CYSTEINE ENGINEERED ANTIBODIES AND CONJUGATES

[0001] REFERENCE TO RELATED APPLICATIONS

[0002] This non-provisional application filed under 37 CFR §1.53(b), claims the benefit under 35 USC §119(e) of U.S. Provisional Application Serial No. 61/352,728 filed on 8 June 2010, which is incorporated by reference in entirety

[0003] FIELD OF THE INVENTION

[0004] The invention relates generally to antibodies engineered with reactive cysteine residues and more specifically to antibodies with therapeutic or diagnostic applications. The cysteine engineered antibodies may be conjugated with chemotherapeutic drugs, toxins, affinity ligands such as biotin, and detection labels such as fluorophores. The invention also relates to methods of using antibodies and antibody-drug conjugate compounds for *in vitro*, *in situ*, and *in vivo* diagnosis or treatment of mammalian cells, or associated pathological conditions.

[0005] BACKGROUND OF THE INVENTION

[0006] Antibody drug conjugates (ADC) are attractive targeted chemo-therapeutic molecules as they combine ideal properties of both antibodies and cytotoxic drugs by targeting potent cytotoxic drugs to the antigen-expressing tumor cells, thereby enhancing their anti-tumor activity. The successful ADC development for a given target antigen depends on optimization of antibody selection, linker stability, cytotoxic drug potency and mode of linker-drug conjugation to the antibody.

[0007] Conventional means of attaching, i.e. linking through covalent bonds, a drug moiety to an antibody generally leads to a heterogeneous mixture of molecules where the drug moieties are attached at a number of sites on the antibody. For example, cytotoxic drugs have typically been conjugated to antibodies through the often-numerous lysine residues of an antibody, generating a heterogeneous antibody-drug conjugate mixture. Depending on reaction conditions, the heterogeneous mixture typically contains a distribution of antibodies with from 0 to about 8, or more, attached drug moieties. In addition, within each subgroup of conjugates with a particular integer ratio of drug moieties to antibody, is a potentially heterogeneous mixture where the drug moiety is attached at various sites on the antibody. Analytical and preparative methods are inadequate to separate and characterize the antibody-

drug conjugate species molecules within the heterogeneous mixture resulting from a conjugation reaction. Antibodies are large, complex and structurally diverse biomolecules, often with many reactive functional groups. Their reactivities with linker reagents and drug-linker intermediates are dependent on factors such as pH, concentration, salt concentration, and co-solvents. Furthermore, the multistep conjugation process may be nonreproducible due to difficulties in controlling the reaction conditions and characterizing reactants and intermediates.

[0008] Cysteine thiols are reactive at neutral pH, unlike most amines which are protonated and less nucleophilic near pH 7. Since free thiol (RSH, sulfhydryl) groups are relatively reactive, proteins with cysteine residues often exist in their oxidized form as disulfide-linked oligomers or have internally bridged disulfide groups. Antibody cysteine thiol groups are generally more reactive, i.e. more nucleophilic, towards electrophilic conjugation reagents than antibody amine or hydroxyl groups. Engineering in cysteine thiol groups by the mutation of various amino acid residues of a protein to cysteine amino acids is potentially problematic, particularly in the case of unpaired (free Cys) residues or those which are relatively accessible for reaction or oxidation. In concentrated solutions of the protein, whether in the periplasm of E. coli, culture supernatants, or partially or completely purified protein, unpaired Cys residues on the surface of the protein can pair and oxidize to form intermolecular disulfides, and hence protein dimers or multimers. Disulfide dimer formation renders the new Cys unreactive for conjugation to a drug, ligand, or other label. Furthermore, if the protein oxidatively forms an intramolecular disulfide bond between the newly engineered Cys and an existing Cys residue, both Cys groups are unavailable for active site participation and interactions. Furthermore, the protein may be rendered inactive or non-specific, by misfolding or loss of tertiary structure (Zhang et al (2002) Anal. Biochem. 311:1-9).

[0009] Antibodies with cysteine substitutions (ThioMabs) at sites where the engineered cysteines are available for conjugation but do not perturb immunoglobulin folding and assembly or alter antigen binding and effector functions (Junutula, et al., 2008b Nature Biotech., 26(8):925-932; Dornan et al (2009) Blood 114(13):2721-2729; US 7521541; US 7723485; WO2009/052249). These ThioMabs can then be conjugated to cytotoxic drugs through the engineered cysteine thiol groups to obtain ThioMab drug conjugates (TDC) with uniform stoichiometry (~2 drugs per antibody). Studies with multiple antibodies against different antigens have shown that TDC are as efficacious as conventional ADC in xenograft models and are tolerated at higher doses in relevant preclinical models. ThioMab drug

conjugates have been engineered with drug attachment at different parts of the antibody (light chain-Fab, heavy chain-Fab and heavy chain-Fc). The *in vitro & in vivo* stability, efficacy and PK properties of TDC provide a unique advantage over conventional ADC due to their homogeneity and site-specific conjugation to cytotoxic drugs.

[0010] SUMMARY

[0011] The invention includes an isolated cysteine engineered antibody comprising a free cysteine amino acid in the heavy chain or light chain.

[0012] An aspect of the invention is a process to prepare the isolated cysteine engineered antibody by mutagenizing a nucleic acid sequence of a parent antibody by replacing one or more amino acid residues by cysteine to encode the cysteine engineered antibody; expressing the cysteine engineered antibody; and isolating the cysteine engineered antibody.

[0013] Another aspect of the invention is a conjugate of the isolated cysteine engineered antibody wherein the antibody is covalently attached to a capture label, a detection label, a drug moiety, or a solid support.

[0014] BRIEF DESCRIPTION OF THE DRAWINGS

[0015] Figure 1A shows a three-dimensional representation of the hu4D5Fabv7 antibody fragment derived by X-ray crystal coordinates. The structure positions of the exemplary engineered Cys residues of the heavy and light chains are numbered (according to a sequential numbering system).

[0016] Figure 1B shows a sequential numbering scheme (top row), starting at the N-terminus in comparison with the Kabat numbering scheme (bottom row) for 4D5v7fabH. Kabat numbering insertions are noted by a,b,c.

[0017] Figures 2A and 2B show binding measurements with detection of absorbance at 450nm of hu4D5Fabv8 and hu4D5Fabv8 Cys mutant (ThioFab) phage variants: (A) non-biotinylated phage-hu4D5Fabv8 and (B) biotinylated phage-hu4D5Fabv8 (B) by the PHESELECTOR assay for interactions with BSA (open bar), HER2 (striped bar) or streptavidin (solid bar).

[0018] Figures 3A and 3B show binding measurements with detection of absorbance at 450nm of hu4D5Fabv8 (left) and hu4D5Fabv8 Cys mutant (ThioFab) variants: (A) non-biotinylated phage-hu4D5Fabv8 and (B) biotinylated phage-hu4D5Fabv8 by the PHESELECTOR assay for interactions with: BSA (open bar), HER2 (striped bar) and

streptavidin (solid bar). Light chain variants are on the left side and heavy chain variants are on the right side. Thiol reactivity = $OD_{450\ nm}$ for streptavidin binding ÷ $OD_{450\ nm}$ for HER2 (antibody) binding

[0019] Figure 4A shows Fractional Surface Accessibility values of residues on wild type hu4D5Fabv8. Light chain sites are on the left side and heavy chain sites are on the right side.

[0020] Figure 4B shows binding measurements with detection of absorbance at 450nm of biotinylated hu4D5Fabv8 (left) and hu4D5Fabv8 Cys mutant (ThioFab) variants for interactions with HER2 (day 2), streptavidin (SA) (day 2), HER2 (day 4), and SA (day 4). Phage-hu4D5Fabv8 Cys variants were isolated and stored at 4 °C. Biotin conjugation was carried out either at day 2 or day 4 followed by PHESELECTOR analyses to monitor their interaction with Her2 and streptavidin as described in Example 2, and probe the stability of reactive thiol groups on engineered ThioFab variants.

