-CH(R¹⁵)₂, wherein said alkyl, alkenyl, alkynyl, aryl and heterocycle radicals are optionally substituted;

m is an integer ranging from 1-1000 or **m** = 0;

R¹³ is -C₂-C₂₀ alkylene, -C₂-C₂₀ alkenylene, or -C₂-C₂₀ alkynylene, each of which is optionally substituted;

R¹⁴ is -H, -C₁-C₂₀ alkyl, -C₂-C₂₀ alkenyl, or -C₂-C₂₀ alkynyl wherein said alkyl, alkenyl and alkynyl radicals are optionally substituted;

each occurrence of **R**¹⁵ is independently -H, -COOH, -(CH₂)_n-N(R¹⁶)₂, -(CH₂)_n-SO₃H, -(CH₂)_n-SO₃-C₁-C₂₀ alkyl, -(CH₂)_n-SO₃-C₂-C₂₀ alkenyl, or -(CH₂)_n-SO₃-C₂-C₂₀ alkynyl wherein said alkyl, alkenyl and alkynyl radicals are

optionally substituted;

each occurrence of R^{16} is independently -H, -C₁-C₂₀ alkyl, -C₂-C₂₀ alkenyl, -C₂-C₂₀ alkynyl or -(CH₂)_n-COOH wherein said alkyl, alkenyl and alkynyl radicals are optionally substituted;

n is an integer ranging from 0 to 6;

or a pharmaceutically acceptable salt thereof.

[0230] In certain of these embodiments, R^{10} is optionally substituted phenyl.

[0231] Auristatins of the formula D_F include those wherein the groups of R^2 , R^3 , R^4 , R^5 , R^6 , R^7 , R^8 , and R^9 are unsubstituted and the groups of R^{10} and R^{11} are as described herein.

[0232] Auristatins of the formula D_F include those wherein said alkyl, alkenyl, alkynyl, alkylene, alkenylene, alkynylene, aryl, carbocycle, and heterocycle radicals are unsubstituted.

[0233] Auristatins of the formula D_F include those wherein

R^2 is -C₁-C₃ alkyl; R^3 is -H or -C₁-C₃ alkyl; R^4 is -C₁-C₅ alkyl; R^5 is -H; R^6 is -C₁-C₃ alkyl; R^7 is -C₁-C₈ alkyl; R^8 is -C₁-C₃ alkoxy; R^9 is -H or -C₁-C₈ alkyl; R^{10} is optionally substituted phenyl; Z is -O-, -S-, or -NH-; R^{11} is as defined herein; or a pharmaceutically acceptable salt thereof.

[0234] Auristatins of the formula D_F include those wherein

R^2 is methyl; R^3 is -H or -C₁-C₃ alkyl; R^4 is -C₁-C₈ alkyl; R^5 is -H; R^6 is methyl; R^7 is isopropyl or sec-butyl; R^8 is methoxy; R^9 is -H or -C₁-C₈ alkyl; R^{10} is optionally substituted phenyl; Z is -O-, -S-, or -NH-; and R^{11} is as defined herein; or a pharmaceutically acceptable salt thereof.

[0235] Auristatins of the formula D_F include those wherein

R^2 is methyl; R^3 is -H or -C₁-C₃ alkyl; R^4 is -C₁-C₅ alkyl; R^5 is -H; R^6 is methyl; R^7 is isopropyl or sec-butyl; R^8 is methoxy; R^9 is -H or -C₁-C₈ alkyl; R^{10} is phenyl; and Z is -O- or -NH- and R^{11} is as defined herein, preferably hydrogen; or a pharmaceutically acceptable salt form thereof.

[0236] Auristatins of the formula D_F include those wherein

R^2 is -C₁-C₃ alkyl; R^3 is -H or -C₁-C₃ alkyl; R^4 is -C₁-C₅ alkyl; R^5 is -H; R^6 is -C₁-C₃ alkyl; R^7 is -C₁-C₅ alkyl; R^8 is -C₁-C₃ alkoxy; R^9 is -H or -C₁-C₈ alkyl; R^{10} is phenyl; and Z is -O- or -NH- and R^{11} is as defined herein, preferably hydrogen; or a pharmaceutically acceptable salt form thereof.

[0237] Auristatins of the formula D_E or D_F include those wherein R^3 , R^4 and R^7 are independently isopropyl or sec-butyl and R^5 is -H. In an exemplary embodiment, R^3 and R^4 are each isopropyl, R^5 is H, and R^7 is sec-butyl. The remainder of the substituents are as defined herein.

[0238] Auristatins of the formula D_E or D_F include those wherein R^2 and R^6 are each methyl, and R^9 is H. The remainder of the substituents are as defined herein.

[0239] Auristatins of the formula D_E or D_F include those wherein each occurrence of R^8 is -OCH₃. The remainder of the substituents are as defined herein.

[0240] Auristatins of the formula D_E or D_F include those wherein R^3 and R^4 are each isopropyl, R^2 and R^6 are each methyl, R^5 is H, R^7 is sec-butyl, each occurrence of R^8 is -OCH₃, and R^9 is H. The remainder of the substituents are as defined herein.

[0241] Auristatins of the formula D_F include those wherein Z is -O- or -NH-. The remainder of the substituents are as defined herein.

[0242] Auristatins of the formula D_F include those wherein R^{10} is aryl. The remainder of the substituents are as defined herein.

[0243] Auristatins of the formula D_F include those wherein R^{10} is -phenyl. The remainder of the substituents are as defined herein.

[0244] Auristatins of the formula D_F include those wherein Z is -O-, and R^{11} is H, methyl or t-butyl. The remainder of the substituents are as defined herein.

[0245] Auristatins of the formula D_F include those wherein, when Z is -NH-, R^{11} is -(R¹³O)_m-CH(R¹⁵)₂, wherein R^{15} is -(CH₂)_n-N(R¹⁶)₂, and R^{16} is -C₁-C₈ alkyl or -(CH₂)_n-COOH. The remainder of the substituents are as defined herein.

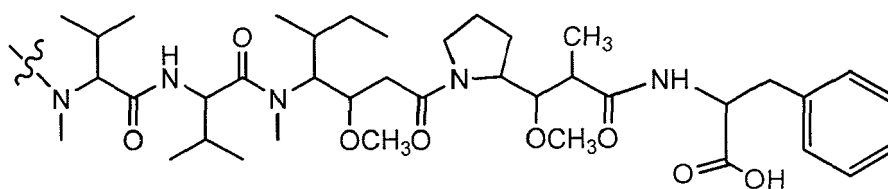
[0246] Auristatins of the formula D_F include those wherein when Z is -NH-, R^{11} is -(R¹³O)_m-CH(R¹⁵)₂, wherein R^{15} is -(CH₂)_n-SO₃H. The remainder of the substituents are as defined herein.

[0247] In preferred embodiments, when D is an auristatin of formula D_E , w is an integer ranging from 1 to 12, preferably 2 to 12, y is 1 or 2, and a is preferably 1.

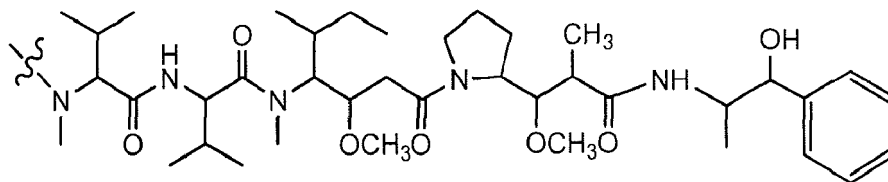
[0248] In some embodiments, wherein D is an auristatin of formula D_F , a is 1 and w and y are 0.

[0249] Illustrative Drug units (-D) include the drug units having the following structures:

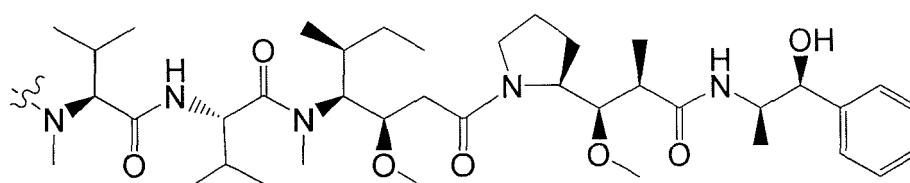
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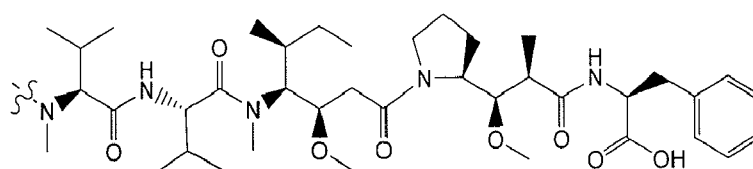
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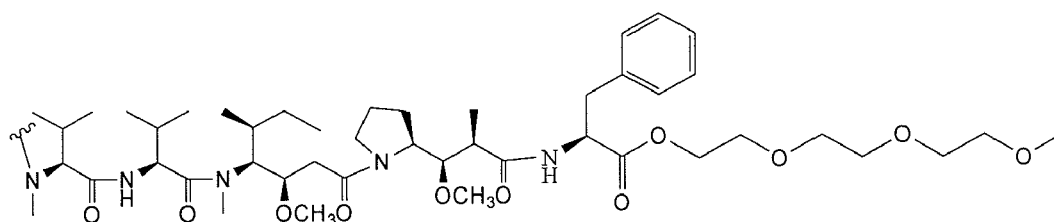


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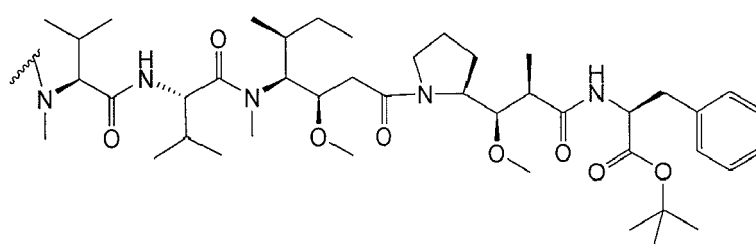
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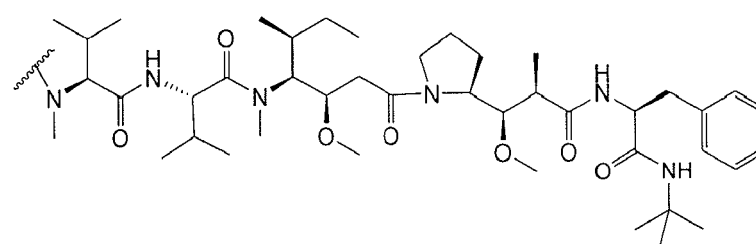
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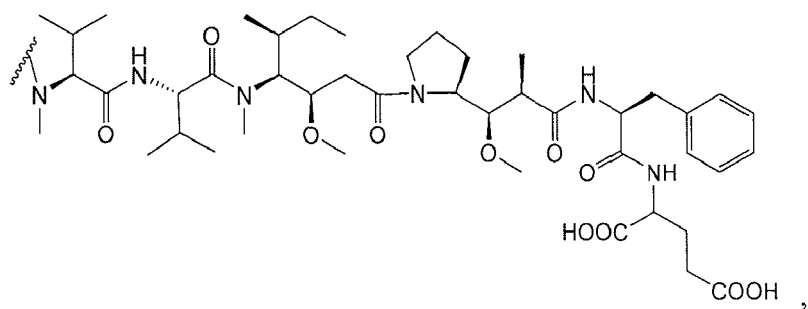
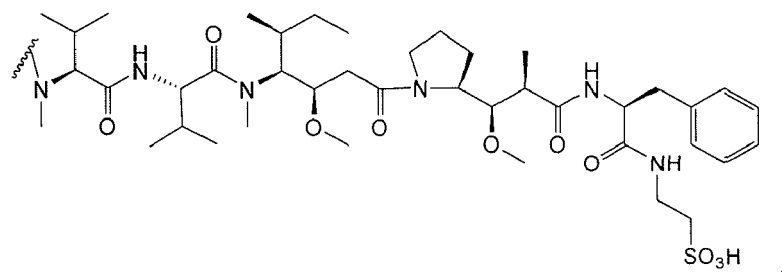
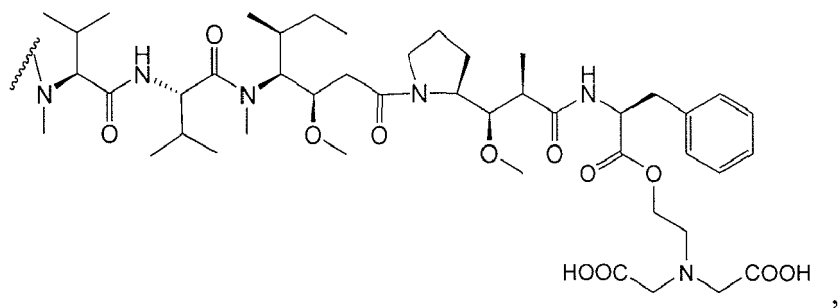
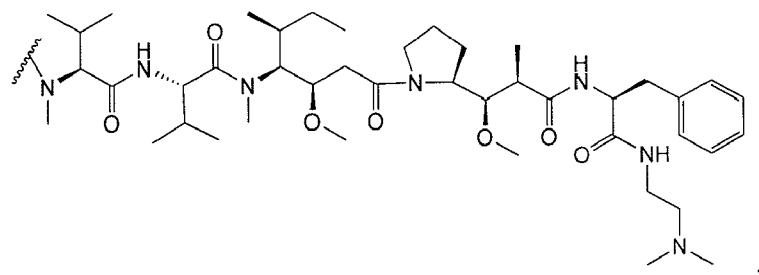
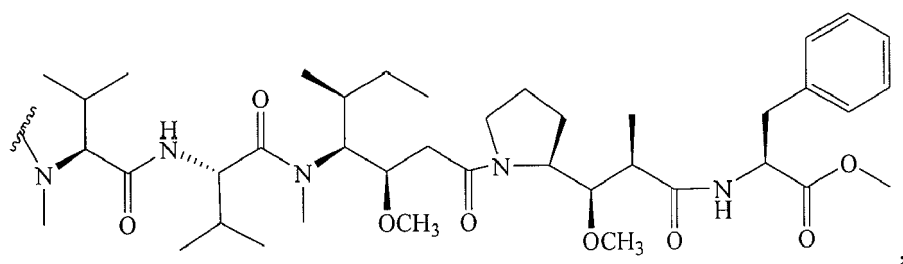


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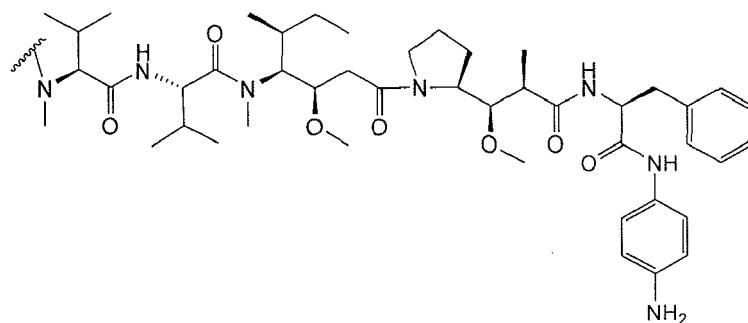
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and

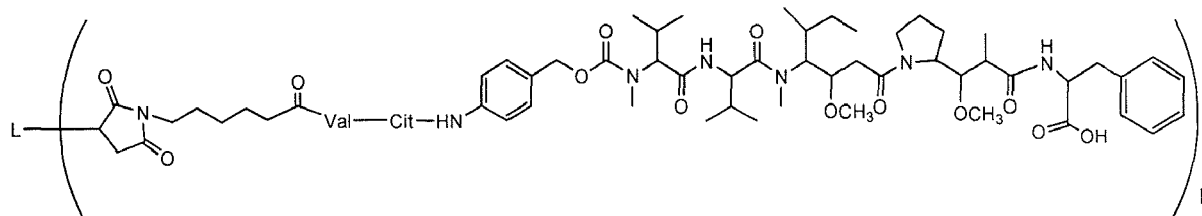


or pharmaceutically acceptable salts or solvates thereof.

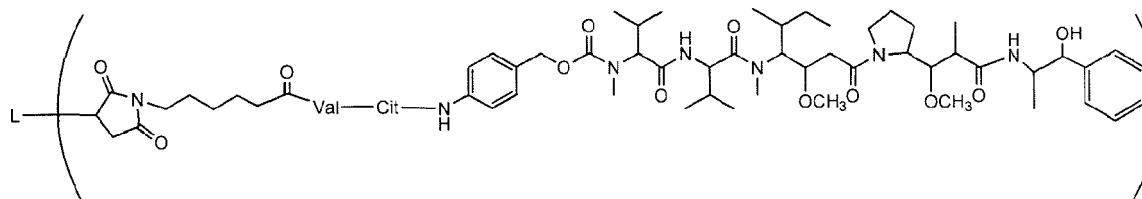
[0250] In one aspect, hydrophilic groups, such as but not limited to triethylene glycol esters (TEG) can be attached to the Drug Unit at R¹¹. Without being bound by theory, the hydrophilic groups assist in the internalization and non-agglomeration of the Drug Unit.

[0251] In some embodiments, the Drug unit is not TZT-1027. In some embodiments, the Drug unit is not auristatin E, dolastatin 10, or auristatin PE.

[0252] Exemplary antibody-drug conjugate compounds have the following structures wherein "L" or "mAb-s-" represents an 191P4D12 MAb designated Ha22-2(2,4)6.1 set forth herein:

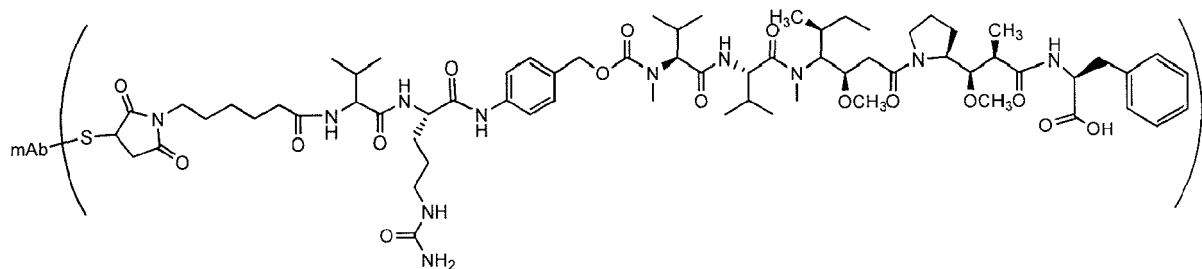


L-MC-vc-PAB-MMAF



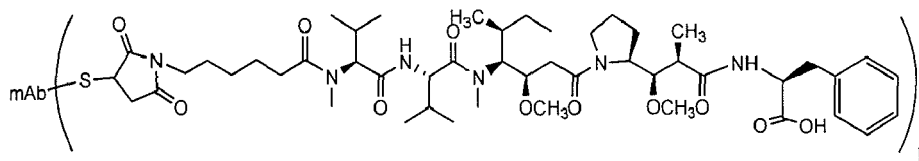
L-MC-vc-PAB-MMAE

or



L-MC-vc-PAB-MMAF

or



L-MC-MMAF

or pharmaceutically acceptable salt thereof.

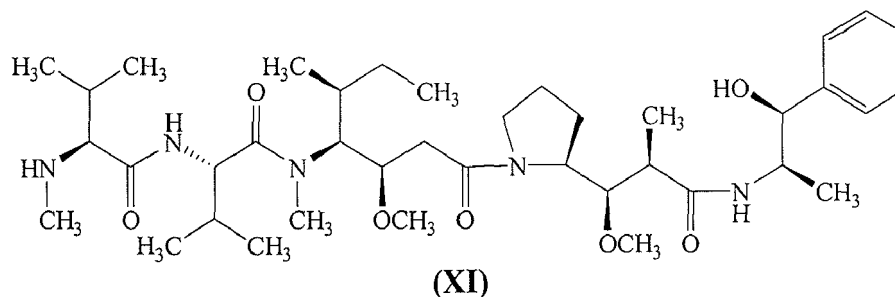
[0253] In some embodiments, the Drug Unit is a calicheamicin, camptothecin, a maytansinoid, or an anthracycline. In some embodiments the drug is a taxane, a topoisomerase inhibitor, a vinca alkaloid, or the like.

[0254] In some typical embodiments, suitable cytotoxic agents include, for example, DNA minor groove binders (e.g., enediyne and lexitropsins, a CBI compound; see also U.S. Patent No. 6,130,237), duocarmycins, taxanes (e.g., paclitaxel and docetaxel), puromycins, and vinca alkaloids. Other cytotoxic agents include, for example, CC-1065, SN-38, topotecan, morpholino-doxorubicin, rhizoxin, cyanomorpholino-doxorubicin, echinomycin, combretastatin, netropsin, epothilone A and B, estramustine, cryptophycins, cemadotin, maytansinoids, discodermolide, eleutherobin, and mitoxantrone.

[0255] In some embodiments, the Drug is an anti-tubulin agent. Examples of anti-tubulin agents include, auristatins, taxanes (e.g., Taxol® (paclitaxel), Taxotere® (docetaxel)), T67 (Tularik) and vinca alkaloids (e.g., vincristine, vinblastine, vindesine, and vinorelbine). Other antitubulin agents include, for example, baccatin derivatives, taxane analogs (e.g., epothilone A and B), nocodazole, colchicine and colchimid, estramustine, cryptophycins, cemadotin, maytansinoids, combretastatins, discodermolide, and eleutherobin.

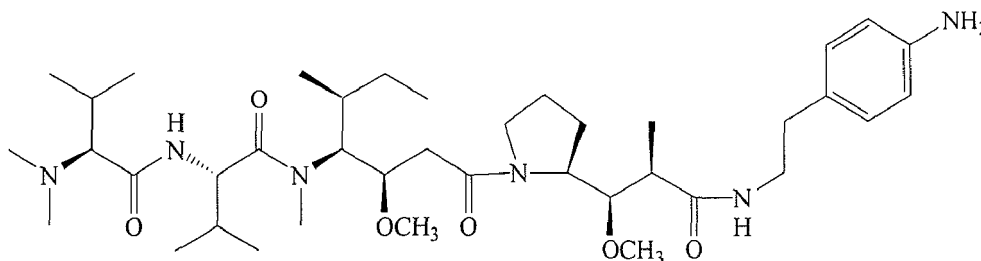
[0256] In certain embodiments, the cytotoxic agent is a maytansinoid, another group of anti-tubulin agents. For example, in specific embodiments, the maytansinoid is maytansine or DM-1 (ImmunoGen, Inc.; see also Chari et al., 1992, Cancer Res. 52:127-131).

[0257] In certain embodiments, the cytotoxic or cytostatic agent is a dolastatin. In certain embodiments, the cytotoxic or cytostatic agent is of the auristatin class. Thus, in a specific embodiment, the cytotoxic or cytostatic agent is MMAE (Formula **XI**). In another specific embodiment, the cytotoxic or cytostatic agent is AFP (Formula **XVI**).

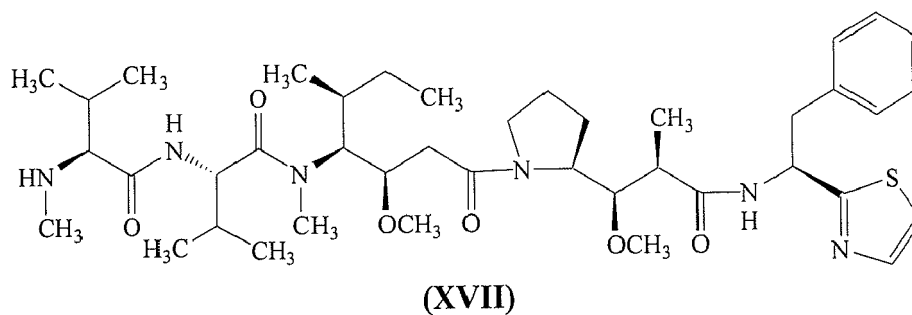
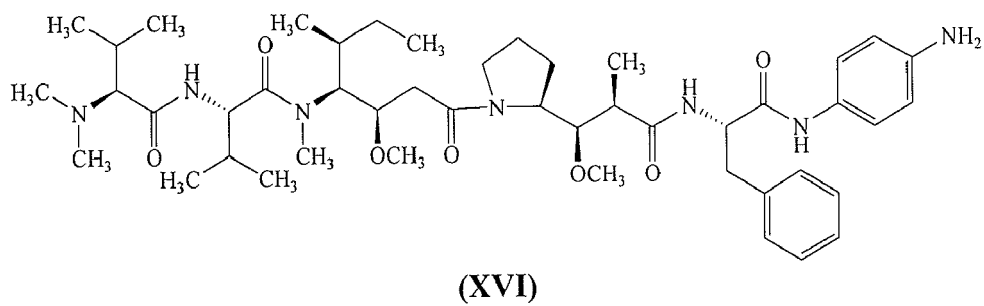
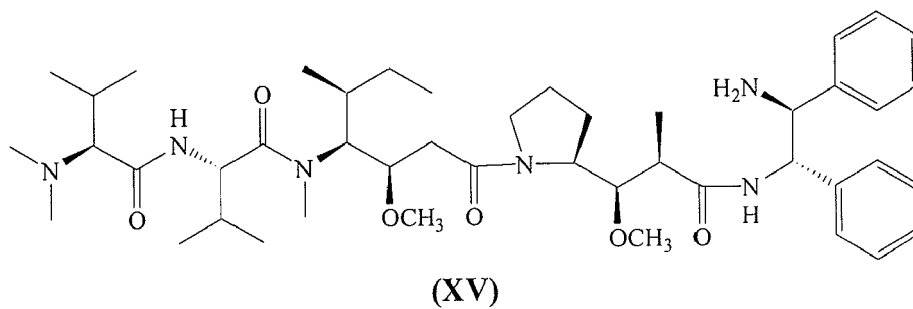
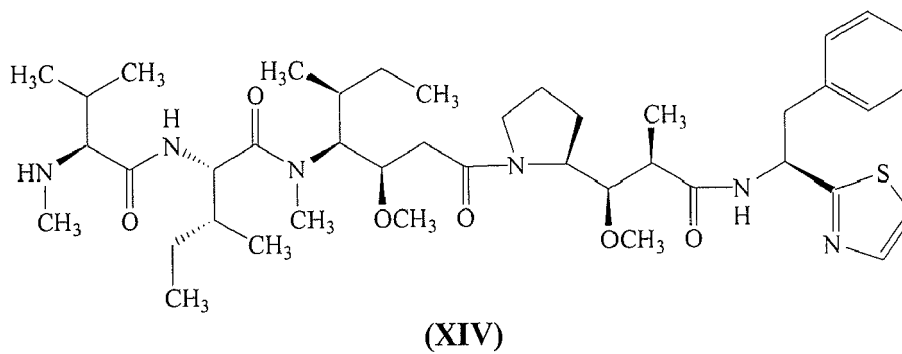
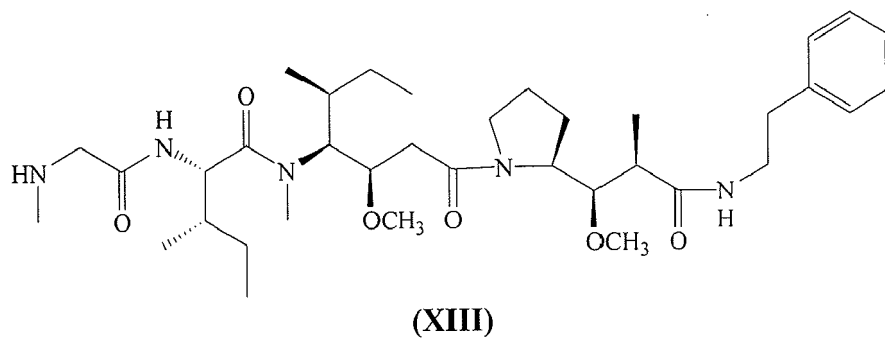


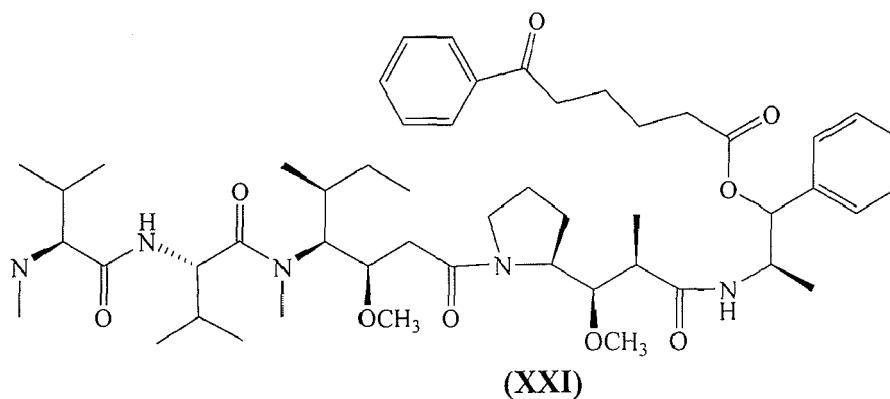
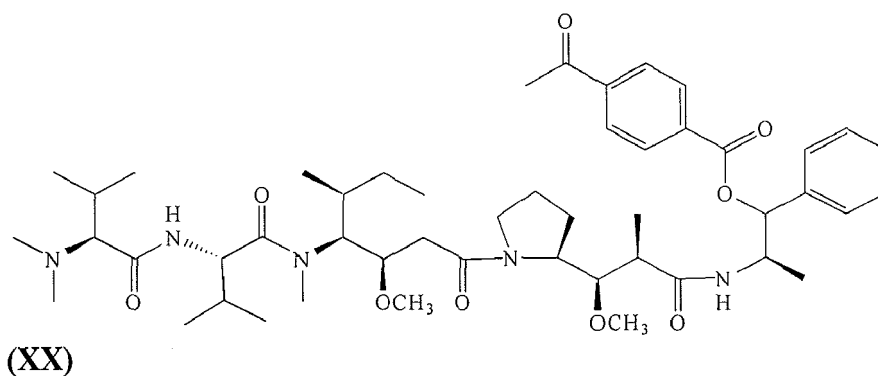
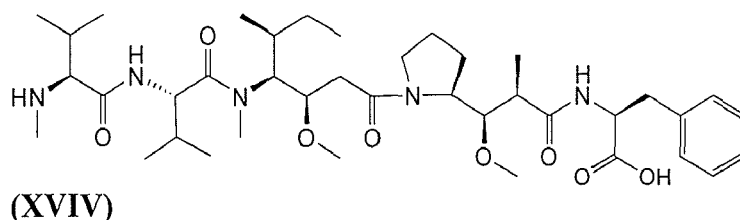
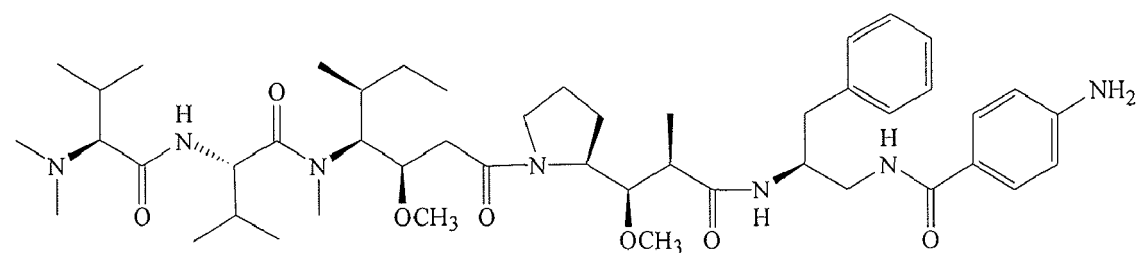
(XI)

[0258] In certain embodiments, the cytotoxic or cytostatic agent is a compound of formulas **XII-XXI** or pharmaceutically acceptable salt thereof:



(XII)





X.) Drug Loading

[0259] Drug loading is represented by p and is the average number of Drug moieties per antibody in a molecule. Drug loading may range from 1 to 20 drug moieties (D) per antibody. ADCs of the invention include collections of antibodies conjugated with a range of drug moieties, from 1 to 20. The average number of drug moieties per antibody in preparations of ADC from conjugation reactions may be characterized by conventional means such as mass spectroscopy and, ELISA assay. The quantitative distribution of ADC in terms of p may also be determined. In some instances, separation, purification, and characterization of homogeneous ADC where p is a certain value from ADC with other drug loadings may be achieved by means such as electrophoresis.

[0260] For some antibody-drug conjugates, p may be limited by the number of attachment sites on the antibody. For example, where the attachment is a cysteine thiol, as in the exemplary embodiments above, an antibody may have only one or several cysteine thiol groups, or may have only one or several sufficiently reactive thiol groups through which a

linker may be attached. In certain embodiments, higher drug loading, e.g. $p > 5$, may cause aggregation, insolubility, toxicity, or loss of cellular permeability of certain antibody-drug conjugates. In certain embodiments, the drug loading for an ADC of the invention ranges from 1 to about 8; from about 2 to about 6; from about 3 to about 5; from about 3 to about 4; from about 3.1 to about 3.9; from about 3.2 to about 3.8; from about 3.2 to about 3.7; from about 3.2 to about 3.6; from about 3.3 to about 3.8; or from about 3.3 to about 3.7. Indeed, it has been shown that for certain ADCs, the optimal ratio of drug moieties per antibody may be less than 8, and may be about 2 to about 5. See US Patent No. 7,498,298 (herein incorporated by reference in its entirety).

