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(54) **Title**: ANTIBODY-DRUG CONJUGATES

(57) **Abstract**: Disclosed are anti-5T4 antibody drug conjugates and methods for preparing and using the same.

ANTIBODY-DRUG CONJUGATES

Field

The present invention generally relates to anti-5T4 antibody-drug conjugates for the treatment of cancer.

Background

Antibody-drug conjugates (ADCs) combine the binding specificity of monoclonal antibodies with the potency of chemotherapeutic agents. The technology associated with the development of monoclonal antibodies to tumor associated target molecules, the use of more effective cytotoxic agents, and the design of chemical linkers to covalently bind these components, has progressed rapidly in recent years (Ducry L., et al. Bioconjugate Chemistry, 21:5-13, 2010).

Promising ADCs such as SGN-75 (US2009/148942) and trastuzumab-DM1 (US2009/0226465) are currently in clinical trials. However, as other tumor associated antigens are considered for targets, numerous challenges remain. Each monoclonal antibody must be characterized separately, an appropriate linker designed, and a suitable cytotoxic agent identified that retains its potency upon delivery to tumor cells. One must consider the antigen density on the cancer target and whether normal tissues express the target antigen. Other considerations include whether the entire ADC is internalized upon binding the target; whether a cytostatic or cytotoxic drug is preferable when considering possible normal tissue exposure and/or the type and stage of the cancer being treated; and, whether the linker connecting the antibody to the drug payload is a cleavable or a non-cleavable linkage. Furthermore, the antibody to drug moiety conjugation ratio must be sufficient without compromising the binding activity of the antibody and/or the potency of the drug. It is evident that ADCs are complex biologics and the challenges to develop an effective ADC remain significant.

The human 5T4 tumor associated antigen is the target antigen of the present invention. It has recently been shown that the 5T4 antigen is expressed in high levels on certain highly tumorigenic cells, also called tumor-initiating cells (WO2010/111659). Tumor-initiating cells show resistance to standard therapies and are believed to be responsible for tumor recurrence and metastasis and therefore present yet another obstacle for ADC development.

The novel anti-5T4 ADCs of the present invention overcome the challenges associated with ADC technology and provide highly specific and potent ADCs that bind to tumor cells expressing the 5T4 antigen and deliver sufficient cytotoxic drug to the cells, thus providing an innovative and effective treatment for cancer.

Summary

In one embodiment, an antibody-drug conjugate of the present invention has the formula: Ab-(LU-D)*p* or a pharmaceutically acceptable salt thereof wherein, Ab is an anti-5T4 antibody or antigen binding portion thereof, comprising a heavy chain variable region having a VH CDR1 region as shown in SEQ ID NO: 5, a VH CDR2 region as shown in SEQ ID NO: 6, and a VH CDR3 region as shown in SEQ ID NO: 7; LU is a linker unit selected from the group consisting of maleimidocaproyl and maleimidocaproyl-Val-Cit-PABA ; *p* is an integer from about 1 to about 8; and D is a Drug unit selected from the group consisting of MMAE, MMAF, and MMAD.

The present invention further provides anti-5T4 antibody-drug conjugates wherein said anti-5T4 antibody or antigen binding portion thereof, comprises a heavy chain variable region having (a) a VH CDR1 region as shown in SEQ ID NO: 5, (b) a VH CDR2 region as shown in SEQ ID NO: 6, and (c) a VH CDR3 region as shown in SEQ ID NO: 7.

The present invention further provides an anti-5T4 antibody-drug conjugate wherein said anti-5T4 antibody or antigen binding portion thereof, comprises a light chain variable region having (a) a VL CDR1 region as shown in SEQ ID NO: 8, (b) a VL CDR2 region as shown in SEQ ID NO: 9, and (c) a VL CDR3 region as shown in SEQ ID NO: 10.

The present invention further provides an anti-5T4 antibody-drug conjugate wherein said anti-5T4 antibody or antigen binding portion thereof, further comprises a heavy chain variable region having (a) a VH CDR1 region as shown in SEQ ID NO: 5, (b) a VH CDR2 region as shown in SEQ ID NO: 6, and (c) a VH CDR3 region as shown in SEQ ID NO: 7 and a light chain variable region having (a) a VL CDR1 region as shown in SEQ ID NO: 8, (b) a VL CDR2 region as shown in SEQ ID NO: 9, and (c) a VL CDR3 region as shown in SEQ ID NO: 10.

The present invention further provides an anti-5T4 antibody-drug conjugate wherein said anti-5T4 antibody or antigen binding portion thereof, comprises the VH region of SEQ ID NO: 3 and the VL region of SEQ ID NO: 4.

The present invention further provides an anti-5T4 antibody-drug conjugate wherein said anti-5T4 antibody consists of a heavy chain having SEQ ID NO: 1 and a light chain having SEQ ID NO: 2.

The present invention further provides an anti-5T4 antibody-drug conjugate wherein:

(a) said anti-5T4 antibody consists of a heavy chain having SEQ ID NO:1 and a light chain having SEQ ID NO: 2, (b) said LU is maleimidocaproyl, (c) said Drug is MMAF, and (d) *p* is an integer of about 4.

The present invention further provides an anti-5T4 antibody-drug conjugate wherein:

(a) said anti-5T4 antibody consists of a heavy chain having SEQ ID NO:1 and a light chain having SEQ ID NO: 2, (b) said LU is maleimidocaproyl-Val-Cit-PABA, (c) said Drug is MMAE, and (d) *p* is an integer of about 4.

The present invention further provides an anti-5T4 antibody-drug conjugate wherein:

(a) said anti-5T4 antibody consists of a heavy chain having SEQ ID NO:1 and a light chain having SEQ ID NO: 2, (b) said LU is maleimidocaproyl-Val-Cit-PABA, (c) said Drug is MMAD, and (d) *p* is an integer from about 1 to about 8.

The present invention further provides an anti-5T4 antibody-drug conjugate wherein: (a) said anti-5T4 antibody consists of a heavy chain having SEQ ID NO:15 and a light chain having SEQ ID NO: 2, (b) said LU is maleimidocaproyl-Val-Cit-PABA, (c) said Drug is MMAE, and (d) *p* is an integer of about 1 to about 8.

The present invention provides an anti-5T4 antibody-drug conjugate wherein said antibody recognizes an epitope on human 5T4 antigen wherein said epitope comprises amino acid residues 173-258 and 282-361 of the amino acid sequence of SEQ ID NO: 11.

The present invention provides a pharmaceutical composition comprising an antibody-drug conjugate indicated above and a pharmaceutically acceptable carrier.

The present invention further provides a method of treating a 5T4-positive cancer in a patient in need thereof, comprising administering to said patient an antibody-drug conjugate indicated above.

The present invention further provides a method of treating a 5T4-positive cancer wherein said cancer is selected from the group consisting of carcinomas of the bladder, breast, cervix, colon, endometrium, kidney, lung, esophagus, ovary, prostate, pancreas, liver, skin, stomach, and testes.

More preferably, the present invention provides a method of treating a 5T4-positive cancer wherein said cancer is selected from the group consisting of colorectal, breast, pancreatic, and non-small cell lung carcinomas.

The invention further provides an antibody-drug conjugate indicated above for use in therapy.

The invention further provides the use of an antibody-drug conjugate indicated above for the manufacture of a medicament.

The invention further provides the use indicated above, wherein said use is for the treatment of a 5T4-positive cancer and wherein said cancer is selected from the group consisting of carcinomas of the bladder, breast, cervix, endometrium, kidney, lung, esophagus, ovary, prostate, pancreas, skin, stomach, and testes.

More preferably, the invention further provides the use indicated above, wherein said use is for the treatment of a 5T4-positive cancer wherein said cancer is selected from the group consisting of colorectal, breast, pancreatic, and non-small cell lung carcinomas.

The invention further provides a nucleic acid that encodes an anti-5T4 antibody, a vector comprising said nucleic acid, and a host cell comprising said vector.

The invention further provides a process for producing an anti-5T4 antibody comprising cultivating the host cell comprising the above mentioned vector and recovering the antibody from the cell culture.

The invention further provides a process for producing an anti-5T4 antibody-drug conjugate comprising: (a) taking the antibody recovered from the cell culture, (b) chemically linking said antibody via a linker unit selected from the group consisting of maleimidocaproyl or maleimidocaproyl-Val-Cit to a Drug unit selected from the group consisting of MMAE, MMAD, or MMAF, and (c) purifying the antibody-drug conjugate.

Detailed Description

The present invention provides anti-5T4 antibody-drug conjugates for the treatment of cancer. In order that the present invention is more readily understood, certain terms are first defined.

All amino acid abbreviations used in this disclosure are those accepted by the United States Patent and Trademark Office as set forth in 37 C.F.R. § 1.822 (B)(I).

5T4 refers to the 5T4 oncofetal antigen, a 72 kDa highly glycosylated transmenbrance glycoprotein comprising a 42 kDa non-glycosylated core (see US 5,869,053). Human 5T4 is expressed in numerous cancer types, including carcinomas of the bladder, breast, cervix, colon, endometrium, kidney, lung, esophagus, ovary, prostate, pancreas, liver, skin, stomach, and testes. Highly tumorigenic cells, also called cancer stem cells or tumor-initiating cells have been shown to have high levels of 5T4 expression (WO2010/111659). Anti-5T4 antibodies of the invention include antibodies that specifically bind the human 5T4 antigen (see US 2007/0231333).