[0021] Figure 5 shows binding measurements with detection of absorbance at 450nm of biotin-maleimide conjugated-hu4D5Fabv8 (A121C) and non-biotinylated wild type hu4D5Fabv8 for binding to streptavidin and HER2. Each Fab was tested at 2 ng and 20 ng.

[0022] Figure 6 shows ELISA analysis with detection of absorbance at 450nm of biotinylated ABP-hu4D5Fabv8 wild type (wt), and ABP-hu4D5Fabv8 cysteine mutants V110C and A121C for binding with rabbit albumin, streptavidin (SA), and HER2.

[0023] Figure 7 shows ELISA analysis with detection of absorbance at 450nm of biotinylated ABP-hu4D5Fabv8 cysteine mutants (ThioFab variants): (left to right) single Cys variants ABP-V110C, ABP-A121C, and double Cys variants ABP-V110C-A88C and ABP-V110C-A121C for binding with rabbit albumin, HER2 and streptavidin (SA), and probing with Fab-HRP or SA-HRP.

[0024] Figure 8 shows binding of biotinylated ThioFab phage and an anti-phage HRP antibody to HER2 (top) and Streptavidin (bottom).

[0025] Figure 9A shows a cartoon depiction of biotinylated antibody binding to immobilized HER2 with binding of HRP labeled secondary antibody for absorbance detection.

[0026] Figure 9B shows binding measurements with detection of absorbance at 450nm of biotin-maleimide conjugated thio-trastuzumab variants and non-biotinylated wild type trastuzumab in binding to immobilized HER2. From left to right: V110C (single cys), A121C (single cys), V110C/A121C (double cys), and trastuzumab. Each thio IgG variant

and trastuzumab was tested at 1, 10, and 100 ng.

[0027] Figure 10A shows a cartoon depiction of biotinylated antibody binding to immobilized HER2 with binding of biotin to anti-IgG-HRP for absorbance detection.

[0028] Figure 10B shows binding measurements with detection of absorbance at 450nm of biotin-maleimide conjugated-thio trastuzumab variants and non-biotinylated wild type trastuzumab in binding to immobilized streptavidin. From left to right: V110C (single cys), A121C (single cys), V110C/A121C (double cys), and trastuzumab. Each thio IgG variant and trastuzumab was tested at 1, 10, and 100 ng.

[0029] Figure 11 shows the general process to prepare a cysteine engineered antibody (ThioMab) expressed from cell culture for conjugation.

[0030] DETAILED DESCRIPTION OF EXEMPLARY EMBODIMENTS

[0031] Reference will now be made in detail to certain embodiments of the invention, examples of which are illustrated in the accompanying structures and formulas. While the invention will be described in conjunction with the enumerated embodiments, it will be understood that they are not intended to limit the invention to those embodiments. On the contrary, the invention is intended to cover all alternatives, modifications, and equivalents, which may be included within the scope of the present invention as defined by the claims.

[0032] One skilled in the art will recognize many methods and materials similar or equivalent to those described herein, which could be used in the practice of the present invention. The present invention is in no way limited to the methods and materials described.

[0033] Unless defined otherwise, technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs, and are consistent with: Singleton et al (1994) Dictionary of Microbiology and Molecular Biology, 2nd Ed., J. Wiley & Sons, New York, NY; and Janeway, C., Travers, P., Walport, M., Shlomchik (2001) Immunobiology, 5th Ed., Garland Publishing, New York.

[0034] DEFINITIONS

[0035] Unless stated otherwise, the following terms and phrases as used herein are intended to have the following meanings:

[0036] When trade names are used herein, applicants intend to independently include the trade name product formulation, the generic drug, and the active pharmaceutical ingredient(s) of the trade name product.

[0037] The term "antibody" herein is used in the broadest sense and specifically

covers monoclonal antibodies, polyclonal antibodies, dimers, multimers, multispecific antibodies (e.g., bispecific antibodies), and antibody fragments, so long as they exhibit the desired biological activity (Miller et al (2003) Jour. of Immunology 170:4854-4861). Antibodies may be murine, human, humanized, chimeric, or derived from other species. An antibody is a protein generated by the immune system that is capable of recognizing and binding to a specific antigen. (Janeway, C., Travers, P., Walport, M., Shlomchik (2001) Immuno Biology, 5th Ed., Garland Publishing, New York). A target antigen generally has numerous binding sites, also called epitopes, recognized by CDRs on multiple antibodies. Each antibody that specifically binds to a different epitope has a different structure. Thus, one antigen may have more than one corresponding antibody. An antibody includes a full-length immunoglobulin molecule or an immunologically active portion of a full-length immunoglobulin molecule, i.e., a molecule that contains an antigen binding site that immunospecifically binds an antigen of a target of interest or part thereof, such targets including but not limited to, cancer cell or cells that produce autoimmune antibodies associated with an autoimmune disease. The immunoglobulin disclosed herein can be of any type (e.g., IgG, IgE, IgM, IgD, and IgA), class (e.g., IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2) or subclass of immunoglobulin molecule. The immunoglobulins can be derived from any species. In one aspect, however, the immunoglobulin is of human, murine, or rabbit origin.

[0038] "Antibody fragments" comprise a portion of a full length antibody, generally the antigen binding or variable region thereof. Examples of antibody fragments include Fab, Fab', $F(ab')_2$, and Fv fragments; diabodies; linear antibodies; minibodies (Olafsen et al (2004) Protein Eng. Design & Sel. 17(4):315-323), fragments produced by a Fab expression library, anti-idiotypic (anti-Id) antibodies, CDR (complementary determining region), and epitope-binding fragments of any of the above which immunospecifically bind to cancer cell antigens, viral antigens or microbial antigens, single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

[0039] 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 site. Furthermore, in contrast to polyclonal antibody preparations which include different antibodies directed against different determinants (epitopes), each monoclonal antibody is directed against a single determinant on the antigen. In addition to

their specificity, the monoclonal antibodies are advantageous in that they may be synthesized uncontaminated by other antibodies. 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 (1975) *Nature* 256:495, or may be made by recombinant DNA methods (see for example: US 4816567; US 5807715). The monoclonal antibodies may also be isolated from phage antibody libraries using the techniques described in Clackson et al (1991) Nature, 352:624-628; Marks et al (1991) J. Mol. Biol., 222:581-597; for example.

[0040] The monoclonal antibodies 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 exhibit the desired biological activity (US 4816567; and Morrison et al (1984) Proc. Natl. Acad. Sci. USA, 81:6851-6855). Chimeric antibodies of interest herein include "primatized" antibodies comprising variable domain antigen-binding sequences derived from a non-human primate (*e.g.*, Old World Monkey, Ape etc) and human constant region sequences.

[0041] An "intact antibody" herein is one comprising a VL and VH domains, as well as a light chain constant domain (CL) and heavy chain constant domains, CH1, CH2 and CH3. The constant domains may be native sequence constant domains (*e.g.*, human native sequence constant domains) or amino acid sequence variant thereof. The intact antibody may have one or more "effector functions" which refer to those biological activities attributable to the Fc constant region (a native sequence Fc region or amino acid sequence variant Fc region) of an antibody. Examples of antibody effector functions include C1q binding; complement dependent cytotoxicity; Fc receptor binding; antibody-dependent cell-mediated cytotoxicity (ADCC); phagocytosis; and down regulation of cell surface receptors such as B cell receptor and BCR.