[0261] In certain embodiments, fewer than the theoretical maximum of drug moieties are conjugated to an antibody during a conjugation reaction. An antibody may contain, for example, lysine residues that do not react with the drug-linker intermediate or linker reagent, as discussed below. Generally, antibodies do not contain many free and reactive cysteine thiol groups which may be linked to a drug moiety; indeed most cysteine thiol residues in antibodies exist as disulfide bridges. In certain embodiments, an antibody may be reduced with a reducing agent such as dithiothreitol (DTT) or tricarboxylethylphosphine (TCEP), under partial or total reducing conditions, to generate reactive cysteine thiol groups. In certain embodiments, an antibody is subjected to denaturing conditions to reveal reactive nucleophilic groups such as lysine or cysteine.

[0262] The loading (drug/antibody ratio) of an ADC may be controlled in different ways, e.g., by: (i) limiting the molar excess of drug-linker intermediate or linker reagent relative to antibody, (ii) limiting the conjugation reaction time or temperature, (iii) partial or limiting reductive conditions for cysteine thiol modification, (iv) engineering by recombinant techniques the amino acid sequence of the antibody such that the number and position of cysteine residues is modified for control of the number and/or position of linker-drug attachments (such as thioMab or thioFab prepared as disclosed herein and in WO2006/034488 (herein incorporated by reference in its entirety)).

[0263] It is to be understood that where more than one nucleophilic group reacts with a drug-linker intermediate or linker reagent followed by drug moiety reagent, then the resulting product is a mixture of ADC compounds with a distribution of one or more drug moieties attached to an antibody. The average number of drugs per antibody may be calculated from the mixture by a dual ELISA antibody assay, which is specific for antibody and specific for the drug. Individual ADC molecules may be identified in the mixture by mass spectroscopy and separated by HPLC, e.g. hydrophobic interaction chromatography (see, e.g., Hamblett, K.J., et al. "Effect of drug loading on the pharmacology, pharmacokinetics, and toxicity of an anti-CD30 antibody-drug conjugate," Abstract No. 624, American Association for Cancer Research, 2004 Annual Meeting, March 27-31, 2004, Proceedings of the AACR, Volume 45, March 2004; Alley, S.C., et al. "Controlling the location of drug attachment in antibody-drug conjugates," Abstract No. 627, American Association for Cancer Research, 2004 Annual Meeting, March 27-31, 2004, Proceedings of the AACR, Volume 45, March 2004). In certain embodiments, a homogeneous ADC with a single loading value may be isolated from the conjugation mixture by electrophoresis or chromatography.

XI.) Methods of Determining Cytotoxic effect of ADCs

[0264] Methods of determining whether a Drug or Antibody-Drug conjugate exerts a cytostatic and/or cytotoxic effect on a cell are known. Generally, the cytotoxic or cytostatic activity of an Antibody Drug conjugate can be measured by: exposing mammalian cells expressing a target protein of the Antibody Drug conjugate in a cell culture medium; culturing the cells for a period from about 6 hours to about 5 days; and measuring cell viability. Cell-based *in vitro* assays can be used to measure viability (proliferation), cytotoxicity, and induction of apoptosis (caspase activation) of the Antibody Drug conjugate.

[0265] For determining whether an Antibody Drug conjugate exerts a cytostatic effect, a thymidine incorporation assay may be used. For example, cancer cells expressing a target antigen at a density of 5,000 cells/well of a 96-well plated can be cultured for a 72-hour period and exposed to 0.5 μ Ci of 3 H-thymidine during the final 8 hours of the 72-hour period. The incorporation of 3 H-thymidine into cells of the culture is measured in the presence and absence of the Antibody Drug conjugate.

[0266] For determining cytotoxicity, necrosis or apoptosis (programmed cell death) can be measured. Necrosis is typically accompanied by increased permeability of the plasma membrane; swelling of the cell, and rupture of the plasma membrane. Apoptosis is typically characterized by membrane blebbing, condensation of cytoplasm, and the activation of endogenous endonucleases. Determination of any of these effects on cancer cells indicates that an Antibody Drug conjugate is useful in the treatment of cancers.

[0267] Cell viability can be measured by determining in a cell the uptake of a dye such as neutral red, trypan blue, or ALAMAR™ blue (see, e.g., Page et al., 1993, Intl. J. Oncology 3:473-476). In such an assay, the cells are incubated in media containing the dye, the cells are washed, and the remaining dye, reflecting cellular uptake of the dye, is measured spectrophotometrically. The protein-binding dye sulforhodamine B (SRB) can also be used to measure cytotoxicity (Skehan et al., 1990, J. Natl. Cancer Inst. 82:1107-12).

[0268] Alternatively, a tetrazolium salt, such as MTT, is used in a quantitative colorimetric assay for mammalian cell

survival and proliferation by detecting living, but not dead, cells (see, e.g., Mosmann, 1983, J. Immunol. Methods 65:55-63).

[0269] Apoptosis can be quantitated by measuring, for example, DNA fragmentation. Commercial photometric methods for the quantitative *in vitro* determination of DNA fragmentation are available. Examples of such assays, including TUNEL (which detects incorporation of labeled nucleotides in fragmented DNA) and ELISA-based assays, are described in Biochemica, 1999, no. 2, pp. 34-37 (Roche Molecular Biochemicals).

[0270] Apoptosis can also be determined by measuring morphological changes in a cell. For example, as with necrosis, loss of plasma membrane integrity can be determined by measuring uptake of certain dyes (e.g., a fluorescent dye such as, for example, acridine orange or ethidium bromide). A method for measuring apoptotic cell number has been described by Duke and Cohen, Current Protocols in Immunology (Coligan et al. eds., 1992, pp. 3.17.1-3.17.16). Cells also can be labeled with a DNA dye (e.g., acridine orange, ethidium bromide, or propidium iodide) and the cells observed for chromatin condensation and margination along the inner nuclear membrane. Other morphological changes that can be measured to determine apoptosis include, e.g., cytoplasmic condensation, increased membrane blebbing, and cellular shrinkage.

[0271] The presence of apoptotic cells can be measured in both the attached and "floating" compartments of the cultures. For example, both compartments can be collected by removing the supernatant, trypsinizing the attached cells, combining the preparations following a centrifugation wash step (e.g., 10 minutes at 2000 rpm), and detecting apoptosis (e.g., by measuring DNA fragmentation). (See, e.g., Piazza et al., 1995, Cancer Research 55:3110-16).

[0272] *In vivo*, the effect of a 191P4D12 therapeutic composition can be evaluated in a suitable animal model. For example, xenogenic cancer models can be used, wherein cancer explants or passaged xenograft tissues are introduced into immune compromised animals, such as nude or SCID mice (Klein et al., 1997, Nature Medicine 3: 402-408). For example, PCT Patent Application WO98/16628 and U.S. Patent 6,107,540 describe various xenograft models of human prostate cancer capable of recapitulating the development of primary tumors, micrometastasis, and the formation of osteoblastic metastases characteristic of late stage disease. Efficacy can be predicted using assays that measure inhibition of tumor formation, tumor regression or metastasis, and the like.

[0273] *In vivo* assays that evaluate the promotion of apoptosis are useful in evaluating therapeutic compositions. In one embodiment, xenografts from tumor bearing mice treated with the therapeutic composition can be examined for the presence of apoptotic foci and compared to untreated control xenograft-bearing mice. The extent to which apoptotic foci are found in the tumors of the treated mice provides an indication of the therapeutic efficacy of the composition.

[0274] The therapeutic compositions used in the practice of the foregoing methods can be formulated into pharmaceutical compositions comprising a carrier suitable for the desired delivery method. Suitable carriers include any material that when combined with the therapeutic composition retains the anti-tumor function of the therapeutic composition and is generally non-reactive with the patient's immune system. Examples include, but are not limited to, any of a number of standard pharmaceutical carriers such as sterile phosphate buffered saline solutions, bacteriostatic water, and the like (see, generally, Remington's Pharmaceutical Sciences 16th Edition, A. Osal., Ed., 1980).

[0275] Therapeutic formulations can be solubilized and administered via any route capable of delivering the therapeutic composition to the tumor site. Potentially effective routes of administration include, but are not limited to, intravenous, parenteral, intraperitoneal, intramuscular, intratumor, intradermal, intraorgan, orthotopic, and the like. A preferred formulation for intravenous injection comprises the therapeutic composition in a solution of preserved bacteriostatic water, sterile unpreserved water, and/or diluted in polyvinylchloride or polyethylene bags containing 0.9% sterile Sodium Chloride for Injection, USP. Therapeutic protein preparations can be lyophilized and stored as sterile powders, preferably under vacuum, and then reconstituted in bacteriostatic water (containing for example, benzyl alcohol preservative) or in sterile water prior to injection.

[0276] Dosages and administration protocols for the treatment of cancers using the foregoing methods will vary with the method and the target cancer, and will generally depend on a number of other factors appreciated in the art.

XII.) Treatment of Cancer(s) Expressing 191P4D12

[0277] The identification of 191P4D12 as a protein that is normally expressed in a restricted set of tissues, but which is also expressed in cancers such as those listed in Table I, opens a number of therapeutic approaches to the treatment of such cancers.

[0278] Of note, targeted antitumor therapies have been useful even when the targeted protein is expressed on normal tissues, even vital normal organ tissues. A vital organ is one that is necessary to sustain life, such as the heart or colon. A non-vital organ is one that can be removed whereupon the individual is still able to survive. Examples of non-vital organs are ovary, breast, and prostate.

[0279] Expression of a target protein in normal tissue, even vital normal tissue, does not defeat the utility of a targeting agent for the protein as a therapeutic for certain tumors in which the protein is also overexpressed. For example, expression in vital organs is not in and of itself detrimental. In addition, organs regarded as dispensable, such as the prostate and ovary, can be removed without affecting mortality. Finally, some vital organs are not affected by normal

organ expression because of an immunoprivilege. Immunoprivileged organs are organs that are protected from blood by a blood-organ barrier and thus are not accessible to immunotherapy. Examples of immunoprivileged organs are the brain and testis.

[0280] Accordingly, therapeutic approaches that inhibit the activity of a 191P4D12 protein are useful for patients suffering from a cancer that expresses 191P4D12. These therapeutic approaches generally fall into three classes. The first class modulates 191P4D12 function as it relates to tumor cell growth leading to inhibition or retardation of tumor cell growth or inducing its killing. The second class comprises various methods for inhibiting the binding or association of a 191P4D12 protein with its binding partner or with other proteins. The third class comprises a variety of methods for inhibiting the transcription of a 191P4D12 gene or translation of 191P4D12 mRNA.

[0281] Accordingly, cancer patients can be evaluated for the presence and level of 191P4D12 expression, preferably using immunohistochemical assessments of tumor tissue, quantitative 191P4D12 imaging, or other techniques that reliably indicate the presence and degree of 191P4D12 expression. Immunohistochemical analysis of tumor biopsies or surgical specimens is preferred for this purpose. Methods for immunohistochemical analysis of tumor tissues are well known in the art.

XIII.) 191P4D12 as a Target for Antibody-based Therapy

[0282] 191P4D12 is an attractive target for antibody-based therapeutic strategies. A number of antibody strategies are known in the art for targeting both extracellular and intracellular molecules (see, e.g., complement and ADCC mediated killing as well as the use of intrabodies). Because 191P4D12 is expressed by cancer cells of various lineages relative to corresponding normal cells, systemic administration of 191P4D12-immunoreactive compositions are prepared that exhibit excellent sensitivity without toxic, non-specific and/or non-target effects caused by binding of the immunoreactive composition to non-target organs and tissues. Antibodies specifically reactive with domains of 191P4D12 are useful to treat 191P4D12-expressing cancers systemically, preferably as antibody drug conjugates (i.e. ADCs) wherein the conjugate is with a toxin or therapeutic agent.

[0283] Those skilled in the art understand that antibodies can be used to specifically target and bind immunogenic molecules such as an immunogenic region of a 191P4D12 sequence shown in Figure 1. In addition, skilled artisans understand that it is routine to conjugate antibodies to cytotoxic agents (see, e.g., Slevers et al. Blood 93:11 3678-3684 (June 1, 1999)). When cytotoxic and/or therapeutic agents are delivered directly to cells, such as by conjugating them to antibodies specific for a molecule expressed by that cell (e.g. 191P4D12), the cytotoxic agent will exert its known biological effect (i.e. cytotoxicity) on those cells.

[0284] A wide variety of compositions and methods for using antibody-cytotoxic agent conjugates to kill cells are known in the art. In the context of cancers, typical methods entail administering to an mammal having a tumor a biologically effective amount of a conjugate comprising a selected cytotoxic and/or therapeutic agent linked to a targeting agent (e.g. a 191P4D12 MAb, preferably Ha22-2(2,4)6.1) that binds to an antigen (e.g. 191P4D12) expressed, accessible to binding or localized on the cell surfaces. A typical embodiment is a method of delivering a cytotoxic and/or therapeutic agent to a cell expressing 191P4D12, comprising conjugating the cytotoxic agent to an antibody that immunospecifically binds to a 191P4D12 epitope, and, exposing the cell to the antibody drug conjugate (ADC). Another illustrative embodiment is a method of treating an individual suspected of suffering from metastasized cancer, comprising a step of administering parenterally to said individual a pharmaceutical composition comprising a therapeutically effective amount of an antibody conjugated to a cytotoxic and/or therapeutic agent.

[0285] Cancer immunotherapy using 191P4D12 antibodies can be done in accordance with various approaches that have been successfully employed in the treatment of other types of cancer, including but not limited to colon cancer (Arlen et al., 1998, Crit. Rev. Immunol. 18:133-138), multiple myeloma (Ozaki et al., 1997, Blood 90:3179-3186, Tsunenari et al., 1997, Blood 90:2437-2444), gastric cancer (Kasprzyk et al., 1992, Cancer Res. 52:2771-2776), B-cell lymphoma (Funakoshi et al., 1996, J. Immunother. Emphasis Tumor Immunol. 19:93-101), leukemia (Zhong et al., 1996, Leuk. Res. 20:581-589), colorectal cancer (Moun et al., 1994, Cancer Res. 54:6160-6166; Velders et al., 1995, Cancer Res. 55:4398-4403), and breast cancer (Shepard et al., 1991, J. Clin. Immunol. 11:117-127). Some therapeutic approaches involve conjugation of naked antibody to a toxin or radioisotope, such as the conjugation of Y⁹¹ or I¹³¹ to anti-CD20 antibodies (e.g., ZevalinTM, IDEC Pharmaceuticals Corp. or BexxarTM, Coulter Pharmaceuticals) respectively, while others involve co-administration of antibodies and other therapeutic agents, such as HerceptinTM (trastuzu MAb) with paclitaxel (Genentech, Inc.). In a preferred embodiment, the antibodies will be conjugated a cytotoxic agent, *supra*, preferably an aurastatin derivative designated MMAE (Seattle Genetics, Inc.).

[0286] Although 191P4D12 antibody therapy is useful for all stages of cancer, antibody therapy can be particularly appropriate in advanced or metastatic cancers. Treatment with the antibody therapy of the invention is indicated for patients who have received one or more rounds of chemotherapy. Alternatively, antibody therapy of the invention is combined with a chemotherapeutic or radiation regimen for patients who have not received chemotherapeutic treatment. Additionally, antibody therapy can enable the use of reduced dosages of concomitant chemotherapy, particularly for

patients who do not tolerate the toxicity of the chemotherapeutic agent very well. Fan et al. (Cancer Res. 53:4637-4642, 1993), Prewett et al. (International J. of Onco. 9:217-224, 1996), and Hancock et al. (Cancer Res. 51:4575-4580, 1991) describe the use of various antibodies together with chemotherapeutic agents.

[0287] 191P4D12 monoclonal antibodies that treat the cancers set forth in Table I include those that initiate a potent immune response against the tumor or those that are directly cytotoxic. In this regard, 191P4D12 monoclonal antibodies (MAbs) can elicit tumor cell lysis by either complement-mediated or antibody-dependent cell cytotoxicity (ADCC) mechanisms, both of which require an intact Fc portion of the immunoglobulin molecule for interaction with effector cell Fc receptor sites on complement proteins. In addition, 191P4D12 MAbs that exert a direct biological effect on tumor growth are useful to treat cancers that express 191P4D12. Mechanisms by which directly cytotoxic MAbs act include: inhibition of cell growth, modulation of cellular differentiation, modulation of tumor angiogenesis factor profiles, and the induction of apoptosis. The mechanism(s) by which a particular 191P4D12 MAb exerts an anti-tumor effect is evaluated using any number of *in vitro* assays that evaluate cell death such as ADCC, complement-mediated cell lysis, and so forth, as is generally known in the art.

[0288] Accordingly, preferred monoclonal antibodies used in the therapeutic methods of the invention are those that are either fully human and that bind specifically to the target 191P4D12 antigen with high affinity.

XIV.) 191P4D12 ADC Cocktails

[0289] Therapeutic methods of the invention contemplate the administration of single 191P4D12 ADCs as well as combinations, or cocktails, of different MAbs (i.e. 191P4D12 MAbs or MAbs that bind another protein). Such MAB cocktails can have certain advantages inasmuch as they contain MAbs that target different epitopes, exploit different effector mechanisms or combine directly cytotoxic MAbs with MAbs that rely on immune effector functionality. Such MAbs in combination can exhibit synergistic therapeutic effects. In addition, 191P4D12 MAbs can be administered concomitantly with other therapeutic modalities, including but not limited to various chemotherapeutic and biologic agents, androgen-blockers, immune modulators (e.g., IL-2, GM-CSF), surgery or radiation. In a preferred embodiment, the 191P4D12 MAbs are administered in conjugated form.

[0290] 191P4D12 ADC formulations are administered via any route capable of delivering the antibodies to a tumor cell. Routes of administration include, but are not limited to, intravenous, intraperitoneal, intramuscular, intratumor, intradermal, and the like. Treatment generally involves repeated administration of the 191P4D12 ADC preparation, via an acceptable route of administration such as intravenous injection (IV), typically at a dose in the range, including but not limited to, 0.1, .2, .3, .4, .5, .6, .7, .8, .9, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, or 25 mg/kg body weight. In general, doses in the range of 10-1000 mg MAb per week are effective and well tolerated.

[0291] Based on clinical experience with the Herceptin® (Trastuzumab) in the treatment of metastatic breast cancer, an initial loading dose of approximately 4 mg/kg patient body weight IV, followed by weekly doses of about 2 mg/kg IV of the MAb preparation represents an acceptable dosing regimen. Preferably, the initial loading dose is administered as a 90-minute or longer infusion. The periodic maintenance dose is administered as a 30 minute or longer infusion, provided the initial dose was well tolerated. As appreciated by those of skill in the art, various factors can influence the ideal dose regimen in a particular case. Such factors include, for example, the binding affinity and half life of the MAbs used, the degree of 191P4D12 expression in the patient, the extent of circulating shed 191P4D12 antigen, the desired steady-state antibody concentration level, frequency of treatment, and the influence of chemotherapeutic or other agents used in combination with the treatment method of the invention, as well as the health status of a particular patient.

[0292] Optionally, patients should be evaluated for the levels of 191P4D12 in a given sample (e.g. the levels of circulating 191P4D12 antigen and/or 191P4D12 expressing cells) in order to assist in the determination of the most effective dosing regimen, etc. Such evaluations are also used for monitoring purposes throughout therapy, and are useful to gauge therapeutic success in combination with the evaluation of other parameters (for example, urine cytology and/or ImmunoCyt levels in bladder cancer therapy, or by analogy, serum PSA levels in prostate cancer therapy).

[0293] An object of the present invention is to provide 191P4D12 ADCs, which inhibit or retard the growth of tumor cells expressing 191P4D12. A further object of this invention is to provide methods to inhibit angiogenesis and other biological functions and thereby reduce tumor growth in mammals, preferably humans, using such 191P4D12 ADCs, and in particular using such 191P4D12 ADCs combined with other drugs or immunologically active treatments.

XV.) Combination Therapy

[0294] In one embodiment, there is synergy when tumors, including human tumors, are treated with 191P4D12 ADCs in conjunction with chemotherapeutic agents or radiation or combinations thereof. In other words, the inhibition of tumor growth by a 191P4D12 ADC is enhanced more than expected when combined with chemotherapeutic agents or radiation or combinations thereof. Synergy may be shown, for example, by greater inhibition of tumor growth with combined treatment than would be expected from a treatment of only 191P4D12 ADC or the additive effect of treatment with a

191P4D12 ADC and a chemotherapeutic agent or radiation. Preferably, synergy is demonstrated by remission of the cancer where remission is not expected from treatment either from a 191P4D12 ADC or with treatment using an additive combination of a 191P4D12 ADC and a chemotherapeutic agent or radiation.

[0295] The method for inhibiting growth of tumor cells using a 191P4D12 ADC and a combination of chemotherapy or radiation or both comprises administering the 191P4D12 ADC before, during, or after commencing chemotherapy or radiation therapy, as well as any combination thereof (*i. e.* before and during, before and after, during and after, or before, during, and after commencing the chemotherapy and/or radiation therapy). For example, the 191P4D12 ADC is typically administered between 1 and 60 days, preferably between 3 and 40 days, more preferably between 5 and 12 days before commencing radiation therapy and/or chemotherapy. However, depending on the treatment protocol and the specific patient needs, the method is performed in a manner that will provide the most efficacious treatment and ultimately prolong the life of the patient.

[0296] The administration of chemotherapeutic agents can be accomplished in a variety of ways including systemically by the parenteral and enteral routes. In one embodiment, the 191P4D12 ADCs and the chemotherapeutic agent are administered as separate molecules. Particular examples of chemotherapeutic agents or chemotherapy include cisplatin, dacarbazine (DTIC), dactinomycin, mechlorethamine (nitrogen mustard), streptozocin, cyclophosphamide, carmustine (BCNU), lomustine (CCNU), doxorubicin (adriamycin), daunorubicin, procarbazine, mitomycin, cytarabine, etoposide, methotrexate, 5-fluorouracil, vinblastine, vincristine, bleomycin, paclitaxel (taxol), docetaxel (taxotere), aldesleukin, asparaginase, busulfan, carboplatin, cladribine, dacarbazine, floxuridine, fludarabine, hydroxyurea, ifosfamide, interferon alpha, leuprolide, megestrol, melphalan, mercaptopurine, plicamycin, mitotane, pegaspargase, pentostatin, pipobroman, plicamycin, streptozocin, tamoxifen, teniposide, testolactone, thioguanine, thiotepa, uracil mustard, vinorelbine, gemcitabine, chlorambucil, taxol and combinations thereof.

[0297] The source of radiation, used in combination with a 191P4D12 ADC, can be either external or internal to the patient being treated. When the source is external to the patient, the therapy is known as external beam radiation therapy (EBRT). When the source of radiation is internal to the patient, the treatment is called brachytherapy (BT).

[0298] The above described therapeutic regimens may be further combined with additional cancer treating agents and/or regimes, for example additional chemotherapy, cancer vaccines, signal transduction inhibitors, agents useful in treating abnormal cell growth or cancer, antibodies (e.g. Anti-CTLA-4 antibodies as described in WO/2005/092380 (Pfizer)) or other ligands that inhibit tumor growth by binding to IGF-1R, and cytokines.

[0299] When the mammal is subjected to additional chemotherapy, chemotherapeutic agents described above may be used. Additionally, growth factor inhibitors, biological response modifiers, anti-hormonal therapy, selective estrogen receptor modulators (SERMs), angiogenesis inhibitors, and anti-androgens may be used. For example, anti-hormones, for example anti-estrogens such as Nolvadex (tamoxifen) or, anti-androgens such as Casodex (4'-cyano-3-(4-fluorophenylsulphonyl)-2-hydroxy-2-methyl-3- (trifluoromethyl)propionanilide) may be used.

[0300] The above therapeutic approaches can be combined with any one of a wide variety of surgical, chemotherapy or radiation therapy regimens. The therapeutic approaches of the invention can enable the use of reduced dosages of chemotherapy (or other therapies) and/or less frequent administration, an advantage for all patients and particularly for those that do not tolerate the toxicity of the chemotherapeutic agent well.

XVI.) Kits/Articles of Manufacture

[0301] For use in the laboratory, prognostic, prophylactic, diagnostic and therapeutic applications described herein, kits are within the scope of the invention. Such kits can comprise a carrier, package, or container that is compartmentalized to receive one or more containers such as vials, tubes, and the like, each of the container(s) comprising one of the separate elements to be used in the method, along with a label or insert comprising instructions for use, such as a use described herein. For example, the container(s) can comprise an antibody that is or can be detectably labeled. Kits can comprise a container comprising a Drug Unit. The kit can include all or part of the amino acid sequences in Figure 2, or Figure 3 or analogs thereof, or a nucleic acid molecule that encodes such amino acid sequences.

[0302] The kit of the invention will typically comprise the container described above and one or more other containers associated therewith that comprise materials desirable from a commercial and user standpoint, including buffers, diluents, filters, needles, syringes; carrier, package, container, vial and/or tube labels listing contents and/or instructions for use, and package inserts with instructions for use.

[0303] A label can be present on or with the container to indicate that the composition is used for a specific therapy or non-therapeutic application, such as a prognostic, prophylactic, diagnostic or laboratory application, and can also indicate directions for either *in vivo* or *in vitro* use, such as those described herein. Directions and or other information can also be included on an insert(s) or label(s) which is included with or on the kit. The label can be on or associated with the container. A label can be on a container when letters, numbers or other characters forming the label are molded or etched into the container itself; a label can be associated with a container when it is present within a receptacle or carrier that also holds the container, *e.g.*, as a package insert. The label can indicate that the composition is used for

diagnosing, treating, prophylaxing or prognosing a condition, such as a cancer of a tissue set forth in Table I.

[0304] The terms "kit" and "article of manufacture" can be used as synonyms.

[0305] In another embodiment of the invention, an article(s) of manufacture containing compositions, such as antibody(s), or antibody drug conjugates (ADCs) e.g., materials useful for the diagnosis, prognosis, prophylaxis and/or treatment of cancers of tissues such as those set forth in Table I is provided. The article of manufacture typically comprises at least one container and at least one label. Suitable containers include, for example, bottles, vials, syringes, and test tubes. The containers can be formed from a variety of materials such as glass, metal or plastic. The container can hold amino acid sequence(s), small molecule(s), nucleic acid sequence(s), cell population(s) and/or antibody(s). In another embodiment a container comprises an antibody, binding fragment thereof or specific binding protein for use in evaluating protein expression of 191P4D12 in cells and tissues, or for relevant laboratory, prognostic, diagnostic, prophylactic and therapeutic purposes; indications and/or directions for such uses can be included on or with such container, as can reagents and other compositions or tools used for these purposes.

[0306] The container can alternatively hold a composition that is effective for treating, diagnosis, prognosing or prophylaxing a condition and can have a sterile access port (for example the container can be an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection needle). The active agents in the composition can be an antibody capable of specifically binding 191P4D12 or an antibody drug conjugate specifically binding to 191P4D12.

[0307] The article of manufacture can further comprise a second container comprising a pharmaceutically-acceptable buffer, such as phosphate-buffered saline, Ringer's solution and/or dextrose solution. It can further include other materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, stirrers, needles, syringes, and/or package inserts with indications and/or instructions for use.

EXAMPLES:

[0308] Various aspects of the invention are further described and illustrated by way of the several examples that follow, none of which is intended to limit the scope of the invention.

Example 1

The 191P4D12 Antigen

[0309] The 191P4D12 gene sequence was discovered using Suppression Subtractive Hybridization (SSH) methods known in the art. The 191P4D12 SSH sequence of 223 bp was identified from a bladder tumor minus cDNAs derived from a pool of nine (9) normal tissues using standard methods. A full length cDNA clone for 191P4D12 was isolated from a bladder cancer cDNA library. The cDNA is 3464 bp in length and encodes a 510 amino acid ORF (See, Figure 1). The 191P4D12 gene shows homology to Nectin-4 gene. For further reference see, US2004/0083497 (Agensys, Inc., Santa Monica, CA) and PCT Publication WO2004/016799 (Agensys, Inc., Santa Monica, CA). For exemplary embodiments of the 191P4D12 antigen, see Figure 1.

Example 2

Generation of 191P4D12 Monoclonal Antibodies (MAbs)

[0310] In one embodiment, therapeutic Monoclonal Antibodies ("MAbs") to 191P4D12 and 191P4D12 variants comprise those that react with epitopes specific for each protein or specific to sequences in common between the variants that would bind, internalize, disrupt or modulate the biological function of 191P4D12 or 191P4D12 variants, for example, those that would disrupt the interaction with ligands, substrates, and binding partners. Immunogens for generation of such MAbs include those designed to encode or contain the extracellular domains or the entire 191P4D12 protein sequence, regions predicted to contain functional motifs, and regions of the 191P4D12 protein variants predicted to be antigenic from computer analysis of the amino acid sequence. Immunogens include peptides and recombinant proteins such as tag5-191P4D12, a purified mammalian cell derived His tagged protein. In addition, cells engineered to express high levels of 191P4D12, such as RAT1-191P4D12 or 300.19-191P4D12, are used to immunize mice.

[0311] MAbs to 191P4D12 were generated using XenoMouse technology® (Amgen Fremont) wherein the murine heavy and kappa light chain loci have been inactivated and a majority of the human heavy and kappa light chain immunoglobulin loci have been inserted. The MAb designated Ha22-2(2,4)6.1 was generated from immunization of human γ 1 producing XenoMice with pTag5/mychis-191P4D12 (amino acids 23-351).

[0312] The 191P4D12 MAb Ha22-2(2,4)6.1 specifically binds to pTag5/mychis-191P4D12 protein by ELISA as well as recombinant 191P4D12 expressing cells and multiple cancer cell lines expressing 191P4D12.

[0313] The hybridoma producing an antibody designated Ha22-2(2,4)6.1 was sent (via Federal Express) to the Amer-

ican Type Culture Collection (ATCC), P.O. Box 1549, Manassas, VA 20108 on 18-August-2010 and assigned Accession number PTA-11267.

[0314] DNA coding sequences for 191P4D12 MAb Ha22-2(2,4)6.1 was determined after isolating mRNA from the respective hybridoma cells with Trizol reagent (Life Technologies, Gibco BRL).

[0315] Anti-191P4D12 Ha22-2(2,4)6.1 heavy and light chain variable nucleic acid sequences were sequenced from the hybridoma cells using the following protocol. Ha22-2(2,4)6.1 secreting hybridoma cells were lysed with Trizol reagent (Life Technologies, Gibco BRL). Total RNA was purified and quantified. First strand cDNAs was generated from total RNA with oligo (dT)12-18 priming using the Gibco-BRL Superscript Preamplification system. First strand cDNA was amplified using human immunoglobulin variable heavy chain primers, and human immunoglobulin variable light chain primers. PCR products were sequenced and the variable heavy and light chain regions determined.

[0316] The nucleic acid and amino acid sequences of the variable heavy and light chain regions are listed in Figure 2 and Figure 3. Alignment of Ha22-2(2,4)6.1 MAb to human Ig germline is set forth in Figure 4A-4B.

Example 3

Expression of Ha22-2(2,4)6.1 using Recombinant DNA Methods

[0317] To express Ha22-2(2,4)6.1 MAb recombinantly in transfected cells, Ha22-2(2,4)6.1 MAb variable heavy and light chain sequences were cloned upstream of the human heavy chain IgG1 and human light chain IgK constant regions respectively. The complete Ha22-2(2,4)6.1 MAb human heavy chain and light chain cassettes were cloned downstream of the CMV promoter/enhancer in a cloning vector. A polyadenylation site was included downstream of the MAb coding sequence. The recombinant Ha22-2(2,4)6.1 MAb expressing constructs were transfected into CHO cells. The Ha22-2(2,4)6.1 MAb secreted from recombinant cells was evaluated for binding to cell surface 191P4D12 by flow cytometry (Figure 5A). RAT-control and RAT-191P4D12 cells were stained with Ha22-2(2,4)6.1 MAb from either hybridoma or from CHO cells transfected with Ha22-2(2,4)6.1 heavy and light chain vector constructs. Binding was detected by flow cytometry.

[0318] Results show that the recombinantly expressed Ha22-2(2,4)6.1 expressed in CHO cells binds 191P4D12 similarly to the Ha22-2(2,4)6.1 purified from hybridoma. The Ha22-2(2,4)6.1 MAb secreted from recombinant cells was also evaluated for binding to 191P4D12 recombinant protein by ELISA. As shown in Figure 5B, binding of Ha22-2(2,4)6.1 to 191P4D12 protein was identical between MAb material derived from CHO and from hybridoma cells.

Example 4

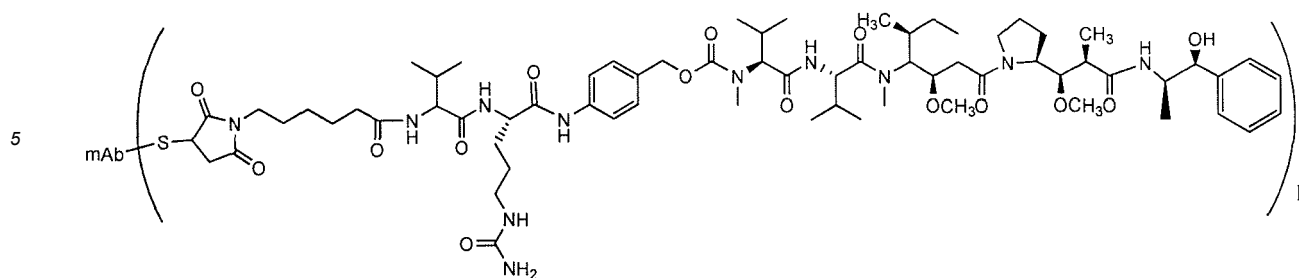
Antibody Drug Conjugation of Ha22-2(2,4)6.1 MAb

[0319] The Ha22-2(2,4)6.1 MAb (Figure 2) was conjugated to an auristatin derivative designated MMAE (Formula XI) using a vc (Val-Cit) linker described herein to create the antibody drug conjugate (ADC) of the invention designated Ha22-2(2,4)6.1 vcMMAE using the following protocols. The conjugation of the vc (Val-Cit) linker to the MMAE (Seattle Genetics, Inc., Seattle, WA) was completed using the general method set forth in Table IV to create the cytotoxic vcMMAE (see, US Patent No. 7,659,241).