An “antibody” is an immunoglobulin molecule capable of specific binding to a target, such as a carbohydrate, polynucleotide, lipid, polypeptide, etc., through at least one antigen recognition site, located in the variable region of the immunoglobulin molecule. As used herein, the term “antibody” encompasses not only intact polyclonal or monoclonal antibodies, but also any antigen binding fragment (i.e., "antigen-binding portion") or single chain thereof, fusion proteins comprising an antibody, and any other modified configuration of the immunoglobulin molecule that comprises an antigen recognition site including, for example without limitation, Fab, Fab’, $F(ab')_2$, an Fd fragment consisting of the VH and CH1 domains, an Fv fragment consisting of the VL and VH domains of a single arm of an antibody, an isolated complementarity determining region (CDR), scFv, single domain antibodies (e.g., shark and camelid antibodies), maxibodies, minibodies, intrabodies, diabodies, triabodies, tetrabodies, v-NAR and bis-scFv.

An antibody includes an antibody of any class, such as IgG, IgA, or IgM (or sub-class thereof), and the antibody need not be of any particular class. Depending on the antibody amino acid sequence of the constant region of its heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2. The heavy-chain constant regions that correspond to the different classes of immunoglobulins are called alpha, delta, epsilon, gamma, and mu, respectively. The subunit structures and three-dimensional configurations of different classes of immunoglobulins are well known.

A “variable region” of an antibody refers to the variable region of the antibody light chain or the variable region of the antibody heavy chain, either alone or in combination. As known in the art, the variable regions of the heavy and light chain each consist of four framework regions (FRs) connected by three complementarity determining regions (CDRs) also known as hypervariable regions, contribute to the formation of the antigen binding site of antibodies. If variants of a subject variable region are desired, particularly with substitution in amino acid residues outside of a CDR region (i.e., in the framework region), appropriate amino acid substitution, preferably, conservative amino acid substitution, can be identified by comparing the subject variable region to the variable regions of other antibodies which contain CDR1 and CDR2 sequences in the same canonincal class as the subject variable region (Chothia and Lesk, J Mol Biol 196(4): 901-917, 1987). When choosing FR to flank subject CDRs, e.g., when humanizing or optimizing an antibody, FRs from antibodies which contain CDR1 and CDR2 sequences in the same canonical class are preferred.

A “CDR” of a variable domain are amino acid residues within the variable region that are identified in accordance with the definitions of the Kabat, Chothia, the cumulation of both Kabat and Chothia, AbM, contact, and/or conformational definitions or any method of CDR determination well known in the art. Antibody CDRs may be identified as the hypervariable regions originally defined by Kabat et al. See, e.g., Kabat et al., 1992, Sequences of Proteins of Immunological Interest, 5th ed., Public Health Service, NIH, Washington, D.C. The positions of the CDRs may also be identified as the structural loop structures originally described by Chothia and others. See, e.g., Chothia et al., 1989, Nature 342:877-883. Other approaches to CDR identification include the “AbM definition,” which is a compromise between Kabat and Chothia and is derived using Oxford Molecular's AbM antibody modeling software (now Accelrys®), or the “contact definition” of CDRs based on observed antigen contacts, set forth in MacCallum et al., 1996, J. Mol. Biol., 262:732-745. In another approach, referred to herein as the “conformational definition” of CDRs, the positions of the CDRs may be identified as the residues that make enthalpic contributions to antigen binding. See, e.g., Makabe et al., 2008, Journal of Biological Chemistry, 283:1156-1166. Still other CDR boundary definitions may not strictly follow one of the above approaches, but will nonetheless overlap with at least a portion of the Kabat CDRs, although they may be shortened or lengthened in light of prediction or experimental findings that particular residues or groups of residues or even entire CDRs do not significantly impact antigen binding. As used herein, a CDR may refer to CDRs defined by any approach known in the art, including combinations of approaches. The methods used herein may utilize CDRs defined according to any of these approaches. For any given embodiment containing more than one CDR, the CDRs may be defined in accordance with any of Kabat, Chothia, extended, AbM, contact, and/or conformational definitions.

The term "monoclonal antibody" (Mab) refers to an antibody that is derived from a single copy or clone, including e.g., any eukaryotic, prokaryotic, or phage clone, and not the method by which it is produced. Preferably, a monoclonal antibody of the invention exists in a homogeneous or substantially homogeneous population.

"Humanized" antibody refers to forms of non-human (e.g. murine) antibodies that are chimeric immunoglobulins, immunoglobulin chains, or fragments thereof (such as Fv, Fab, Fab', $F(ab')_2$ or other antigen-binding subsequences of antibodies) that contain minimal sequence derived from non-human immunoglobulin. Preferably, humanized antibodies are human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat, or rabbit having the desired specificity, affinity, and capacity.

The term “chimeric antibody” is intended to refer to antibodies in which the variable region sequences are derived from one species and the constant region sequences are derived from another species, such as an antibody in which the variable region sequences are derived from a mouse antibody and the constant region sequences are derived from a human antibody.

Antibodies of the invention can be produced using techniques well known in the art, e.g., recombinant technologies, phage display technologies, synthetic technologies or combinations of such technologies or other technologies readily known in the art (see, for example, Jayasena, S.D., Clin. Chem., 45: 1628-50 (1999) and Fellouse, F.A., et al, J. Mol. Biol., 373(4):924-40 (2007)).

Tables 1 and 2 below depict preferred CDRs for the antibodies of the present invention.

Table 1

Antibody	**LCDR1**	**LCDR2**	**LCDR3**
A1	KASQSVSNDVA SEQ ID NO: 8	FATNRYT SEQ ID NO: 9	QQDYSSPWT SEQ ID NO: 10
A3	KASQDVDTAVA SEQ ID NO: 17	WASTRLT SEQ ID NO: 18	QQYSSYPYT SEQ ID NO: 19

Table 2

Antibody	**HCDR1**	**HCDR2**	**HCDR3**
A1	NFGMN SEQ ID NO: 5	WINTNTGEPRYAEEFKG SEQ ID NO: 6	DWDGAYFFDY SEQ ID NO: 7
A1-IgG4	GYTFTNFGMN SEQ ID NO: 14	WINTNTGEPRYAEEFKG SEQ ID NO: 6	DWDGAYFFDY SEQ ID NO: 7
A3	TYAMN SEQ ID NO: 22	RIRSKSNNYATYYADSVKD SEQ ID NO: 23	QWDYDVRAMNY SEQ ID NO: 24

The present invention includes an antibody or antigen binding portion thereof, that comprises:

a) a light chain variable region comprising:

i) a LCDR1 having an amino acid sequence selected from the group consisting of SEQ ID NOs: 8 and 17;

ii) a LCDR2 having an amino acid sequence selected from the group consisting of SEQ ID NOs: 9 and 18; and

iii) a LCDR3 having an amino acid sequence selected from the group consisting of SEQ ID NOs: 10 and 19; and

b) a heavy chain variable region comprising:

i) a HCDR1 having an amino acid sequence selected from the group consisting of SEQ ID NOs: 5 and 22;

ii) a HCDR2 having an amino acid sequence selected from the group consisting of SEQ ID NOs: 6 and 23; and

iii) a LCDR1 having an amino acid sequence selected from the group consisting of SEQ ID NOs: 7 and 24.

A preferred antibody or antigen binding portion thereof, of the invention comprises:

a) a LCVR comprising: a LCDR1 of SEQ ID NO: 8, a LCDR2 of SEQ ID NO: 9, and a LCDR3 of SEQ ID NO: 10; and

b) a HCVR comprising: a HCDR1 of SEQ ID NO: 5, a HCDR2 of SEQ ID NO: 6, and a HCDR3 of SEQ ID NO: 7.

Preferred monoclonal antibodies of the invention are referred to herein as A1 (a humanized anti-5T4 IgG1 antibody); A1-IgG4 (a humanized anti-5T4 IgG4 antibody); A3 (a mouse/human chimeric antibody); and A3hu (a humanized anti-5T4 IgG1 antibody). The SEQ ID NOs of the amino acid sequences encoding Mabs A1,A1-IgG4 and A3 are provided in Table 3 below:

Table 3

Mab	LC	HC	LCVR	LCDR1	LCDR2	LCDR3	HCVR	HCDR1	HCDR2	HCDR3
A1	2	1	4	8	9	10	3	5	6	7
A1-IgG4	2	12	4	8	9	10	13	5	6	7
A3	2	15	21	22	23	24	16	17	18	19
A3hu	30	25	31	32	33	34	26	27	28	29

The phrases "an antibody recognizing an antigen" and "an antibody specific for an antigen" are used interchangeably herein with the term "an antibody which binds specifically to an antigen."

Anti-5T4 Antibody-Drug conjugate refers to an anti-5T4 antibody or antigen binding portion thereof, as described herein linked to a cytotoxic drug moiety (D) via a linker unit molecule (LU).

Linker Unit (LU): LU describes the direct or indirect linkage of the antibody to the drug. Attachment of a linker to a mAb can be accomplished in a variety of ways, such as through surface lysines, reductive-coupling to oxidized carbohydrates, and through cysteine residues liberated by reducing interchain disulfide linkages. A variety of ADC linkage systems are known in the art, including hydrazone-, disulfide- and peptide-based linkages.

Drug (D): A drug is any substance having biological or detectable activity, for example, therapeutic agents, detectable labels, binding agents, etc., and prodrugs, which are metabolized to an active agent *in vivo*. The terms drug and payload are used interchangeably. 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 Nos. 6,884,869, 7,098,308, 7,256,257, 7,423,116, 7,498,298 and 7,745,394, each of which is incorporated by reference herein in its entirety and for all purposes.