[0042] Depending on the amino acid sequence of the constant domain of their heavy chains, intact antibodies can be assigned to different "classes." There are five major classes of intact immunoglobulin antibodies: IgA, IgD, IgE, IgG, and IgM, and several of these may

be further divided into "subclasses" (isotypes), *e.g.*, IgG1, IgG2, IgG3, IgG4, IgA, and IgA2. The heavy-chain constant domains that correspond to the different classes of antibodies are called α, δ, ε, γ, and μ, respectively. The subunit structures and three-dimensional configurations of different classes of immunoglobulins are well known. Ig forms include hinge-modifications or hingeless forms (Roux et al (1998) J. Immunol. 161:4083-4090; Lund et al (2000) Eur. J. Biochem. 267:7246-7256; US 2005/0048572; US 2004/0229310).

[0043] An "ErbB receptor" is a receptor protein tyrosine kinase which belongs to the ErbB receptor family whose members are important mediators of cell growth, differentiation and survival. The ErbB receptor family includes four distinct members including epidermal growth factor receptor (EGFR, ErbB1, HER1), HER2 (ErbB2 or p185neu), HER3 (ErbB3) and HER4 (ErbB4 or tyro2). A panel of anti-ErbB2 antibodies has been characterized using the human breast tumor cell line SKBR3 (Hudziak et al (1989) Mol. Cell. Biol. 9(3):1165-1172. Maximum inhibition was obtained with the antibody called 4D5 which inhibited cellular proliferation by 56%. Other antibodies in the panel reduced cellular proliferation to a lesser extent in this assay. The antibody 4D5 was further found to sensitize ErbB2-overexpressing breast tumor cell lines to the cytotoxic effects of TNF-α (US 5677171). The anti-ErbB2 antibodies discussed in Hudziak et al. are further characterized in Fendly et al (1990) Cancer Research 50:1550-1558; Kotts et al. (1990) In Vitro 26(3):59A; Sarup et al. (1991) Growth Regulation 1:72-82; Shepard et al. J. (1991) Clin. Immunol. 11(3):117-127; Kumar et al. (1991) Mol. Cell. Biol. 11(2):979-986; Lewis et al. (1993) Cancer Immunol. Immunother. 37:255-263; Pietras et al. (1994) Oncogene 9:1829-1838; Vitetta et al. (1994) Cancer Research 54:5301-5309; Sliwkowski et al. (1994) J. Biol. Chem. 269(20):14661-14665; Scott et al. (1991) J. Biol. Chem. 266:14300-5; D'souza et al. Proc. Natl. Acad. Sci. (1994) 91:7202-7206; Lewis et al. (1996) Cancer Research 56:1457-1465; and Schaefer et al. (1997) Oncogene 15:1385-1394.

[0044] The ErbB receptor will generally comprise an extracellular domain, which may bind an ErbB ligand; a lipophilic transmembrane domain; a conserved intracellular tyrosine kinase domain; and a carboxyl-terminal signaling domain harboring several tyrosine residues which can be phosphorylated. The ErbB receptor may be a "native sequence" ErbB receptor or an "amino acid sequence variant" thereof. Preferably, the ErbB receptor is native sequence human ErbB receptor. Accordingly, a "member of the ErbB receptor family" includes EGFR (ErbB1), ErbB2, ErbB3, ErbB4.

[0045] The term "amino acid sequence variant" refers to polypeptides having amino acid sequences that differ to some extent from a native sequence polypeptide. Ordinarily,

amino acid sequence variants will possess at least about 70% sequence identity with at least one receptor binding domain of a native ErbB ligand or with at least one ligand binding domain of a native ErbB receptor, and preferably, they will be at least about 80%, more preferably, at least about 90% homologous by sequence with such receptor or ligand binding domains. The amino acid sequence variants possess substitutions, deletions, and/or insertions at certain positions within the amino acid sequence of the native amino acid sequence. Amino acids are designated by the conventional names, one-letter and three-letter codes.

[0046] "Sequence identity" is defined as the percentage of residues in the amino acid sequence variant that are identical after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Methods and computer programs for the alignment are well known in the art. One such computer program is "Align 2," authored by Genentech, Inc., which was filed with user documentation in the United States Copyright Office, Washington, DC 20559, on December 10, 1991.

[0047] "Native antibodies" are usually heterotetrameric glycoproteins of about 150,000 daltons, composed of two identical light (L) chains and two identical heavy (H) chains. Each light chain is linked to a heavy chain by one covalent disulfide bond, while the number of disulfide linkages varies among the heavy chains of different immunoglobulin isotypes. Each heavy and light chain also has regularly spaced intrachain disulfide bridges. Each heavy chain has at one end a variable domain (V_H) followed by a number of constant domains. Each light chain has a variable domain at one end (V_L) and a constant domain at its other end. The constant domain of the light chain is aligned with the first constant domain of the heavy chain, and the light-chain variable domain is aligned with the variable domain of the heavy chain. Particular amino acid residues are believed to form an interface between the light chain and heavy chain variable domains.

[0048] The term "variable" refers to the fact that certain portions of the variable domains differ extensively in sequence among antibodies and are used in the binding and specificity of each particular antibody for its particular antigen. However, the variability is not evenly distributed throughout the variable domains of antibodies. It is concentrated in three segments called hypervariable regions both in the light chain and the heavy chain variable domains. The more highly conserved portions of variable domains are called the framework regions (FRs). The variable domains of native heavy and light chains each comprise four FRs, largely adopting a β-sheet configuration, connected by three hypervariable regions, which form loops connecting, and in some cases forming part of, the β-sheet structure. The hypervariable regions in each chain are held together in close

proximity by the FRs and, with the hypervariable regions from the other chain, contribute to the formation of the antigen-binding site of antibodies (see Kabat et al (1991) Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD). The constant domains are not involved directly in binding an antibody to an antigen, but exhibit various effector functions, such as participation of the antibody in antibody dependent cellular cytotoxicity (ADCC).

[0049] The term "hypervariable region" when used herein refers to the amino acid residues of an antibody which are responsible for antigen-binding. The hypervariable region generally comprises amino acid residues from a "complementarity determining region" or "CDR" (*e.g.*, residues 24-34 (L1), 50-56 (L2) and 89-97 (L3) in the light chain variable domain and 31-35 (H1), 50-65 (H2) and 95-102 (H3) in the heavy chain variable domain; Kabat et al *supra*) and/or those residues from a "hypervariable loop" (*e.g.*, residues 26-32 (L1), 50-52 (L2) and 91-96 (L3) in the light chain variable domain and 26-32 (H1), 53-55 (H2) and 96-101 (H3) in the heavy chain variable domain; Chothia and Lesk (1987) J. Mol. Biol., 196:901-917). "Framework Region" or "FR" residues are those variable domain residues other than the hypervariable region residues as herein defined.

[0050] Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, whose name reflects its ability to crystallize readily. Pepsin treatment yields an F(ab')2 fragment that has two antigen-binding sites and is still capable of cross-linking antigen.

[0051] "Fv" is the minimum antibody fragment which contains a complete antigen-recognition and antigen-binding site. This region consists of a dimer of one heavy chain and one light chain variable domain in tight, non-covalent association. It is in this configuration that the three hypervariable regions of each variable domain interact to define an antigen-binding site on the surface of the V_H-V_L dimer. Collectively, the six hypervariable regions confer antigen-binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three hypervariable regions specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

[0052] The Fab fragment also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab' fragments differ from Fab fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear at least one free

thiol group. F(ab')2 antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

[0053] The "light chains" of antibodies from any vertebrate species can be assigned to one of two clearly distinct types, called kappa (κ) and lambda (λ), based on the amino acid sequences of their constant domains.