[0320] Next, the antibody drug conjugate (ADC) of the invention designated Ha22-2(2,4)6.1vcMMAE was made using the following protocols.

[0321] Briefly, a 15 mg/mL solution of the Ha22-2(2,4)6.1MAb in 10 mM acetate at pH 5.0, 1% sorbitol, 3% L-arginine is added with a 20% volume of 0.1 M TrisCl at pH 8.4, 25mM EDTA and 750 mM NaCl to adjust the pH of the solution to 7.5, 5mM EDTA and 150 mM sodium chloride. The MAb is then partially reduced by adding 2.3 molar equivalents of TCEP (relative to moles of MAb) and then stirred at 37°C for 2 hours. The partially reduced MAb solution is then cooled to 5°C and 4.4 molar equivalents of vcMMAE (relative to moles of antibody) are added as a 6% (v/v) solution of DMSO. The mixture is stirred for 60 minutes at 5°C, then for 15 additional minutes following the addition of 1 molar equivalents of N-acetylcysteine relative to vcMMAE. Excess quenched vcMMAE and other reaction components are removed by ultrafiltration/diafiltration of the antibody drug conjugate (ADC) with 10 volumes of 20 mM histidine, pH 6.0.

[0322] The resulting antibody drug conjugate (ADC) is designated Ha22-2(2,4)6.1vcMMAE and has the following formula:



wherein MAb is Ha22-2(2,4)6.1 (Figure 2 and Figure 3) and p is from 1 to 8. The p value of the antibody drug conjugate set forth in this Example was about 3.8.

Example 5

Characterization of Ha22-2(2,4)6.1vcMMAE

[0323] Antibody Drug Conjugates that bind 191P4D12 were generated using the procedures set forth in the example entitled "Antibody Drug Conjugation of Ha22-2(2,4)6.1 MAb" and were screened, identified, and characterized using a combination of assays known in the art.

A. Affinity Determination by FACS

[0324] Ha22-2(2,4)6.1 vcMMAE was tested for its binding affinity to 191P4D12 expressed on the surface of PC3-human-191P4D12, PC3-Cynomolgus-191P4D12, and PC3-rat-191P4D12 cells respectively. Briefly, eleven (11) dilutions of Ha22-2(2,4)6.1vcMMAE were incubated with each of the cell types (50,000 cells per well) overnight at 4°C at a final concentration of 160 nM to 0.011 nM. At the end of the incubation, cells are washed and incubated with anti-hIgG-PE detection antibody for 45 min at 4°C. After washing the unbound detection antibodies, the cells are analyzed by FACS. Mean Fluorescence Intensity (MFI) values were obtained as listed in Figure(s) 6-8. MFI values were entered into Graphpad Prism software and analyzed using the one site binding (hyperbola) equation of $Y = B_{max} * X / (K_d + X)$ to generate Ha22-2(2,4)6.1vcMMAE saturation curves shown also in Figure(s) 6-8 respectively. B_{max} is the MFI value at maximal binding of Ha22-2(2,4)6.1vcMMAE to 191P4D12; K_d is the Ha22-2(2,4)6.1vcMMAE binding affinity which is the concentration of Ha22-2(2,4)6.1vcMMAE required to reach half-maximal binding.

[0325] The calculated affinity (K_d) of Ha22-2(2,4)6.1vcMMAE to 191P4D12 expressed on the surface of PC3-human-191P4D12, PC3-Cynomolgus-191P4D12, and PC3-rat-191P4D12 cells respectively is 0.69 nM (Figure 6), 0.34 nM (Figure 7), and 1.6 nM (Figure 8).

B. Affinity Determination by SPR

[0326] The affinity of Ha22-2(2,4)6.1 MAb and Ha22-2(2,4)6.1vcMMAE to purified recombinant 191P4D12 (ECD amino acids 1-348) was performed by Surface Plasmon Resonance (SPR) (Biacore). Briefly, goat-anti-human Fey polyclonal Abs (Jackson Immuno Research Labs, Inc.) were covalently immobilized on the surface of a CM5 sensor chip (Biacore). Purified Ha22-2(2,4)6.1 MAb or Ha22-2(2,4)6.1vcMMAE were then captured on the surface of said chip. On average, approximately 300 RUs of test Ha22-2(2,4)6.1 MAb or Ha22-2(2,4)6.1vcMMAE was captured in every cycle. Subsequently, a series of five (5) to six (6) dilutions of recombinant 191P4D12 (ECD amino acids 1-348) ranging from 1 nM to 100 nM was injected over such surface to generate binding curves (sensograms) that were processed and globally fit to a 1:1 interaction model using BIAevaluation 3.2 and CLAMP software (Myszka and Morton, 1998) (Figure 22). Table V summarizes association and dissociation rate constants as well as affinities of Ha22-2(2,4)6.1 MAb and Ha22-2(2,4)6.1vcMMAE to recombinant 191P4D12 (ECD amino acids 1-348).

C. Domain Mapping of Ha22-2(2,4)6.1 MAb

[0327] To map the binding site of Ha22-2(2,4)6.1 MAb to a specific domain of 191P4D12 protein, several Rat1(E) recombinant cell lines expressing such domains (or a combination thereof) were generated (Table VI). Binding of Ha22-2(2,4)6.1 to cell surface was assessed by FACS using standard protocols. As shown in Figure 10, Ha22-2(2,4)6.1 MAb binds to VC1 domain expressing cells as well as wild-type 191P4D12, but not to C1C2 domain expressing cells. Additionally, another 191P4D12 MAb entitled Ha22-8e6.1 recognizes C1C2 domain of 191P4D12 on cell surface, but not the VC1 domain. This suggests that the binding site for Ha22-2(2,4)6.1 MAb is located in the 1-147 aa domain of

191P4D12, but that not every MAb which binds to 191P4D12 recognizes this domain.

[0328] To further corroborate the results set forth in Figure 10, a Western Blot analysis was performed. Briefly, the entire extracellular portion of 191P4D12 (full length), as well as specific domains set forth in Table VI were expressed in 293T cells as murine Fc fusion proteins and purified. Goat anti-mouse-HRP were used as a control. As shown in Figure 11, when resolved on SDS-PAGE (non-reduced) and probed with Ha22-2(2,4)6.1-biotin followed by streptavidin-HRP, bands corresponding to full-length 191P4D12 (lane 1), V (lane 2) and VC1 (lane 3) fusion constructs, but not C1C2 fusion construct (lane 4) are recognized. This further suggests that the binding epitope for Ha22-2(2,4)6.1 MAb is located within 1-147 aa domain of 191P4D12.

Example 6

Cell Cytotoxicity Mediated by Ha22-2(2,4)6.1vcMMAE

[0329] The ability of Ha22-2(2,4)6.1vcMMAE to mediate 191P4D12-dependent cytotoxicity was evaluated in PC3 cells engineered to express human 191P4D12, Cynomolgus 191P4D12 and rat 191P4D12. Briefly, PC3-Neo, PC3-human-191P4D12 cells, PC3-Cynomolgus-191P4D12 or PC3-rat-191P4D12 cells (1500 cells/well) were seeded into a 96 well plate on day 1. The following day an equal volume of medium containing the indicated concentration of Ha22-2(2,4)6.1 vcMMAE or a Control MAb conjugated with vcMMAE (i.e. Control-vcMMAE) was added to each well. The cells were allowed to incubate for 4 days at 37 degrees C. At the end of the incubation period, Alamar Blue was added to each well and incubation continued for an additional 4 hours. The resulting fluorescence was detected using a Biotek plate reader with an excitation wavelength of 620 nM and an emission wavelength of 540 nM.

[0330] The results in Figure 9A-9D show that Ha22-2(2,4)6.1vcMMAE mediated cytotoxicity in PC3-human-191P4D12 (Figure 9A), PC3-Cynomolgus-191P4D12 (Figure 9B), and PC3-rat-191P4D12 cells (Figure 9C) while a control human IgG conjugated with vcMMAE had no effect. The specificity of Ha22-2(2,4)6.1 vcMMAE was further demonstrated by the lack of toxicity for PC3-Neo cells that do not express 191P4D12 (Figure 9D). Thus, these results indicate that Ha22-2(2,4)6.1 vcMMAE can selectively deliver a cytotoxic drug to 191P4D12 expressing cells leading to their killing.

Example 7

Ha22-2(2,4)6.1vcMMAE Inhibit Growth of Tumors *In Vivo*

[0331] The significant expression of 191P4D12 on the cell surface of tumor tissues, together with its restrictive expression in normal tissues makes 191P4D12 a good target for antibody therapy and similarly, therapy via ADC. Thus, the therapeutic efficacy of Ha22-2(2,4)6.1vcMMAE in human bladder, lung, breast, and pancreatic cancer xenograft mouse models is evaluated.

[0332] Antibody drug conjugate efficacy on tumor growth and metastasis formation is studied in mouse cancer xenograft models (e.g. subcutaneous and orthotopically).

[0333] Subcutaneous (s.c.) tumors are generated by injection of 5×10^4 - 10^6 cancer cells mixed at a 1:1 dilution with Matrigel (Collaborative Research) in the right flank of male SCID mice. To test ADC efficacy on tumor formation, ADC injections are started on the same day as tumor-cell injections. As a control, mice are injected with either purified human IgG or PBS; or a purified MAb that recognizes an irrelevant antigen not expressed in human cells. In preliminary studies, no difference is found between control IgG or PBS on tumor growth. Tumor sizes are determined by caliper measurements, and the tumor volume is calculated as $\text{width}^2 \times \text{Length}/2$, wherein width is the smallest dimension and length is the largest dimension. Mice with subcutaneous tumors greater than 1.5 cm in diameter are sacrificed.

[0334] Ovarian tumors often metastasize and grow within the peritoneal cavity. Accordingly, intraperitoneal growth of ovarian tumors in mice are performed by injection of 2 million cells directly into the peritoneum of female mice. Mice are monitored for general health, physical activity, and appearance until they become moribund. At the time of sacrifice, the peritoneal cavity can be examined to determine tumor burden and lungs harvested to evaluate metastasis to distant sites. Alternatively, death can be used as an endpoint. The mice are then segregated into groups for the appropriate treatments, with 191P4D12 or control MAbs being injected i.p.

[0335] An advantage of xenograft cancer models is the ability to study neovascularization and angiogenesis. Tumor growth is partly dependent on new blood vessel development. Although the capillary system and developing blood network is of host origin, the initiation and architecture of the neovasculature is regulated by the xenograft tumor (Davidoff et al., Clin Cancer Res. (2001) 7:2870; Solesvik et al., Eur J Cancer Clin Oncol. (1984) 20:1295). The effect of antibody and small molecule on neovascularization is studied in accordance with procedures known in the art, such as by IHC analysis of tumor tissues and their surrounding microenvironment.

[0336] Ha22-2(2,4)6.1ADC inhibits formation lung, bladder, breast, and pancreatic cancer xenografts. These results indicate the utility of Ha22-2(2,4)6.1ADC in the treatment of local and advanced stages of cancer and preferably those

cancers set forth in Table I.

191P4D12 ADCs:

[0337] Monoclonal antibodies were raised against 191P4D12 as described in the Example entitled "Generation of 191P4D12 Monoclonal Antibodies (MAbs)." Further the MAbs are conjugated to a toxin as described in the Example entitled "Antibody Drug Conjugation of Ha22-2(2,4)6.1 MAb" to form Ha22-2(2,4)6.1vcMMAE. The Ha22-2(2,4)6.1vcMMAE is characterized by FACS, and other methods known in the art to determine its capacity to bind 191P4D12.

Cell Lines and Xenografts:

[0338] The BT-483 and HPAC cells are maintained in DMEM, supplemented with L-glutamine and 10% FBS, as known in the art. AG-B8, AG-Panc4, AG-Panc2, AG-B1, AG-L4, and AG-Panc3 xenografts are maintained by serial propagation in SCID mice.

Evaluation of Ha22-2(2,4)6.1vcMMAE MAb in the subcutaneous tumor formation model of human lung cancer xenograft AG-L4 in SCID mice

[0339] In this experiment, patient-derived lung cancer xenograft AG-L4 was maintained by serial passages in SCID mice. Stock tumors were harvested sterilely and enzymatically digested into single cell suspensions. Two (2) million cells were implanted into the flank of individual SCID mice. Animals were then randomly assigned to seven groups: six (6) 191P4D12 antibody treated groups and a control antibody H3-1.10.1.2 group (n=10). All antibodies were dosed intraperitoneally at 750 μ g/animal twice a week until the end of the study. Tumor growth was monitored using caliper measurements every 3 to 4 days. Tumor volume was calculated as $\text{Width}^2 \times \text{Length}/2$, where width is the smallest dimension and length is the largest dimension.

[0340] The results show that the 191P4D12 MAb did not significantly inhibit tumor growth in human lung cancer xenograft AG-L4 in SCID mice. Additionally, other 191P4D12 MAbs were utilized in this study. The results are not shown. (Figure 12).

Evaluation of Ha22-2(2,4)6.1 MAb in the subcutaneous tumor formation model of human pancreatic cancer xenograft HPAC in SCID mice

[0341] In another experiment, human pancreatic cancer HPAC cells (2.0 millions/mouse) were injected into the flank of individual SCID mice. Animals were then randomly assigned to eight groups: seven (7) 191P4D12 antibody treated groups and a control antibody H3-1.4.1.2 group (n=10). All antibodies were dosed intraperitoneally at 500 μ g/animal twice a week until the end of the study. Tumor growth was monitored using caliper measurements every 3 to 4 days. Tumor volume was calculated as $\text{Width}^2 \times \text{Length}/2$, where width is the smallest dimension and length is the largest dimension.

[0342] The results show that the 191P4D12 MAb did not inhibit tumor growth in a human pancreatic xenograft in SCID mice when compared to the control antibody. Additionally, other 191P4D12 MAbs were utilized in this study. The results are not shown. (Figure 13).

[0343] Evaluation of Ha22-2(2,4)6.1 MAb in the subcutaneous tumor formation model of human pancreatic cancer xenograft AG-Panc3 in SCID mice.

[0344] In another experiment, patient-derived pancreatic cancer xenograft AG-Panc3 was maintained by serial passages in SCID mice. Stock tumors were harvested sterilely and minced into 1 mm³ pieces. Six pieces were implanted into the flank of individual SCID mice. Animals were then randomly assigned to the following cohorts (n=10): two (2) 191P4D12 MAb treated groups and a control antibody H3-1.4.1.2 group. All antibodies were dosed intraperitoneally at 500 μ g/animal twice a week until the end of the study. Tumor growth was monitored using caliper measurements every 3 to 4 days. Tumor volume was calculated as $\text{Width}^2 \times \text{Length}/2$, where width is the smallest dimension and length is the largest dimension.

[0345] The results show that the 191P4D12 MAb did not inhibit tumor growth in a human pancreatic xenograft in SCID mice when compared to the control antibody. Additionally, other 191P4D12 MAbs were utilized in this study. The results are not shown. (Figure 14).

Efficacy of Ha22-2(2,4)6.1-vcMMAE in subcutaneous established human lung cancer xenograft AG-L4 in SCID mice

[0346] In another experiment, patient-derived lung cancer xenograft AG-L13 was maintained by serial passages in

SCID mice. Stock tumors were harvested sterilely and minced into 1 mm³ pieces. Six (6) pieces were implanted into the flank of individual SCID mice. Tumors were allowed to grow untreated until they reached an approximate volume of 200 mm³. The Ha22-2(2,4)6.1vcMMAE and the control ADC were dosed at 10 mg/kg every seven (7) days for two doses by intravenous bolus injection. The amount of ADC administered was based on the individual body weight of each animal obtained immediately prior to dosing. Tumor growth was monitored using caliper measurements every 3 to 4 days. Tumor volume was calculated as $\text{Width}^2 \times \text{Length}/2$, where width is the smallest dimension and length is the largest dimension.

[0347] The results show that treatment with Ha22-2(2,4)6.1-vcMMAE significantly inhibited the growth of AG-L4 lung cancer xenografts implanted subcutaneously in nude mice compared to the control ADC. Additionally, other 191P4D12 MAbs were utilized in this study. The results are not shown. (Figure 15).

Efficacy of Ha22-2(2,4)6.1-vcMMAE in subcutaneous established human breast cancer xenograft BT-483 in SCID mice

[0348] In this experiment, human breast cancer BT-483 cells were used to generate stock xenografts, which were maintained by serial passages in SCID mice. Stock tumors were harvested sterilely and minced into 1 mm³ pieces. Six (6) pieces were implanted into the flank of individual SCID mice. Tumors were allowed to grow untreated until they reached an approximate volume of 100 mm³. The Ha22-2(2,4)6.1vcMMAE and the control ADC were dosed at 5 mg/kg every four (4) days for four (4) doses by intravenous bolus injection. The amount of ADC administered was based on the individual body weight of each animal obtained immediately prior to dosing. Tumor growth was monitored using caliper measurements every 3 to 4 days. Tumor volume was calculated as $\text{Width}^2 \times \text{Length}/2$, where width is the smallest dimension and length is the largest dimension.

[0349] The results show that treatment with Ha22-2(2,4)6.1-vcMMAE significantly inhibited the growth of BT-483 breast tumor xenografts implanted subcutaneously in SCID mice compared to the control ADC. Additionally, other 191P4D12 MAbs were utilized in this study. The results are not shown. (Figure 16).

Efficacy of Ha22-2(2,4)6.1-vcMMAE in subcutaneous established human bladder cancer xenograft AG-B1 in SCID mice

[0350] In another experiment, patient-derived bladder cancer xenograft AG-B1 was maintained by serial passages in SCID mice. Stock tumors were harvested sterilely and minced into 1 mm³ pieces. Six (6) pieces were implanted into the flank of individual SCID mice. Tumors were allowed to grow untreated until they reached an approximate volume of 230 mm³. The Ha22-2(2,4)6.1vcMMAE and the control ADC were dosed at 4 mg/kg once by intravenous bolus injection. The amount of ADC administered was based on the individual body weight of each animal obtained immediately prior to dosing. Tumor growth was monitored using caliper measurements every 3 to 4 days. Tumor volume was calculated as $\text{Width}^2 \times \text{Length}/2$, where width is the smallest dimension and length is the largest dimension.

[0351] The results show that treatment with Ha22-2(2,4)6.1-vcMMAE significantly inhibited the growth of AG-B1 bladder cancer xenografts as compared to the control ADC. Additionally, other 191P4D12 MAbs were utilized in this study. The results are not shown. (Figure 17).

Efficacy of Ha22-2(2,4)6.1-vcMMAE in subcutaneous established human pancreatic cancer xenograft AG-Panc2 in SCID mice

[0352] In another experiment, patient-derived pancreatic cancer xenograft AG-Panc2 was maintained by serial passages in SCID mice. Stock tumors were harvested sterilely and minced into 1 mm³ pieces. Five (5) pieces were implanted into the flank of individual SCID mice. Tumors were allowed to grow untreated until they reached an approximate volume of 100 mm³. The Ha22-2(2,4)6.1vcMMAE and control ADC were dosed at 5 mg/kg every four (4) days for four (4) doses by intravenous bolus injection. The amount of ADC administered was based on the individual body weight of each animal obtained immediately prior to dosing. Tumor growth was monitored using caliper measurements every 3 to 4 days. Tumor volume was calculated as $\text{Width}^2 \times \text{Length}/2$, where width is the smallest dimension and length is the largest dimension.

[0353] The results show that treatment with Ha22-2(2,4)6.1-vcMMAE significantly inhibited the growth of AG-Panc2 pancreatic cancer xenografts as compared to the control ADC. Additionally, other 191P4D12 MAbs were utilized in this study. The results are not shown. (Figure 18).

Efficacy of Ha22-2(2,4)6.1-vcMMAE in subcutaneous established human pancreatic cancer xenograft AG-Panc4 in SCID mice

[0354] In another experiment, patient-derived pancreatic cancer xenograft AG-Panc4 was maintained by serial passages in SCID mice. Stock tumors were harvested sterilely and minced into 1 mm³ pieces. Six (6) pieces were implanted

into the flank of individual SCID mice. The Ha22-2(2,4)6.1 vcMMAE and control ADC were dosed at 5 mg/kg every seven (7) days for three doses by intravenous bolus injection. The amount of ADC administered was based on the individual body weight of each animal obtained immediately prior to dosing. Tumor growth was monitored using caliper measurements every 3 to 4 days. Tumor volume was calculated as $\text{Width}^2 \times \text{Length}/2$, where width is the smallest dimension and length is the largest dimension.

[0355] The results show that treatment with Ha22-2(2,4)6.1-vcMMAE significantly inhibited the growth of AG-Panc4 pancreatic cancer xenografts as compared to the control ADC. Additionally, other 191P4D12 MABs were utilized in this study. The results are not shown. (Figure 19).

Efficacy of Ha22-2(2,4)6.1-vcMMAE at comparative dosage in subcutaneous established human bladder cancer xenograft AG-B8 in SCID mice

[0356] In this experiment, patient-derived bladder cancer xenograft AG-B8 was maintained by serial passages in SCID mice. Stock tumors were harvested sterilely and minced into 1 mm³ pieces. Six (6) pieces were implanted into the flank of individual SCID mice. Tumors were allowed to grow untreated until they reached an approximate volume of 200 mm³. Animals were then randomly assigned to the following three cohorts (n=6): two (2) Ha22-2(2,4)6.1-vcMMAE treated groups and a control ADC VCD37-5ce5p-vcMMAE group. Ha22-2(2,4)6.1-vcMMAE was dosed at 5 mg/kg or 10 mg/kg and the control ADC was given at 5 mg/kg. All ADCs were dosed once by intravenous bolus injection. The amount of ADC administered was based on the individual body weight of each animal obtained immediately prior to dosing. Tumor growth was monitored using caliper measurements every 3 to 4 days. Tumor volume was calculated as $\text{Width}^2 \times \text{Length}/2$, where width is the smallest dimension and length is the largest dimension.

[0357] The results show that treatment with Ha22-2(2,4)6.1 vcMMAE at 10mg/kg inhibited the growth of AG-B8 bladder cancer xenografts as compared to the Ha22-2(2,4)6.1 vcMMAE at 5mg/kg. (Figure 20).

Conclusion

[0358] In summary, Figures 12-20, show that the 191P4D12 ADC entitled Ha22-2(2,4)6. 1vcMMAE significantly inhibited the growth of tumors cells that express 191P4D12 when compared to control ADCs. Thus, the Ha22-2(2,4)6.1 vcMMAE can be used for therapeutic purposes to treat and manage cancers set forth in Table I.

Example 8

Human Clinical Trials for the Treatment and Diagnosis of Human Carcinomas through use of 191P4D12 ADCs

[0359] 191P4D12 ADCs are used in accordance with the present invention which specifically bind to 191P4D12, and are used in the treatment of certain tumors, preferably those listed in Table I. In connection with each of these indications, two clinical approaches are successfully pursued.

[0360] I.) Adjunctive therapy: In adjunctive therapy, patients are treated with 191P4D12 ADCs in combination with a chemotherapeutic or anti-neoplastic agent and/or radiation therapy or a combination thereof. Primary cancer targets, such as those listed in Table I, are treated under standard protocols by the addition of 191P4D12 ADCs to standard first and second line therapy. Protocol designs address effectiveness as assessed by the following examples, including but not limited to, reduction in tumor mass of primary or metastatic lesions, increased progression free survival, overall survival, improvement of patients health, disease stabilization, as well as the ability to reduce usual doses of standard chemotherapy and other biologic agents. These dosage reductions allow additional and/or prolonged therapy by reducing dose-related toxicity of the chemotherapeutic or biologic agent. 191P4D12 ADCs are utilized in several adjunctive clinical trials in combination with the chemotherapeutic or anti-neoplastic agents.

[0361] II.) Monotherapy: In connection with the use of the 191P4D12 ADCs in monotherapy of tumors, the 191P4D12 ADCs are administered to patients without a chemotherapeutic or anti-neoplastic agent. In one embodiment, monotherapy is conducted clinically in end-stage cancer patients with extensive metastatic disease. Protocol designs address effectiveness as assessed by the following examples, including but not limited to, reduction in tumor mass of primary or metastatic lesions, increased progression free survival, overall survival, improvement of patients health, disease stabilization, as well as the ability to reduce usual doses of standard chemotherapy and other biologic agents.

Dosage

[0362] Dosage regimens may be adjusted to provide the optimum desired response. For example, a single bolus may be administered, several divided doses may be administered over time or the dose may be proportionally reduced or increased as indicated by the exigencies of the therapeutic situation. It is especially advantageous to formulate parenteral

compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the mammalian subjects to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on (a) the unique characteristics of the antibody and/or ADC and the particular therapeutic or prophylactic effect to be achieved, and (b) the limitations inherent in the art of compounding such an active compound for the treatment of sensitivity in individuals.

[0363] An exemplary, non limiting range for a therapeutically effective amount of an 191P4D12 ADC administered in combination according to the invention is about 0.5 to about 10 mg/kg, about 1 to about 5 mg/kg, at least 1 mg/kg, at least 2 mg/kg, at least 3 mg/kg, or at least 4 mg/kg. Other exemplary non-limiting ranges are for example about 0.5 to about 5 mg/kg, or for example about 0.8 to about 5 mg/kg, or for example about 1 to about 7.5mg/kg. The high dose embodiment of the invention relates to a dosage of more than 10 mg/kg. It is to be noted that dosage values may vary with the type and severity of the condition to be alleviated, and may include single or multiple doses. It is to be further understood that for any particular subject, specific dosage regimens should be adjusted over time according to the individual need and the professional judgment of the person administering or supervising the administration of the compositions, and that dosage ranges set forth herein are exemplary only and are not intended to limit the scope or practice of the claimed composition.

Clinical Development Plan (CDP)

[0364] The CDP follows and develops treatments of 191 P4D12 ADCs in connection with adjunctive therapy or monotherapy. Trials initially demonstrate safety and thereafter confirm efficacy in repeat doses. Trials are open label comparing standard chemotherapy with standard therapy plus 191P4D12 ADCs. As will be appreciated, one non-limiting criteria that can be utilized in connection with enrollment of patients is 191P4D12 expression levels in their tumors as determined by biopsy.

[0365] As with any protein or antibody infusion-based therapeutic, safety concerns are related primarily to (i) cytokine release syndrome, *i.e.*, hypotension, fever, shaking, chills; (ii) the development of an immunogenic response to the material (*i.e.*, development of human antibodies by the patient to the antibody therapeutic, or HAMA response); and, (iii) toxicity to normal cells that express 191P4D12. Standard tests and follow-up are utilized to monitor each of these safety concerns. 191P4D12 ADCs are found to be safe upon human administration.

Example 9

Detection of 191P4D12 protein in cancer patient specimens by IHC

[0366] Expression of 191P4D12 protein by immunohistochemistry was tested in patient tumor specimens from (i) bladder, (ii) breast, (iii) pancreatic, (iv) lung, (v) ovarian cancer, (vi) esophageal, and (vii) head and neck patients. Briefly, formalin fixed, paraffin wax-embedded tissues were cut into four (4) micron sections and mounted on glass slides. The sections were de-waxed, rehydrated and treated with EDTA antigen retrieval solution (Biogenex, San Ramon, CA) in the EZ-Retriever microwave (Biogenex, San Ramon, CA) for 30 minutes at 95°C. Sections were then treated with 3% hydrogen peroxide solution to inactivate endogenous peroxidase activity. Serum-free protein block (Dako, Carpinteria, CA) was used to inhibit non-specific binding prior to incubation with monoclonal mouse anti-191P4D12 antibody or an isotype control. Subsequently, the sections were treated with the Super Sensitive™ Polymer-horseradish peroxidase (HRP) Detection System which consists of an incubation in Super Enhancer™ reagent followed by an incubation with polymer-HRP secondary antibody conjugate (BioGenex, San Ramon, CA). The sections were then developed using the DAB kit (BioGenex, San Ramon, CA). Nuclei were stained using hematoxylin, and analyzed by bright field microscopy. Specific staining was detected in patient specimens using the 191P4D12 immunoreactive antibody, as indicated by the brown staining. (See, Figure 21(A), 21(C), 21(E), 21(G), 21(I), 21(K), and 21(M)). In contrast, the control antibody did not stain either patient specimen. (See, Figure 21(B), 21(D), 21(F), 21(H), 21(J), 21(L), and 21(N)).

[0367] The results show expression of 191P4D12 in the tumor cells of patient bladder, breast, pancreatic, lung, ovarian, esophageal, and head and neck cancer tissues. These results indicate that 191P4D12 is expressed in human cancers and that antibodies directed to this antigen and the antibody drug conjugate designated Ha22-2(2,4)6.1vcMMAE are useful for diagnostic and therapeutic purposes. (Figure 21).

Example 10

Determining the Binding Epitope of Ha22-2(2,4)6.1 MAb

[0368] The 191P4D12 protein of human, cynomolgus, rat and murine origin was overexpressed recombinantly in a PC3 cell line to determine cross-reactivity of Ha22-2(2,4)6.1 to these orthologs. It was shown that Ha22-2(2,4)6.1 strongly cross-reacts with cynomolgus and rat orthologs of 191P4D12 (Figure 23). EC50 binding values are shown in Table VII. Binding of Ha22-2(2,4)6.1 to murine ortholog shows a significant reduction in binding EC50 value, which shows important amino acid substitutions in the V domain (as compared to human and rat sequences) affected affinity of Ha22-2(2,4)6.1 to 191P4D12.

[0369] Table VIII shows aa 1-180 protein sequence alignment of 191P4D12 orthologs containing the V-domain. Only two amino acids in the rat ortholog sequence, Thr-75 and Ser-90, are substituted in the murine ortholog sequence for Ile and Asn respectively (marked in bold text). It should be noted that the corresponding amino acids in the human sequence are Ala-76 and Ser-91. To determine if these amino acids comprise the binding epitope of Ha22-2(2,4)6.1, several mutant constructs of 191P4D12 and its murine ortholog were generated and expressed in PC3 cells (Table IX). "Murine" amino acids were introduced instead of a standard alanine substitution mutagenesis into human sequence and vice versa in the mouse sequence.

[0370] It was shown that mutation of Ser-91 to Asn in the 191P4D12 severely impairs the binding of Ha22-2(2,4)6.1 confirming that this amino acid, Ser-91, is essential for binding and must comprise the epitope recognized by the Ha22-2(2,4)6.1 MAb. Additional mutation of Ala in position 76 (A76I, S91N double mutant) was also introduced into 191P4D12. It was shown that binding of Ha22-2(2,4)6.1 to the double mutant A76I, S91N is very similar to murine ortholog binding (Figure 24). Conversely, mutation of Asn-90 in the murine sequence to Ser dramatically improves binding of Ha22-2(2,4)6.1 to the murine mutant ortholog further confirming the importance of the amino acid in this position for binding of Ha22-2(2,4)6.1. Binding of Ha22-2(2,4)6.1 to the murine ortholog double mutant A90S, I75A appears very similar to human ortholog of 191P4D12.

[0371] Taken together, these data prove that Ser-91 and Ala-76 play a crucial role in binding of Ha22-2(2,4)6.1 to 191P4D12 protein on cell surface and constitute part of the epitope recognized by Ha22-2(2,4)6.1 on the surface of 191P4D12.

[0372] To visualize this concept, we generated a computer model of the V-domain of 191P4D12 based on published crystal structure data for family members of 191P4D12 and Ig-domain containing proteins using PyMOL (Figure 25). The positions of Ala-76 (stippled) and Ser-91 (crosshatched) are shown.

[0373] Additionally, to further refine the binding site of Ha22-2(2,4)6.1 on 191P4D12 molecule, we designed and expressed a fragment of 191P4D12 corresponding to the V-domain on the surface of Rat(1)E cells. The following construct was generated in retroviral vector:

191P4D12 (aa1-150,347-510)

[0374] Binding of Ha22-2(2,4)6.1 MAb was assessed by FACS. As shown in Figure 26, Ha22-2(2,4)6.1 binds to V-domain expressing cells (A) as well as wild-type 191P4D12 (B), but not to C1C2 domain expressing cells generated earlier (C). This proves the binding site for this antibody is located in the V-domain of 191P4D12 within first 150 amino acids.

[0375] The results show that the Ha22-2(2,4)6.1 MAb binds to the v-domain of the 191P4D12 protein from position aa 1-150 and additionally shows that the specific epitope comprising aa Ser-91 and aa Ala-76 are critical for binding the Ha22-2(2,4)6.1 MAb.

[0376] Throughout this application, various website data content, publications, patent applications and patents are referenced. (Websites are referenced by their Uniform Resource Locator, or URL, addresses on the World Wide Web.) The disclosures of each of these references are hereby incorporated by reference herein in their entireties.

[0377] The present invention is not to be limited in scope by the embodiments disclosed herein, which are intended as single illustrations of individual aspects of the invention, and any that are functionally equivalent are within the scope of the invention. Various modifications to the models and methods of the invention, in addition to those described herein, will become apparent to those skilled in the art from the foregoing description and teachings, and are similarly intended to fall within the scope of the invention. Such modifications or other embodiments can be practiced without departing from the true scope and spirit of the invention.

TABLES

[0378]

TABLE I: Tissues that express 191P4D12 when malignant.