Auristatins have been shown to interfere with microtubule dynamics and nuclear and cellular division and have anticancer activity. Auristatins of the present invention bind tubulin and can exert a cytotoxic or cytostatic effect on a 5T4 expressing cell or cell line. There are a number of different assays, known in the art, that can be used for determining whether an auristatin or resultant antibody-drug conjugate exerts a cytostatic or cytotoxic effect on a desired cell or cell line. 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.

Examples of drugs or payloads are selected from the group consisting of DM1 (maytansine, N2'-deacetyl-N2'-(3-mercapto-1-oxopropyl)- or N2'-deacetyl-N2'-(3-mercapto-1-oxopropyl)-maytansine), mc-MMAD (6-maleimidocaproyl-monomethylauristatin-D or N-methyl-L-valyl-N-[(1S,2R)-2-methoxy-4-[(2S)-2-[(1R,2R)-1-methoxy-2-methyl-3-oxo-3-[[(1S)-2-phenyl-1-(2-thiazolyl)ethyl]amino]propyl]-1-pyrrolidinyl]-1-[(1S)-1-methylpropyl]-4-oxobutyl]-N-methyl- (9Cl)- L-valinamide), mc-MMAF (maleimidocaproyl-monomethylauristatin F or N-[6-(2,5-dihydro-2,5-dioxo-1H-pyrrol-1-yl)-1-oxohexyl]-N-methyl-L-valyl-L-valyl-(3R,4S,5S)-3-methoxy-5-methyl-4-(methylamino)heptanoyl-(αR,βR,2S)-β-methoxy-α-methyl-2-pyrrolidinepropanoyl-L-phenylalanine) and mc-Val-Cit-PABA-MMAE (6-maleimidocaproyl –ValcCit-(p-aminobenzyloxycarbonyl)-monomethylauristatin E or N-[[[4-[[N-[6-(2,5-dihydro-2,5-dioxo-1H-pyrrol-1-yl)-1-oxohexyl]-L-valyl-N5-(aminocarbonyl)-L-ornithyl]amino]phenyl]methoxy]carbonyl]-N-methyl-L-valyl-N-[(1S,2R)-4-[(2S)-2-[(1R,2R)-3-[[(1R,2S)-2-hydroxy-1-methyl-2-phenylethyl]amino]-1-methoxy-2-methyl-3-oxopropyl]-1-pyrrolidinyl]-2-methoxy-1-[(1S)-1-methylpropyl]-4-oxobutyl]-N-methyl-L-valinamide). DM1 is a derivative of the tubulin inhibitor maytansine while MMAD, MMAE, and MMAF are auristatin derivatives. The preferred payloads of the present invention are selected from the group consisting of mc-MMAF and mc-Val-Cit-PABA-MMAE.

The term "epitope" refers to that portion of a molecule capable of being recognized by and bound by an antibody at one or more of the antibody's antigen-binding regions. Epitopes often consist of a chemically active surface grouping of molecules such as amino acids or sugar side chains and have specific three-dimensional structural characteristics as well as specific charge characteristics. The term "antigenic epitope" as used herein, is defined as a portion of a polypeptide to which an antibody can specifically bind as determined by any method well known in the art, for example, by conventional immunoassays. A "nonlinear epitope" or "conformational epitope" comprises noncontiguous polypeptides (or amino acids) within the antigenic protein to which an antibody specific to the epitope binds.

The term "binding affinity (K_D)" as used herein, is intended to refer to the dissociation rate of a particular antigen-antibody interaction. The K_D is the ratio of the rate of dissociation, also called the "off-rate (k_{off})", to the association rate, or "on- rate (k_{on})". Thus, K_D equals k_{off} / k_{on} and is expressed as a molar concentration (M). It follows that the smaller the K_D, the stronger the affinity of binding. Therefore, a K_D of 1 μM indicates weak binding affinity compared to a K_D of 1 nM. K_D values for antibodies can be determined using methods well established in the art. One method for determining the K_D of an antibody is by using surface plasmon resonance (SPR), typically using a biosensor system such as a Biacore® system.

The term "specifically binds" as used herein in reference to the binding between an antibody and a 5T4 antigen and the antibody binds the 5T4 antigen with a K_D less than about 30 nM as determined by SPR at 25°C.

Pharmaceutically acceptable salt as used herein refers to pharmaceutically acceptable organic or inorganic salts of a molecule or macromolecule.

The term "potency" is a measurement of biological activity and may be designated as IC_{50}, or effective concentration of antibody needed to inhibit 50% of growth of a 5T4 positive cell line as described in Example 3. Alternatively, potency may refer to anti-tumor activity as determined in an *in vivo* tumor xenograph model as shown in Example 4.

The terms "polynucleotide" or "nucleic acid molecule", as used herein, are intended to include DNA molecules and RNA molecules. A nucleic acid molecule may be single-stranded or double-stranded, but preferably is double-stranded DNA.

The polynucleotides that encode the antibodies of the present invention may include the following: only the coding sequence for the variant, the coding sequence for the variant and additional coding sequences such as a functional polypeptide, or a signal or secretory sequence or a pro-protein sequence; the coding sequence for the antibody and non-coding sequence, such as introns or non-coding sequence 5' and/or 3' of the coding sequence for the antibody. The term 'polynucleotide encoding an antibody" encompasses a polynucleotide which includes additional coding sequence for the variant but also a polynucleotide which includes additional coding and/or non-coding sequence. It is known in the art that a polynucleotide sequence that is optimized for a specific host cell/expression system can readily be obtained from the amino acid sequence of the desired protein (see GENEART® AG, Regensburg, Germany).

The polynucleotides encoding the antibodies of the present invention will typically include an expression control polynucleotide sequence operably linked to the antibody coding sequences, including naturally-associated or heterologous promoter regions known in the art. Preferably, the expression control sequences will be eukaryotic promoter systems in vectors capable of transforming or transfecting eukaryotic host cells, but control sequences for prokaryotic hosts may also be used. Once the vector has been incorporated into the appropriate host cell line, the host cell is propagated under conditions suitable for expressing the nucleotide sequences, and, as desired, for the collection and purification of the antibodies. Preferred eukaryotic cell lines include the CHO cell lines, various COS cell lines, HeLa cells, myeloma cell lines, transformed B-cells, or human embryonic kidney cell lines. The most preferred host cell is a CHO cell line.

The present invention encompasses antibodies or antigen-binding portions thereof that bind to a specific epitope on the 5T4 antigen. The epitope identified is a nonlinear or conformational epitope comprising a first contact with the human 5T4 antigen (SEQ ID NO: 11) between amino acid residues 173 and 252 and comprising a second contact between amino acid residues 276 and 355 (see Example 7). Thus, the CDRs and heavy and light chain variable regions described herein are used to make full-length antibodies as well as functional fragments and analogs that maintain the binding affinity of the protein employing the CDRs specific for the above mentioned epitope of the 5T4 antigen.

The binding affinity of antibodies of the present invention is determined using SPR (Example 6). In these experiments the 5T4 antigens are immobilized at low densities onto a BIAcore® chip and antibodies are flowed past. Build up of mass at the surface of the chip is measured. This analytical method allows the determination in real time of both on and off rates to obtain affinity (K_D) for binding. The humanized antibodies of the present invention have a K_D of between about 0.30 and about 30 nM; about 0.30 and about 20 nM; about 0.30 and about 10 nM; about 0.5 and about 7 nM; about 1.0 and about 5 nM; and about 1.0 and about 3 nM.

Conjugation of Drugs to an Antibody

The drug has, or is modified to include, a group reactive with a conjugation point on the antibody. For example, a drug can be attached by alkylation (e.g., at the epsilon-amino group lysines or the N-terminus of antibodies), reductive amination of oxidized carbohydrate, transesterification between hydroxyl and carboxyl groups, amidation at amino groups or carboxyl groups, and conjugation to thiols. In some embodiments, the number of drug moieties, *p*, conjugated per antibody molecule ranges from an average of 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 an average of 2 to 8, 2 to 7, 2 to 6, 2 to 5, 2 to 4 or 2 to 3. In other embodiments, *p* is an average of 1, 2, 3, 4, 5, 6, 7 or 8. In some embodiments, *p* ranges from an average of about 1 to about 8; about 1 to about 7, about 1 to about 6, about 1 to about 5, about 1 to about 4, about 1 to about 3, or about 1 to about 2. In some embodiments, *p* ranges from about 2 to about 8, about 2 to about 7, about 2 to about 6, about 2 to about 5, about 2 to about 4 or about 2 to about 3. For examples of chemistries that can be used for conjugation, see, e.g., Current Protocols in Protein Science (John Wiley & Sons, Inc.), Chapter 15 (Chemical Modifications of Proteins) (the disclosure of which is incorporated by reference herein in its entirety.)

For example, when chemical activation of the protein results in formation of free thiol groups, the protein may be conjugated with a sulfhydryl reactive agent. In one aspect, the agent is one which is substantially specific for free thiol groups. Such agents include, for example, malemide, haloacetamides (e.g., iodo, bromo or chloro), haloesters (e.g., iodo, bromo or chloro), halomethyl ketones (e.g., iodo, bromo or chloro), benzylic halides (e.g., iodide, bromide or chloride), vinyl sulfone and pyridylthio.