[0054] "Single-chain Fv" or "scFv" antibody fragments comprise the V_H and V_L domains of antibody, wherein these domains are present in a single polypeptide chain. Preferably, the Fv polypeptide further comprises a polypeptide linker between the VH and VL domains which enables the scFv to form the desired structure for antigen binding. For a review of scFv, see Plückthun in The Pharmacology of Monoclonal Antibodies, vol. 113, Rosenburg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994). Anti-ErbB2 antibody scFv fragments are described in WO 93/16185; US Patent Nos. 5571894; and 5587458.

[0055] "Humanized" forms of non-human (*e.g.,* rodent) antibodies are chimeric antibodies that contain minimal sequence derived from non-human immunoglobulin. Humanization is a method to transfer the murine antigen binding information to a non-immunogenic human antibody acceptor, and has resulted in many therapeutically useful drugs. The method of humanization generally begins by transferring all six murine complementarity determining regions (CDRs) onto a human antibody framework (Jones et al, (1986) Nature 321:522-525). These CDR-grafted antibodies generally do not retain their original affinity for antigen binding, and in fact, affinity is often severely impaired. Besides the CDRs, select non-human antibody framework residues must also be incorporated to maintain proper CDR conformation (Chothia et al (1989) Nature 342:877). The transfer of key mouse framework residues to the human acceptor in order to support the structural conformation of the grafted CDRs has been shown to restore antigen binding and affinity (Riechmann et al (1992) J. Mol. Biol. 224, 487-499; Foote and Winter, (1992) J. Mol. Biol. 224:487-499; Presta et al (1993) J. Immunol. 151, 2623-2632; Werther et al (1996) J. Immunol. Methods 157:4986-4995; and Presta et al (2001) Thromb. Haemost. 85:379-389). For the most part, humanized antibodies are human immunoglobulins (recipient antibody) in which residues from a hypervariable region of the recipient are replaced by residues from a hypervariable region of a non-human species (donor antibody) such as mouse, rat, rabbit or nonhuman primate having the desired specificity, affinity, and capacity. In some instances, framework region (FR) residues of the human immunoglobulin are replaced by

corresponding non-human residues. Furthermore, humanized antibodies may comprise residues that are not found in the recipient antibody or in the donor antibody. These modifications are made to further refine antibody performance. 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 FRs 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. For further details, see US 6407213; Jones et al (1986) Nature, 321:522-525; Riechmann et al (1988) Nature 332:323-329; and Presta, (1992) Curr. Op. Struct. Biol., 2:593-596.

[0056] A "free cysteine amino acid" refers to a cysteine amino acid residue which has been engineered into a parent antibody, has a thiol functional group (-SH), and is not paired as an intramolecular or intermolecular disulfide bridge.

[0057] The term "thiol reactivity value" is a quantitative characterization of the reactivity of free cysteine amino acids. The thiol reactivity value is the percentage of a free cysteine amino acid in a cysteine engineered antibody which reacts with a thiol-reactive reagent, and converted to a maximum value of 1. For example, a free cysteine amino acid on a cysteine engineered antibody which reacts in 100% yield with a thiol-reactive reagent, such as a biotin-maleimide reagent, to form a biotin-labelled antibody has a thiol reactivity value of 1.0. Another cysteine amino acid engineered into the same or different parent antibody which reacts in 80% yield with a thiol-reactive reagent has a thiol reactivity value of about 0.8. Another cysteine amino acid engineered into the same or different parent antibody which fails totally to react with a thiol-reactive reagent has a thiol reactivity value of 0. Determination of the thiol reactivity value of a particular cysteine may be conducted by ELISA assay, mass spectroscopy, liquid chromatography, autoradiography, or other quantitative analytical tests.

[0058] A "parent antibody" is an antibody comprising an amino acid sequence from which one or more amino acid residues are replaced by one or more cysteine residues. The parent antibody may comprise a native or wild type sequence. The parent antibody may have pre-existing amino acid sequence modifications (such as additions, deletions and/or substitutions) relative to other native, wild type, or modified forms of an antibody. A parent antibody may be directed against a target antigen of interest, e.g. a biologically important polypeptide. Antibodies directed against nonpolypeptide antigens (such as tumor-associated

glycolipid antigens; see US 5091178) are also contemplated.

[0059] Exemplary parent antibodies include antibodies having affinity and selectivity for cell surface and transmembrane receptors and tumor-associated antigens (TAA).

[0060] An "isolated" antibody is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody in situ within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

[0061] An antibody "which binds" a molecular target or an antigen of interest, *e.g.*, ErbB2 antigen, is one capable of binding that antigen with sufficient affinity such that the antibody is useful in targeting a cell expressing the antigen. Where the antibody is one which binds ErbB2, it will usually preferentially bind ErbB2 as opposed to other ErbB receptors, and may be one which does not significantly cross-react with other proteins such as EGFR, ErbB3 or ErbB4. In such embodiments, the extent of binding of the antibody to these non-ErbB2 proteins (*e.g.*, cell surface binding to endogenous receptor) will be less than 10% as determined by fluorescence activated cell sorting (FACS) analysis or radioimmunoprecipitation (RIA). Sometimes, the anti-ErbB2 antibody will not significantly cross-react with the rat neu protein, *e.g.*, as described in Schecter et al. (1984) Nature 312:513 and Drebin et al (1984) Nature 312:545-548.

[0062] Molecular targets for antibodies encompassed by the present invention include CD proteins and their ligands, such as, but not limited to: (i) CD3, CD4, CD8, CD19, CD20, CD22, CD34, CD40, CD79α (CD79a), and CD79β (CD79b); (ii) members of the ErbB receptor family such as the EGF receptor, HER2, HER3 or HER4 receptor; (iii) cell adhesion molecules such as LFA-1, Mac1, p150,95, VLA-4, ICAM-1, VCAM and αv/β3 integrin, including either alpha or beta subunits thereof (*e.g.* anti-CD11a, anti-CD18 or anti-CD11b antibodies); (iv) growth factors such as VEGF; IgE; blood group antigens; flk2/flt3 receptor;

obesity (OB) receptor; *mpl* receptor; CTLA-4; protein C, BR3, c-met, tissue factor, β7 etc; and (v) cell surface and transmembrane tumor-associated antigens (TAA).

[0063] Unless indicated otherwise, the term "monoclonal antibody 4D5" refers to an antibody that has antigen binding residues of, or derived from, the murine 4D5 antibody (ATCC CRL 10463). For example, the monoclonal antibody 4D5 may be murine monoclonal antibody 4D5 or a variant thereof, such as a humanized 4D5. Exemplary humanized 4D5 antibodies include huMAb4D5-1, huMAb4D5-2, huMAb4D5-3, huMAb4D5-4, huMAb4D5-5, huMAb4D5-6, huMAb4D5-7 and huMAb4D5-8 (trastuzumab, HERCEPTIN®) as in US Patent No. 5821337.

[0064] The terms "treat" and "treatment" refer to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) an undesired physiological change or disorder, such as the development or spread of cancer. For purposes of this invention, beneficial or desired clinical results include, but are not limited to, alleviation of symptoms, diminishment of extent of disease, stabilized (*i.e.,* not worsening) state of disease, delay or slowing of disease progression, amelioration or palliation of the disease state, and remission (whether partial or total), whether detectable or undetectable. "Treatment" can also mean prolonging survival as compared to expected survival if not receiving treatment. Those in need of treatment include those already with the condition or disorder as well as those prone to have the condition or disorder or those in which the condition or disorder is to be prevented.