Colon
 Pancreas
 Ovarian
 Breast
 Lung
 Bladder

TABLE II: Amino Acid Abbreviations

SINGLE LETTER	THREE LETTER	FULL NAME
F	Phe	phenylalanine
L	Leu	leucine
s	Ser	serine
Y	Tyr	tyrosine
C	Cys	cysteine
W	Trp	tryptophan
P	Pro	proline
H	His	histidine
Q	Gln	glutamine
R	Arg	arginine
I	Ile	isoleucine
M	Met	methionine
T	Thr	threonine
N	Asn	asparagine
K	Lys	lysine
V	Val	valine
A	Ala	alanine
D	Asp	aspartic acid
E	Glu	glutamic acid
G	Gly	glycine

TABLE III: Amino Acid Substitution Matrix

Adapted from the GCG Software 9.0 BLOSUM62 amino acid substitution matrix (block substitution matrix). The higher the value, the more likely a substitution is found in related, natural proteins.

	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y	.	
10	4	0	-2	-1	-2	0	-2	-1	-1	-1	-1	-2	-1	-1	-1	1	0	0	-3	-2	A	
		9	-3	-4	-2	-3	-3	-1	-3	-1	-1	-3	-3	-3	-3	-1	-1	-1	-2	-2	C	
			6	2	-3	-1	-1	-3	-1	-4	-3	1	-1	0	-2	0	-1	-3	-4	-3	D	
				5	-3	-2	0	-3	1	-3	-2	0	-1	2	0	0	-1	-2	-3	-2	E	
15				6	-3	-1	0	-3	0	0	-3	-4	-3	-3	-2	-2	-1	1	3	F		
					6	-2	-4	-2	-4	-3	0	-2	-2	-2	0	-2	-3	-2	-3	G		
						8	-3	-1	-3	-2	1	-2	0	0	-1	-2	-3	-2	2	H		
							4	-3	2	1	-3	-3	-3	-3	-2	-1	3	-3	-1	I		
20									5	-2	-1	0	-1	1	2	0	-1	-2	-3	-2	K	
										4	2	-3	-3	-2	-2	-2	-1	1	-2	-1	L	
											5	-2	-2	0	-1	-1	-1	1	-1	-1	M	
												6	-2	0	0	1	0	-3	-4	-2	N	
25														7	-1	-2	-1	-1	-2	-4	-3	P
															5	1	0	-1	-2	-2	-1	Q
																5	-1	-1	-3	-3	-2	R
																	4	1	-2	-3	-2	S
30																		5	0	-2	-2	T
																			4	-3	-1	V
																				11	2	W
																					7	Y

TABLE IV: General Method for Synthesis of vcMMAE

Where:

AA1 = Amino Acid 1
 AA2 = Amino Acid 2
 AA5 = Amino Acid 5
 DIL = Dolaisoleuine
 DAP = Dolaproine
 Linker = Val-Cit (vc)

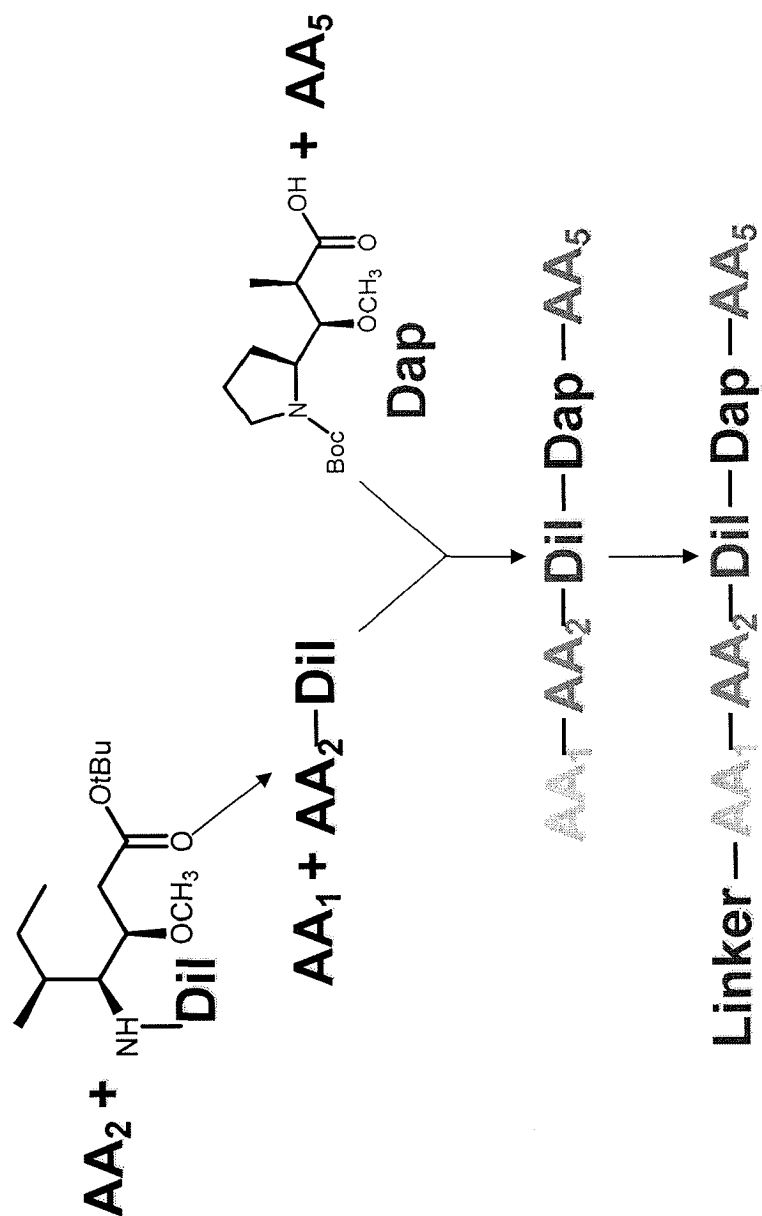


TABLE V: Biacore association and dissociation rates and resulting affinity calculation

	kon, M-1s-1	koff, s-1	KD, M
Ha22-2(2,4)6.1	3.8E+05	5.8E-03	1.6E-08
Ha22-2(2,4)6.1 vcMMAE	4.5E+05	5.2E-03	1.1 E-08

TABLE VI: 191P4D12 constructs used in domain mapping assay

Constructs	Name
191P4D12 (aa 1-242, 347-510)	VC1, Rat1(E) expressing line
191P4D12 (aa 1-31, 147-510)	C1C2, Rat 1(E) expressing line
191P4D12 (aa 1-242)	mFc-VC1, fusion protein
191P4D12 (aa 1-31, 147-346)	mFc-C1C2, fusion protein
191P4D12 (aa 1-141)	mFc-V, fusion protein

TABLE VII

	PC3-191P4D12	Cyno ortholog	Rat ortholog	Murine ortholog
Bmax (MFI)	816	1146	679	325
EC₅₀ (nM)	0.28	0.30	0.44	70.3

TABLE VIII (SEQ ID NOS:11-13, in order of appearance)

mouse	MPLSLGAEMWGPEAWLR-LLFLASFTGQYSAGELETSDVVTVLGQDAKLPCFYRGDPDE	59
rat	MPLSLGAEMWGPEAWLL-LLFLASFTGRYSAGELETSDLVTWLGQDAKLPCFYRGDPDE	59
human	MPLSLGAEMWGPEAWLLLLLLLASFTGRCPAGELETSDWTWLGQDAKLPCFYRGDSGE	60
***** ** .*****. *****.*****.***** *		
mouse	QVGQVAWARVDPNEGIRELALLHSKYGLHVNPAVEDRVEQPPPPRDPLDGSVLLRNAVQA	119
rat	QVGQVAWARVDPNEGIRELALLHSKYGLHVSPAYEDRVEQPPPPRDPLDGSILLRNAVQA	119
human	QVGQVAWARVDAGEGAQELALLHSKYGLHVSPAYEGRVEQPPPPRNPLDGSVLLRNAVQA	120
***** .*.*****.*** *****.*****.*****		
mouse	DEGEYECRVSTFPAGSFQARMRLRVLPPLPSLNPGPPLLEEGQGLTLAASCTAEGSPAPS	179
rat	DEGEYECRVSTFPAGSFQARMRLRVLPPLPSLNPGPPLLEEGQGLTLAASCTAEGSPAPS	179
human	DEGEYECRVSTFPAGSFQARLRLRVLPPLPSLNPGPALEEGQGLTLAASCTAEGSPAPS	180
***** .*****.***** *****.*****.*****		

TABLE IX

Wild type constructs	Mutant constructs	Double-mutant constructs
191P4D12, wild type	S91N	S91N, A76I
Murine ortholog of 191P4D12, wild type	N90S	N90S, I75A

SEQUENCE LISTING

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SEATTLE GENETICS, INC.

<120> ANTIBODY DRUG CONJUGATES (ADC) THAT BIND
TO 191P4D12 PROTEINS

<130> 104909PCEPT1

<140> Divisional Application based on EP 11831345.1

<141> 2011-09-29

<150> US 61/387,933

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cagttcctta ttcaagtctg cagccggctc ccaggagat ctgggtggaa cttcagaaac 240
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Met Pro Leu Ser Leu Gly Ala Glu Met Trp
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75 80 85 90

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	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu					
				205					210					215							
50	gtc	acc	cat	cag	ggc	ctg	agc	tcg	ccc	gtc	aca	aag	agc	ttc	aac	agg					723
	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg					
			220					225					230								
55	gga	gag	tgt	tag																	735
	Gly	Glu	Cys	*																	
		235																			

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 <223> Ha22-2(2,4)6.1 light chain

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 20 25 30
 Val Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
 35 40 45
 Gln Gly Ile Ser Gly Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
 50 55 60
 Ala Pro Lys Phe Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val
 65 70 75 80
 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 85 90 95
 Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
 100 105 110
 Ala Asn Ser Phe Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
 115 120 125
 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
 130 135 140
 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
 145 150 155 160
 Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
 165 170 175
 Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
 180 185 190
 Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
 195 200 205
 Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
 210 215 220
 Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235

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 1 5 10 15
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 20 25 30
 Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
 35 40 45
 Ser Ser Tyr Asn Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 50 55 60
 Glu Trp Val Ser Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala

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	65				70				75				80
	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn
					85					90			Lys
5	Ser	Leu	Ser	Leu	Gln	Met	Asn	Ser	Leu	Arg	Asp	Glu	Asp
				100					105				110
	Tyr	Tyr	Cys	Ala	Arg	Ala	Tyr	Tyr	Tyr	Gly	Met	Asp	Val
			115					120				125	Trp
	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly
			130				135					140	Pro
10	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly
	145					150					155		Thr
	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val
				165						170			Thr
	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe
			180						185				Pro
15	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val
			195					200					Thr
	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val
			210				215					220	Asn
	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys
20	225				230						235		Ser
	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu
				245						250			Leu
	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr
			260						265				Leu
25	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val
			275					280					Ser
	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val
			290				295					300	Glu
	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser
	305				310						315		Thr
30	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu
				325						330			Asn
	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala
			340						345				Pro
	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro
			355					360					Gln
35	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln
			370				375					380	Val
	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala
	385				390						395		Val
	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr
				405						410			Pro
40	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu
				420					425				Thr
	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser
			435					440					Val
	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser
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	Gly	Lys											
	465												

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 <223> Ha22-2(2,4)6.1 light chain

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 20 25 30
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 35 40 45
 Gln Gly Ile Ser Gly Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
 50 55 60
 Ala Pro Lys Phe Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val
 65 70 75 80
 Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 85 90 95
 Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
 100 105 110
 Ala Asn Ser Phe Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
 115 120 125
 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
 130 135 140
 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
 145 150 155 160
 Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
 165 170 175
 Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
 180 185 190
 Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
 195 200 205
 Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
 210 215 220
 Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235

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 20 25 30
 Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Tyr Ile Ser Ser Ser Ser Ser Thr Ile Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg

 <210> 10
 <211> 96
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<213> Homo sapiens

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<222> (1)...(96)

<223> Human Ig germline L5

<400> 10

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          20           25           30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35           40           45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
          50           55           60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65           70           75           80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Pro
          85           90           95

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<210> 11

<211> 179

<212> PRT

<213> Mus musculus

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<221> misc_feature

<222> (1)...(179)

<223> 191P4D12 ortholog containing the V-domain

<400> 11

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Met Pro Leu Ser Leu Gly Ala Glu Met Trp Gly Pro Glu Ala Trp Leu
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          20           25           30
Leu Glu Thr Ser Asp Val Val Thr Val Val Leu Gly Gln Asp Ala Lys
          35           40           45
Leu Pro Cys Phe Tyr Arg Gly Asp Pro Asp Glu Gln Val Gly Gln Val
          50           55           60
Ala Trp Ala Arg Val Asp Pro Asn Glu Gly Ile Arg Glu Leu Ala Leu
65           70           75           80
Leu His Ser Lys Tyr Gly Leu His Val Asn Pro Ala Tyr Glu Asp Arg
          85           90           95
Val Glu Gln Pro Pro Pro Pro Arg Asp Pro Leu Asp Gly Ser Val Leu
          100          105          110
Leu Arg Asn Ala Val Gln Ala Asp Glu Gly Glu Tyr Glu Cys Arg Val
          115          120          125
Ser Thr Phe Pro Ala Gly Ser Phe Gln Ala Arg Met Arg Leu Arg Val
45           130          135          140
Leu Val Pro Pro Leu Pro Ser Leu Asn Pro Gly Pro Pro Leu Glu Glu
145           150          155          160
Gly Gln Gly Leu Thr Leu Ala Ala Ser Cys Thr Ala Glu Gly Ser Pro
          165          170          175
Ala Pro Ser

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<210> 12

<211> 179

<212> PRT

<213> Rattus norvegicus

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 <222> (1)...(179)
 <223> 191P4D12 ortholog containing the V-domain

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<400> 12

10

15

20

25

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Met Pro Leu Ser Leu Gly Ala Glu Met Trp Gly Pro Glu Ala Trp Leu
 1           5           10           15
Leu Leu Leu Phe Leu Ala Ser Phe Thr Gly Arg Tyr Ser Ala Gly Glu
           20           25           30
Leu Glu Thr Ser Asp Leu Val Thr Val Val Leu Gly Gln Asp Ala Lys
           35           40           45
Leu Pro Cys Phe Tyr Arg Gly Asp Pro Asp Glu Gln Val Gly Gln Val
 50           55           60
Ala Trp Ala Arg Val Asp Pro Asn Glu Gly Thr Arg Glu Leu Ala Leu
65           70           75           80
Leu His Ser Lys Tyr Gly Leu His Val Ser Pro Ala Tyr Glu Asp Arg
           85           90           95
Val Glu Gln Pro Pro Pro Pro Arg Asp Pro Leu Asp Gly Ser Ile Leu
           100          105          110
Leu Arg Asn Ala Val Gln Ala Asp Glu Gly Glu Tyr Glu Cys Arg Val
           115          120          125
Ser Thr Phe Pro Ala Gly Ser Phe Gln Ala Arg Met Arg Leu Arg Val
130          135          140
Leu Val Pro Pro Leu Pro Ser Leu Asn Pro Gly Pro Pro Leu Glu Glu
145          150          155          160
Gly Gln Gly Leu Thr Leu Ala Ala Ser Cys Thr Ala Glu Gly Ser Pro
           165          170          175
Ala Pro Ser

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<220>
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 <222> (1)...(180)
 <223> 191P4D12 ortholog containing the V-domain

40

45

50

55

<400> 13

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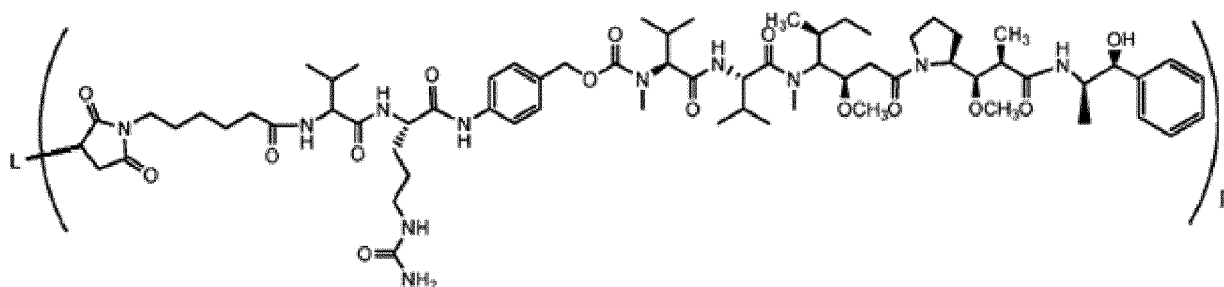
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 1           5           10           15
Leu Leu Leu Leu Leu Leu Ala Ser Phe Thr Gly Arg Cys Pro Ala Gly
           20           25           30
Glu Leu Glu Thr Ser Asp Val Val Thr Val Val Leu Gly Gln Asp Ala
           35           40           45
Lys Leu Pro Cys Phe Tyr Arg Gly Asp Ser Gly Glu Gln Val Gly Gln
 50           55           60
Val Ala Trp Ala Arg Val Asp Ala Gly Glu Gly Ala Gln Glu Leu Ala
65           70           75           80
Leu Leu His Ser Lys Tyr Gly Leu His Val Ser Pro Ala Tyr Glu Gly
           85           90           95
Arg Val Glu Gln Pro Pro Pro Pro Arg Asn Pro Leu Asp Gly Ser Val
           100          105          110
Leu Leu Arg Asn Ala Val Gln Ala Asp Glu Gly Glu Tyr Glu Cys Arg
           115          120          125
Val Ser Thr Phe Pro Ala Gly Ser Phe Gln Ala Arg Leu Arg Leu Arg
130          135          140
Val Leu Val Pro Pro Leu Pro Ser Leu Asn Pro Gly Pro Ala Leu Glu

```

145		150		155		160									
Glu	Gly	Gln	Gly	Leu	Thr	Leu	Ala	Ala	Ser	Cys	Thr	Ala	Glu	Gly	Ser
				165					170					175	
5	Pro	Ala	Pro	Ser											
				180											

Claims

1. An anti-191P4D12 antibody or antigen binding fragment thereof comprising a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises a CDRH1 consisting of the amino acid sequence ranging from 45 to 52 of SEQ ID NO:7, a CDRH2 consisting of the amino acid sequence ranging from 70 to 77 of SEQ ID NO:7, and a CDRH3 consisting of the amino acid sequence ranging from 116 to 125 of SEQ ID NO:7, and wherein the light chain variable region comprises a CDRL1 consisting of the amino acid sequence ranging from 49 to 54 of SEQ ID NO:8, a CDRL2 consisting of the amino acid sequence ranging from 72 to 74 of SEQ ID NO:8, and a CDRL3 consisting of the amino acid sequence ranging from 111 to 119 of SEQ ID NO:8.
2. The antibody or antigen binding fragment thereof of claim 1, wherein the heavy chain variable region comprises amino acid residue 20 to amino acid residue 136 of SEQ ID NO: 7 and the light chain variable region comprises amino acid residue 23 to amino acid residue 130 of SEQ ID NO:8.
3. The antibody of claim 1 or 2, wherein the antibody comprises a heavy chain comprising amino acid residue 20 to amino acid residue 466 of SEQ ID NO: 7 and a light chain comprising amino acid residue 23 to amino acid residue 236 of SEQ ID NO:8.
4. An antibody or antigen binding fragment thereof comprising a heavy chain variable region comprising the amino acid sequence of the heavy chain variable region of an antibody produced by a hybridoma deposited under American Type Culture Collection (ATCC) Accession No. PTA-11267, and a light chain variable region comprising the amino acid sequence of the light chain variable region of an antibody produced by a hybridoma deposited under ATCC Accession No. PTA-11267.
5. The antibody of claim 4, wherein the antibody comprises a heavy chain comprising the amino acid sequence of the heavy chain of an antibody produced by a hybridoma deposited under ATCC Accession No. PTA-11267, and a light chain comprising the amino acid sequence of the light chain of an antibody produced by a hybridoma deposited under ATCC Accession No. PTA-11267.
6. The antigen binding fragment of any one of claims 1, 2, or 4, wherein the antigen binding fragment is an Fab, F(ab')², Fv or scFv.
7. The antibody or antigen binding fragment thereof of any one of claims 1 to 6, wherein the antibody or antigen binding fragment thereof is a fully human antibody or antigen binding fragment thereof.
8. An antibody drug conjugate comprising the antibody or antigen binding fragment thereof of any one of claims 1 to 7 conjugated to monomethyl auristatin E (MMAE), wherein the antibody drug conjugate has the following structure:



wherein L is the antibody, and

wherein p ranges from about 3 to about 5.

9. The antibody drug conjugate of claim 8, wherein p is about 3.8.

10. A pharmaceutical composition comprising the antibody or antigen binding fragment thereof of any one of claims 1 to 7, or the antibody drug conjugate of claim 8 or 9, and a pharmaceutically acceptable excipient.

11. An antibody or antigen binding fragment thereof as defined in any one of claims 1 to 7, or an antibody drug conjugate as defined in claim 8 or 9 for use in a method of treating cancer.

12. The antibody or antigen binding fragment thereof, or the antibody drug conjugate for use of claim 11, wherein the cancer expresses 191P4D12.

13. The antibody or antigen binding fragment thereof, or the antibody drug conjugate for use of claim 11 or 12, wherein the cancer is bladder cancer, breast cancer, pancreatic cancer, lung cancer, ovarian cancer, esophageal cancer, or head and neck cancer.

14. The antibody or antigen binding fragment thereof, or the antibody drug conjugate for use of claim 13, wherein the cancer is bladder cancer.

15. The antibody or antigen binding fragment thereof for use of claim 14, wherein the bladder cancer is advanced bladder cancer.

Patentansprüche

1. Anti-191P4D12-Antikörper oder antigenbindendes Fragment davon, umfassend eine variable Region der schweren Kette und eine variable Region der leichten Kette, wobei die variable Region der schweren Kette eine CDRH1, bestehend aus der Aminosäuresequenz, die zwischen 45 und 52 von SEQ-ID-Nr. 7 liegt, eine CDRH2, bestehend aus der Aminosäuresequenz, die zwischen 70 und 77 von SEQ-ID-Nr. 7 liegt, und eine CDRH3, bestehend aus der Aminosäuresequenz, die zwischen 116 und 125 von SEQ-ID-Nr. 7 liegt, umfasst und wobei die variable Region der leichten Kette eine CDRL1, bestehend aus der Aminosäuresequenz, die zwischen 49 und 54 von SEQ-ID-Nr. 8 liegt, eine CDRL2, bestehend aus der Aminosäuresequenz, die zwischen 72 und 74 von SEQ-ID-Nr. 8 liegt, und eine CDRL3, bestehend aus der Aminosäuresequenz, die zwischen 111 und 119 von SEQ-ID-Nr. 8 liegt, umfasst.

2. Antikörper oder antigenbindendes Fragment davon nach Anspruch 1, wobei die variable Region der schweren Kette Aminosäureresiduum 20 bis Aminosäureresiduum 136 von SEQ-ID-Nr. 7 umfasst und die variable Region der leichten Kette Aminosäureresiduum 23 bis Aminosäureresiduum 130 von SEQ-ID-Nr. 8 umfasst.

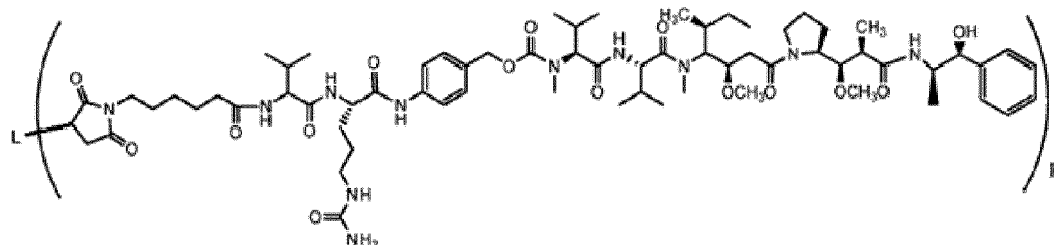
3. Antikörper nach Anspruch 1 oder 2, wobei der Antikörper eine schwere Kette, die Aminosäureresiduum 20 bis Aminosäureresiduum 466 von SEQ-ID-Nr. 7 umfasst, und eine leichte Kette umfasst, die Aminosäureresiduum 23 bis Aminosäureresiduum 236 von SEQ-ID-Nr. 8 umfasst.

4. Antikörper oder antigenbindendes Fragment davon, umfassend eine variable Region der schweren Kette, umfassend die Aminosäuresequenz der variablen Region der schweren Kette eines Antikörpers, der von einem in der Amerikanischen Typus-Kultursammlung (American Type Culture Collection; ATCC) unter Vermehrungsnummer PTA-11267 hinterlegten Hybridom erzeugt wurde, und eine variable Region der leichten Kette, umfassend die Aminosäuresequenz der variablen Region der leichten Kette eines Antikörpers, der von einem unter der ATCC-Vermehrungsnummer PTA-11267 hinterlegten Hybridom erzeugt wurde.

5. Antikörper nach Anspruch 4, wobei der Antikörper eine schwere Kette umfasst, umfassend die Aminosäuresequenz der schweren Kette eines Antikörpers, der von einem unter der ATCC-Vermehrungsnummer PTA-11267 hinterlegten Hybridom erzeugt wurde, und eine leichte Kette, umfassend die Aminosäuresequenz der leichten Kette eines Antikörpers, der von einem unter der ATCC-Vermehrungsnummer PTA-11267 hinterlegten Hybridom erzeugt wurde.

6. Antigenbindendes Fragment eines der Ansprüche 1, 2 oder 4, wobei das antigenbindende Fragment ein Fab-, F(ab')²-, Fv-, oder scFv-Fragment ist.

7. Antikörper oder antigenbindendes Fragment davon nach einem der Ansprüche 1 bis 6, wobei der Antikörper oder das antigenbindende Fragment ein vollständig humaner Antikörper oder ein antigenbindendes Fragment davon ist.
8. Antikörper-Arzneistoff-Konjugat, umfassend den Antikörper oder ein antigenbindendes Fragment davon nach einem der Ansprüche 1 bis 7, das an Monomethylauristatin E (MMAE) konjugiert ist, wobei das Antikörper-Arzneistoff-Konjugat die folgende Struktur aufweist:



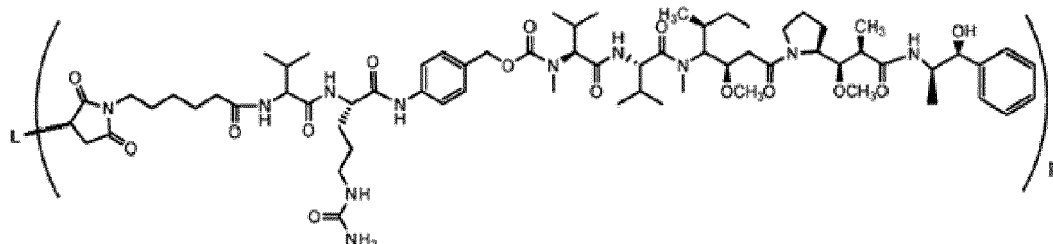
wobei L der Antikörper ist und
wobei p zwischen etwa 3 und etwa 5 liegt.

9. Antikörper-Arzneistoff-Konjugat nach Anspruch 8, wobei p etwa 3,8 ist.
10. Pharmazeutische Zusammensetzung, umfassend den Antikörper oder ein antigenbindendes Fragment davon nach einem der Ansprüche 1 bis 7, oder das Antikörper-Arzneistoff-Konjugat nach Anspruch 8 oder 9 und einen pharmazeutisch verträglichen Trägerstoff.
11. Antikörper oder antigenbindendes Fragment davon nach einem der Ansprüche 1 bis 7, oder ein Antikörper-Arzneistoff-Konjugat nach Anspruch 8 oder 9 zur Verwendung in einem Verfahren zur Behandlung von Krebs.
12. Antikörper oder antigenbindendes Fragment davon oder das Antikörper-Arzneistoff-Konjugat zur Verwendung nach Anspruch 11, wobei der Krebs 191P4D12 exprimiert.
13. Antikörper oder antigenbindendes Fragment davon oder das Antikörper-Arzneistoff-Konjugat zur Verwendung nach Anspruch 11 oder 12, wobei der Krebs Blasenkrebs, Brustkrebs, Bauchspeicheldrüsenkrebs, Lungenkrebs, Eierstockkrebs, Speiseröhrenkrebs oder Kopf- und Halskrebs ist.
14. Antikörper oder antigenbindendes Fragment davon oder das Antikörper-Arzneistoff-Konjugat zur Verwendung nach Anspruch 13, wobei der Krebs Blasenkrebs ist.
15. Antikörper oder antigenbindendes Fragment davon zur Verwendung nach Anspruch 14, wobei der Blasenkrebs ein fortgeschrittener Blasenkrebs ist.

Revendications

1. Anticorps anti-191P4D12 ou fragment de liaison à l'antigène de celui-ci, comprenant une région variable de chaîne lourde et une région variable de chaîne légère, dans lequel la région variable de chaîne lourde comprend un CDRH1 constitué de la séquence d'acides aminés allant de 45 à 52 de la SEQ ID NO: 7, un CDRH2 constitué de la séquence d'acides aminés allant de 70 à 77 de la SEQ ID NO: 7, et un CDRH3 constitué de la séquence d'acides aminés allant de 116 à 125 de la SEQ ID NO: 7, et dans lequel la région variable de chaîne légère comprend un CDRL1 constitué de la séquence d'acides aminés allant de 49 à 54 de la SEQ ID NO: 8, un CDRL2 constitué de la séquence d'acides aminés allant de 72 à 74 de la SEQ ID NO: 8, et un CDRL3 constitué de la séquence d'acides aminés allant de 111 à 119 de la SEQ ID NO: 8.
2. Anticorps ou fragment de liaison à l'antigène de celui-ci selon la revendication 1, dans lequel la région variable de chaîne lourde comprend le résidu d'acide aminé 20 au résidu d'acide aminé 136 de la SEQ ID NO: 7 et la région variable de chaîne légère comprend le résidu d'acide aminé 23 au résidu d'acide aminé 130 de la SEQ ID NO: 8.

3. Anticorps selon la revendication 1 ou 2, dans lequel l'anticorps comprend une chaîne lourde comprenant le résidu d'acide aminé 20 au résidu d'acide aminé 466 de la SEQ ID NO: 7 et une chaîne légère comprenant le résidu d'acide aminé 23 au résidu d'acide aminé 236 de la SEQ ID NO: 8.
4. Anticorps ou fragment de liaison à l'antigène de celui-ci comprenant une région variable de chaîne lourde comprenant la séquence d'acides aminés de la région variable de chaîne lourde d'un anticorps produit par un hybridome déposé sous le numéro d'accès PTA-11267 à l'American Type Culture Collection (ATCC), et une région variable de chaîne légère comprenant la séquence d'acides aminés de la région variable de chaîne légère d'un anticorps produit par un hybridome déposé sous le numéro d'accès ATCC. PTA-11267.
5. Anticorps selon la revendication 4, dans lequel l'anticorps comprend une chaîne lourde comprenant la séquence d'acides aminés de la chaîne lourde d'un anticorps produit par un hybridome déposé sous le numéro d'accès ATCC. PTA-11267, et une chaîne légère comprenant la séquence d'acides aminés de la chaîne légère d'un anticorps produit par un hybridome déposé sous le numéro d'accès ATCC. PTA-11267.
6. Fragment de liaison à l'antigène selon l'une quelconque des revendications 1, 2 ou 4, dans lequel le fragment de liaison à l'antigène est un Fab, F(ab')₂, Fv ou scFv.
7. Anticorps ou fragment de liaison à l'antigène de celui-ci selon l'une quelconque des revendications 1 à 6, dans lequel l'anticorps ou le fragment de liaison à l'antigène de celui-ci est un anticorps entièrement humain ou un fragment de liaison à l'antigène de celui-ci.
8. Conjugué anticorps-médicament comprenant l'anticorps ou le fragment de liaison à l'antigène de celui-ci selon l'une quelconque des revendications 1 à 7 conjugué à la monométhyl auristatine E (MMAE), dans lequel le conjugué anticorps-médicament a la structure suivante :



dans lequel L est l'anticorps, et
dans lequel p va d'environ 3 à environ 5.

9. Conjugué anticorps-médicament selon la revendication 8, dans lequel p est environ 3,8.
10. Composition pharmaceutique comprenant l'anticorps ou le fragment de liaison à l'antigène de celui-ci selon l'une quelconque des revendications 1 à 7, ou le conjugué anticorps-médicament selon la revendication 8 ou 9, et un excipient pharmaceutiquement acceptable.
11. Anticorps ou fragment de liaison à l'antigène de celui-ci selon l'une quelconque des revendications 1 à 7, ou conjugué anticorps-médicament selon la revendication 8 ou 9 pour utilisation dans un procédé de traitement du cancer.
12. Anticorps ou fragment de liaison à l'antigène de celui-ci, ou conjugué anticorps-médicament pour utilisation selon la revendication 11, dans lequel le cancer exprime le 191P4D12.
13. Anticorps ou fragment de liaison à l'antigène de celui-ci, ou conjugué anticorps-médicament pour utilisation selon la revendication 11 ou 12, dans lequel le cancer est le cancer de la vessie, le cancer du sein, le cancer du pancréas, le cancer du poumon, le cancer de l'ovaire, le cancer de l'œsophage, ou le cancer de la tête et du cou.
14. Anticorps ou fragment de liaison à l'antigène de celui-ci, ou conjugué anticorps-médicament pour utilisation selon la revendication 13, dans lequel le cancer est un cancer de la vessie.

- 15.** Anticorps ou fragment de liaison à l'antigène de celui-ci pour utilisation selon la revendication 14, dans lequel le cancer de la vessie est un cancer avancé de la vessie.

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**Figure 1: The cDNA (SEQ ID NO:1) and amino acid sequence (SEQ ID NO:2) of 191P4D12.
The start methionine is underlined. The open reading frame extends from nucleic acid 264-1796 including the stop codon.**