Linkers

The drug can be linked to an antibody by a linker. Suitable linkers include, for example, cleavable and non-cleavable linkers. A cleavable linker is typically susceptible to cleavage under intracellular conditions. Suitable cleavable linkers include, for example, a peptide linker cleavable by an intracellular protease, such as lysosomal protease or an endosomal protease. In exemplary embodiments, the linker can be a dipeptide linker, such as a valine-citrulline (val-cit), a phenylalanine-lysine (phe-lys) linker, or maleimidocapronic –valine-citruline-p-aminobenzyloxycarbonyl (mc-Val-Cit-PABA) linker. Another linker is Sulfosuccinimidyl-4-[N-maleimidomethyl]cyclohexane-1-carboxylate (smcc). Sulfo-smcc conjugation occurs via a maleimide group which reacts with sulfhydryls (thiols, -SH), while its Sulfo-NHS ester is reactive toward primary amines (as found in Lysine and the protein or peptide N-terminus). Yet another linker is maleimidocaproyl (mc). Other suitable linkers include linkers hydrolyzable at a specific pH or a pH range, such as a hydrazone linker. Additional suitable cleavable linkers include disulfide linkers. The linker may be covalently bound to the antibody to such an extent that the antibody must be degraded intracellularly in order for the drug to be released e.g. the mc linker and the like.

A linker can include a group for linkage to the antibody. For example, linker can include an amino, hydroxyl, carboxyl or sulfhydryl reactive groups (e.g., malemide, haloacetamides (e.g., iodo, bromo or chloro), haloesters (e.g., iodo, bromo or chloro), halomethyl ketones (e.g., iodo, bromo or chloro), benzylic halides (e.g., iodide, bromide or chloride), vinyl sulfone and pyridylthio). See generally Wong, Chemistry of Protein Conjugation and Cross-linking; CRC Press, Inc., Boca Raton, 1991.

Immunotherapy

For immunotherapy, an antibody can be conjugated to a suitable drug, such as a cytotoxic or cytostatic agent, an immunosuppressive agent, a radioisotope, a toxin, or the like. The conjugate can be used for inhibiting the multiplication of a tumor cell or cancer cell, causing apoptosis in a tumor or cancer cell, or for treating cancer in a patient. The conjugate can be used accordingly in a variety of settings for the treatment of animal cancers. The conjugate can be used to deliver a drug to a tumor cell or cancer cell. Without being bound by theory, in some embodiments, the conjugate binds to or associates with a cancer-cell or a tumor-associated antigen, and the conjugate and/or drug can be taken up inside a tumor cell or cancer cell through receptor-mediated endocytosis. The antigen can be attached to a tumor cell or cancer cell or can be an extracellular matrix protein associated with the tumor cell or cancer cell. Once inside the cell, one or more specific peptide sequences within the conjugate (e.g., in a linker) are hydrolytically cleaved by one or more tumor-cell or cancer-cell-associated proteases, resulting in release of the drug. The released drug is then free to migrate within the cell and induce cytotoxic or cytostatic or other activities. In some embodiments, the drug is cleaved from the antibody outside the tumor cell or cancer cell, and the drug subsequently penetrates the cell, or acts at the cell surface.

Therapy for Cancer

As discussed above, cancers, including, but not limited to, a tumor, metastasis, or other disease or disorder characterized by uncontrolled cell growth, can be treated or prevented by administration of a protein-drug conjugate.

In other embodiments, methods for treating or preventing cancer are provided, including administering to a patient in need thereof an effective amount of a conjugate and a chemotherapeutic agent. In some embodiments, the chemotherapeutic agent is that with which treatment of the cancer has not been found to be refractory. In some embodiments, the chemotherapeutic agent is that with which the treatment of cancer has been found to be refractory. The conjugate can be administered to a patient that has also undergone a treatment, such as surgery for treatment for the cancer. In another embodiment, the additional method of treatment is radiation therapy.

Multi-Drug Therapy for Cancer

Methods for treating cancer include administering to a patient in need thereof an effective amount of an antibody-drug conjugate and another therapeutic agent that is an anti-cancer agent. Suitable anticancer agents include, but are not limited to, methotrexate, taxol, L-asparaginase, mercaptopurine, thioguanine, hydroxyurea, cytarabine, cyclophosphamide, ifosfamide, nitrosoureas, cisplatin, carboplatin, mitomycin, dacarbazine, procarbizine, topotecan, nitrogen mustards, cytoxan, etoposide, 5-fluorouracil, BCNU, irinotecan, camptothecins, bleomycin, doxorubicin, idarubicin, daunorubicin, dactinomycin, plicamycin, mitoxantrone, asparaginase, vinblastine, vincristine, vinorelbine, paclitaxel, calicheamicin, and docetaxel.

The ADCs of the present invention can be in the form of a pharmaceutical composition for administration that are formulated to be appropriate for the selected mode of administration, and pharmaceutically acceptable diluent or excipients, such as buffers, surfactants, preservatives, solubilizing agents, isotonicity agents, stabilizing agents, carriers, and the like. Remington's Pharmaceutical Sciences, Mack Publishing Co., Easton Pa., 18^{th} ed., 1995, incorporated herein by reference, provides a compendium of formulation techniques as are generally known to practitioners.

These pharmaceutical compositions may be administered by any means known in the art that achieve the generally intended purpose to treat cancer. The preferred route of administration is parenteral, defined herein as referring to modes of administration that include but not limited to intravenous, intramuscular, intraperitoneal, subcutaneous, and intraarticular injection and infusion. The dosage administered will be dependent upon the age, health, and weight of the recipient, kind of concurrent treatment, if any, frequency of treatment, and the nature of the effect desired.

Compositions within the scope of the invention include all compositions wherein an ADC is present in an amount that is effective to achieve the desired medical effect for treating cancer. While individual needs may vary from one patient to another, the determination of the optimal ranges of effective amounts of all of the components is within the ability of the clinician of ordinary skill.

Example 1

Preparation of an anti-5T4 ADC

5T4-A1 antibody drug conjugate (ADC) is prepared via partial reduction of the mAb with tris(2-carboxyethyl)phosphine (TCEP) followed by reaction of reduced Cys residues with the desired maleimide terminated linker-payload. In particular, 5T4-A1 mAb is partially reduced via addition of 2.8 molar excess of tris(2-carboxyethyl)phosphine (TCEP) in 100 mM HEPES (4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid buffer), pH 7.0 and

1 mM diethylenetriaminepentaacetic acid (DTPA) for 2 h at 37 °C. The desired linker-payload is then added to the reaction mixture at a linker-payload/mAb-thiol molar ratio of 5.5 (maleimidocapronic-monomethylauristatin F [mc-MMAF]) or 8 (maleimidocapronic – valine-citruline-p-aminobenzyloxycarbonyl- monomethylauristatin E [mc-Val-Cit-PABA-MMAE]) and reacted for an additional 1 h at 25°C in the presence of 15% v/v of dimethylacetamide (DMA). After the 1 h incubation period, N-ethylmaleimide (4.5 fold excess for mc-MMAF and 2 fold excess for mc-Val-Cit-PABA-MMAE) is added to cap the unreacted thiols and is allowed to react for 15 minutes followed by addition of 6 fold excess L-Cys to quench any unreacted linker-payload. The reaction mixture is dialyzed overnight at 4 °C in phosphate buffered saline (PBS), pH 7.4, and purified via SEC (AKTA explorer, Superdex 200 10/30 GL column). The ADC is further characterized via size exclusion chromatography (SEC) for purity, hydrophobic interaction chromatography (HIC), and liquid chromatography electrospray ionisation tandem mass spectrometry (LC-ESI MS) to calculate loading, and the concentration is determined via UV spectrophotometer.

Example 2

Binding Studies

Cells expressing the 5T4 antigen, and the negative control Raji cells, are plated at a density of 500,000 cells/well on non-tissue culture treated 96 well plates and kept on ice. Dilutions of the A1 and A1-IgG4 antibodies or A1-mcMMAF ADC are made in 3% bovine serum albumin BSA in Dulbecco's phosphate buffered saline (DPBS) and added to the plate at a final concentration of 10μg/mL. The plates are then incubated on ice for 1 hour followed by 2 washes. The secondary antibody, PE (phycoerythrin) conjugated Goat Anti-Human IgG Fc is added to the wells. After 30 minutes of incubation at 4°C, the mean fluorescence intensity is then measured using a flow cytometer.

The data in Table 4 indicates that the A1 antibody binds a diverse panel of 5T4 positive cell lines. The data in Table 5 indicates that similar binding on several different cell lines is observed with the A1 and A1-IgG4 antibodies as well as the A1-mcMMAF ADC.

Table 4

Human Cell Lines	A1 antibody Mean Fluorescent Intensity
MDAMB435/5T4 (melanoma)	15000
MDAMB468 (breast)	3000
MDAMD361-DYT2 (breast)	4500
NCI-H157 (lung)	4100
A431 (epithelial)	2000
Caki (kidney)	2500
PC3mm2 (prostate)	4500
PC14PE6 (lung)	3200
Panc1 (pancreatic)	3500
BxPC3 (pancreatic	1000
Su8686 (pancreatic)	3700
H1975	1600
37622A – (Primary Lung cancer cells)	10600
Raji (negative control)	<100

Table 5

Mean Fluorescent Intensity					
Cell Lines	**A1**	**A1-mcMMAF**	**A1-IGG4**	**A1-IGG4-CM**	**IgG control**
MDAMD361-DYT2	7000	6900	5500	4800	<100
A431	3900	3400	2400	2000	<100
MDAMB468	3500	2800	2500	1800	<100
PC3mm2	3400	2700	2100	1500	<100
Raji	<200	<200	<200	<100	<100

Example 3

Cytotoxicity Assay

Cell lines expressing 5T4, and the negative control Raji cell line, are cultured with increasing concentrations of ADC. After four days, viability of each culture is assessed. IC_{50} values are calculated by logistic non-linear regression and are presented as ng Ab/mL. A1-mcMMAF, A1-vcMMAE, A3-mcMMAF and A3-mcMMAE are shown to inhibit the growth of 5T4 expressing cell lines (MDAMB435/5T4, MDAMB468, and MDAMB361DYT2), while being inactive on 5T4 negative cells (Raji), Table 6.