[0065] The term "therapeutically effective amount" refers to an amount of a drug effective to treat a disease or disorder in a mammal. In the case of cancer, the therapeutically effective amount of the drug may reduce the number of cancer cells; reduce the tumor size; inhibit (*i.e.,* slow to some extent and preferably stop) cancer cell infiltration into peripheral organs; inhibit (*i.e.,* slow to some extent and preferably stop) tumor metastasis; inhibit, to some extent, tumor growth; and/or relieve to some extent one or more of the symptoms associated with the cancer. To the extent the drug may prevent growth and/or kill existing cancer cells, it may be cytostatic and/or cytotoxic. For cancer therapy, efficacy can, for example, be measured by assessing the time to disease progression (TTP) and/or determining the response rate (RR).

[0066] The terms "cancer" and "cancerous" refer to or describe the physiological condition in mammals that is typically characterized by unregulated cell growth. A "tumor" comprises one or more cancerous cells. Examples of cancer include, but are not limited to,

carcinoma, lymphoma, blastoma, sarcoma, and leukemia or lymphoid malignancies. More particular examples of such cancers include squamous cell cancer (*e.g.,* epithelial squamous cell cancer), lung cancer including small- cell lung cancer, non-small cell lung cancer ("NSCLC"), adenocarcinoma of the lung and squamous carcinoma of the lung, cancer of the peritoneum, hepatocellular cancer, gastric or stomach cancer including gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, hepatoma, breast cancer, colon cancer, rectal cancer, colorectal cancer, endometrial or uterine carcinoma, salivary gland carcinoma, kidney or renal cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma, anal carcinoma, penile carcinoma, as well as head and neck cancer.

[0067] An "ErbB-expressing cancer" is one comprising cells which have ErbB protein present at their cell surface. An "ErbB2-expressing cancer" is one which produces sufficient levels of ErbB2 at the surface of cells thereof, such that an anti-ErbB2 antibody can bind thereto and have a therapeutic effect with respect to the cancer.

[0068] A cancer which "overexpresses" an antigenic receptor is one which has significantly higher levels of the receptor, such as ErbB2, at the cell surface thereof, compared to a noncancerous cell of the same tissue type. Such overexpression may be caused by gene amplification or by increased transcription or translation. Receptor overexpression may be determined in a diagnostic or prognostic assay by evaluating increased levels of the receptor protein present on the surface of a cell (*e.g.,* via an immunohistochemistry assay; IHC). Alternatively, or additionally, one may measure levels of receptor-encoding nucleic acid in the cell, *e.g.,* via fluorescent in situ hybridization (FISH; see WO 98/45479), southern blotting, or polymerase chain reaction (PCR) techniques, such as real time quantitative PCR (RT-PCR).

[0069] The term "cytotoxic agent" as used herein refers to a substance that inhibits or prevents the function of cells and/or causes destruction of cells. The term is intended to include radioactive isotopes (*e.g.,* ^{211}At, ^{131}I, ^{125}I, ^{90}Y, ^{186}Re, ^{188}Re, ^{153}Sm, ^{212}Bi, ^{32}P, ^{60}C, and radioactive isotopes of Lu), chemotherapeutic agents, and toxins such as small molecule toxins or enzymatically active toxins of bacterial, fungal, plant or animal origin, including synthetic analogs and derivatives thereof.

[0070] "Phage display" is a technique by which variant polypeptides are displayed as fusion proteins to a coat protein on the surface of phage, *e.g.*, filamentous phage, particles. One utility of phage display lies in the fact that large libraries of randomized protein variants can be rapidly and efficiently sorted for those sequences that bind to a target molecule with

high affinity. Display of peptide and protein libraries on phage has been used for screening millions of polypeptides for ones with specific binding properties. Polyvalent phage display methods have been used for displaying small random peptides and small proteins, typically through fusions to either pIII or pVIII of filamentous phage (Wells and Lowman, (1992) Curr. Opin. Struct. Biol., 3:355-362, and references cited therein). In monovalent phage display, a protein or peptide library is fused to a phage coat protein or a portion thereof, and expressed at low levels in the presence of wild type protein. Avidity effects are reduced relative to polyvalent phage so that sorting is on the basis of intrinsic ligand affinity, and phagemid vectors are used, which simplify DNA manipulations. Lowman and Wells, *Methods: A companion to Methods in Enzymology,* 3:205-0216 (1991). Phage display includes techniques for producing antibody-like molecules (Janeway, C., Travers, P., Walport, M., Shlomchik (2001) *Immunobiology, 5th Ed.*, Garland Publishing, New York, p627-628; Lee et al).

[0071] A "phagemid" is a plasmid vector having a bacterial origin of replication, *e.g.*, Co1E1, and a copy of an intergenic region of a bacteriophage. The phagemid may be used on any known bacteriophage, including filamentous bacteriophage and lambdoid bacteriophage. The plasmid will also generally contain a selectable marker for antibiotic resistance. Segments of DNA cloned into these vectors can be propagated as plasmids. When cells harboring these vectors are provided with all genes necessary for the production of phage particles, the mode of replication of the plasmid changes to rolling circle replication to generate copies of one strand of the plasmid DNA and package phage particles. The phagemid may form infectious or non-infectious phage particles. This term includes phagemids which contain a phage coat protein gene or fragment thereof linked to a heterologous polypeptide gene as a gene fusion such that the heterologous polypeptide is displayed on the surface of the phage particle.

[0072] "Linker", "Linker Unit", or "link" means a chemical moiety comprising a covalent bond or a chain of atoms that covalently attaches an antibody to a drug moiety. In various embodiments, a linker is specified as L. Linkers include a divalent radical such as an alkyldiyl, an arylene, a heteroarylene, moieties such as: $-(CR_2)_nO(CR_2)_n-$, repeating units of alkyloxy (e.g. polyethylenoxy, PEG, polymethyleneoxy) and alkylamino (e.g. polyethyleneamino, Jeffamine™); and diacid ester and amides including succinate, succinamide, diglycolate, malonate, and caproamide.

[0073] The term "label" means any moiety which can be covalently attached to an

antibody and that functions to: (i) provide a detectable signal; (ii) interact with a second label to modify the detectable signal provided by the first or second label, e.g. FRET (fluorescence resonance energy transfer); (iii) stabilize interactions or increase affinity of binding, with antigen or ligand; (iv) affect mobility, e.g. electrophoretic mobility, or cell-permeability, by charge, hydrophobicity, shape, or other physical parameters, or (v) provide a capture moiety, to modulate ligand affinity, antibody/antigen binding, or ionic complexation.

[0074] Stereochemical definitions and conventions used herein generally follow S. P. Parker, Ed., *McGraw-Hill Dictionary of Chemical Terms* (1984) McGraw-Hill Book Company, New York; and Eliel, E. and Wilen, S., *Stereochemistry of Organic Compounds* (1994) John Wiley & Sons, Inc., New York. Many organic compounds exist in optically active forms, i.e., they have the ability to rotate the plane of plane-polarized light. In describing an optically active compound, the prefixes D and L, or *R* and *S,* are used to denote the absolute configuration of the molecule about its chiral center(s). The prefixes d and l or (+) and (-) are employed to designate the sign of rotation of plane-polarized light by the compound, with (-) or l meaning that the compound is levorotatory. A compound prefixed with (+) or d is dextrorotatory. For a given chemical structure, these stereoisomers are identical except that they are mirror images of one another. A specific stereoisomer may also be referred to as an enantiomer, and a mixture of such isomers is often called an enantiomeric mixture. A 50:50 mixture of enantiomers is referred to as a racemic mixture or a racemate, which may occur where there has been no stereoselection or stereospecificity in a chemical reaction or process. The terms "racemic mixture" and "racemate" refer to an equimolar mixture of two enantiomeric species, devoid of optical activity.