```

1  ggccgctcgttgttggccacagcgtgggaagcagctctgggggagctcggagctcccgatc
61  acggcttcttgggggtagctacggctgggtgtgtagaacggggccggggctggggctggg
121  tccccctagtgagacccaagtgcgagaggcaagaactctgcagcttctctgcttctgggt
181  cagttccttattcaagttctgcagccggctcccagggagatctcgggtggaacttcagaaac
1      M P L S L G A E M W G P E
241  gctgggcagttctgcctttcaaccATGCCCCCTGTCCCTGGGAGCCGAGATGTGGGGCCCTG
14   A W L L L L L L L A S F T G R C P A G E
301  AGGCCTGGCTGCTGCTGCTGCTACTGCTGGCATCATTTACAGGCCGGTGCCCCGCGGGTG
34   L E T S D V V T V V L G Q D A K L P C F
361  AGCTGGAGACCTCAGACGTGGTAACCTGTGGTGTGGGCCAGGACGCAAACTGCCCTGCT
54   Y R G D S G E Q V G Q V A W A R V D A G
421  TCTACCGAGGGGACTCCGGCGAGCAAGTGGGGCAAGTGGCATGGGCTCGGGGTGGACGCGG
74   E G A Q E L A L L H S K Y G L H V S P A
481  GCGAAGGCGCCCAGGAACTAGCGCTACTGCACTCCAAATACGGGCTTCATGTGAGCCCGG
94   Y E G R V E Q P P P P R N P L D G S V L
541  CTTACGAGGGCCCGCTGGAGCAGCCGCCGCCCCCACGCAACCCCTGGACGGCTCAGTGC
114  L R N A V Q A D E G E Y E C R V S T F P
601  TCCTGCGCAACGCAGTGCAGGCGGATGAGGGCGAGTACGAGTGGCGGGTGCAGCACCTTCC
134  A G S F Q A R L R L R V L V P P L P S L
661  CCGCCGGCAGCTTCCAGGCGCGGCTGGGCTCCGAGTGTGGTGGCTCCCCCTGCCCTCAC
154  N P G P A L E E G Q G L T L A A S C T A
721  TGAATCCTGGTCCAGCACTAGAAAGAGGGCCAGGGCCTGACCCCTGGCAGCCTCCTGCACAG
174  E G S P A P S V T W D T E V K G T T S S
781  CTGAGGGCAGCCCAGCCCCCAGCGTGACCTGGGACACGGAGGTCAAAGGCACAACGTCCA
194  R S F K H S R S A A V T S E F H L V P S
841  GCCGTTCCCTCAAGCACTCCCGCTCTGCTGCGGTACCTCAGAGTTCCACTTGGTGCCTA
214  R S M N G Q P L T C V V S H P G L L Q D
901  GCGCAGCATGAATGGGCAGCCACTGACTTGTGTGGTGTCCCATCCTGGCCTGCTCCAGG
234  Q R I T H I L H V S F L A E A S V R G L
961  ACCAAAGGATCACCCACATCCTCCACGTGTCCTTCCTTGCTGAGGCCTCTGTGAGGGGCC
254  E D Q N L W H I G R E G A M L K C L S E
1021 TTGAAGACCAAAATCTGTGGCACATTTGGCAGAGAAGGAGCTATGCTCAAGTGCCTGAGTG
274  G Q P P P S Y N W T R L D G P L P S G V
1081 AAGGGCAGCCCCCTCCCTCATACTGGACACGGCTGGATGGGCCTCTGCCAGTGGGG
294  R V D G D T L G F P P L T T E H S G I Y
1141 TACGAGTGGATGGGACACTTTGGGCTTTCCCCCACTGACCACTGAGCACAGCGGCATCT
314  V C H V S N E F S S R D S Q V T V D V L
1201 ACGTCTGCCATGTCAGCAATGAGTTCTCCTCAAGGGATTCTCAGGTCACTGTGGATGTTT
334  D P Q E D S G K Q V D L V S A S V V V V

```

1261 TTGACCCCCAGGAAGACTCTGGGAAGCAGGTGGACCTAGTGTGACCCTCGGTGGTGGTGG
 354 G V I A A L L F C L L V V V V V L M S R
 1321 TGGGTGTGATCGCCGCACTCTTGTCTGCTCTGGTGGTGGTGGTGGTGGTGCATGTCCC
 374 Y H R R K A Q Q M T Q K Y E E E L T L T
 1381 GATACCATCGGCGCAAGGCCAGCAGATGACCCAGAAATATGAGGAGGAGCTGACCCCTGA
 394 R E N S I R R L H S H H T D P R S Q P E
 1441 CCAGGGAGAACTCCATCCGGAGGCTGCATTCCCATCACACGGACCCAGGAGCCAGCCGG
 414 E S V G L R A E G H P D S L K D N S S C
 1501 AGGACAGTGTAGGGCTGAGAGCCGAGGGCCACCCTGATAGTCTCAAGGACAACAGTAGCT
 434 S V M S E E P E G R S Y S T L T T V R E
 1561 GCTCTGTGATGAGTGAAGAGCCCCGAGGGCCGAGTTACTCCACGCTGACCACGGTGAGGG
 454 I E T Q T E L L S P G S G R A E E E E D
 1621 AGATAGAAACACAGACTGAACTGCTGTCTCCAGGCTCTGGCGGGCCGAGGAGGAGGAAG
 474 Q D E G I K Q A M N H F V Q E N G T L R
 1681 ATCAGGATGAAGGCATCAAACAGGCCATGAACCATTTTGTTCAGGAGAATGGGACCCCTAC
 494 A K P T G N G I Y I N G R G H L V *
 1741 GGGCCAAGCCACGGGCAATGGCATCTACATCAATGGGCGGGGACACCTGGTCTGAcccc
 1801 ggcootgcotccotccotccotagggcootggctcctctgttgacatgggagatttttagctcatc
 1861 ttggggggcctccctaaacaaccccatcttcttgcggaagatgctcccccacccactgactg
 1921 cttgacctttacccccaacccctctgttccatgggagggctccaccaattgagctctctcc
 1981 caccatgcacgcaggtcactgtgtgtgtgcacatgtgtgcctgtgtgagtggtgactgactg
 2041 tgtgtgtgtgtggaggggtgactgtccgtggaggggtgactgtgtccgtgggtgtgtattatg
 2101 ctgtcatatcagagtcaggtgaactgtgggtgtatgtgccaagggatttgagtggttgctg
 2161 gggcaaacactgtcaggggttggggtgtgtgtcatgtgggtgtgtgtgacctctgcctgaa
 2221 aaagcaggtattttctcagaccccagagcagctattaatgatgcagaggttgaggagagaga
 2281 ggtggagactgtgggtcagacccaggtgtgcgggcatagctggagctggaatctgcctcc
 2341 ggtgtgagggaaacctgtctcctaccacttcggagccatgggggcaagtgtgaagcagcca
 2401 gtccctgggtcagccagagggcttgaaactgttaacagaagccctctgcctctgggtggctc
 2461 tgggcctgtgtcatgtacatatattttctgtaaatatacatgcgcgggagcttcttgacagg
 2521 aatactgtccgaatcacttttaattttttcttttttttttttgcctttccattagt
 2581 tgtattttttattttattttttatttttttttagagatggagctctcactatgttgc
 2641 tcaggctggccttgaaactcctgggctcaagcaatcctcctgcctcagcctccctagtagc
 2701 tgggaactttaagtgtacaccactgtgcctgctttgaatcctttaagaagagaaaaaaaaa
 2761 attaaagaaagccttttagatttatccaatgtttactactgggattgcttaasagtgaggcc
 2821 cctccaacaccagggggttaattcctgtgattgtgaaaggggctacttccaaggcatctt
 2881 catgcaggcagcccttgggagggcactgagagctggtagagctctgaaattagggatgt
 2941 gagcctcgtgggttactgagtaaggtaaaattgcacccaccattgtttgtgataccttagg
 3001 gaattgcttggacctggtagacaagggtcctgttcaatagtgggtgttggggagagagaga
 3061 gcagtgattatagaccgagagagtaggagttgaggtgaggtgaaggaggtgctgggggtg
 3121 agaatgtgcctttcccccctgggttttggatcactaatcgaagctctcttgatgtttc
 3181 tctgggttggggctggagttcaatgaggtttatcttttagctggcccccagatacactc
 3241 agccagaataactagatttagtaccocaaactctcttagctctgaaatctgtggattttct
 3301 ggccaaagggagaggtcccatccttcgttcocccagccactaggacttcgaatgtgga
 3361 gcctgaagatctaagatcctaacatgtacattttatgtaaatatgtgcatactttgtacat
 3421 aaaatgatattctgttttttaataaacagacaaaaacttgaaaaa

Figure 1
(Continued)

Figure 2A: The cDNA (SEQ ID NO:3) and amino acid sequence (SEQ ID NO:4) of Ha22-2(2,4)6.1 heavy chain. Double-underlined is the leader sequence, underlined is the heavy chain variable region, and underlined with a dashed line is the human IgG1 constant region.

M E L G L C W V F L V A I L E

```

1  G3TGATCAGCACTGAACACAGAGGACTCACCATGGAGTTGGGGCTGTGCTGGGTTTTCCTTGTTCCTATTTAGAA
   · G V Q C E V Q L V E S G G G L V Q F G G S L R L S
76  AGGTGTCCATGTGTAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTCAGACTCTC
   · C A A S G F T F S S Y N M N W V R Q A P G K G L E
151  CTGTGCAGCCTCTGGATTCACTTCAGTAGCTATAACATGAACCTGGGTCCGCCAGGCTCCAGGGAAGGGCTGGA
   · W V S Y I S S S S S S T I Y Y A D S V K G R F T I S
226  GTGGGTTTCACATAGTAGTAGTAGTAGTACCATATACTACGCAGACTCTGTGAAGGGCCGATTCAACATCTC
   · R D N A K N S L S L Q M N S L R D E D T A V Y Y C
301  CAGAGACAATGCCAAGAACTCACTGTCTCTGCAAAATGAACAGCTGTGAGAGACAGGACACGGCTGTGTATTACTG
   · A R A Y Y Y G M D V W G Q G T T V T V S S A S T K
376  TGGAGAGACATACTACTACGCTATGGAGCTCTGGGGGCAAGGGACCAAGGTCACTGTCTCTCAGCCTCCACCAA
   · G F S S V F P L A P S S K S T S G G T A A L G C L V
451  GGGCCCATCTTCCCCCTGGCAGCCCTCCCTCCAGAGCACTCTGGGGGACAGCGGCCCTGGGCTCCCTGTG
   · K D Y F P E P V T V S W N S G A L T S G V H T F P
526  CAAGGACTACTTCCCGAAGCCGGTGAAGGTGTCTGGGAAGTCAAGCGCCTGACAGCGGGCTGCACAGCTTCCC
   · A V L Q S S G L Y S L S S V V T V P S S S L G T Q
601  GGCTCTCTCACTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAAGCTGCCCTCCAGCAGCTTGGGACCCCA
   · T Y I C N V N H K P S N T K V D K R V E P K S C D
676  GACCTACACTCTGCAAGGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAGAGTGAAGCCCAATCTTGTGA
   · K T H T C P P C P A P E L L G G P S V F L F P P K
751  CAAAAGTCAACATGCCAGCCTGGCCAGCACTGAAGTCTGGGGGACCGTCAGTCTTCCCTCTTCCCGCCAAA
   · P K D T L M I S R T P E V T C V V V D V S H E D P
826  ACCCAAGGACACCTTCATGATCTCCCGGACCCCTGAGCTCAGATGCTTGGTGTGGAGCTGAGGCAAGAGACCC
   · E V K F N W Y V D G V E V H N A K T K P R E E Q Y
901  TGAGGTCACTTCAACTGGTACCGTGGAGCGCTGGAGTGCATATGCGAAGACAAAGCCCGGAGGAGGAGCTA
   · N S T Y R V V S V L T V L H Q D W L N G K E Y K C
976  CAACAGCAGCTACCGTGTGGTCAAGCTCTCTCAGCTCTCTGACCCAGGACTGGTGAATGGCAAGGAGTACAAGTG
   · K V S N N K A L P A P I E K T I S K A K G G Q P R E P
1051  CAAGCTCTCCCAAGAAAGCTTCCAGCCCTCCATCGAAGAAATCTCTCAAGCCCAAGGAGGAGGAGGAGGAG
   · Q V Y T L P P S R E E M T K N Q V S L T C L V K G
1126  ACAGGTGTACACCTTCCCTCCATCCCGGAGGAGATGACCAAGAACAGGTCAAGCTGACCTGCTGTGTAAGG
   · F Y P S D I A V E W E S N G Q P E N N Y K T P P P
1201  CTTCTATCCAGGACATCCCGCTGGAGTGGAGGCAATGGGCAAGCCGAGAACAACTACAGAGCCAGCCCTCC
   · V L D S D G S F F L Y S K L T V D K S R W Q Q G N
1276  CGTCTGGACTTCCGAGGGCTCTCTCTCTCTATAGCAAGCTACCGTGGACAGAGCAGGTGGCAGCAGGGGAA
   · V F T S C S V M H E A L H N H Y T Q K S L S L S P G
1351  CGTCTGATCTCCCTGGATGCAATGAGGCTCTGCAACACCTACAGCAGAGAGGCTCTCTCTCTTCCCGGG
   · K *
1426  TAAATGA

```

Figure 2B: The cDNA (SEQ ID NO:5) and amino acid sequence (SEQ ID NO:6) of Ha22-2(2,4)6.1 light chain. Double-underlined is the leader sequence, underlined is the light chain variable region, and underlined with a dashed line is the human kappa constant region.

M D M R V P A Q L L G L L L L W F

```

1  AGTCAGACCCAGTCAGGACACAGCATGGACATGAGGGTCCCGGCTCAGCTCCCTGGGGCTCCCTGCTGCTGTGGTTC
   P G S R C D I Q M T Q S P S S V S A S V S D R V T
76  CCAGGTTCCAGATGGACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCACTCTGTGGAGACAGAGCTCAC
   I T C R A S Q G I S G W L A W Y Q Q K P G K A P K
151  ATCACTTGTCTGGCTGAGTCAGGGTATTAGCGGCTTGGTATGCTGATCAGCAGAAACAGGGGAAGCCCTTAAG
   F L I Y A A S T L Q S G V P S R F S G S G S G T D
226  TTCTTGATCTATGCTGCACCCACTTTGCAAGGTGGGTCTCCCATCAAGGTTTCAAGCGGCACTGGATCTGGGACAGAT
   F T L T I S S L Q P E D F A T Y Y C Q Q A N S F P
301  TTCACCTCTCAACATCAGCAGCCTGCAGCCTGAAGATTCTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCT
   P T F G G G G K V E I K R T V A A P S V F I F P P
376  CCCACTTTCCGGGGAGGGACCAAGGTGGAGATCAAAAGCACTGTGGCTGACCATCTGTCTCATCTTCCCGCA
   S D E Q L K S G T A S V V C L L N N F Y P R E A K
451  TCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGGTGTGGTGCCTGCTGAATAACTTCTATCCCGAGAGAGCCAAA
   V Q W K V D N A L Q S G N S Q E S V T E Q D S K D
526  GTACAGTGGAAAGGTGATAACGCCCTCCAATCGGGTAAGTCCAGGAGAGTGTACAGAGACAGGACAGCAAGGAC
   S T Y S L S S T L T L S K A D Y E K H K V Y A C E
601  AGCAGCTACAGCCTCAGCAGCAGCCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAA
   V T H Q G L S S P V T K S F N R G E C *
676  GTCACCCATCAGGGGCTGAGCTGCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG

```

Figure 3A: The amino acid sequence (SEQ ID NO:7) of Ha22-2(2,4)6.1 heavy chain.
Double-underlined is the leader sequence, underlined is the heavy chain variable region, and underlined with a dashed line is the human IgG1 constant region.

```

1  MELGLCWVFLVAILEGVOCEVQLVESGGGLVQPGGSLRLSCAASGFTFSS
51 YNMNWVRQAPGKGLEWVSYISSSSSTIYYADSVKGRFTISRDNAKNSLSL
101 QMNSLRDEDTAVYYCARAYYYGMDVWGQGTITVTVSSASTKGPSVFPLAPS
151 SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS
201 LSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPA
251 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDG
301 VEVHNAKTKPREEQYNSTYRVVSVLTVTLHQDWLNGKEYKCKVSNKALPAP
351 IEKTIISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
401 ESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEA
451 LHNHYTQKSLSLSPGK

```

Figure 3B: The amino acid sequence (SEQ ID NO:8) of Ha22-2(2,4)6.1 light chain.
Double-underlined is the leader sequence, underlined is the light chain variable region, and underlined with a dashed line is the human kappa constant region.