Table 6

	IC_{50} (ng Ab/ml)			
ADC	MDAMB435/5T4	MDAMB361DYT2	MDAMB468	Raji (5T4-)
A1-mcMMAF	1.3	104.2	534.2	>45,000
A1-vcMMAE	6.8	157.7	7667	>45,000
A3-mcMMAF	0.3	31.0	27.7	>45,000
A3-vcMMAE	3.5	86.8	160.6	>45,000
Nonbinding Ab-mcMMAF	21258	~50,000	73059	>45,000
Nonbinding Ab- vcMMAE	7979	27650	23819	>45,000

Additionally, 5T4+ primary lung tumor 37622a cells are isolated and grown in culture. Cells are cultured with increasing concentrations of ADC. Ten days later, viability of each culture is assessed using the MTS method. IC_{50} values were calculated by logistic non-linear regression and are presented as ng Ab/ml. A1-mcMMAF, A1-vcMMAE, A3-mcMMAF, and A3-vcMMAE inhibit the growth of the primary lung tumor cells, Table 7.

Table 7

ADC	37622a primary lung IC_{50} (ng Ab/ml)
A1-mcMMAF	504.1
A1-vcMMAE	443.1
A3-mcMMAF	77.2
A3-vcMMAE	78.1
Nonbinding Ab-mcMMAF	>45,000

Example 4

Subcutaneous Xenograft Model

Female, athymic (nude) mice (or another strain of immunosupressed mice) are injected s.c. with MDAMB435/5T4, MDAMB361DYT2, or H1975 tumor cells. Mice with staged tumors, approximately 0.1 to 0.3 g (n=6 to 10 mice/treatment group) are administered intravenously Q4Dx4 with normal saline (vehicle), A1-mcMMAF, A1-vcMMAE, A1-mcMMAD, A1-smccDM1, A3-mcMMAF, A3-vcMMAE, or a nonbinding control antibody conjugated to either mcMMAF or vcMMAE, at the dose of 3 mg Ab/kg. All ADCs are dosed based on Ab content. Tumors are measured at least once a week and their size ($mm^2 \pm$ SEM) is calculated as $mm^2 = 0.5 \times (\text{tumor width}^2) \times (\text{tumor length})$.

The data in Table 8 indicates that A1-mcMMAF, A1-vcMMAE, A1-vcMMAD, A3-mcMMAF, and A3-vcMMAE inhibit the growth of MDAMB435/5T4 xenografts while A1-mcMMAD and A1-smccDM1 were not active in this model.

The data in Table 9 indicates that A1-mcMMAF, A1-vcMMAE, A1-vcMMAD, A1-smccDM1, A3-mcMMAF, and A3-vcMMAE inhibit the growth of MDAMB361DYT2 xenografts while A1-mcMMAD was not active in this model.

The data in Table 10 indicates that A1-mcMMAF, A1-vcMMAE, A1-vcMMAD, A3-mcMMAF, and A3-vcMMAE inhibit the growth of H1975 xenografts while A1-mcMMAD and A1-smccDM1 were not active in this model.

Table 8

	MDAMB435/5T4 xenografts Tumor volume (mm^3, x ± sem)				
Compound (3 mg/kg Q4dx4)	Day 0	Day 17	Day 42	Day 65	Day 85
Vehicle	169 ± 8	531 ± 73	1255 ± 190	GT	GT
A1 mcMMAF	168 v 15	53 ± 12	67 ± 56	174 ± 119	364 ± 278
A1 vcMMAE	168 ± 8	4 ± 4	10 ± 10	91 ± 91	200 ± 200
A1 mcMMAD	168 ± 12	390 ± 112	GT	GT	GT
A1 smccDM1	174 ± 10	429 ± 62	1255 ± 227	1781 ± 388	GT
A1 vcMMAD	169 ± 12	17 ± 7	0 ± 0	0 ± 0	0 ± 0
A3 mcMMAF	174 ± 12	105 ± 27	216 ± 143	448 ± 220	GT
A3 vcMMAE	172 ± 13	0 ± 0	0 ± 0	0 ± 0	0 ± 0
Nonbinding Ab mcMMAF	170 ± 11	100 ± 15	314 ± 121	838 ± 381	GT
Nonbinding Ab vcMMAE	172 ± 11	168 ± 53	461 ± 178	GT	GT

GT= group terminated due to large tumor size

Table 9

	MDAMB361DYT2 xenografts Tumor volume (mm^3, x ± sem)				
Compound (3 mg/kg Q4dx4)	Day 0	Day 19	Day 47	Day 90	Day 131
Vehicle	353 ± 10	363 ± 58	558 ± 149	1117 ± 348	GT
A1 mcMMAF	348 ± 14	76 ± 32	0 ± 0	7 ± 7	11 ± 11
A1 vcMMAE	356 ± 11	86 ± 8	0 ± 0	9 ± 9	34 ± 27
A1 vcMMAD	352 ± 26	130 ± 15	0 ± 0	0 ± 0	0 ± 0
A3 mcMMAF	342 ± 23	128 ± 10	79 ± 30	105 ± 49	353 ± 234
A3 vcMMAE	354 ± 21	111 ± 20	21 ± 21	72 ± 72	155 ± 155
A1 mcMMAD	347 ± 15	380 ± 66	775 ± 199	GT	GT
A1 vcMMAD	352 ± 26	130 ± 15	0 ± 0	0 ± 0	0 ± 0
A1 smccDM1	353 ± 25	123 ± 9	51 ± 25	98 ± 41	330 ± 146
Nonbinding Ab mcMMAF	342 ± 38	407 ± 93	869 ± 198	GT	GT
Nonbinding Ab vcMMAE	344 ± 20	303 ± 78	346 ± 185	595 ± 362	GT

GT= group terminated due to large tumor size

Table 10

		H1975 Xenografts Tumor volume (mm^3, x ± sem)				
Compound	Dose (mg/kg) Q4dx4	Day 0	Day 8	Day 15	Day 22	Day 40
Vehicle		423 ± 14	1154 ± 136	2229 ± 240	GT	GT
A1 mcMMAF	3	425 ± 14	619 ± 46	519 ± 45	581 ± 79	2840 ± 207
A1 vcMMAE	3	425 ± 12	702 ± 45	929 ± 90	926 ± 116	GT
A1 vcMMAD	3	427 ± 18	739 ± 59	467 ± 19	240 ± 14	625 ± 317
A3 mcMMAF	3	426 ± 10	980 ± 79	1343 ± 140	1261 ± 203	GT
A3 vcMMAE	3	431 ± 14	944 ± 52	993 ± 71	GT	GT
A1 mcMMAD	3	427 ± 16	837 ± 69	1468 ±139	GT	GT
A1 smccDM1	3	423 ± 18	901 ± 83	1852 ± 167	GT	GT
Nonbinding Ab-mcMMAF	3	423 ± 16	1026 ± 68	1861 ± 224	GT	GT
Nonbinding Ab-vcMMAE	3	427 ± 13	1213 ± 67	1959 ± 139	GT	GT

GT= group terminated due to large tumor size

Alternatively, nude mice with 37622a primary tumor cell xenografts established subcutaneously are treated iv Q4Dx4 with A1-mcMMAF, A1-mcMMAD, A1-vcMMAD, or A3-mcMMAF at the dose of 3 mg Ab/kg and the tumor growth is monitored over the period of 96 days. Table 11 demonstrates that A1-mcMMAF, A1-vcMMAD and A3-mcMMAF inhibit the growth of 37622a primary tumor xenografts compared to vehicle control treated animals while A1-mcMMAD was not active in this model.

Table 11

	37622a Primary Tumor Xenografts Tumor volume (mm^3, x ± sem)					
Compound	Dose (mg/kg) Q4dx4	Day 1	Day 22	Day 46	Day 68	Day 96
Vehicle		111 ± 18	503 ± 155	1174 ± 247	GT	GT
A1-mcMMAF	3	111 ± 18	67 ± 11	124 ± 47	233 ± 105	357 ± 150
A1-mcMMAD	3	127 ± 28	376 ± 119	862 ± 377	GT	GT
A1-vcMMAD	3	108 ± 14	52 ± 14	13 ± 5	50 ± 37	160 ± 121
A3-mcMMAF	3	131 ± 28	99 ± 26	211 ± 128	463 ± 210	GT

GT= group terminated due to large tumor size

Unexpectedly, the data in Tables 8-11 show that ADCs with the same antibody and drug payload but with different linkers had a dissimilar efficacy profile i.e. A1-mcMMAD vs A1-vcMMAD in all four xenograft models. In addition, the data show that ADCs with the same antibody and linker but with different drug payloads also had a different efficacy profile i.e. A1-mcMMAF vs A1-mcMMAD, in all four xenograft models. Thus, the drug MMAD is effective in all four xenograft models when linked to the A1 antibody by the vc linker but has no activity in any of the xenograft models tested when linked by the mc linker. In contrast, the drug MMAF is highly effective in all 4 xenograft models when linked to the A1 antibody with the mc linker while the chemically related drug MMAD has no activity in all 4 xenograft models when linked to the same antibody by the same linker.

Yet another unexpected observation is seen with the ADC A1-smccDM1 (Tables 8-10). This ADC was very effective against the MDAMB361DYT2 xenograft but had essentially no effect against the MDAMB435/5T4 and the H1975 xenografts even though all the xenografts have a high expression of the 5T4 target antigen. This data illustrates that the effectiveness of the linker-payload could not be predicted even when the same high affinity antibody is utilized or even when the same ADC is used.