[0075] The phrase "pharmaceutically acceptable salt," as used herein, refers to pharmaceutically acceptable organic or inorganic salts of an ADC. Exemplary salts include, but are not limited, to sulfate, citrate, acetate, oxalate, chloride, bromide, iodide, nitrate, bisulfate, phosphate, acid phosphate, isonicotinate, lactate, salicylate, acid citrate, tartrate, oleate, tannate, pantothenate, bitartrate, ascorbate, succinate, maleate, gentisinate, fumarate, gluconate, glucuronate, saccharate, formate, benzoate, glutamate, methanesulfonate, ethanesulfonate, benzenesulfonate, *p*-toluenesulfonate, and pamoate (*i.e.*, 1,1'-methylene-bis -(2-hydroxy-3- naphthoate)) salts. A pharmaceutically acceptable salt may involve the inclusion of another molecule such as an acetate ion, a succinate ion or other counterion. The counterion may be any organic or inorganic moiety that stabilizes the charge on the parent compound. Furthermore, a pharmaceutically acceptable salt may have more than one charged atom in its structure. Instances where multiple charged atoms are part of the

pharmaceutically acceptable salt can have multiple counter ions. Hence, a pharmaceutically acceptable salt can have one or more charged atoms and/or one or more counterion.

[0076] "Pharmaceutically acceptable solvate" refers to an association of one or more solvent molecules and an ADC. Examples of solvents that form pharmaceutically acceptable solvates include, but are not limited to, water, isopropanol, ethanol, methanol, DMSO, ethyl acetate, acetic acid, and ethanolamine.

[0077] CYSTEINE ENGINEERED ANTIBODIES

[0078] The compounds of the invention include cysteine engineered antibodies where one or more amino acids of a wild-type or parent antibody are replaced with a cysteine amino acid. Any form of antibody may be so engineered, i.e. mutated. For example, a parent Fab antibody fragment may be engineered to form a cysteine engineered Fab, referred to herein as "ThioFab." Similarly, a parent monoclonal antibody may be engineered to form a "ThioMab." It should be noted that a single site mutation yields a single engineered cysteine residue in a ThioFab, while a single site mutation yields two engineered cysteine residues in a ThioMab, due to the dimeric nature of the IgG antibody. Mutants with replaced ("engineered") cysteine (Cys) residues are evaluated for the reactivity of the newly introduced, engineered cysteine thiol groups. The thiol reactivity value is a relative, numerical term in the range of 0 to 1.0 and can be measured for any cysteine engineered antibody. Thiol reactivity values of cysteine engineered antibodies of the invention are in the ranges of 0.6 to 1.0; 0.7 to 1.0; or 0.8 to 1.0.

[0079] The design, selection, and preparation methods of the invention enable cysteine engineered antibodies which are reactive with electrophilic functionality. These methods further enable antibody conjugate compounds such as antibody-drug conjugate (ADC) compounds with drug molecules at designated, designed, selective sites. Reactive cysteine residues on an antibody surface allow specifically conjugating a drug moiety through a thiol reactive group such as maleimide or haloacetyl. The nucleophilic reactivity of the thiol functionality of a Cys residue to a maleimide group is about 1000 times higher compared to any other amino acid functionality in a protein, such as amino group of lysine residues or the N-terminal amino group. Thiol specific functionality in iodoacetyl and maleimide reagents may react with amine groups, but higher pH (>9.0) and longer reaction times are required (Garman, 1997, Non-Radioactive Labelling: A Practical Approach, Academic Press, London).

[0080] Cysteine engineered antibodies of the invention preferably retain the antigen

binding capability of their wild type, parent antibody counterparts. Thus, cysteine engineered antibodies are capable of binding, preferably specifically, to antigens. Such antigens include, for example, tumor-associated antigens (TAA), cell surface receptor proteins and other cell surface molecules, transmembrane proteins, signalling proteins, cell survival regulatory factors, cell proliferation regulatory factors, molecules associated with (for e.g., known or suspected to contribute functionally to) tissue development or differentiation, lymphokines, cytokines, molecules involved in cell cycle regulation, molecules involved in vasculogenesis and molecules associated with (for e.g., known or suspected to contribute functionally to) angiogenesis. The tumor-associated antigen may be a cluster differentiation factor (i.e., a CD protein). An antigen to which a cysteine engineered antibody is capable of binding may be a member of a subset of one of the above-mentioned categories, wherein the other subset(s) of said category comprise other molecules/antigens that have a distinct characteristic (with respect to the antigen of interest).

[0081] The parent antibody may also be a humanized antibody selected from huMAb4D5-1, huMAb4D5-2, huMAb4D5-3, huMAb4D5-4, huMAb4D5-5, huMAb4D5-6, huMAb4D5-7 and huMAb4D5-8 (Trastuzumab, HERCEPTIN®) as described in Table 3 of US 5821337, expressly incorporated herein by reference; humanized 520C9 (WO 93/21319) and humanized 2C4 antibodies as described herein.

[0082] Cysteine engineered antibodies of the invention may be site-specifically and efficiently coupled with a thiol-reactive reagent. The thiol-reactive reagent may be a multifunctional linker reagent, a capture, i.e. affinity, label reagent (e.g. a biotin-linker reagent), a detection label (e.g. a fluorophore reagent), a solid phase immobilization reagent (e.g. SEPHAROSE™, polystyrene, or glass), or a drug-linker intermediate. One example of a thiol-reactive reagent is N-ethyl maleimide (NEM). In an exemplary embodiment, reaction of a ThioFab with a biotin-linker reagent provides a biotinylated ThioFab by which the presence and reactivity of the engineered cysteine residue may be detected and measured. Reaction of a ThioFab with a multifunctional linker reagent provides a ThioFab with a functionalized linker which may be further reacted with a drug moiety reagent or other label. Reaction of a ThioFab with a drug-linker intermediate provides a ThioFab drug conjugate.

[0083] The exemplary methods described here may be applied generally to the identification and production of antibodies, and more generally, to other proteins through application of the design and screening steps described herein.

[0084] Such an approach may be applied to the conjugation of other thiol-reactive agents in which the reactive group is, for example, a maleimide, an iodoacetamide, a pyridyl

disulfide, or other thiol-reactive conjugation partner (Haugland, 2003, Molecular Probes Handbook of Fluorescent Probes and Research Chemicals, Molecular Probes, Inc.; Brinkley, 1992, Bioconjugate Chem. 3:2; Garman, 1997, Non-Radioactive Labelling: A Practical Approach, Academic Press, London; Means (1990) Bioconjugate Chem. 1:2; Hermanson, G. in Bioconjugate Techniques (1996) Academic Press, San Diego, pp. 40-55, 643-671). The partner may be a cytotoxic agent (e.g. a toxin such as doxorubicin or pertussis toxin), a fluorophore such as a fluorescent dye like fluorescein or rhodamine, a chelating agent for an imaging or radiotherapeutic metal, a peptidyl or non-peptidyl label or detection tag, or a clearance-modifying agent such as various isomers of polyethylene glycol, a peptide that binds to a third component, or another carbohydrate or lipophilic agent.

[0085] The sites identified on the exemplary antibody fragment, hu4D5Fabv8, herein are primarily in the constant domain of an antibody which is well conserved across all species of antibodies. These sites should be broadly applicable to other antibodies, without further need of structural design or knowledge of specific antibody structures, and without interference in the antigen binding properties inherent to the variable domains of the antibody.

[0086] Cysteine engineered antibodies which may be useful in the treatment of cancer include, but are not limited to, antibodies against cell surface receptors and tumor-associated antigens (TAA). Such antibodies may be used as naked antibodies (unconjugated to a drug or label moiety) or as Formula **I** antibody-drug conjugates (ADC). Tumor-associated antigens are known in the art, and can prepared for use in generating antibodies using methods and information which are well known in the art. In attempts to discover effective cellular targets for cancer diagnosis and therapy, researchers have sought to identify transmembrane or otherwise tumor-associated polypeptides that are specifically expressed on the surface of one or more particular type(s) of cancer cell as compared to on one or more normal non-cancerous cell(s). Often, such tumor-associated polypeptides are more abundantly expressed on the surface of the cancer cells as compared to on the surface of the non-cancerous cells. The identification of such tumor-associated cell surface antigen polypeptides has given rise to the ability to specifically target cancer cells for destruction via antibody-based therapies.