```

1  MDMRVPAQLLGLLLLWFGSRCDIQMTQSPSSVSASVGDRVTITCRASQG
51 ISGWLAWYQQKPGKAPKFLIYAASLTQSGVPSRFSGSGSGTDFTLTISL
101 QPEDFATYYCQQAANSFPPTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSG
151 TASVVCLLNMFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST
201 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

```

Figure 4A: Alignment of Ha22-2(2,4)6.1 heavy chain (a portion of SEQ ID NOS:3, 4) to human Ig germline VH3-48 (SEQ ID NO:9).

<u>ID#</u>		<-----FWR1----->	
		E V Q L V E S G G G L V Q P G G S L R L S C A	
	<u>2(2,4)6.1</u>	GAGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTACAGCCCTGGGGGTCCCTGAGACTCTCCTGTGCAG	158
		E V Q L V E S G G G L V Q P G G S L R L S C A	
99.3 (293/295)	<u>VH3-48</u>		70
100 (6/6)	<u>D2-21</u>	-----	
98.2 (54/55)	<u>JH6</u>	-----	
<u>ID#</u>			
	<u>2(2,4)6.1</u>	-----CDR1-----> <-----FWR2-----	
		CCTCT GGATTCACCTTCAGTAGCTATAAC ATGAAGTGGTCCGCCAGGCTCCAGGGAAGGGCTGGAGTG	228
		A S G F T F S S Y N M N W V R Q A P G K G L E W	
		G.	140
99.3 (293/295)	<u>VH3-48</u>	-----	
100 (6/6)	<u>D2-21</u>	-----	
98.2 (54/55)	<u>JH6</u>	-----	
<u>ID#</u>			
		-----> <-----CDR2-----> <-----	
	<u>2(2,4)6.1</u>	V S Y I S S S S T I Y Y A D S V K G R F T I	
		GGTTTCATAC ATTAGTAGTAGTAGTAGTACATA TACTACGAGACTCTGTGAAGGCCGATTCACCATC	298
		V S Y I S S S S T I Y Y A D S V K G R F T I	
			210
99.3 (293/295)	<u>VH3-48</u>	-----	
100 (6/6)	<u>D2-21</u>	-----	
98.2 (54/55)	<u>JH6</u>	-----	
<u>ID#</u>			
	<u>2(2,4)6.1</u>	-----FWR3-----	
		S R D N A K N S L S L Q M N S L R D E D T A V	
		TCCAGAGACAATGCCAAGAACTCACTGTCTCTGCAAAATGAACAGCTGAGAGACGAGGACACGGCTGTGT	368
		S R D N A K N S L Y L Q M N S L R D E D T A V	
		A.....	280
99.3 (293/295)	<u>VH3-48</u>	-----	
100 (6/6)	<u>D2-21</u>	-----	
98.2 (54/55)	<u>JH6</u>	-----	

<u>ID%</u>		<u>2(2,4)6.1</u>	369	Y Y C	A R A Y Y Y G M D V W G Q G T T V T V S S		
	99.3(293/295)	<u>VH3-48</u>	281	ATTACTGT	GGGAGCATACTACTACGGTATGGACGTCTGGGGCCGAGGACCGGTACCGTCTCCTC	438	
	100(6/6)	<u>D2-21</u>	1	Y Y C	A R		
	98.2(54/55)	<u>JH6</u>	9		G.....		
<u>ID%</u>		<u>2(2,4)6.1</u>	439	AG	440		
	99.3(293/295)	<u>VH3-48</u>		--			
	100(6/6)	<u>D2-21</u>		--			
	98.2(54/55)	<u>JH6</u>	62	..	63		

Figure 4A
(Continued)

ID#		<-----FWR1----->	D I Q M T Q S P S S V S A S V G D R V T I T C	
	<u>2(2,4)6.1</u>		GACATCCAGATGACCAGCTCCTCCATCTTCGGTGTCTGCATTGTGGAGACAGATCACCATCTGTC	160
			D I Q M T Q S P S S V S A S V G D R V T I T C	
98.6(283/287)	L5		A.....	70
100(35/35)	Jk4		-----	
ID#		<-----CDR1-----> <-----FWR2-----	R A S Q G I S G W L A W Y Q Q K P G K A P K F L	
	<u>2(2,4)6.1</u>		GGCGAGT CAGGTATTAGGGCTGG TTAGCTGTATCAGCAGAAACAGGGAAGCCCTAAGTTCT	230
			R A S Q G I S S W L A W Y Q Q K P G K A P K L L	
98.6(283/287)	L5		A.....	140
100(35/35)	JK4		-----	
ID#		<-----CDR2-----> <-----F-----	I Y A A S T L Q S G V P S R F S G S G S G T D	
	<u>2(2,4)6.1</u>		GATCTAT GCTGCATCC ACTTGCAAGTGGGTCCATCAAGTTCAGGGCAGTGGATCTGGACAGAT	300
			I Y A A S S L Q S G V P S R F S G S G S G T D	
98.6(283/287)	L5		G.....	210
100(35/35)	JK4		-----	
ID#		WR3----->	F T L T I S S L Q P E D F A T Y Y C Q Q A N S	