Example 5

Antibody Dependent Cell-Mediated Cytotoxicity (ADCC)

ADCC assay:

Blood from a healthy volunteer is collected into a BD Vacutainer CPT cell preparation tube with sodium heparin. Human peripheral blood mononucleocytes (PBMC) are harvested and resuspended in assay buffer (RPMI 1640 supplemented with 10 mM HEPES) at 2.5 x 10^7 cells/ml. Target cells (MDAMB435/5T4 or MDAMB435/neo) are seeded at a density of 1 x 10^4 cells/well in a 96 well assay plate. A1 antibody or A1-mcMMAF are added, then human PBMC effector cells (5 x 10^5) are dispensed into the wells for an effector:target cell ratio (E:T) of 50:1. The assay plate is incubated at 37 °C for 4 hours for ADCC activity. The plate is harvested by adding equal volume of CytoTox-One reagent (Promega). Stop solution (Promega; 50 ul) is added to each well and lactate dehydrogenase release was quantified by measuring fluorescence intensity. As a positive control, 2 µl of lysis buffer per well is added to generate a maximum LDH release (100% cytotoxicity) in control wells. Percent cytotoxicity is calculated using the following equation:

$$\text{\% Specific Cytotoxicity} = \frac{\text{experimental} - \text{effector spontaneous} - \text{target spontaneous}}{\text{target maximum} - \text{target spontaneous}} \times 100$$

Where “experimental” corresponds to the signal measured in one of the experimental conditions, “effector spontaneous” corresponds to the signal measured in the presence of PBMC alone, “target spontaneous” corresponds to the signal measured in the presence of target cells alone, and “target maximum” corresponds to the signal measured in the presence of detergent-lysed target cells alone.

The ADCC activity of A1-IgG1 Ab and A1-mcMMAF compared to A1-IgG4 Ab is shown in Table 12. Both the A1 antibody and A1-mcMMAF demonstate comparable ADCC activity indicating that the ADCC activity of A1-mcMMAF may contribute to its anti-tumor activity.

Table 12

Compound	% Cytotoxicity
A1-IgG1	37 ± 8
A1-mcMMAF	34 ± 1
A1-IgG4	9 ± 5

Example 6
Binding Affinity

Surface plasmon resonance (SPR) analysis is performed utilizing the BIAcore® to determine the affinity constants for A1-IgG1 and A1-IgG4 binding to either human or cynomolgus 5T4 at pH 6.0 and pH 7.4. BIAcore® technology utilizes changes in the refractive index at the surface layer upon binding of the huA1 antibody variants to the human 5T4 protein immobilized on the surface layer. Binding is detected by SPR of laser light refracting from the surface. Analysis of the signal kinetics on-rate and off-rate allows the discrimination between non-specific and specific interactions. The 5T4 proteins used for this analysis consisted of the human or cynomolgus 5T4 ectodomain fused to the human IgG1-Fc domain and low densities (45.1 and 45.4 RU for human and cynomolgus respectively) are immobilized onto a CM5 chip to accurately measure affinity constants.

The measurement of specific binding to the 5T4 ectodomain is attained by subtracting binding to a reference surface that had only human IgG1-Fc protein immobilized onto the CM5 chip at the same density to that on the 5T4-Fc surfaces. Next, various concentrations of A1, A1-IgG4, or A3 antibodies in either HBS-EP pH 7.4 or MES-EP pH 6.0 buffer are injected over the surface. The surface is regenerated two times with Glycine pH 1.7 + 0.05% Surfactant P20 (GE Healthcare, BR-1000-54) between injection cycles.

Results show that the A1 has a slightly higher affinity for human 5T4 using the low-density 5T4 surface at both pH 6.0 and pH 7.4 relative to A1-IgG4 (1.5-fold and 1.2-fold respectively, Table 13). Additionally, A1 exhibited slightly better binding to cynomolgus 5T4 at both pH 6.0 and pH 7.4 compared to A1-IgG4 (1.7-fold and 1.2-fold respectively) and both A1 and A1-IgG4 bound human 5T4, 3 – 4 fold better than cynomolgus 5T4 (Table 12).

Table 13

Antibody	Antigen	pH	ka (1/Ms)	kd (1/s)	KD (nM)
A1-IgG1	hu5T4	6.0	4.31E+05	4.59E-04	1.06
A1-IgG4	hu5T4	6.0	6.26E+05	8.93E-04	1.43
A1-IgG1	cyno5T4	6.0	2.33E+05	6.41E-04	2.76
A1-IgG4	cyno5T4	6.0	2.02E+05	9.50E-04	4.70
A1-IgG1	hu5T4	7.4	2.75E+05	1.32E-04	0.48
A1-IgG4	hu5T4	7.4	3.28E+05	1.72E-04	0.52
A1-IgG1	cyno5T4	7.4	1.51E+05	2.73E-04	1.80
A1-IgG4	cyno5T4	7.4	1.81E+05	3.82E-04	2.11

Comparing the A1 and A3 antibodies, it is apparent that the A1 antibody binds human and cynomolgus 5T4 better at pH 7.4 relative to pH 6.0 while the A3 antibody exhibits enhanced binding at pH 6.0 compared to pH 7.4, Table 14.

Table 14

Antibody	Antigen	pH	ka (1/Ms)on	kd (1/s)off	KD (nM)
A1	hu5T4	6.0	4.31E+05	4.59E-04	1.06
A3	hu5T4	6.0	3.51E+05	4.17E-05	0.12
A1	cyno5T4	6.0	2.33E+05	6.41E-04	2.76
A3	cyno5T4	6.0	4.58E+05	1.87E-04	0.41
A1	hu5T4	7.4	2.75E+05	1.32E-04	0.48
A3	hu5T4	7.4	1.79E+05	3.06E-05	0.17
A1	cyno5T4	7.4	1.51E+05	2.73E-04	1.80
A3	cyno5T4	1.98E+05	1.62E-04	0.82	1.98E+05

Example 7
Epitope Mapping Using 5T4 Chimeras

To identify the epitopes to which each of the A1 and A3 antibodies bind, an enzyme linked immunosorbent assay (ELISA) is performed using (1) 5T4 ectodomain Fc construct and (2) human/mouse 5T4 chimera constructs transiently expressed in COS-1 cells. The ectodomain includes the amino-terminal region, two leucine-rich repeats, and the intervening hydrophilic region. Mouse and rat 5T4 ectodomains contain a 6 amino acid direct repeat within their hydrophilic region.

Fusion proteins containing a 5T4 ectodomain and a Fc constant region from human IgG1 are prepared using human 5T4 (amino acids 1-355), mouse 5T4 (amino acids 1-361), rat 5T4 (amino acids 1-361), cynomologus monkey 5T4 (amino acids 1-355), chimpanzee 5T4 (amino acids 1-355), and black-tailed marmoset (amino acids 1-355). The binding results with human/mouse 5T4 chimera constructs are summarized in Table 14, which indicates specific binding, partial binding, or lack of binding, by the A1 and A3 antibodies.

Table 15 refers to binding ability of the antibodies to the various human/mouse chimeras and the nomenclature is designated by mouse 5T4 content. When no binding is observed, this indicates where the antibody binds human 5T4 since these antibodies do not bind mouse 5T4. For example, the A3 antibody has the most N-terminal binding epitope (between 83 – 163) and this is shown by lack of binding to the 5T4 chimera that has residues 83 – 163 replaced by mouse 5T4, hence A3 can no longer bind. Based upon these results, it is determined that humanized A1 antibody has a first contact with human 5T4 between amino acid residues 173 and 252 and a second contact with human 5T4 between amino acid residues 276 and 355. The A3 antibody binds the first leucine-rich repeat region of human 5T4 between amino acid residues 83 through 163. The number of amino acid residues corresponds to the human 5T4 antigen amino acid sequence of SEQ ID NO: 11.

Table 15

	Antibody	
5T4 Antigen Construct	**A1**	**A3**
Human/mouse 83-163	+	-
Human/mouse 173-361	-	+
Human/mouse 173-258	+/-	+
Human/mouse 282-361	+/-	+

Example 8

Comparison of A1-mcMMAF ADC with A1-IgG4-CM ADC

A1-mcMMAF is compared to A1-IgG4-AcBut calicheamicin (A1-IGG4-CM) for both safety and efficacy. A1-4-CM is comprised of the A1-IgG4 antibody conjugated with the linker, AcBut [-(4’ acetylphenoxy) butanoic acid], to a calicheamicin payload. The calicheamicins are potent antitumor agents of a class of enediyne antibiotics derived from the bacterium *Micromonospora echinospora*.

The cell binding activity of A1 Ab, A1-IgG4 Ab, A1-mcMMAF ADC and A1-IgG4-CM ADC are compared using several 5T4 positive cell lines (see Example 2, Table 5). The data indicates that similar binding is observed with the A1 and A1-IgG4 antibodies as well as the A1-mcMMAF ADC, all of which have a higher mean fluorescent intensity than A1-IgG4-CM for all the 5T4 positive cell lines tested.

A1-mcMMAF and A1-IgG4-CM are tested side-by-side in the MDAMB435/5T4 subcutaneous xenograft model. Both ADCs are given *iv* (Q4dx2) when the tumors reach approximately 200 mm^2 in size. The anti-tumor activity of A1-IgG4-CM at a dose of 3 mg/kg is similar to the anti-tumor activity of A1-mcMMAF administered at dose of 10 mg/kg (Table 16). Based upon these results, the anti-tumor activity of A1-IgG4-CM is approximately 3.3 fold more potent than A1-mcMMAF.