[0087] Examples of TAA include, but are not limited to, TAA (1)-(36) listed below. For convenience, information relating to these antigens, all of which are known in the art, is listed below and includes names, alternative names, Genbank accession numbers and primary reference(s), following nucleic acid and protein sequence identification conventions of the National Center for Biotechnology Information (NCBI). Nucleic acid and protein sequences

corresponding to TAA (1)-(36) are available in public databases such as GenBank. Tumor-associated antigens targeted by antibodies include all amino acid sequence variants and isoforms possessing at least about 70%, 80%, 85%, 90%, or 95% sequence identity relative to the sequences identified in the cited references, or which exhibit substantially the same biological properties or characteristics as a TAA having a sequence found in the cited references. For example, a TAA having a variant sequence generally is able to bind specifically to an antibody that binds specifically to the TAA with the corresponding sequence listed. The sequences and disclosure in the reference specifically recited herein are expressly incorporated by reference.

[0088] TUMOR-ASSOCIATED ANTIGENS (1)-(36):

[0089] (1) BMPR1B (bone morphogenetic protein receptor-type IB, Genbank accession no. NM_001203) ten Dijke,P., et al Science 264 (5155):101-104 (1994), Oncogene 14 (11):1377-1382 (1997)); WO2004063362 (Claim 2); WO2003042661 (Claim 12); US2003134790-A1 (Page 38-39); WO2002102235 (Claim 13; Page 296); WO2003055443 (Page 91-92); WO200299122 (Example 2; Page 528-530); WO2003029421 (Claim 6); WO2003024392 (Claim 2; Fig 112); WO200298358 (Claim 1; Page 183); WO200254940 (Page 100-101); WO200259377(Page 349-350); WO200230268 (Claim 27; Page 376); WO200148204 (Example; Fig 4); NP_001194 bone morphogenetic protein receptor, type IB /pid=NP_001194.1. Cross-references: MIM:603248; NP_001194.1; AY065994

[0090] (2) E16 (LAT1, SLC7A5, Genbank accession no. NM_003486) Biochem. Biophys. Res. Commun. 255 (2), 283-288 (1999), Nature 395 (6699):288-291 (1998), Gaugitsch, H.W., et al (1992) J. Biol. Chem. 267 (16):11267-11273); WO2004048938 (Example 2); WO2004032842 (Example IV); WO2003042661 (Claim 12); WO2003016475 (Claim 1); WO200278524 (Example 2); WO200299074 (Claim 19; Page 127-129); WO200286443 (Claim 27; Pages 222, 393); WO2003003906 (Claim 10; Page 293); WO200264798 (Claim 33; Page 93-95); WO200014228 (Claim 5; Page 133-136); US2003224454 (Fig 3); WO2003025138 (Claim 12; Page 150); NP_003477 solute carrier family 7 (cationic amino acid transporter, y+system), member 5 /pid=NP_003477.3 - Homo sapiens; Cross-references: MIM:600182; NP_003477.3; NM_015923; NM_003486_1

[0091] (3) STEAP1 (six transmembrane epithelial antigen of prostate, Genbank accession no. NM_012449); Cancer Res. 61 (15), 5857-5860 (2001), Hubert, R.S., et al (1999) Proc. Natl. Acad. Sci. U.S.A. 96 (25):14523-14528); WO2004065577 (Claim 6); WO2004027049 (Fig 1L); EP1394274 (Example 11); WO2004016225 (Claim 2);

WO2003042661 (Claim 12); US2003157089 (Example 5); US2003185830 (Example 5); US2003064397 (Fig 2); WO200289747 (Example 5; Page 618-619); WO2003022995 (Example 9; Fig 13A, Example 53; Page 173, Example 2; Fig 2A); NP_036581 six transmembrane epithelial antigen of the prostate
Cross-references: MIM:604415; NP_036581.1; NM_012449_1

[0092] (4) 0772P (CA125, MUC16, Genbank accession no. AF361486); J. Biol. Chem. 276 (29):27371-27375 (2001)); WO2004045553 (Claim 14); WO200292836 (Claim 6; Fig 12); WO200283866 (Claim 15; Page 116-121); US2003124140 (Example 16); Cross-references: GI:34501467; AAK74120.3; AF361486_1

[0093] (5) MPF (MPF, MSLN, SMR, megakaryocyte potentiating factor, mesothelin, Genbank accession no. NM_005823) Yamaguchi, N., et al Biol. Chem. 269 (2), 805-808 (1994), Proc. Natl. Acad. Sci. U.S.A. 96 (20):11531-11536 (1999), Proc. Natl. Acad. Sci. U.S.A. 93 (1):136-140 (1996), J. Biol. Chem. 270 (37):21984-21990 (1995)); WO2003101283 (Claim 14); (WO2002102235 (Claim 13; Page 287-288); WO2002101075 (Claim 4; Page 308-309); WO200271928 (Page 320-321); WO9410312 (Page 52-57); Cross-references: MIM:601051; NP_005814.2; NM_005823_1

[0094] (6) Napi3b (NAPI-3B, NPTIIb, SLC34A2, solute carrier family 34 (sodium phosphate), member 2, type II sodium-dependent phosphate transporter 3b, Genbank accession no. NM_006424) J. Biol. Chem. 277 (22):19665-19672 (2002), Genomics 62 (2):281-284 (1999), Feild, J.A., et al (1999) Biochem. Biophys. Res. Commun. 258 (3):578-582); WO2004022778 (Claim 2); EP1394274 (Example 11); WO2002102235 (Claim 13; Page 326); EP875569 (Claim 1; Page 17-19); WO200157188 (Claim 20; Page 329); WO2004032842 (Example IV); WO200175177 (Claim 24; Page 139-140); Cross-references: MIM:604217; NP_006415.1; NM_006424_1

[0095] (7) Sema 5b (FLJ10372, KIAA1445, Mm.42015, SEMA5B, SEMAG, Semaphorin 5b Hlog, sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5B, Genbank accession no. AB040878); Nagase T., et al (2000) DNA Res. 7 (2):143-150); WO2004000997 (Claim 1); WO2003003984 (Claim 1); WO200206339 (Claim 1; Page 50); WO200188133 (Claim 1; Page 41-43, 48-58); WO2003054152 (Claim 20); WO2003101400 (Claim 11); Accession: Q9P283; EMBL; AB040878; BAA95969.1. Genew; HGNC:10737

[0096] (8) PSCA hlg (2700050C12Rik, C530008O16Rik, RIKEN cDNA 2700050C12, RIKEN cDNA 2700050C12 gene, Genbank accession no. AY358628); Ross et al (2002) Cancer Res. 62:2546-2553; US2003129192 (Claim 2); US2004044180 (Claim 12);

US2004044179 (Claim 11); US2003096961 (Claim 11); US2003232056 (Example 5); WO2003105758 (Claim 12); US2003206918 (Example 5); EP1347046 (Claim 1); WO2003025148 (Claim 20); Cross-references: GI:37182378; AAQ88991.1; AY358628_1