	<u>2(2,4)6.1</u>		TTCACTCTCACCATCAGCAGCCCTGCAGCTGAAGATTTCGAATTACTATTCT CAACAGGCTAACAGTT	370
			F T L T I S S L Q P E D F A T Y Y C Q Q A N S	
98.6(283/287)	L5			280
100(35/35)	JK4		-----	
ID#			F P P T F G G G T K V E I K	
	<u>2(2,4)6.1</u>		TCCCTCCCACITTCGGCGGAGGACCAAGGTGGAGATCAAAC	412
			F P P	
98.6(283/287)	L5			287
100(35/35)	JK4		-----	
ID#				38

Figure 5A: Binding of Ha22-2(2,4)6.1 Mab using Flow Cytometry

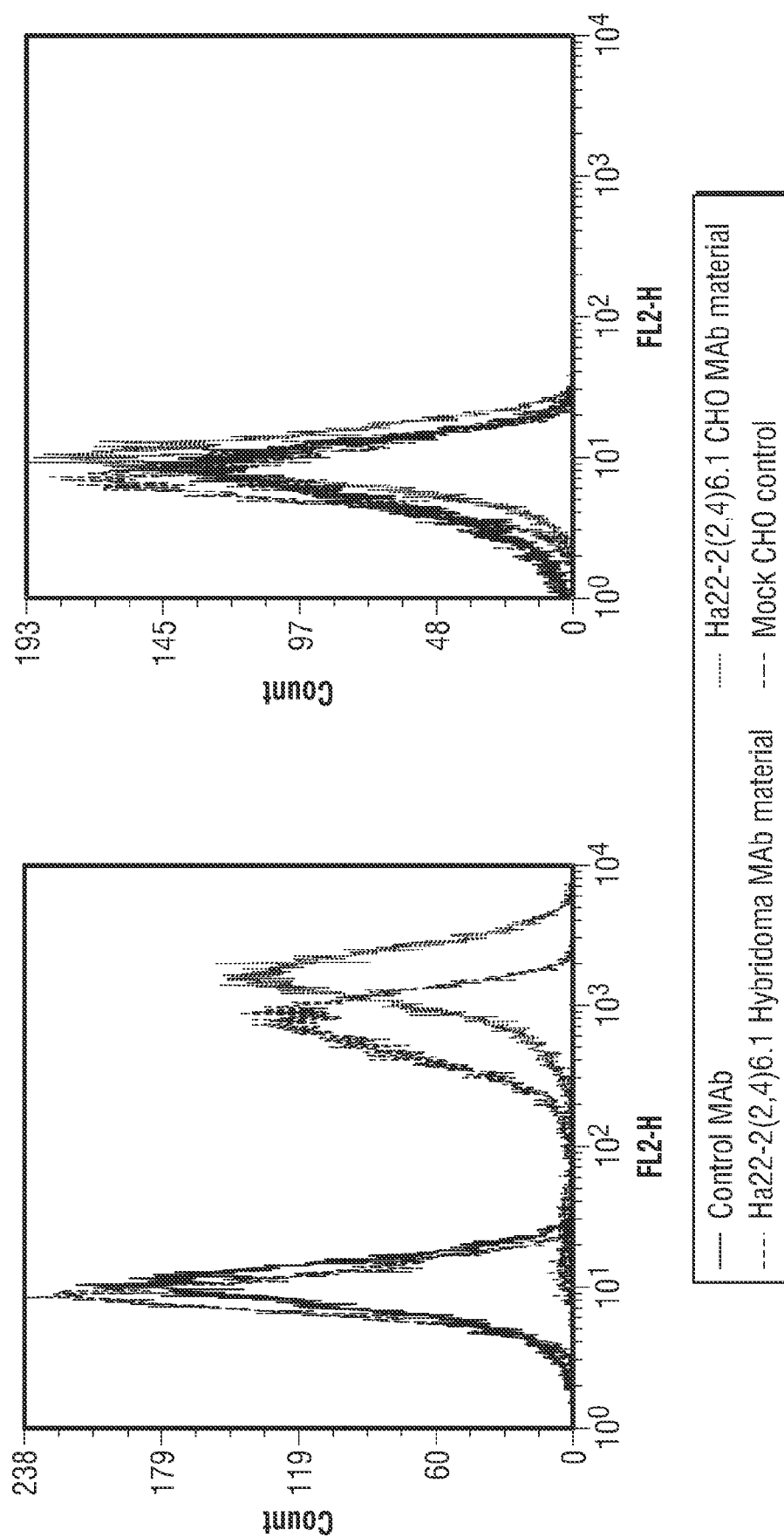


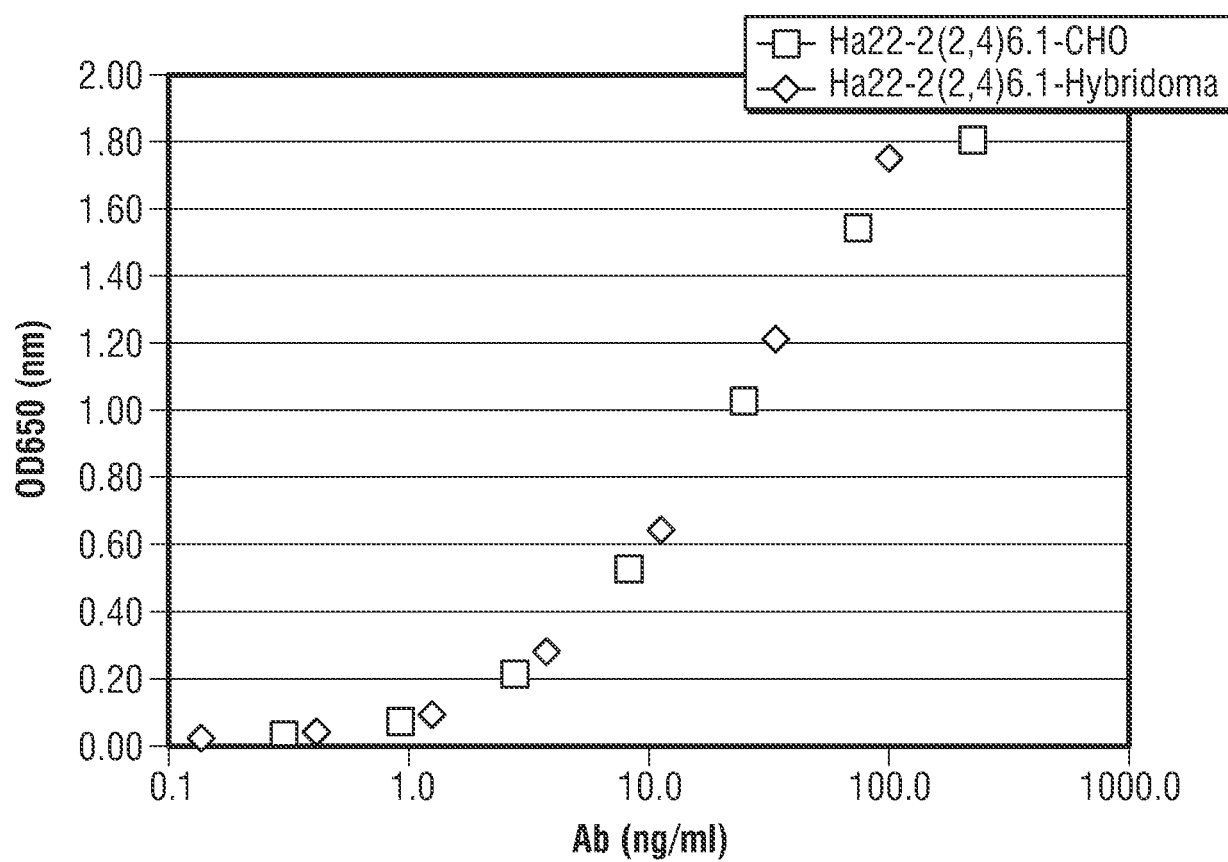
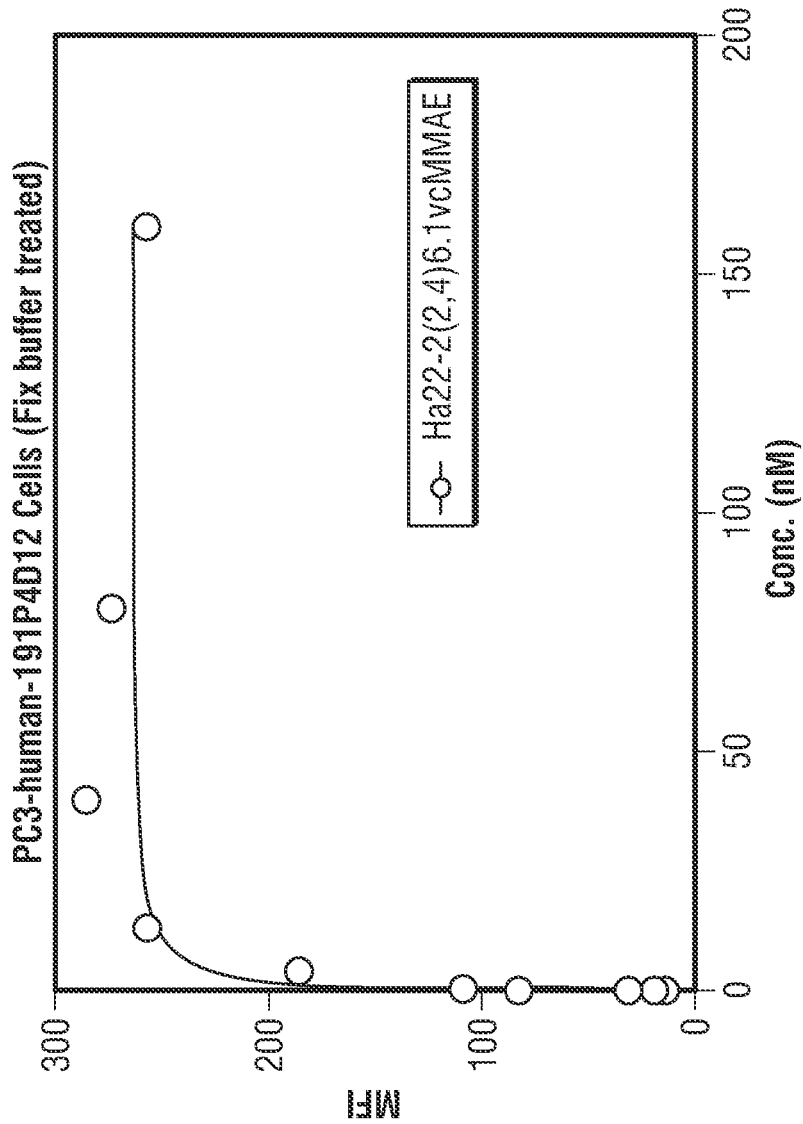
Figure 5B: Binding of Ha22-2(2,4)6.1 Mab using ELISA

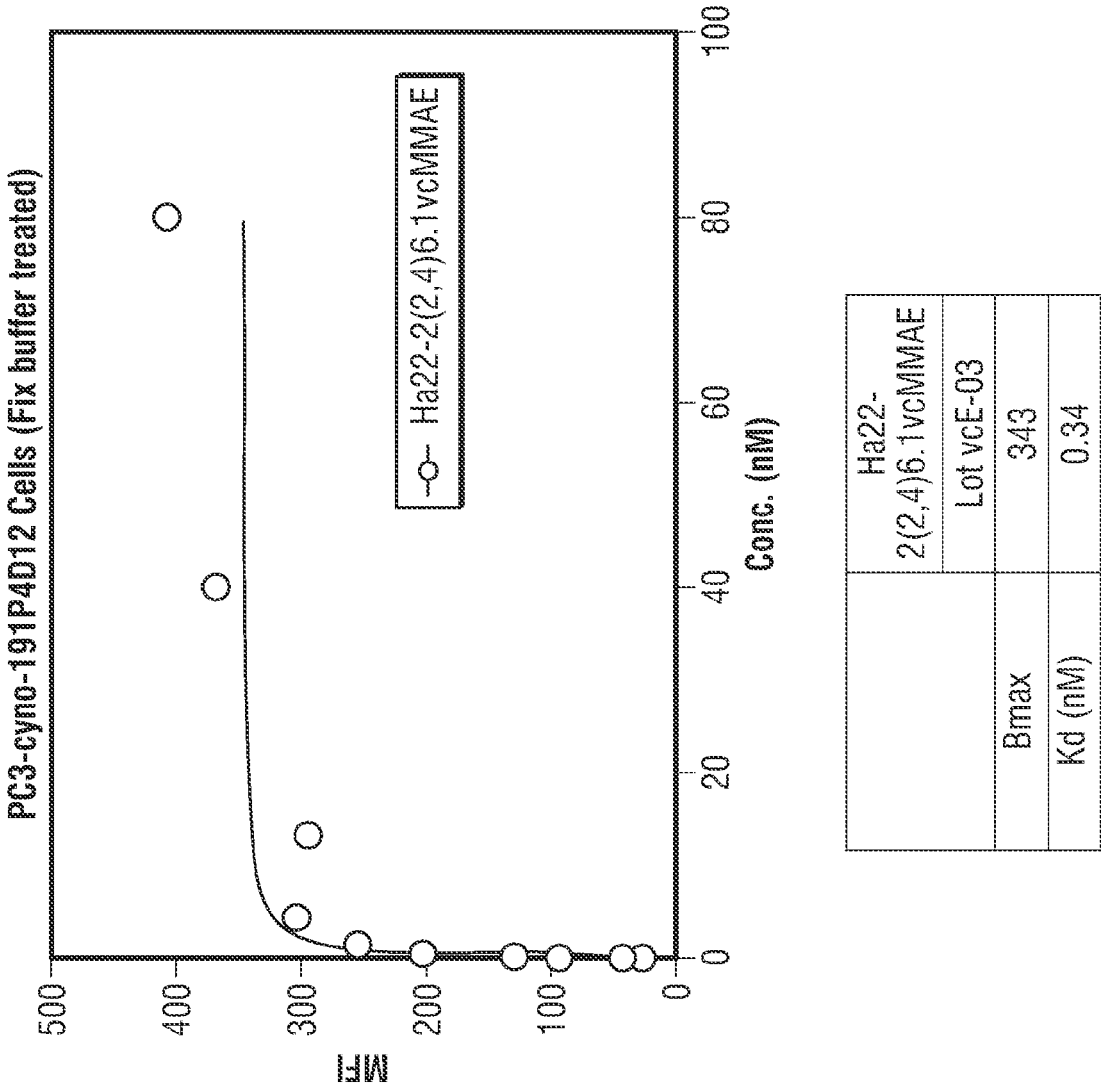
Figure 6: Ha22-2(2,4)6.1vcMMAE Affinity Determination by FACS using PC3-human-191P4D12



MFI Values (nM)	Ha22-2(2,4)6.1 vcMMAE
	Lot vcE-03
160	257
80	273
40	285
13.33	256
4.44	183
1.48	183
0.49	105
0.16	78
0.05	26
0.02	14
0.01	9
0.000	1

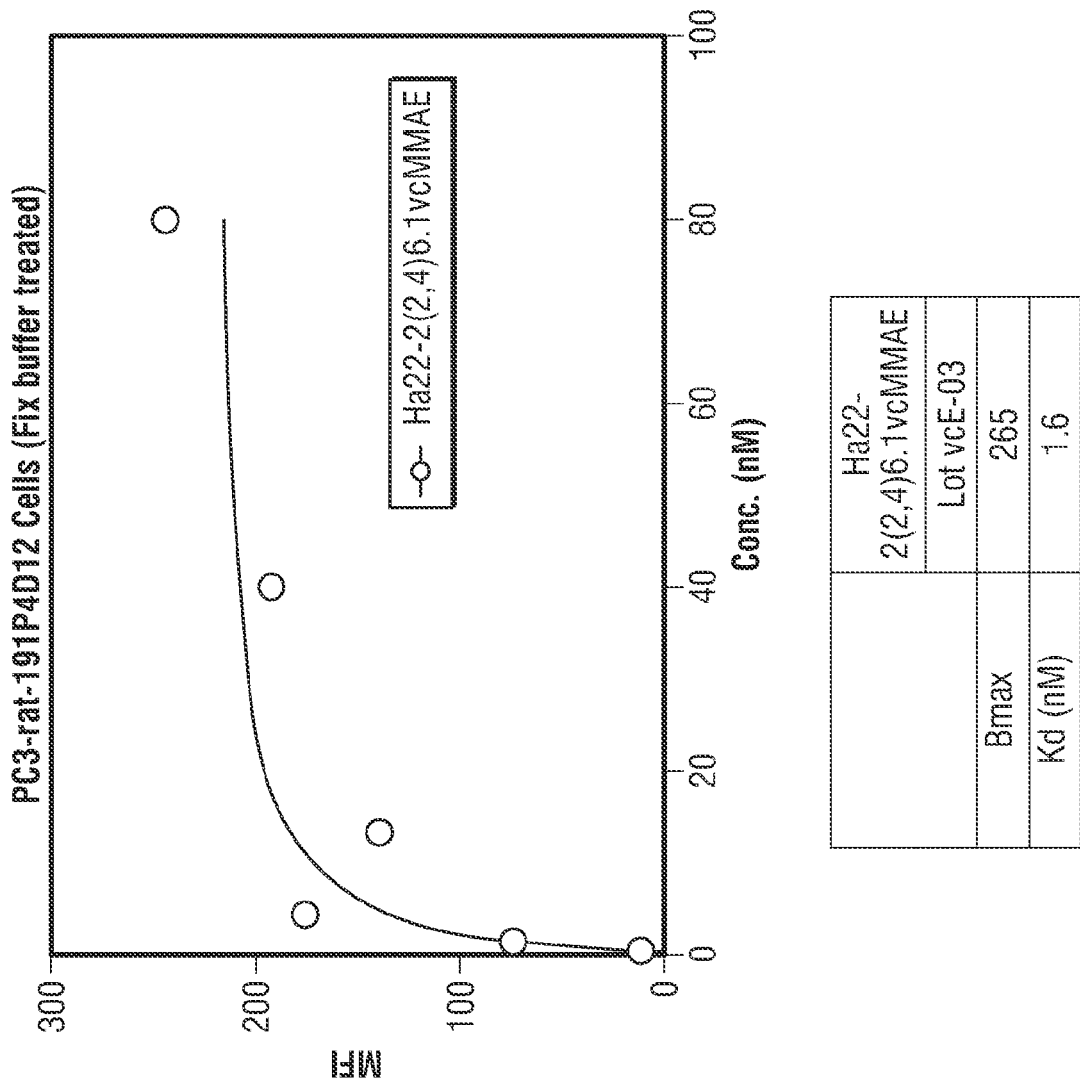
	Ha22- 2(2,4)6.1vcMMAE
	Lot vcE-03
Bmax	265
Kd (nM)	0.69

Figure 7: Ha22-2(2,4)6.1vcMMAE Affinity Determination by FACS using PC3-cynomolgus-191P4D12



MFI Values (nM)	Ha22-2(2,4)6.1vcMMAE
	Lot vcE-03
160	375
80	403
40	364
13.33	288
4.44	298
1.48	248
0.49	196
0.16	122
0.05	86
0.02	34
0.01	19
0.000	1

Figure 8: Ha22-2(2,4)6.1vcMMAE Affinity Determination by FACS using PC3-rat-191P4D12



MFI Values (nM)	Ha22-2(2,4)6.1vcMMAE
	Lot vcE-03
160	205
80	296
40	243
13.33	192
4.44	224
1.48	121
0.49	56
0.16	40
0.05	22
0.02	11
0.01	8
0.000	4

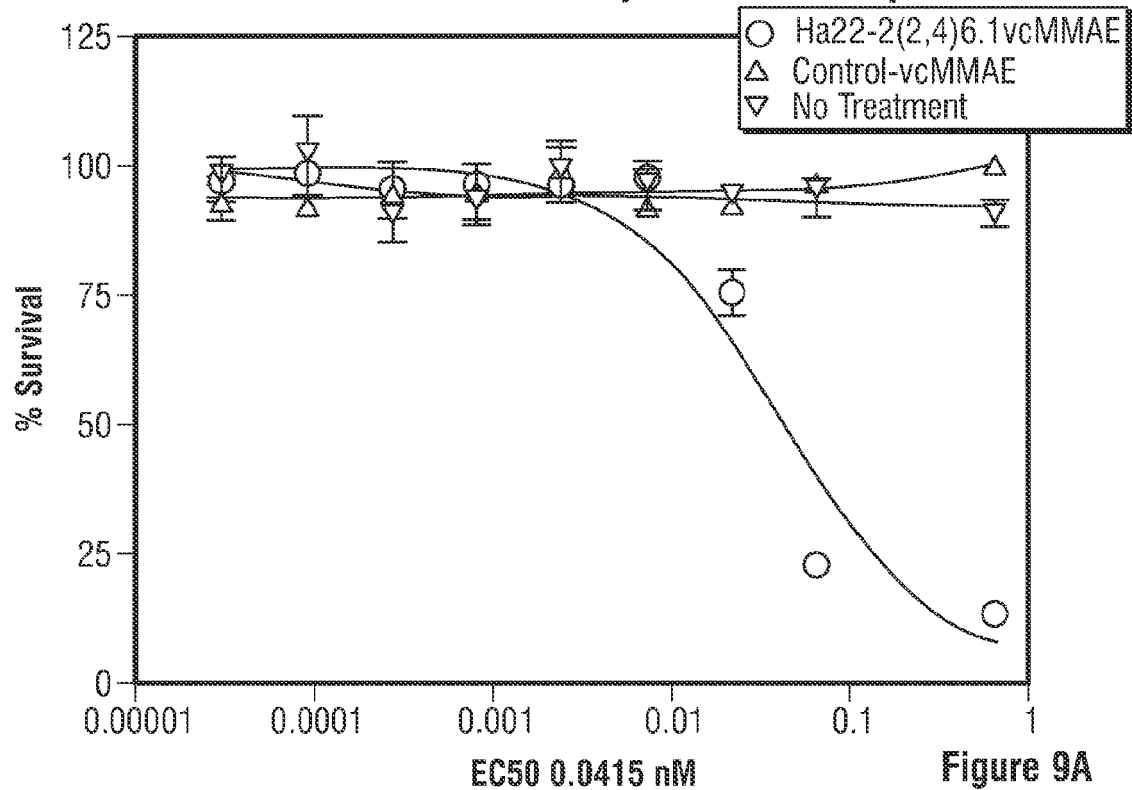
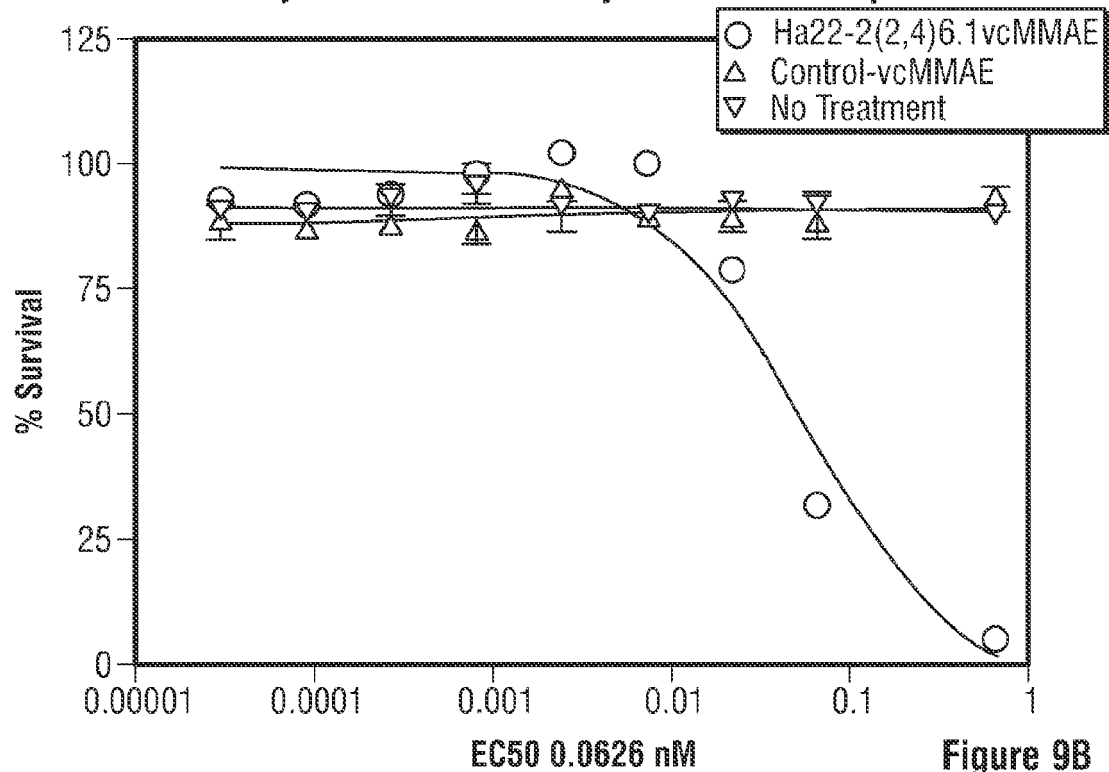
Figure 9: Cell Cytotoxicity Mediated by Ha22-2(2,4)6.1vcMMAE**PC-3 Human-191P4D12: 4 day kill/ 1500 cells per well****Figure 9A****PC-3 cyno-191P4D12: 4 day kill/ 1500 cells per well****Figure 9B**

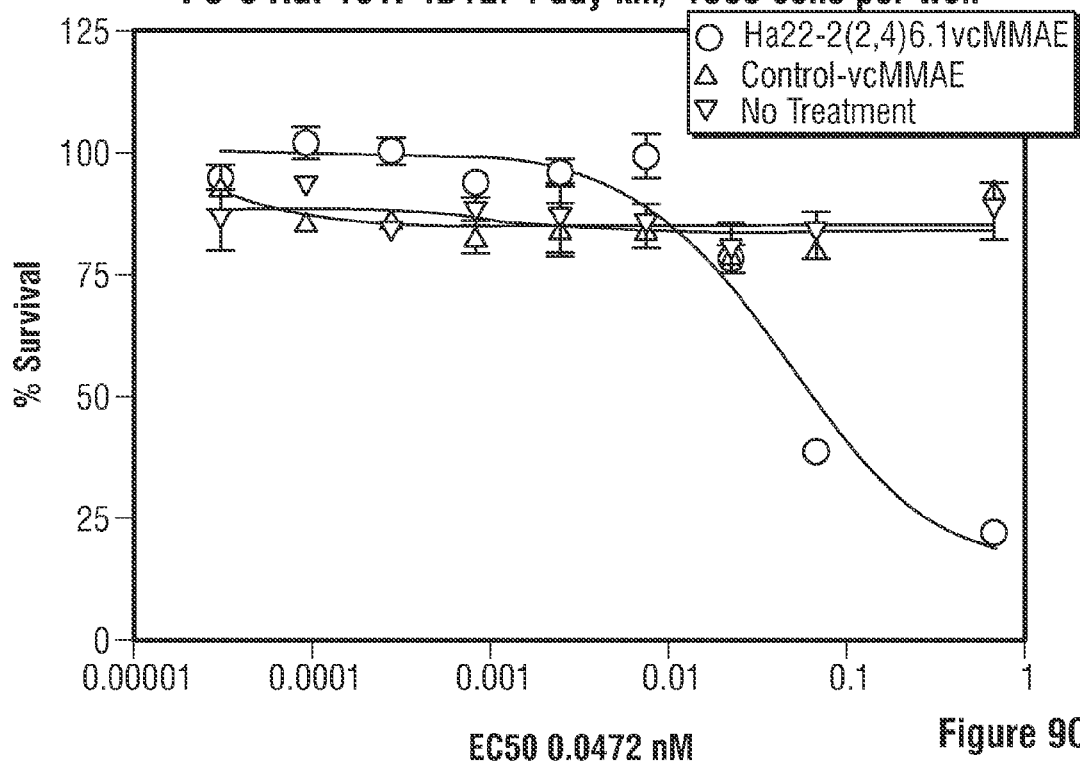
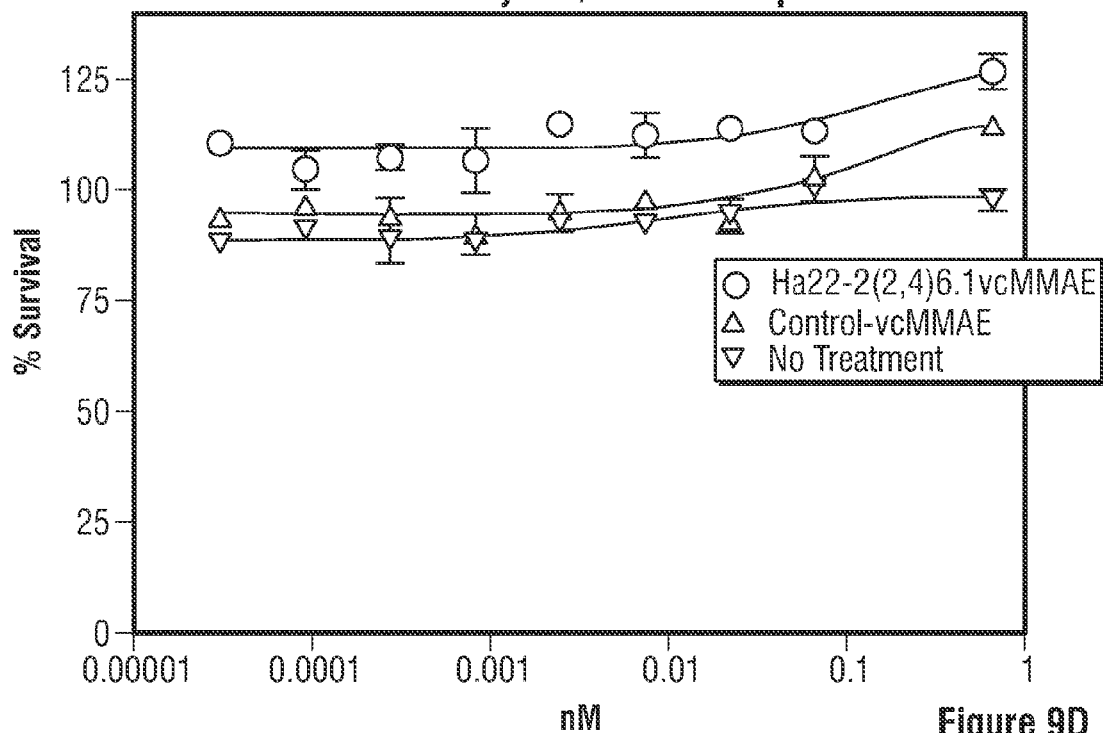
Figure 9: Cell Cytotoxicity Mediated by Ha22-2(2,4)6.1vcMMAE**PC-3 Rat-191P4D12: 4 day kill/ 1500 cells per well****Figure 9C****PC-3 Neo: 4 day kill/ 1500 cells per well****Figure 9D**

Figure 10: Domain Mapping of Ha22-(2,4)6.1 MAb by FACS

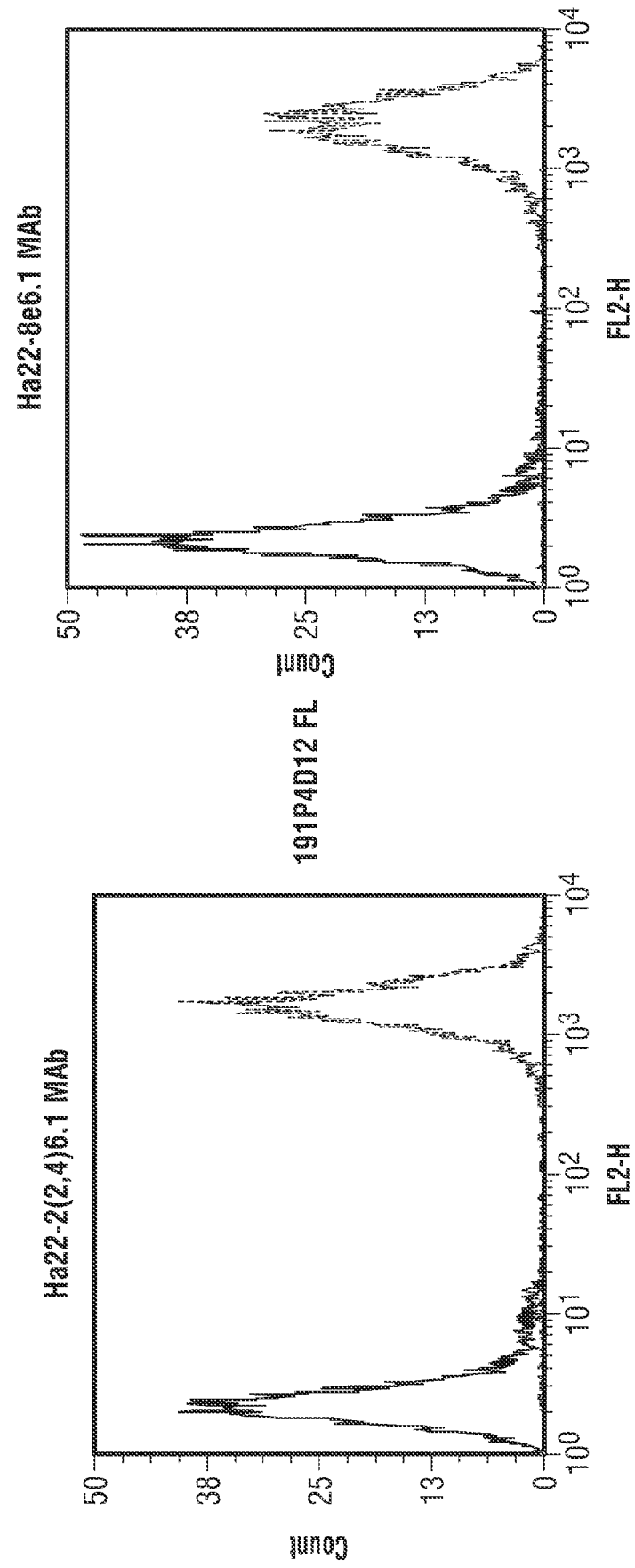


Figure 10 (Continued): Domain Mapping of Ha22-(2,4)6.1 MAb by FACS

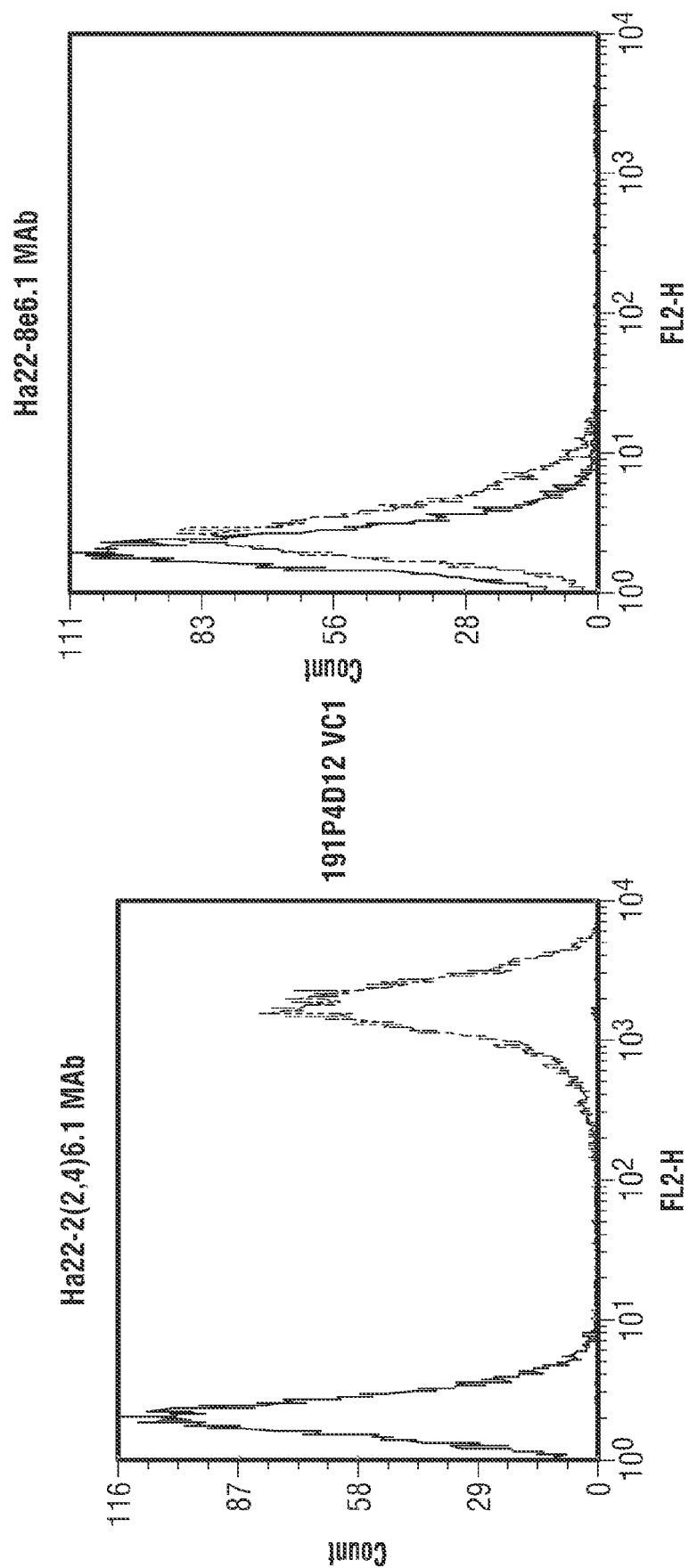


Figure 10 (Continued): Domain Mapping of Ha22-(2,4)6.1 MAb by FACS

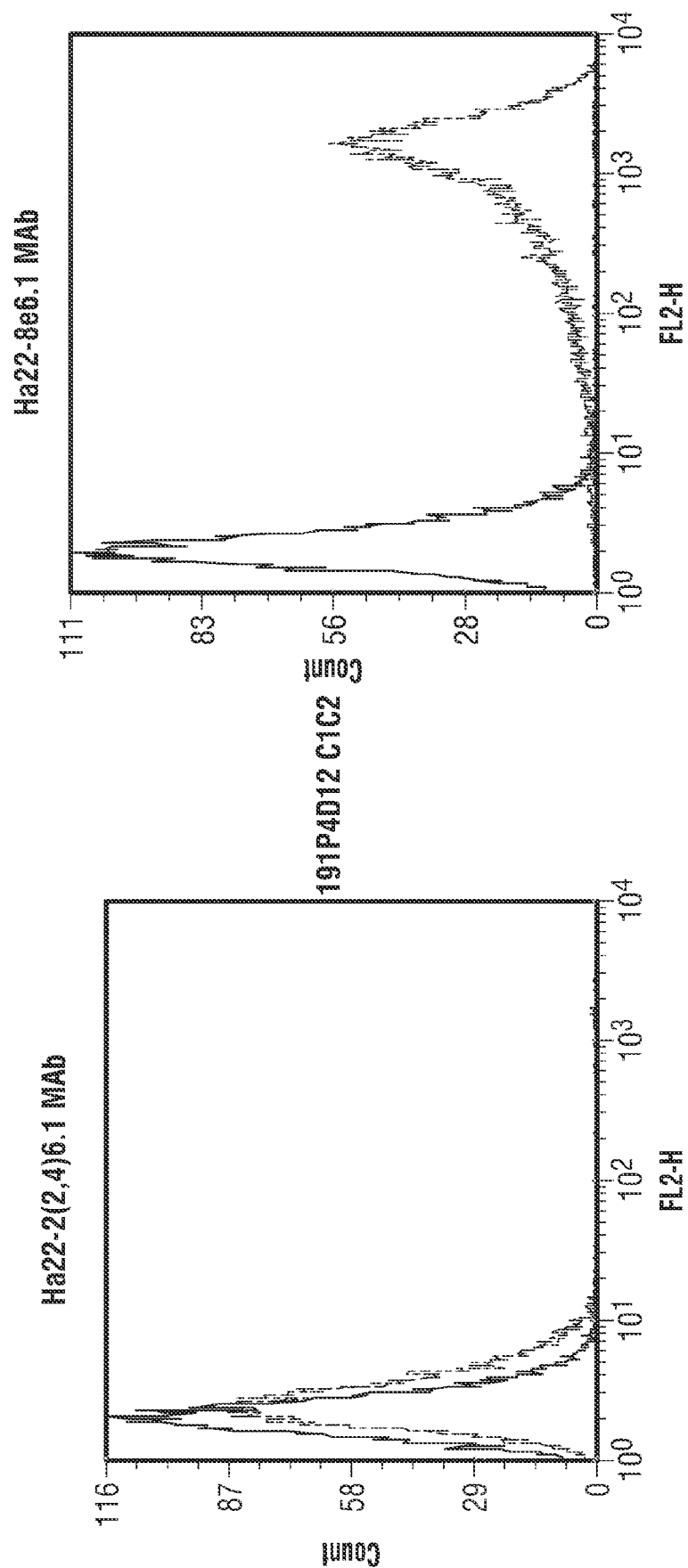


Figure 11: Ha22-2(2,4)6.1 MAb Domain Mapping by Western Blot Analysis.

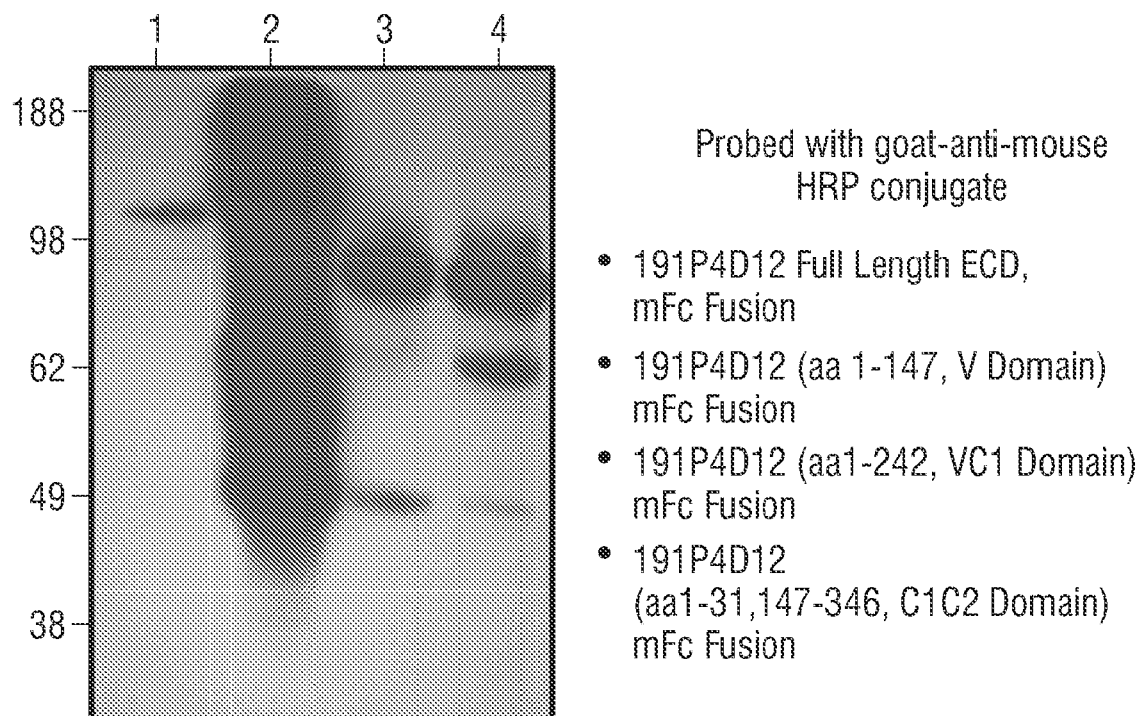
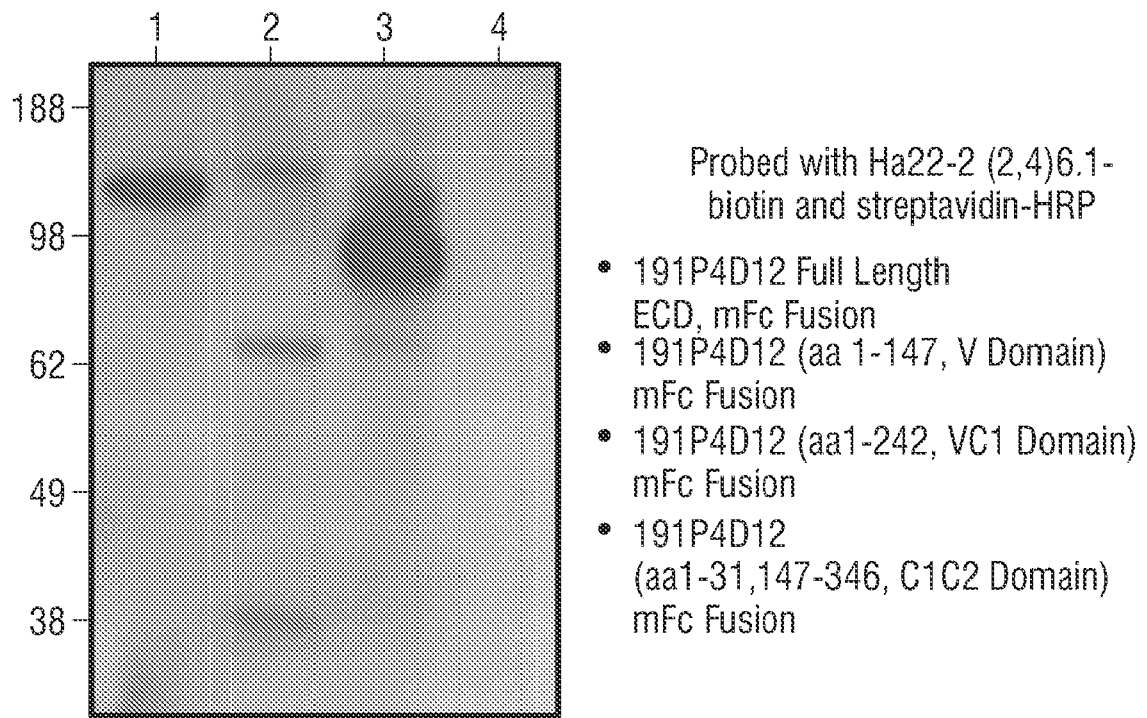
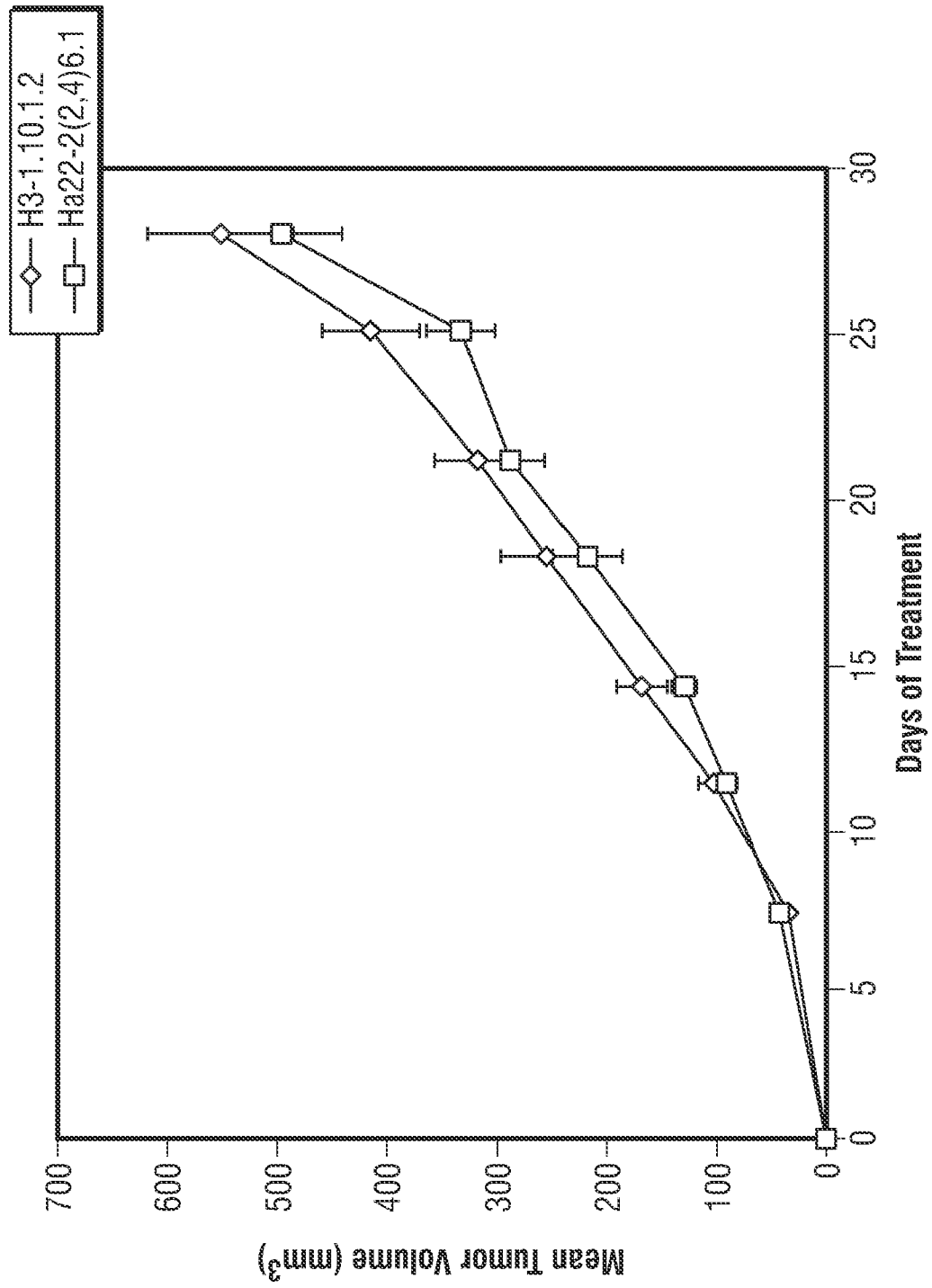


Figure 12: Evaluation of Ha22-2(2,4)6.1 MAb in the Subcutaneous tumor formation model of human lung cancer xenograft AG-L4 in SCID mice



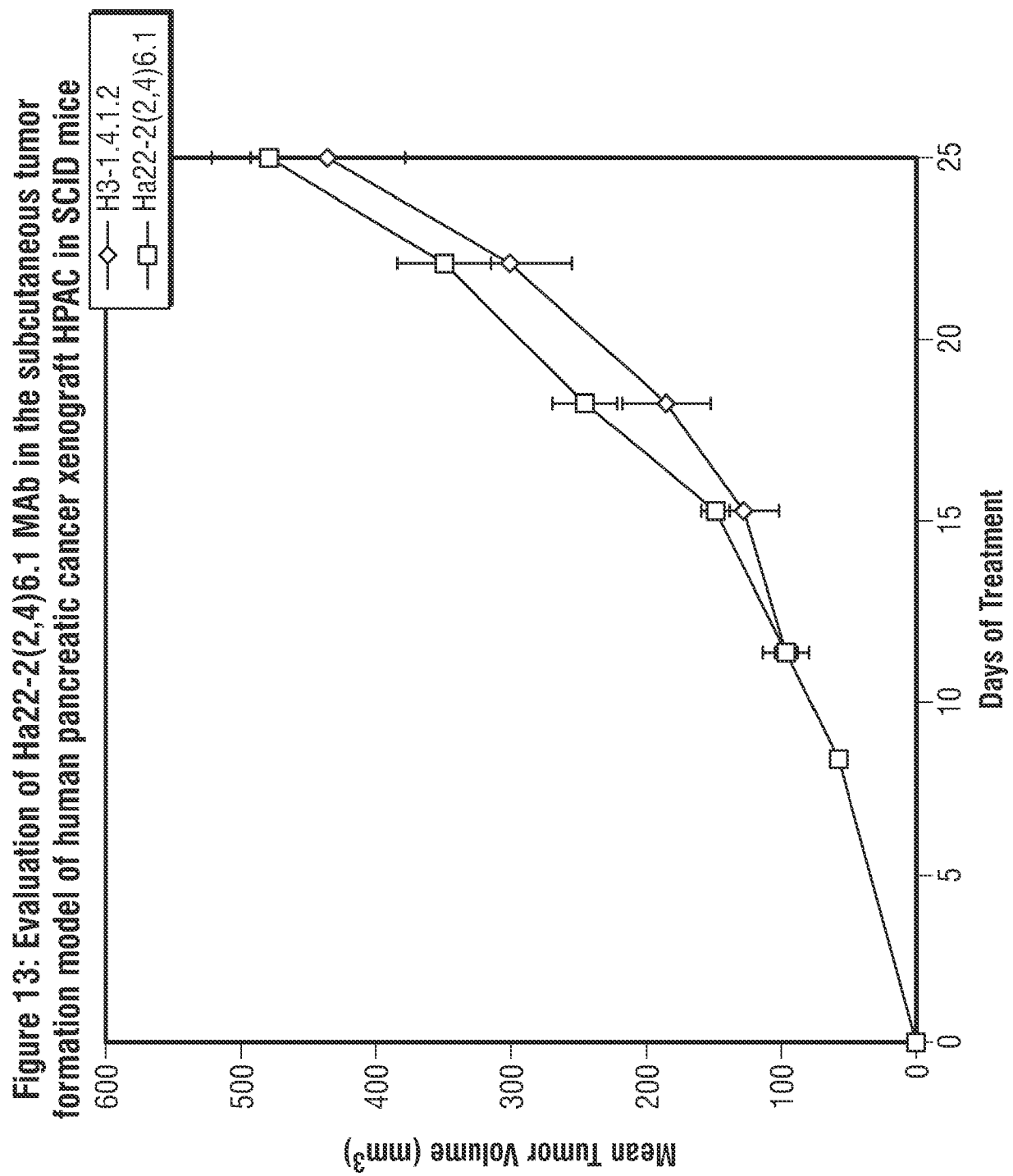


Figure 14: Evaluation of Ha22-2(2,4)6.1 MAb in the subcutaneous tumor formation model of human pancreatic cancer xenograft AG-Panc3 in SCID mice

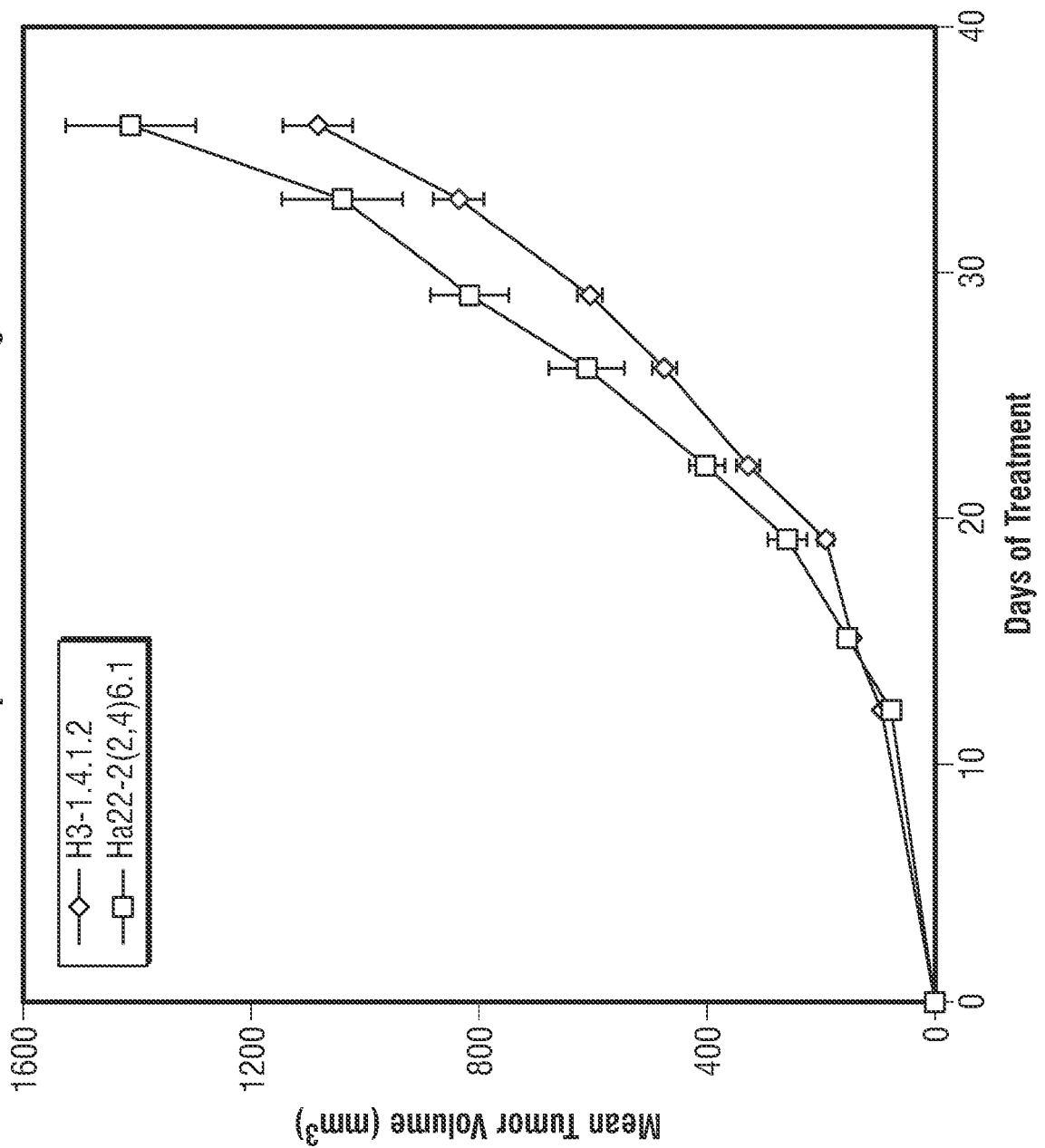


Figure 15: Efficacy of Ha22-2(2,4)6.1-vcMMAE in subcutaneous established human lung cancer xenograft AG-L4 in SCID mice

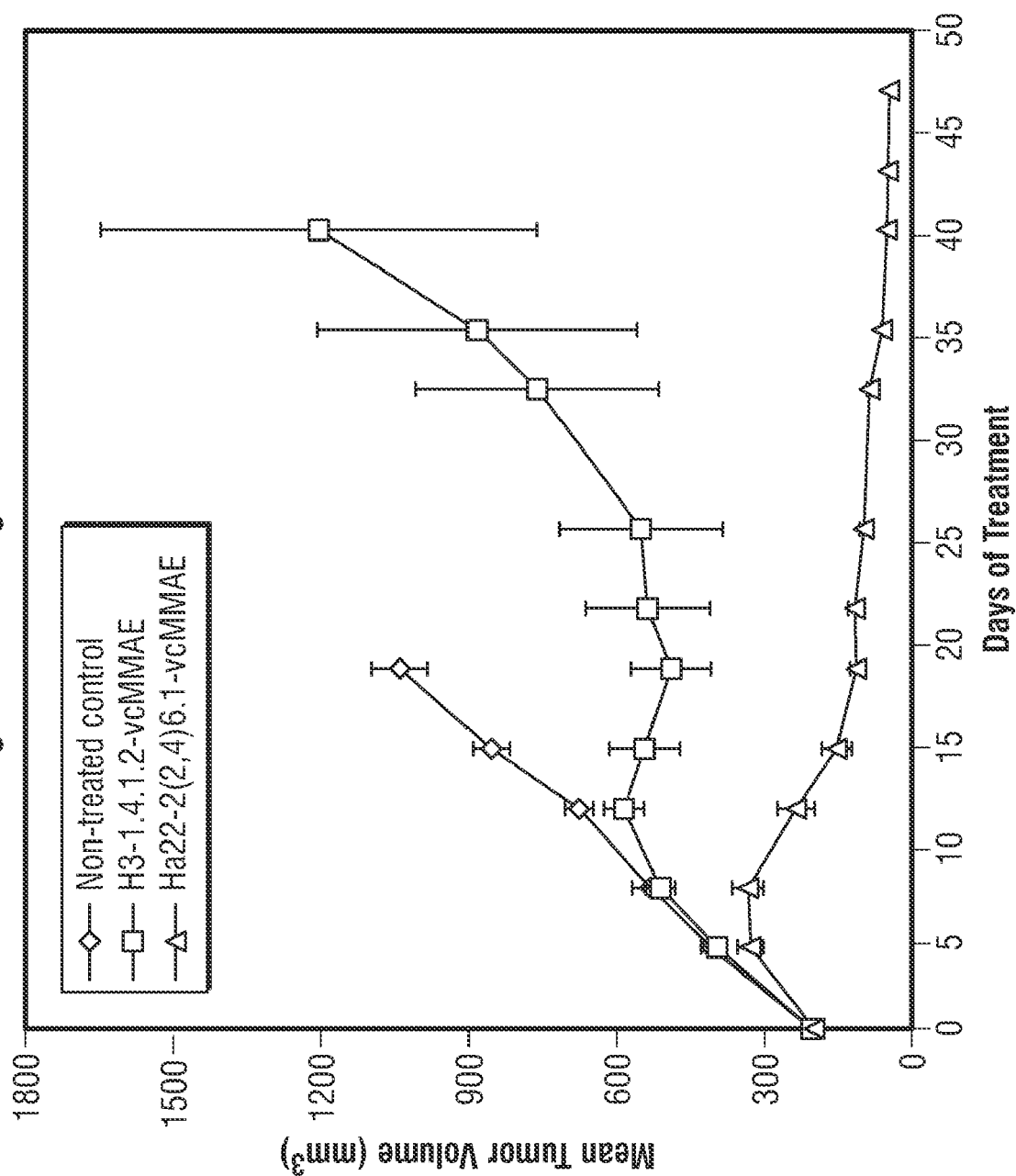


Figure 16: Efficacy of Ha22-2(2,4)6.1-vcMMAE in subcutaneous established human breast cancer xenograft BT-483 in SCID mice