Table 16

	Tumor volume (mm^3, x ± sem)					
Compound	Dose (mg/kg) Q4dx4	Day 0	Day 7	Day 21	Day 31	Day 45
Vehicle	0	123 ± 8	195 ± 36	402 ± 56	635 ± 111	1309 ± 332
A1-mcMMAF	3	124 ± 11	121 ± 8	166 ± 29	227 ± 42	361 ± 89
A1-mcMMAF	10	123 ± 14	76 ± 11	0 ± 0	3 ± 3	2 ± 1
A1-IGG4-CM	3	121 ± 12	140 ± 15	32 ± 10	24 ± 10	26 ± 15

It could be expected that the 3.3 fold enhanced potency of A1-IgG4-CM over that of A1-mcMMAF would translate into a 3.3 fold enhanced safety margin of A1-mcMMAF over that of A1-IgG4-CM in an animal toxicity study. However, when the safety profile of A1-IgG4-CM in cynomolgus macques is reviewed, it is determined that A1-IgG4-CM is at least 100 fold more toxic than A1-mcMMAF in the cynomolgus macque. When A1-IgG4-CM is administered at 0.032, 0.095 and 0.32 mg Ab/kg/cycle (2, 6, 20 µg calicheamicin/kg/cycle) to male (n=3) and female (n=3) cynomolgus macques, toxicity is observed at each dose level. After 2 cycles (2 doses), 4 out of 6 animals in the 0.095 treatment group are either euthanized or found dead. On the other hand, no deaths are observed at dosages up to 10 mg/kg with A1-mcMMAF (247 µg mcMMAF/kg/cycle), after 2 cycles (2 doses), over the same 4 week time period. In summary, the 10 mg/kg dosage group of A1-mcMMAF is safe while the 0.096 mg/kg dosage group of A1-IgG4-CM is deemed toxic when both are administered twice to cynomolgus macques in a 4 week observation period.

Unexpectedly, these results demonstrate a 105 fold (10/0.095=105) safety margin of A1-mcMMAF over that of A1-IgG4-CM, rather than the expected 3.3 fold safety margin based on the relative anti-tumor potency of each ADC. This data reveals the unpredictable nature of antibody-drug conjugates that utilize antibodies to the same antigen target but are conjugated to a different drug payload.

Example 9

A1-mcMMAF Mouse PK/PD Modeling and Clinical Dose Predictions

PK/PD modeling has been used to quantify the tumor response of A1-mcMMAF in mouse xenograft studies, in order to determine efficacious concentration across cell lines. The transit compartment tumor kill PK/PD model used was previously described by Simeoni *et al.* (*Simeoni et al, Cancer Res,* 64:1094, (2004)). The model has been modified to account for linear, exponential and logistic growth of tumor, and saturative killing by the drug. PK/PD model parameters include:

$k_{g\ ex}$	*exponential growth*
k_g	*logistic growth*
w_0	*initial tumor volume*
tau	*transduction rate*
k_{max}	*maximum kill rate*
kC_{50}	*concentration at half max kill rate*

The PK/PD modeling results are used to calculate the Tumor Static Concentration (TSC, Equation 1). This is the drug concentration where tumor growth is equal to tumor death rates and tumor volume remains unchanged. TSC can be defined as the minimal concentration required for efficacy. TSC is used to give guidance on clinical dose selection, with concentrations of >TSC required for efficacy in the clinic.

For A1-mcMMAF, mouse PK was determined in a separate study (3mg/kg IV, female athymic nu/nu mice). Mouse xenograft studies were completed using 3 different 5T4 cell lines with A1-mcMMAF administered at dose levels between 1 and 30 mg/kg every 4 days: cell line MDAMB435/5T4 (dosed at 1, 3, 10, and 30 mg/kg), cell line H1975 (dosed at 1, 3, and 10 mg/kg) and cell line 37622A (dosed at 1 and 10 mg/kg). PK/PD modeling was performed as described and TSCs are reported in Table 17.

Mouse PK/PD parameters for each xenograft cell line were combined with predicted human PK of A1-mcMMAF to simulate doses required for efficacy in the clinic. Using this methodology, A1-mcMMAF has a predicted minimally efficacious clinical dose of about 0.22 to about 2.3 mg/kg Q3 weeks [every three weeks] (Table 17).

In an embodiment of the present invention, dose ranges can be in the range from about 0.18 mg/kg to about 2.7 mg/kg, from about 0.22 mg/kg to about 2.6 mg/kg, from about 0.27 mg/kg to about 2.5 mg/kg, from about 0.32 mg/kg to about 2.3 mg/kg, from about 0.37 mg/kg to about 2.15 mg/kg, from about 0.42 mg/kg to about 2.10 mg/kg, from about 0.47 mg/kg to about 2.05 mg/kg, from about 0.52 mg/kg to about 2.00 mg/kg, from about 0.57 mg/kg to about 1.95 mg/kg, from about 0.62 mg/kg to about 1.90 mg/kg, from about 0.67 mg/kg to about 1.85 mg/kg, from about 0.72 mg/kg to about 1.80 mg/kg, from about 0.82 mg/kg to about 1.70 mg/kg, from about 0.92 mg/kg to about 1.60 mg/kg, from about 1.02 mg/kg to about 1.50 mg/kg, from about 1.12 mg/kg to about 1.40 mg/kg, or from about 1.20 mg/kg to about 1.30 mg/kg, with dosing at Q3 weeks. Preferably, dose ranges can be in the range from about 0.22 mg/kg to about 2.3 mg/kg.

Equation 1

1.1

If $\frac{k_{gEx}}{k_g} w_0 \leq 1$, $TSC = \frac{k_{gEx} \cdot k_{C50}}{k_{max} - k_{gEx}}$

1.2

If $\frac{k_{gEx}}{k_g} w_0 > 1$, $TSC = \frac{k_g \cdot k_{C50}}{w_0 \cdot k_{max} - k_g}$

Table 17

Cell Line	TSC [80% confidence] (ug/ml)	Predicted Stasis Dose [80% confidence] (mg/kg Q3 weeks)
MDAMB435/5T4	1.1 [0.9, 1.4]	0.22 [0.18, 0.28]
37622A	5.1 [2.1, 9.9]	1.1 [0.6, 2.0]
H1975	11.6 [9.6, 14.1]	2.3 [2.0, 2.7]

SEQUENCE LISTING

SEQ ID NO:1 Humanized A1 human IgG1 heavy chain

EVQLVESGGGLVQPGGSLRLSCAASGYTFTNFGMNWVRQAPGKGLEWVAWINTNTGEPRYAEEFKG
RFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDWDGAYFFDYWGQGTLVTVSSASTKGPSVFPLAP
SSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQ
TYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL
PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO:2 Humanized A1 human Kappa light chain:

DIQMTQSPSSLSASVGDRVTITCKASQSVSNDVAWYQQKPGKAPKLLIYFATNRYTGVPSRFSGSG
YGTDFTLTISSLQPEDFATYYCQQDYSSPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASV
VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTH
QGLSSPVTKSFNRGEC

SEQ ID NO:3 A1-VH

EVQLVESGGGLVQPGGSLRLSCAASGYTFTNFGMNWVRQAPGKGLEWVAWINTNTGEPRYAEEFKG
RFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDWDGAYFFDYWGQGTLVTVSS

SEQ ID NO:4 A1-VL

DIQMTQSPSSLSASVGDRVTITCKASQSVSNDVAWYQQKPGKAPKLLIYFATNRYTGVPSRFSGSG
YGTDFTLTISSLQPEDFATYYCQQDYSSPWTFGQGTKVEIK

SEQ ID NO:5 A1-HC CDR1

NFGMN

SEQ ID NO:6 A1-HC CDR2
WINTNTGEPRYAEEFKG

SEQ ID NO:7 A1-HC CDR3
DWDGAYFFDY

SEQ ID NO:8 A1-LC-CDR1
KASQSVSNDVA

SEQ ID NO:9 A1-LC-CDR2
FATNRYT

SEQ ID NO:10 A1-LC-CDR3
QQDYSSPWT

SEQ ID NO:11 Human 5T4 antigen
MPGGCSRGPAAGDGRLRLARLALVLLGWVSSSSPTSSASS
FSSSAPFLASAVSAQPPLPDQCPALCECSEAARTVKCVNR
NLTEVPTDLPAYVRNLFLTGNQLAVLPAGAFARRPPLAEL
AALNLSGSRLDEVRAGAFEHLPSLRQLDLSHNPLADLSPF
AFSGSNASVSAPSPLVELILNHIVPPEDERQNRSFEGMVV
AALLAGRALQGLRRLELASNHFLYLPRDVLAQLPSLRHLD
LSNNSLVSLTYVSFRNLTHLESLHLEDNALKVLHNGTLAE
LQGLPHIRVFLDNNPWVCDCHMADMVTWLKETEVVQGKDR
LTCAYPEKMRNRVLLELNSADLDCDPILPPSLQTSYVFLG
IVLALIGAIFLLVLYLNRKGIKKWMHNIRDACRDHMEGYH
YRYEINADPRLTNLSSNSDV

SEQ ID NO:12 Humanized A1 human IgG4m heavy chain:
EVQLVESGGGLVQPGGSLRLSCAASGYTFTNFGMNWVRQAPGKGLEWVAWINTNTGEPRYAEEFKG
RFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDWDGAYFFDYWGQGTLVTVSSASTKGPSVFPLAP
CSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTK
TYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD
VSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSS
IEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
LDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK