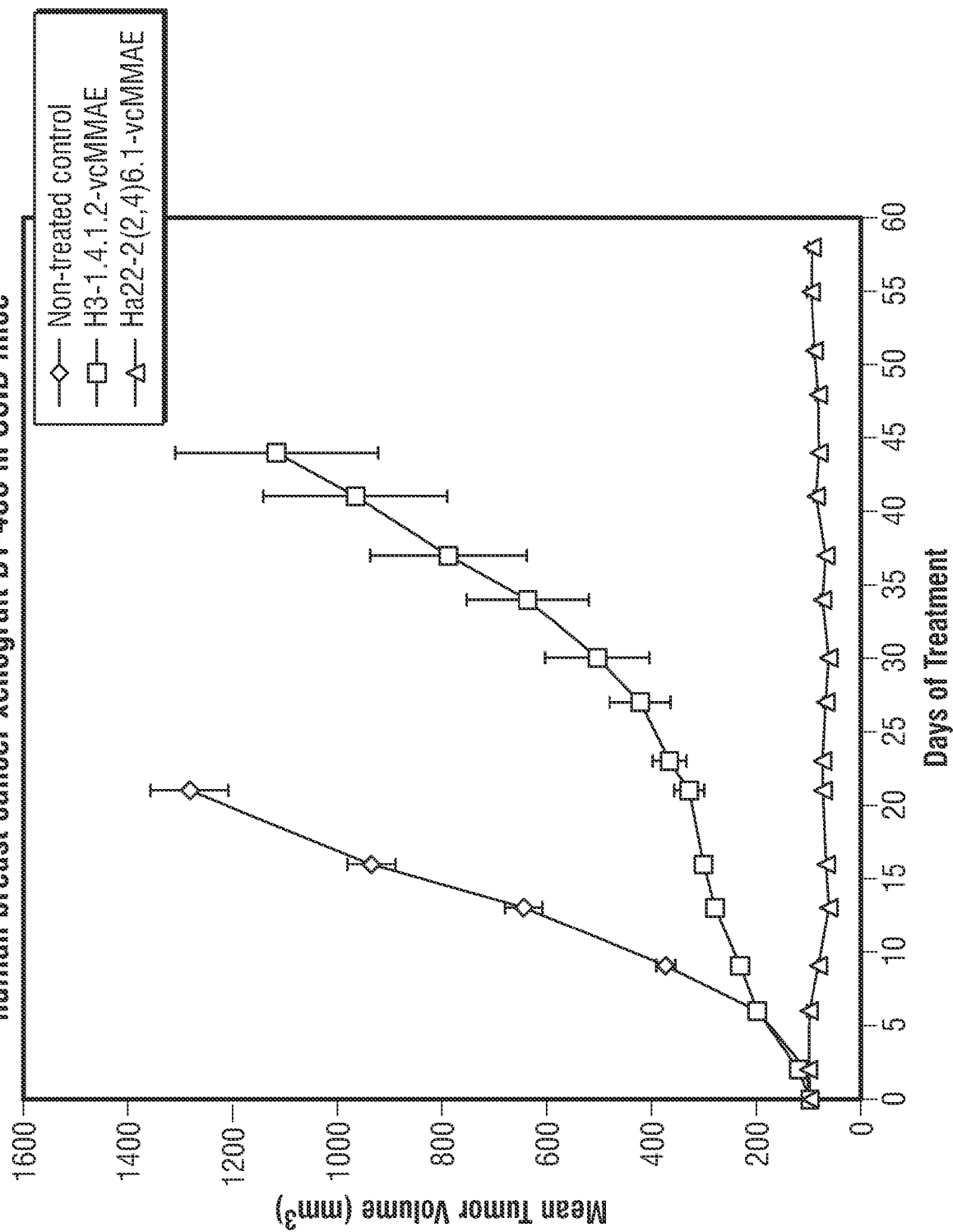


Figure 17: Efficacy of Ha22-2(2,4)6.1-vcMMAE in subcutaneous established human bladder cancer xenograft AG-B1 in SCID mice

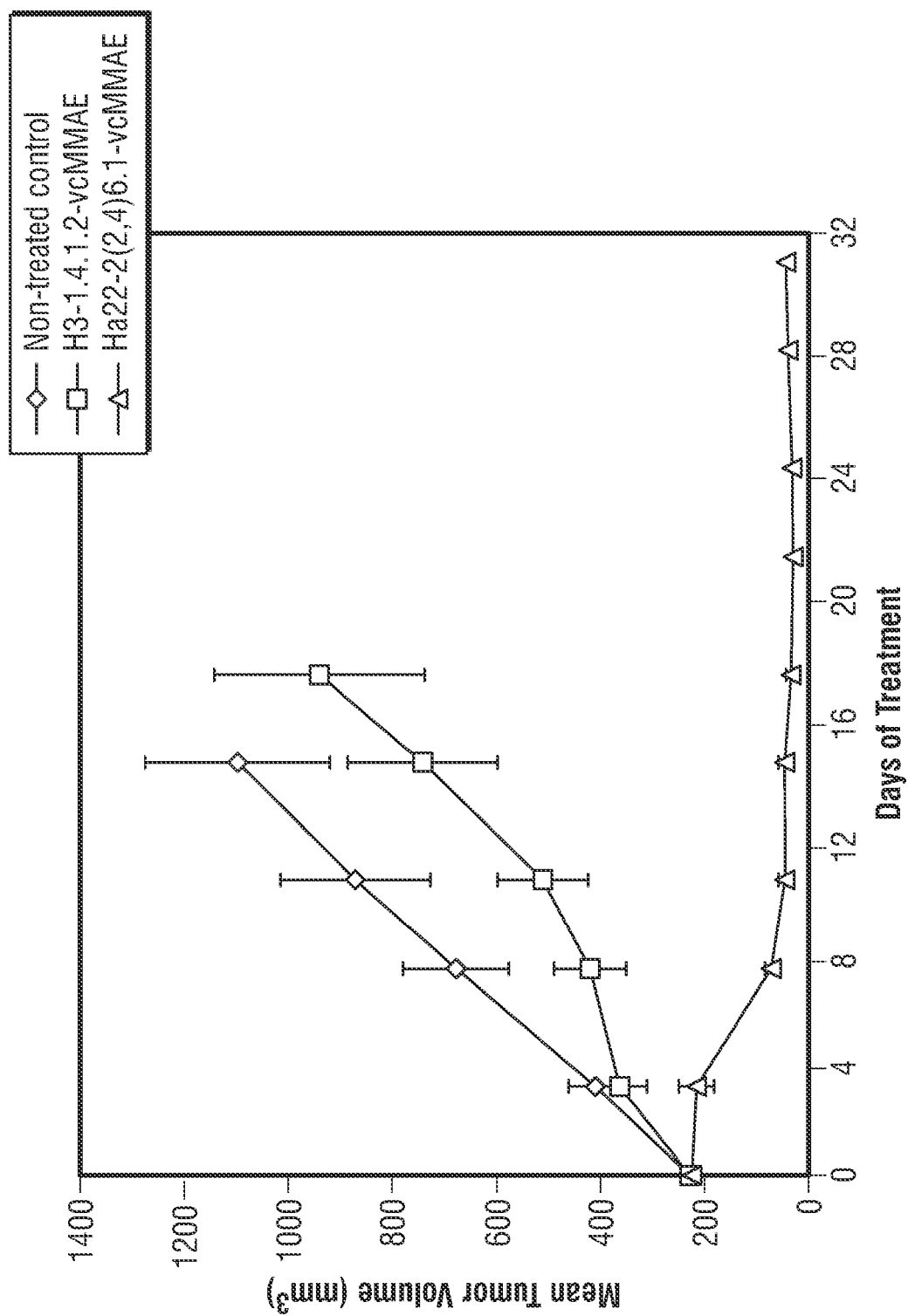


Figure 18: Efficacy of Ha22-2(2,4)6.1-vcMMAE in subcutaneous established human pancreatic cancer xenograft AG-Panc2 in SCID mice

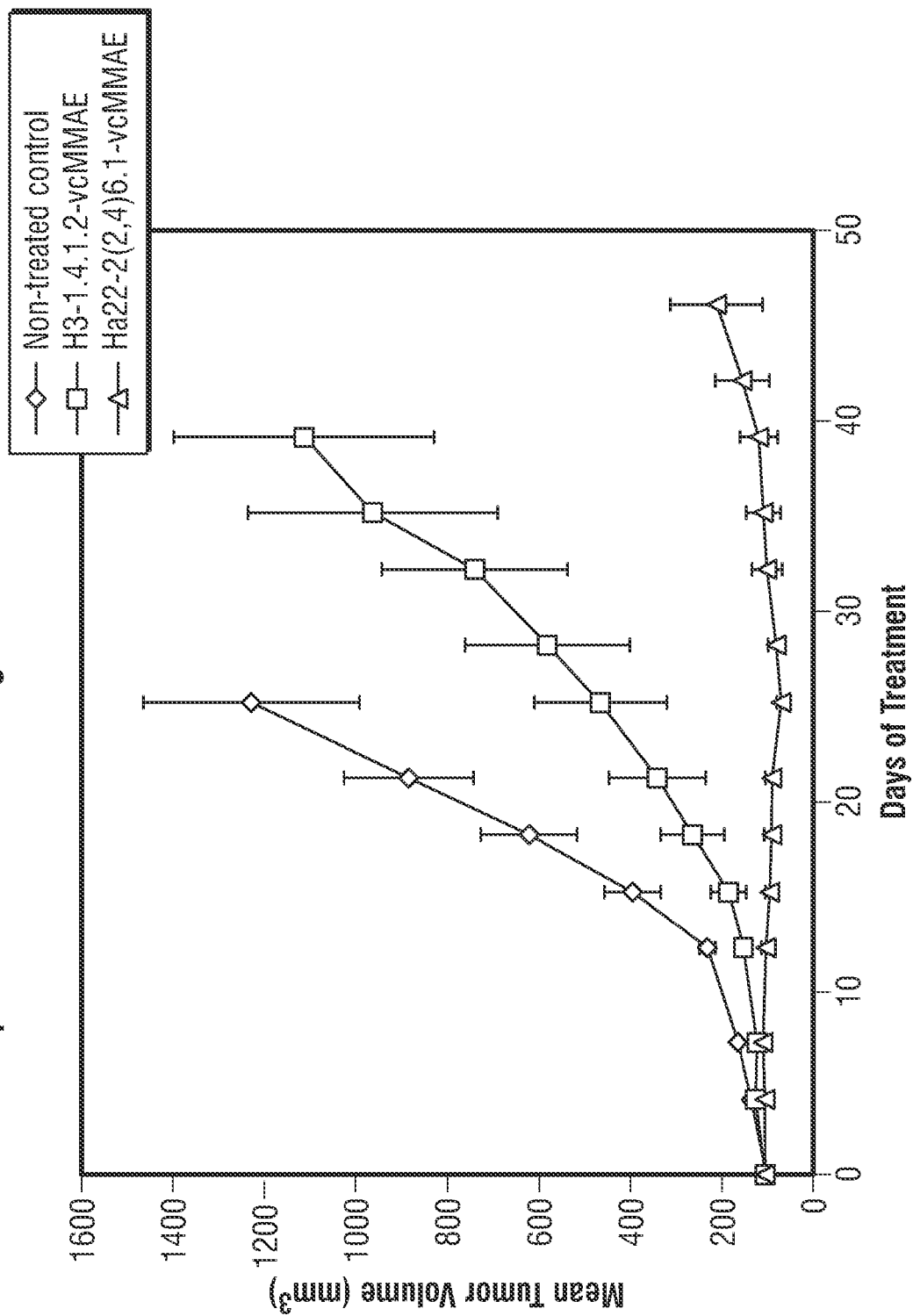


Figure 19: Efficacy of Ha22-2(2,4)6.1-vcMMAE in subcutaneous established human pancreatic cancer xenograft AG-Panc4 in SCID mice

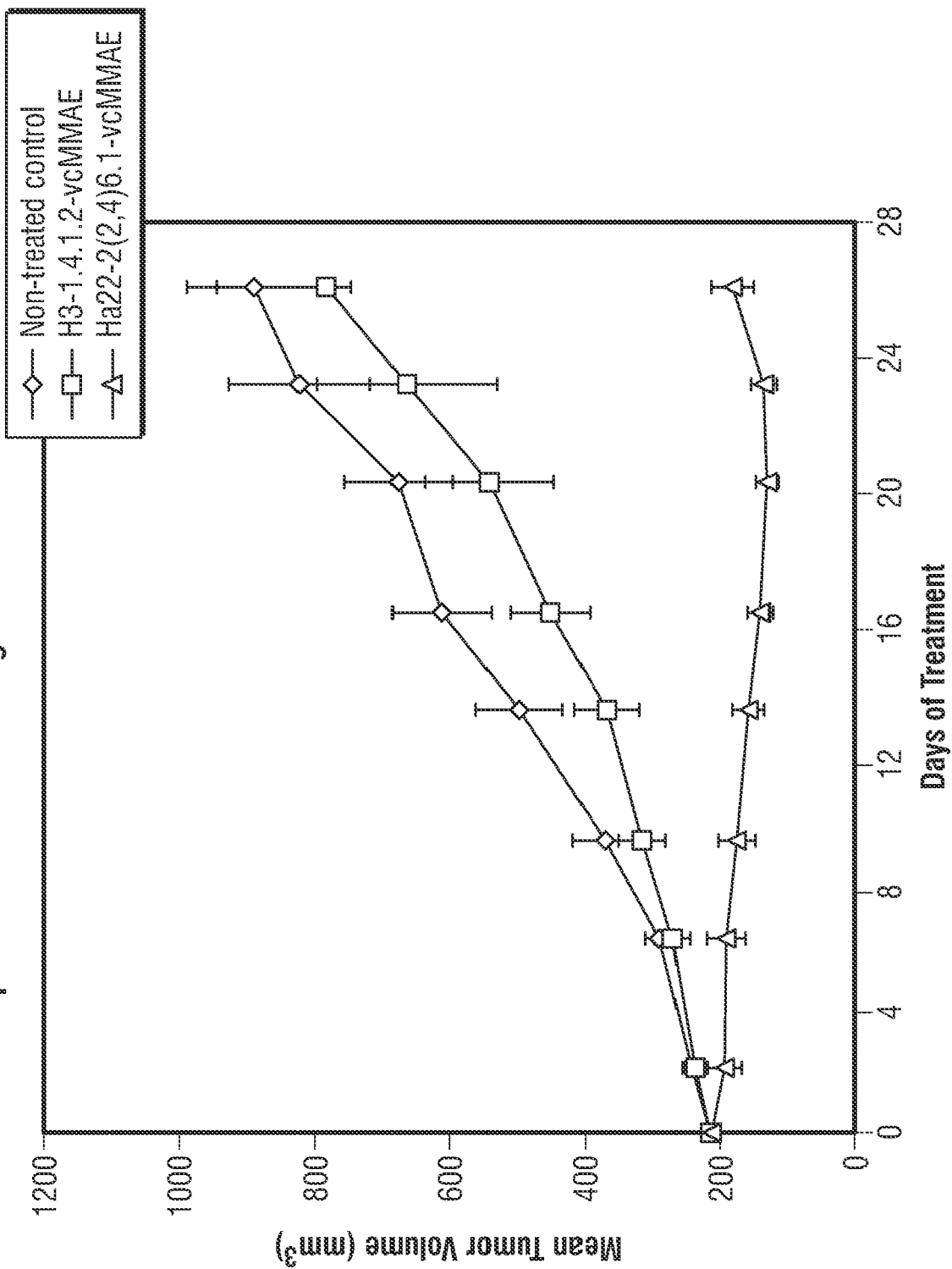


Figure 20: Efficacy of Ha22-2(2,4)6.1-vcMMAE at comparative dosage in subcutaneous established human bladder cancer xenograft AG-B8 in SCID Mice

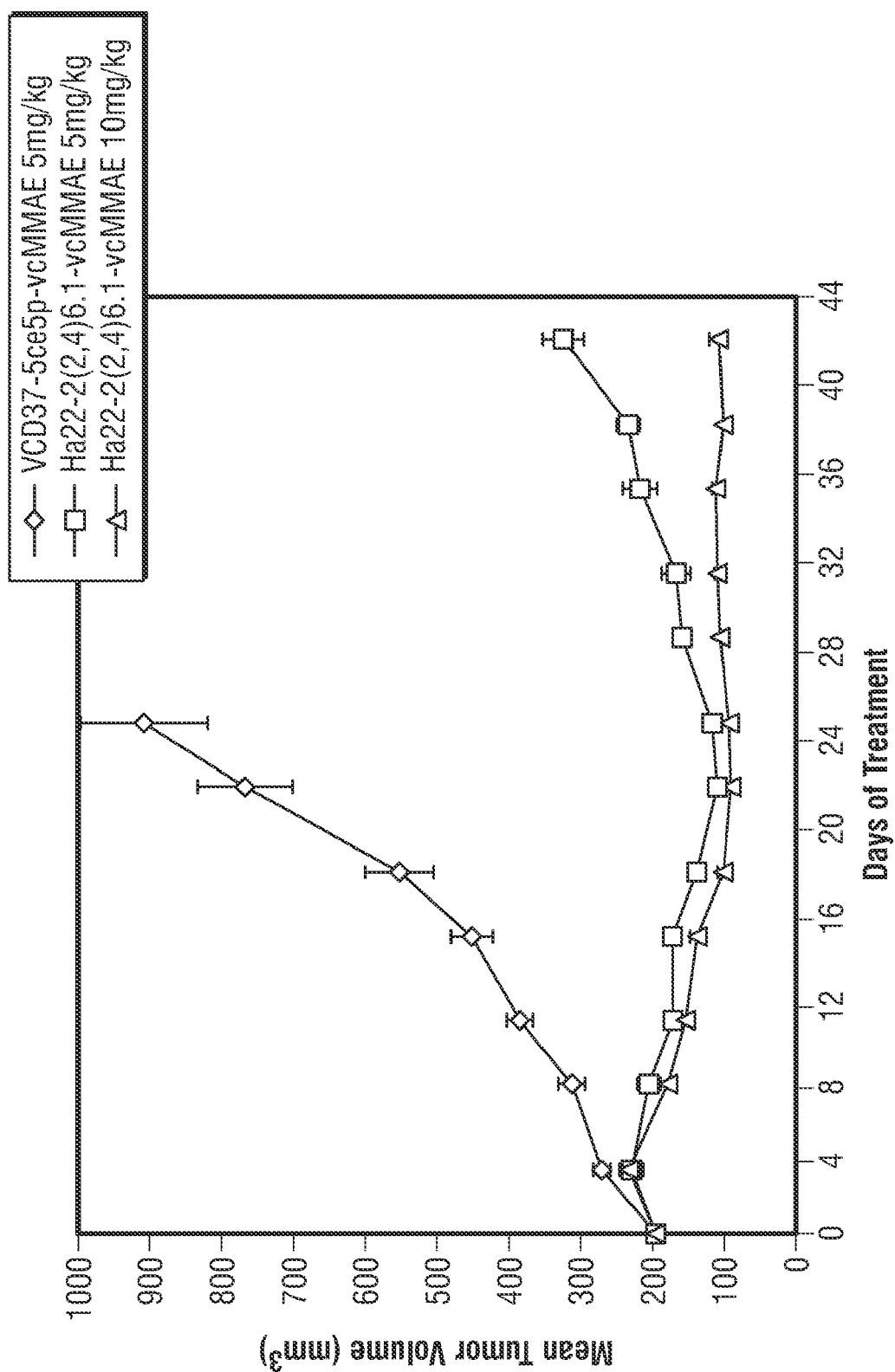


Figure 21: Detection of 191P4D12 protein in cancer patient specimens by immunohistochemistry.

Bladder cancer specimen

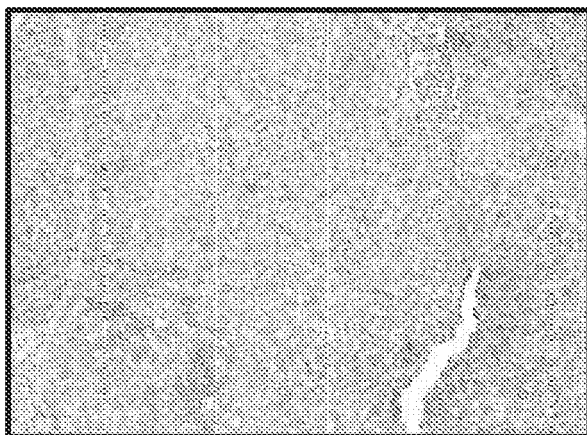


Figure 21A

Bladder cancer specimen



Figure 21B

Breast cancer specimen

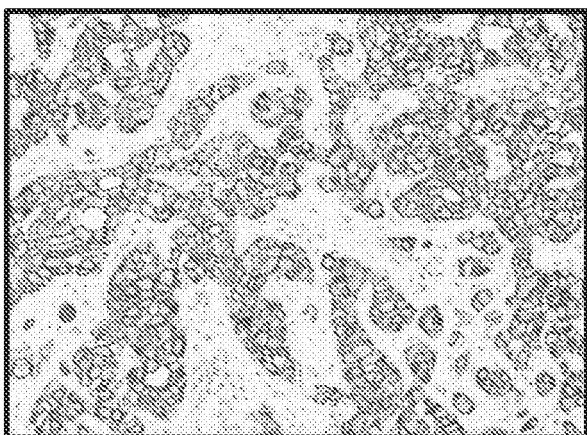


Figure 21C

Breast cancer specimen



Figure 21D

Pancreatic cancer specimen

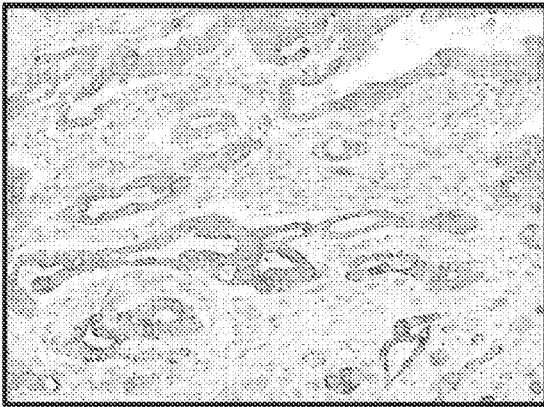


Figure 21E

Pancreatic cancer specimen

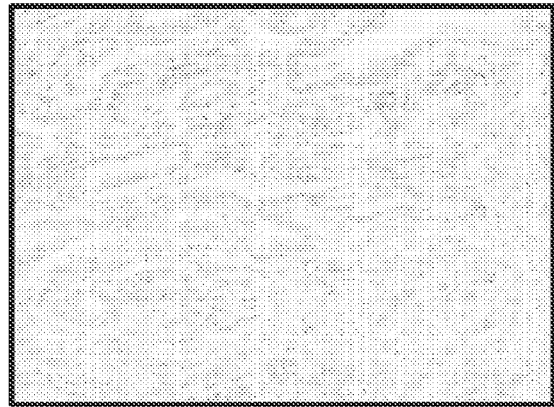


Figure 21F

Lung cancer specimen

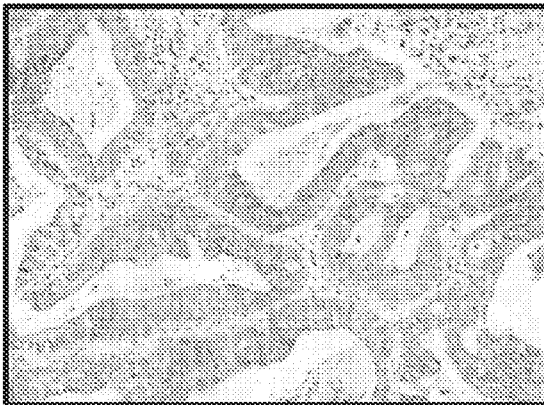


Figure 21G

Lung cancer specimen

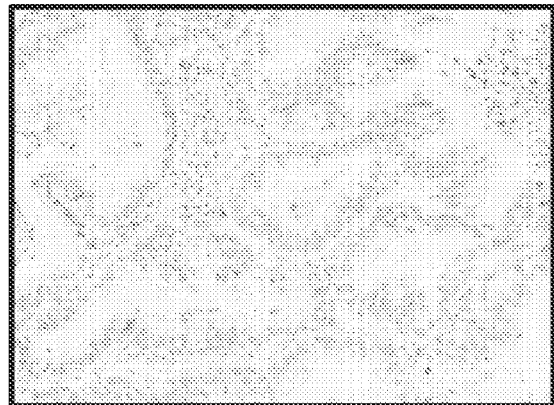


Figure 21H

Ovarian cancer specimen

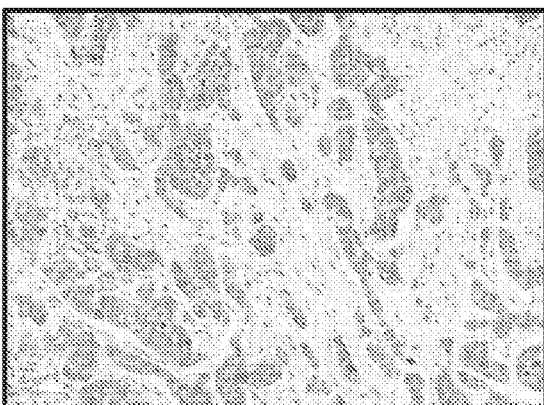


Figure 21I

Ovarian cancer specimen

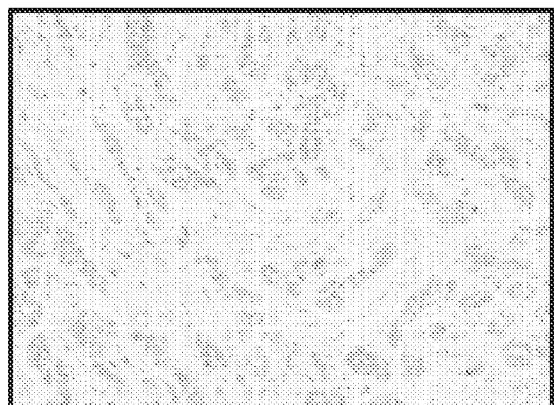


Figure 21J

Esophageal cancer specimens



Figure 21K

Esophageal cancer specimens



Figure 21L

Head and neck cancer specimens

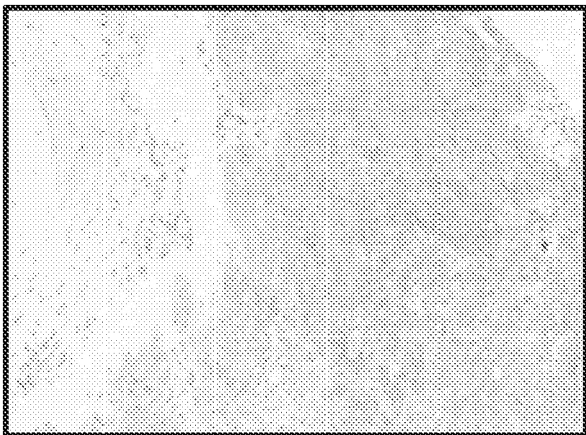


Figure 21M

Head and neck cancer specimens

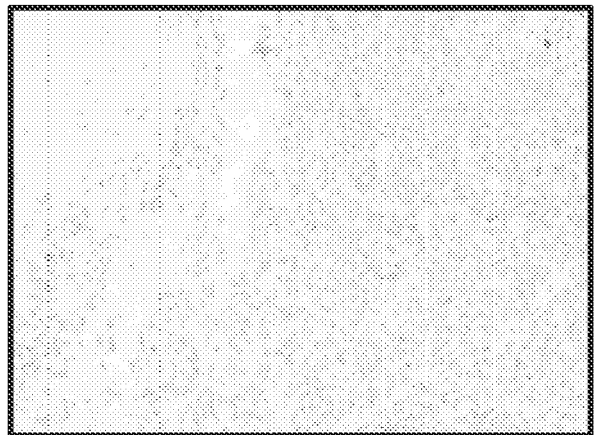


Figure 21N

Figure 22: Binding Curves (Sensograms) Used to Determine Affinity via SPR

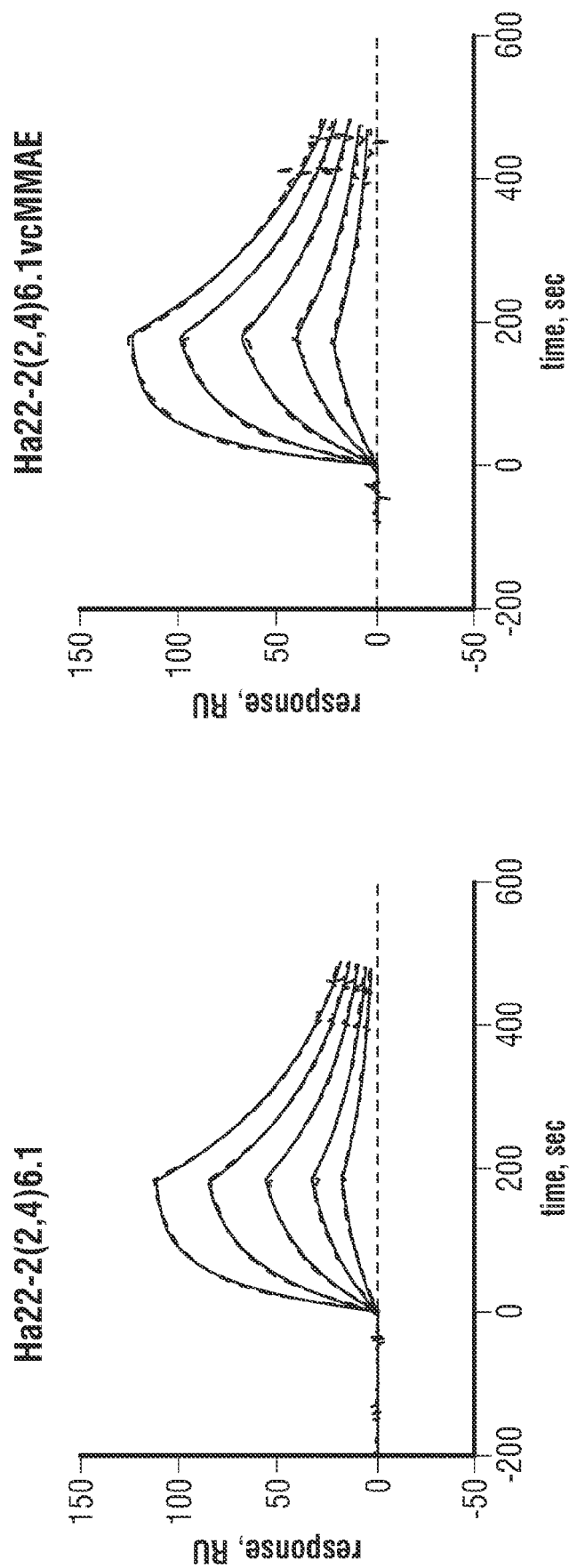


Figure 22A

Figure 22B

Figure 23: Ha22-2(2,4)6.1 binds to PC3 cells expressing 191P4D12 (A) and orthologs from cynomolgus monkey (B), rat (C) and mouse (D)

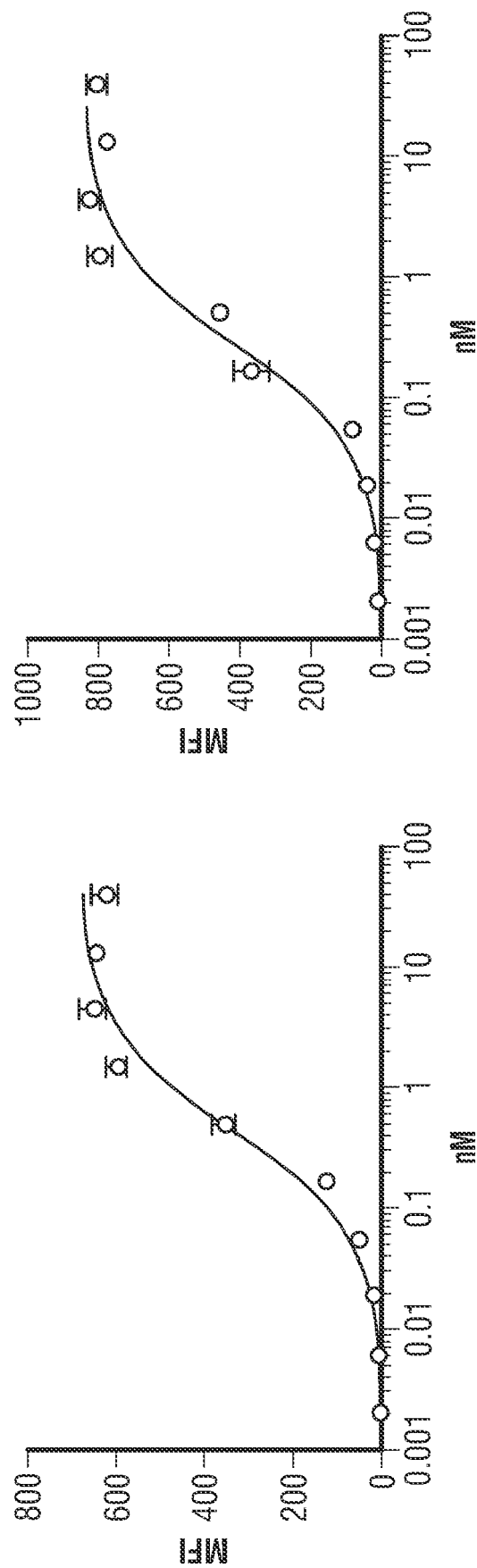


Figure 23A

Figure 23B

Figure 23 (Continued): Ha22-2(2,4)6.1 binds to PC3 cells expressing 191P4D12 (A) and orthologs from cynomolgus monkey (B), rat (C) and mouse (D)

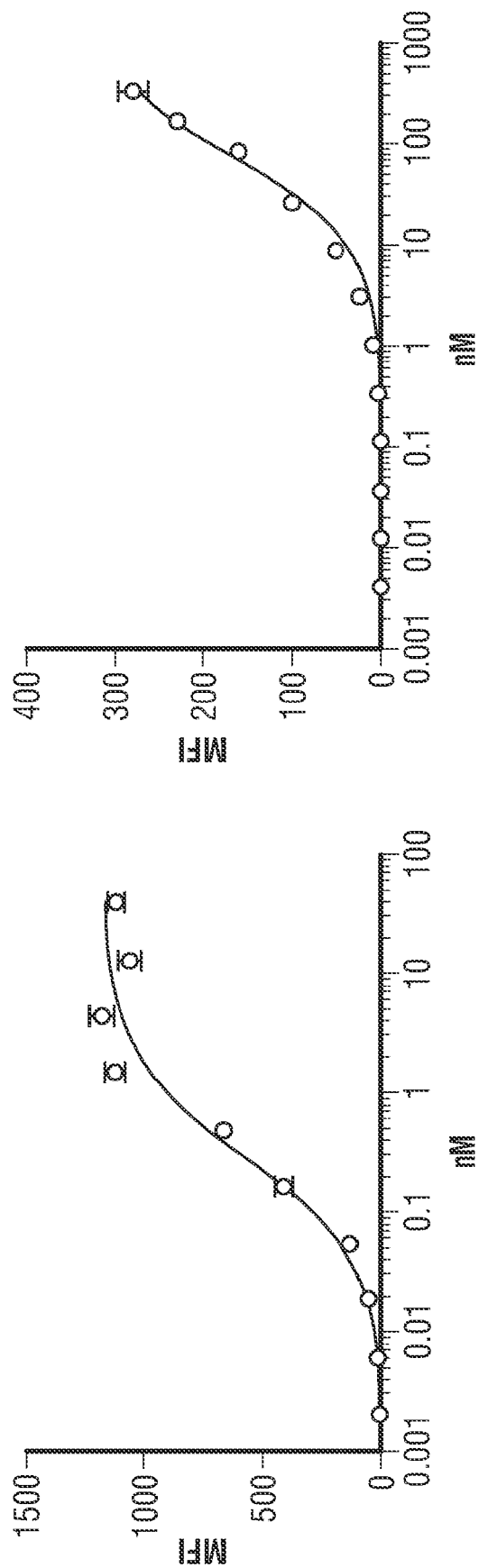


Figure 23D

Figure 23C

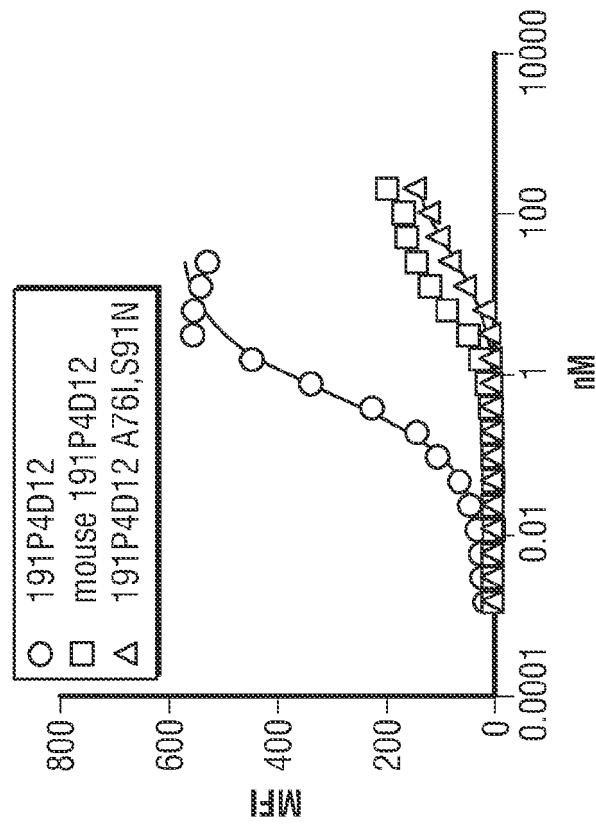


Figure 24B

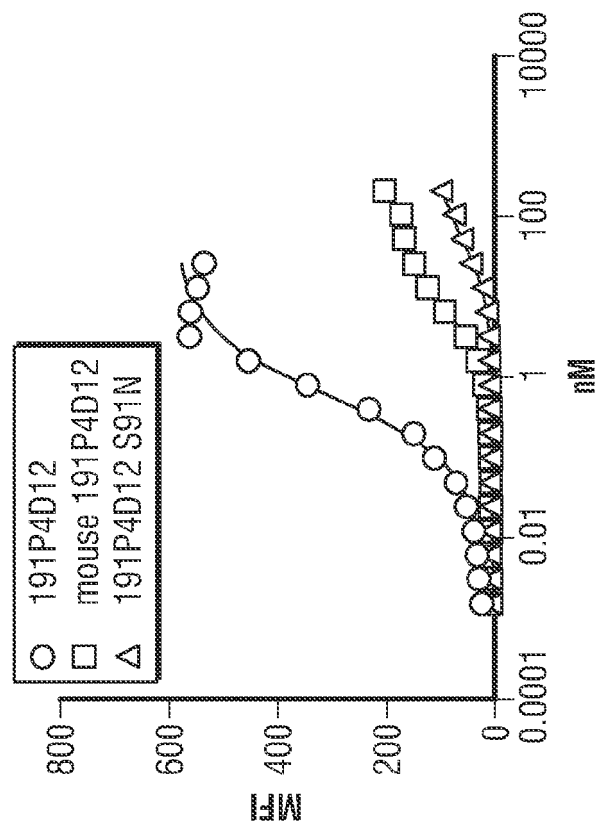


Figure 24A

Figure 24 (Continued):

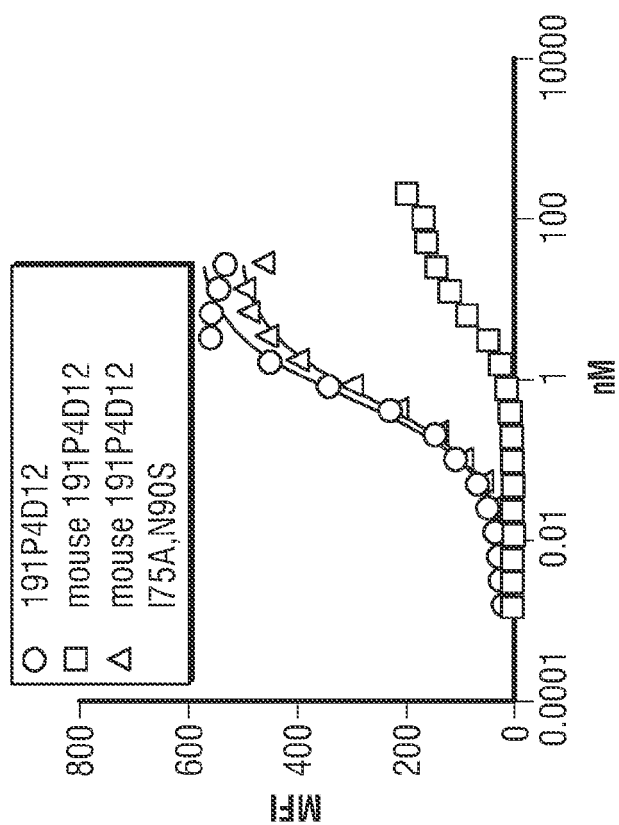


Figure 24D

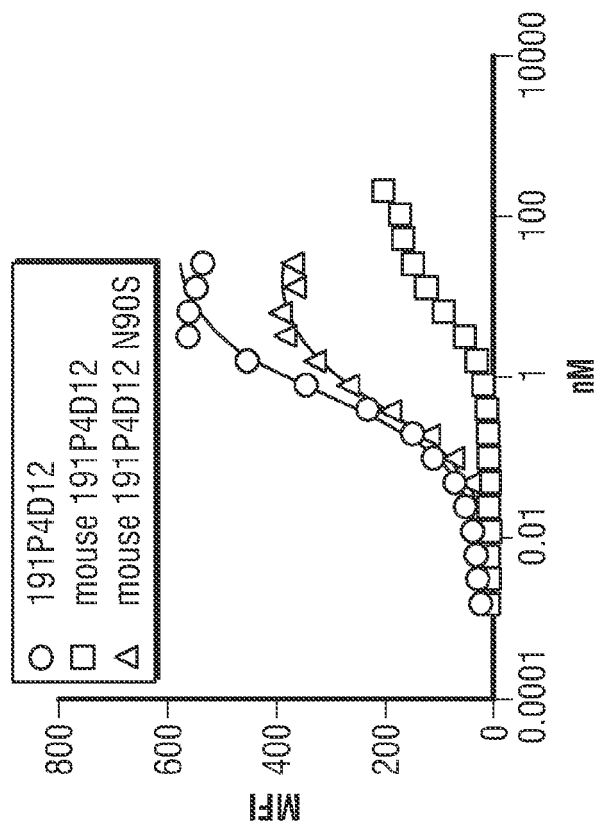


Figure 24C

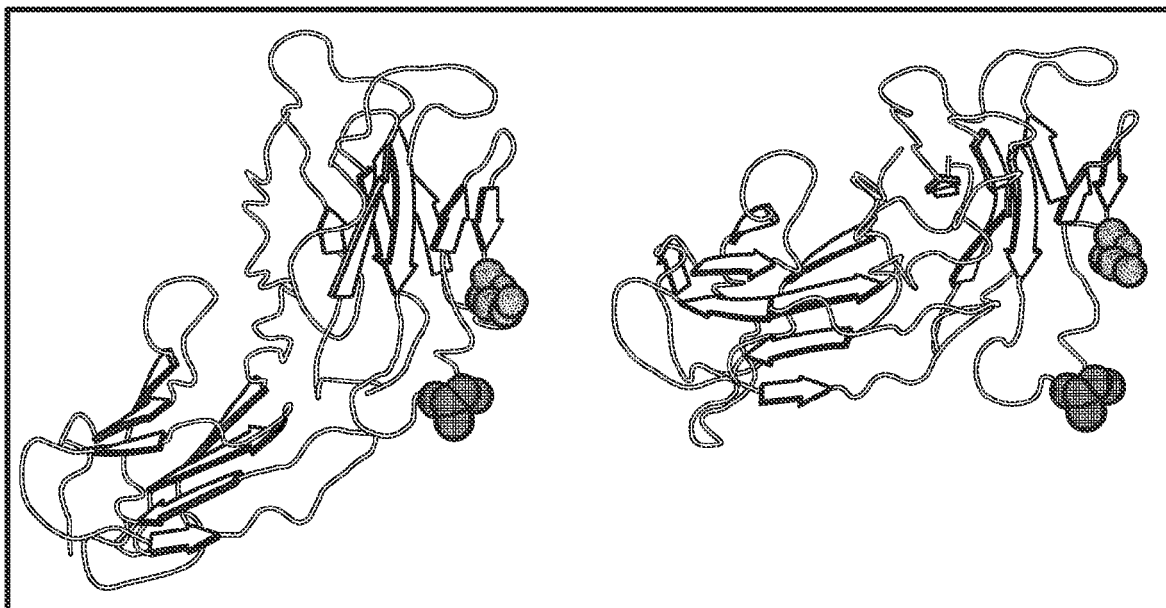


Figure 25

Figure 26: Binding of Ha22-2(2,4)6.1 Mab assessed by FACS

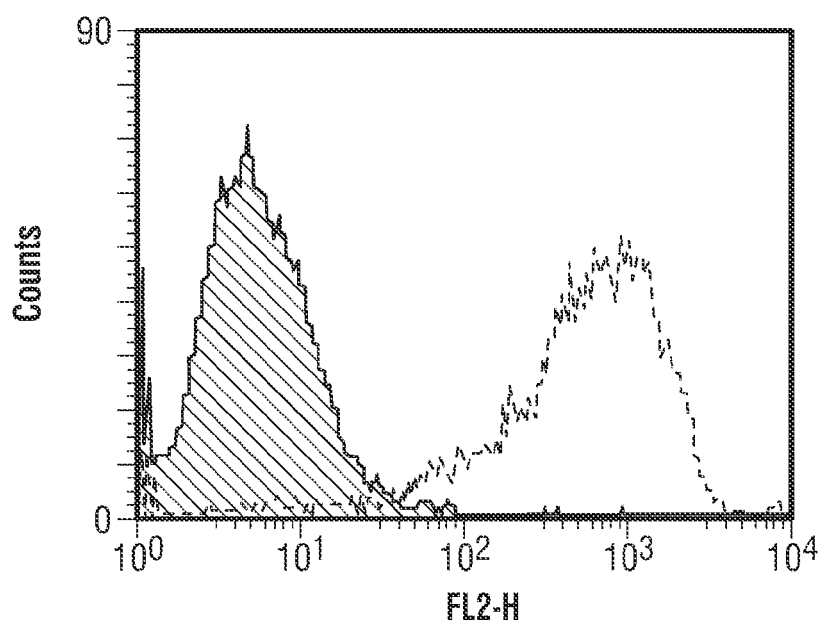


Figure 26A

Figure 26(Continued): Binding of Ha22-2(2,4)6.1 Mab assessed by FACS

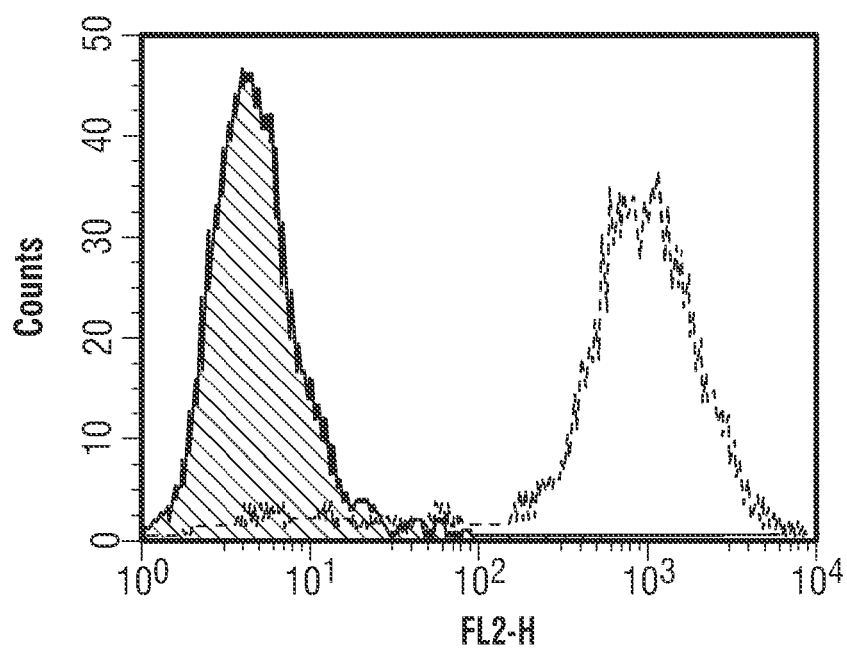


Figure 26B

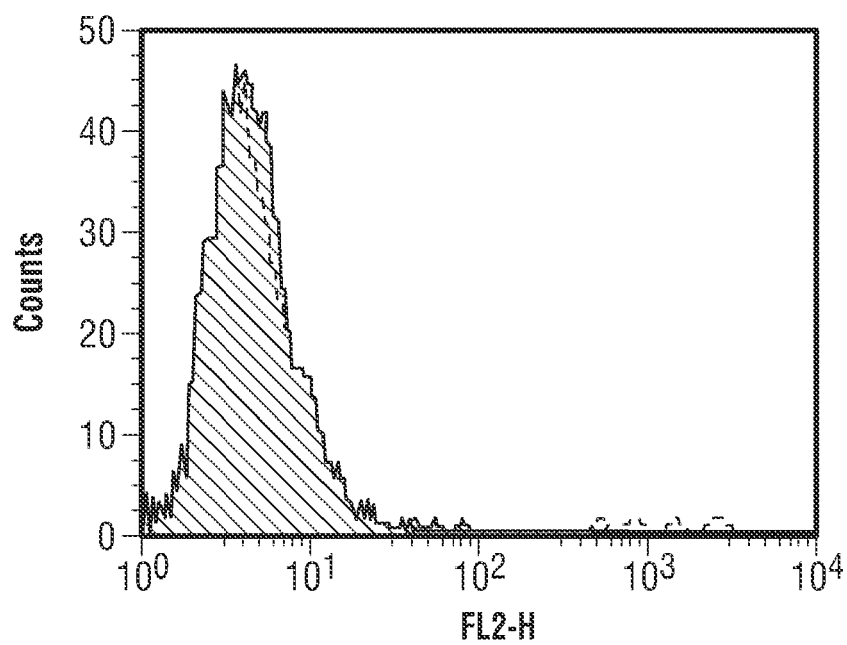


Figure 26C

REFERENCES CITED IN THE DESCRIPTION

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