SEQ ID NO:13 A1 human IgG4m VH (A1-IGG4-VH)
EVQLVESGGGLVQPGGSLRLSCAASGYTFTNFGMNWVRQAPGKGLEWVAWINTNTGEPRYAEEFKG
RFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDWDGAYFFDYWGQGTLVTVSS

SEQ ID NO:14 A1-IgG4-VH-CDR1
NFGMN

SEQ ID NO:15 Chimeric A3 heavy chain (muA3-huIgG1)
EVQLVESGGGLVQPKGSLKLSCAASGFTFNTYAMNWVRQAPGKGLEWVARIRSKSNNYATYYADSV
KDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRQWDYDVRAMNYWGQGTLVTVSSASTKGPSVFP
LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL
GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN
KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO:16 Chimeric A3 VH
EVQLVESGGGLVQPKGSLKLSCAASGFTFNTYAMNWVRQAPGKGLEWVARIRSKSNNYATYYADSV
KDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRQWDYDVRAMNYWGQGTLVTVSS

SEQ ID NO:17 Chimeric A3 VH-CDR1
TYAMN

SEQ ID NO:18 Chimeric A3 VH-CDR2
RIRSKSNNYATYYADSVKD

SEQ ID NO:19 Chimeric A3 VH-CDR3
QWDYDVRAMNY

SEQ ID NO:20 Chimeric A3 light chain (muA3-huKappa)
DIVMTQSHIFMSTSVGDRVSITCKASQDVDTAVAWYQQKPGQSPKLLIYWASTRLTGVPDRFTGSG
SGTDFTLTISNVQSEDLADYFCQQYSSYPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASV
VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTH
QGLSSPVTKSFNRGEC

SEQ ID NO:21 Chimeric A3 VL
DIVMTQSHIFMSTSVGDRVSITCKASQDVDTAVAWYQQKPGQSPKLLIYWASTRLTGVPDRFTGSG
SGTDFTLTISNVQSEDLADYFCQQYSSYPYTFGQGTKLEIK

SEQ ID NO:22 Chimeric A3 VL-CDR1
KASQDVDTAVA

SEQ ID NO:23 Chimeric A3 VL-CDR2
WASTRLT

SEQ ID NO:24 Chimeric A3 VL-CDR3
QQYSSYPYT

SEQ ID NO:25 Humanized A3 human IgG1 heavy chain:

EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVARIRSKSNNYATYYADSV
KDRFTISRDDAKNSLYLQMNSLRAEDTAVYYCVRQWDYDVRAMNYWGQGTLVTVSSASTKGPSVFP
LAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL
GTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN
KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO:26 Humanized A3 VH:
EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMNWVRQAPGKGLEWVARIRSKSNNYATYYADSV
KDRFTISRDDAKNSLYLQMNSLRAEDTAVYYCVRQWDYDVRAMNYWGQGTLVTVSS

SEQ ID NO:27 Humanized A3 VH-CDR1:
TYAMN

SEQ ID NO:28 Humanized A3 VH-CDR2:
RIRSKSNNYATYYADSVKD

SEQ ID NO:29 Humanized A3 VH-CDR3:
QWDYDVRAMNY

SEQ ID NO:30 Humanized A3 human Kappa light chain:
DIQMTQSPSSLSASVGDRVTITCKASQDVDTAVAWYQQKPGKAPKLLIYWASTRLTGVPSRFSGSG
SGTDFTLTISSLQPEDFATYYCQQYSSYPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASV
VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTH
QGLSSPVTKSFNRGEC

SEQ ID NO:31 Humanized A3 VL:

DIQMTQSPSSLSASVGDRVTITCKASQDVDTAVAWYQQKPGKAPKLLIYWASTRLTGVPSRFSGSG
SGTDFTLTISSLQPEDFATYYCQQYSSYPYTFGQGTKLEIK

SEQ ID NO:32 Humanized A3 VL-CDR1:
KASQDVDTAVA

SEQ ID NO:33 Humanized A3 VL-CDR2:
WASTRLT

SEQ ID NO:34 Humanized A3 VL-CDR3:
QQYSSYPYT

We Claim:

1. An antibody-drug conjugate of the formula:

Ab-(LU-D)*p*

or a pharmaceutically acceptable salt thereof wherein;

(a) Ab is an anti-5T4 antibody or antigen binding portion thereof, comprising a heavy chain variable region having:

(i) a VH CDR1 region as shown in SEQ ID NO: 5,

(ii) a VH CDR2 region as shown in SEQ ID NO: 6, and

(iii) a VH CDR3 region as shown in SEQ ID NO: 7;

(b) LU is a linker unit selected from the group consisting of maleimidocaproyl and maleimidocaproyl-Val-Cit,

(c) *p* is an integer from about 1 to about 8, and

(d) D is a Drug unit selected from the group consisting of MMAE, MMAD, and MMAF.

2. The antibody-drug conjugate of Claim 1 wherein said anti-5T4 antibody or antigen binding portion thereof, comprises a light chain variable region having:

(a) a VL CDR1 region as shown in SEQ ID NO: 8,

(b) a VL CDR2 region as shown in SEQ ID NO: 9, and

(c) a VL CDR3 region as shown in SEQ ID NO: 10.

3. The antibody-drug conjugate of Claims 1 or 2 wherein said anti-5T4 antibody or antigen binding portion thereof, further comprises:

1) a heavy chain variable region having

(a) a VH CDR1 region as shown in SEQ ID NO: 5,

(b) a VH CDR2 region as shown in SEQ ID NO: 6, and

(c) a VH CDR3 region as shown in SEQ ID NO: 7.

2) a light chain variable region having

(a) a VL CDR1 region as shown in SEQ ID NO: 8,

(b) a VL CDR2 region as shown in SEQ ID NO: 9, and

(c) a VL CDR3 region as shown in SEQ ID NO: 10.

4. The antibody-drug conjugate of any one of Claims 1-3, wherein said anti-5T4 antibody or antigen binding portion thereof, comprises the VH region of SEQ ID NO: 3 and the VL region of SEQ ID NO: 4.

5. The antibody-drug conjugate of any one of Claims 1-4 wherein said anti-5T4 antibody or antigen binding portion thereof, consists of a heavy chain having SEQ ID NO:1 and a light chain having SEQ ID NO: 2.

6. The antibody-drug conjugate of any one of Claims 1-5, wherein said antibody or antigen binding portion thereof, recognizes an epitope on human 5T4 antigen, wherein said epitope comprises amino acid residues 173-258 and 282-361 of the amino acid sequence of SEQ ID NO:11.

7. The antibody-drug conjugate of any one of Claims 1-6, wherein said LU is maleimidocaproyl.

8. The antibody-drug conjugate of any one of Claims 1-7, wherein said Drug is MMAF.

9. The antibody-drug conjugate of any one of Claims 1-8, wherein *p* is an integer from about 1 to about 4.

10. The antibody-drug conjugate of Claim 1 wherein:

(a) said anti-5T4 antibody consists of a heavy chain having SEQ ID NO:1 and a light chain having SEQ ID NO: 2,

(b) said LU is maleimidocaproyl,

(c) said Drug is MMAF, and
(d) *p* is 4.

11. A pharmaceutical composition comprising the antibody-drug conjugate of any one of Claims 1-10 and a pharmaceutically acceptable carrier.

12. A method of treating 5T4-positive cancer in a patient in need thereof, comprising administering to said patient the antibody-drug conjugate according to any one of Claims 1-11.

13. The method of Claim 12 wherein said cancer is selected from the group consisting of colorectal, breast, pancreatic, and non-small cell lung carcinomas.

14. The antibody-drug conjugate of any one of Claims 1-11 for use in therapy.

15. The use of the antibody-drug conjugate of any one of Claims 1-11 for the manufacture of a medicament.

16. The use according to Claims 14 or 15, wherein said use is for the treatment of 5T4-positive cancer.

17. A nucleic acid that encodes the anti-5T4 antibody of any one of Claims 1-6.

18. A vector comprising the nucleic acid of Claim 17.

19. A host cell comprising the vector according to Claim 18.

20. A process for producing an antibody comprising cultivating the host cell of Claim 19 and recovering the antibody from the culture.

21. A process for producing an anti-5T4 antibody-drug conjugate comprising:
(a) chemically linking a linker unit selected from the group consisting of maleimidocaproyl or maleimidocaproyl-Val-Cit to a Drug unit selected from the group consisting of MMAE, MMAD, or MMAF;
(b) conjugating said linker-drug to the antibody recovered from the cell culture of Claim 20 , and;
(c) purifying the antibody-drug conjugate.

INTERNATIONAL SEARCH REPORT

International application No
PCT/IB2012/051304

A. CLASSIFICATION OF SUBJECT MATTER
INV. A61K47/48 A61P35/00
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EPO-Internal, BIOSIS, EMBASE, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2007/106744 A2 (WYETH CORP [US]; BOGHAERT ERWIN R [US]; DAMLE NITIN K [US]; HAMANN PHI) 20 September 2007 (2007-09-20) Claims 46, 47. Figures 1A-1C; Example 1 pages 62-62; Example 6 pages 72-74. -----	17-21
A	WO 2007/067602 A1 (WYETH CORP [US]; DAMLE NITIN K [US]; DIJOSEPH JOHN [US]; SCHENDEL PAUL) 14 June 2007 (2007-06-14) claim 33 -----	1-21

☐ Further documents are listed in the continuation of Box C.

☒ See patent family annex.

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"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
4 June 2012	13/06/2012

Name and mailing address of the ISA/	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Bettio, Andrea

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/IB2012/051304

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