[0097] (9) ETBR (Endothelin type B receptor, Genbank accession no. AY275463); Nakamuta M., et al Biochem. Biophys. Res. Commun. 177, 34-39, 1991; Ogawa Y., et al Biochem. Biophys. Res. Commun. 178, 248-255, 1991; Arai H., et al Jpn. Circ. J. 56, 1303-1307, 1992; Arai H., et al J. Biol. Chem. 268, 3463-3470, 1993; Sakamoto A., Yanagisawa M., et al Biochem. Biophys. Res. Commun. 178, 656-663, 1991; Elshourbagy N.A., et al J. Biol. Chem. 268, 3873-3879, 1993; Haendler B., et al J. Cardiovasc. Pharmacol. 20, s1-S4, 1992; Tsutsumi M., et al Gene 228, 43-49, 1999; Strausberg R.L., et al Proc. Natl. Acad. Sci. U.S.A. 99, 16899-16903, 2002; Bourgeois C., et al J. Clin. Endocrinol. Metab. 82, 3116-3123, 1997; Okamoto Y., et al Biol. Chem. 272, 21589-21596, 1997; Verheij J.B., et al Am. J. Med. Genet. 108, 223-225, 2002; Hofstra R.M.W., et al Eur. J. Hum. Genet. 5, 180-185, 1997; Puffenberger E.G., et al Cell 79, 1257-1266, 1994; Attie T., et al, Hum. Mol. Genet. 4, 2407-2409, 1995; Auricchio A., et al Hum. Mol. Genet. 5:351-354, 1996; Amiel J., et al Hum. Mol. Genet. 5, 355-357, 1996; Hofstra R.M.W., et al Nat. Genet. 12, 445-447, 1996; Svensson P.J., et al Hum. Genet. 103, 145-148, 1998; Fuchs S., et al Mol. Med. 7, 115-124, 2001; Pingault V., et al (2002) Hum. Genet. 111, 198-206; WO2004045516 (Claim 1); WO2004048938 (Example 2); WO2004040000 (Claim 151); WO2003087768 (Claim 1); WO2003016475 (Claim 1); WO2003016475 (Claim 1); WO200261087 (Fig 1); WO2003016494 (Fig 6); WO2003025138 (Claim 12; Page 144); WO200198351 (Claim 1; Page 124-125); EP522868 (Claim 8; Fig 2); WO200177172 (Claim 1; Page 297-299); US2003109676; US6518404 (Fig 3); US5773223 (Claim 1a; Col 31-34); WO2004001004

[0098] (10) MSG783 (RNF124, hypothetical protein FLJ20315, Genbank accession no. NM_017763); WO2003104275 (Claim 1); WO2004046342 (Example 2); WO2003042661 (Claim 12); WO2003083074 (Claim 14; Page 61); WO2003018621 (Claim 1); WO2003024392 (Claim 2; Fig 93); WO200166689 (Example 6); Cross-references: LocusID:54894; NP_060233.2; NM_017763_1

[0099] (11) STEAP2 (HGNC_8639, IPCA-1, PCANAP1, STAMP1, STEAP2, STMP, prostate cancer associated gene 1, prostate cancer associated protein 1, six transmembrane epithelial antigen of prostate 2, six transmembrane prostate protein, Genbank accession no. AF455138); Lab. Invest. 82 (11):1573-1582 (2002)); WO2003087306; US2003064397 (Claim 1; Fig 1); WO200272596 (Claim 13; Page 54-55); WO200172962 (Claim 1; Fig 4B); WO2003104270 (Claim 11); WO2003104270 (Claim 16); US2004005598

(Claim 22); WO2003042661 (Claim 12); US2003060612 (Claim 12; Fig 10); WO200226822 (Claim 23; Fig 2); WO200216429 (Claim 12; Fig 10); Cross-references: GI:22655488; AAN04080.1; AF455138_1

[00100] (12) TrpM4 (BR22450, FLJ20041, TRPM4, TRPM4B, transient receptor potential cation channel, subfamily M, member 4, Genbank accession no. NM_017636); Xu, X.Z., et al Proc. Natl. Acad. Sci. U.S.A. 98 (19):10692-10697 (2001), Cell 109 (3):397-407 (2002), J. Biol. Chem. 278 (33):30813-30820 (2003)); US2003143557 (Claim 4); WO200040614 (Claim 14; Page 100-103); WO200210382 (Claim 1; Fig 9A); WO2003042661 (Claim 12); WO200230268 (Claim 27; Page 391); US2003219806 (Claim 4); WO200162794 (Claim 14; Fig 1A-D); Cross-references: MIM:606936; NP_060106.2; NM_017636_1

[00101] (13) CRIPTO (CR, CR1, CRGF, CRIPTO, TDGF1, teratocarcinoma-derived growth factor, Genbank accession no. NP_003203 or NM_003212); Ciccodicola, A., et al EMBO J. 8 (7):1987-1991 (1989), Am. J. Hum. Genet. 49 (3):555-565 (1991)); US2003224411 (Claim 1); WO2003083041 (Example 1); WO2003034984 (Claim 12); WO200288170 (Claim 2; Page 52-53); WO2003024392 (Claim 2; Fig 58); WO200216413 (Claim 1; Page 94-95, 105); WO200222808 (Claim 2; Fig 1); US5854399 (Example 2; Col 17-18); US5792616 (Fig 2); Cross-references: MIM:187395; NP_003203.1; NM_003212_1

[00102] (14) CD21 (CR2 (Complement receptor 2) or C3DR (C3d/Epstein Barr virus receptor) or Hs.73792 Genbank accession no. M26004); Fujisaku et al (1989) J. Biol. Chem. 264 (4):2118-2125); Weis J.J., et al J. Exp. Med. 167, 1047-1066, 1988; Moore M., et al Proc. Natl. Acad. Sci. U.S.A. 84, 9194-9198, 1987; Barel M., et al Mol. Immunol. 35, 1025-1031, 1998; Weis J.J., et al Proc. Natl. Acad. Sci. U.S.A. 83, 5639-5643, 1986; Sinha S.K., et al (1993) J. Immunol. 150, 5311-5320; WO2004045520 (Example 4); US2004005538 (Example 1); WO2003062401 (Claim 9); WO2004045520 (Example 4); WO9102536 (Fig 9.1-9.9); WO2004020595 (Claim 1); Accession: P20023; Q13866; Q14212; EMBL; M26004; AAA35786.1.

[00103] (15) CD79b (CD79B, CD79β, IGb (immunoglobulin-associated beta), B29, Genbank accession no. NM_000626 or 11038674); Proc. Natl. Acad. Sci. U.S.A. (2003) 100 (7):4126-4131, Blood (2002) 100 (9):3068-3076, Muller et al (1992) Eur. J. Immunol. 22 (6):1621-1625); WO2004016225 (claim 2, Fig 140); WO2003087768, US2004101874 (claim 1, page 102); WO2003062401 (claim 9); WO200278524 (Example 2); US2002150573 (claim 5, page 15); US5644033; WO2003048202 (claim 1, pages 306 and 309); WO 99/558658,

US6534482 (claim 13, Fig 17A/B); WO200055351 (claim 11, pages 1145-1146); Cross-references: MIM:147245; NP_000617.1; NM_000626_1

[00104] (16) FcRH2 (IFGP4, IRTA4, SPAP1A (SH2 domain containing phosphatase anchor protein 1a), SPAP1B, SPAP1C, Genbank accession no. NM_030764, AY358130); Genome Res. 13 (10):2265-2270 (2003), Immunogenetics 54 (2):87-95 (2002), Blood 99 (8):2662-2669 (2002), Proc. Natl. Acad. Sci. U.S.A. 98 (17):9772-9777 (2001), Xu, M.J., et al (2001) Biochem. Biophys. Res. Commun. 280 (3):768-775; WO2004016225 (Claim 2); WO2003077836; WO200138490 (Claim 5; Fig 18D-1-18D-2); WO2003097803 (Claim 12); WO2003089624 (Claim 25); Cross-references: MIM:606509; NP_110391.2; NM_030764_1

[00105] (17) HER2 (ErbB2, Genbank accession no. M11730); Coussens L., et al Science (1985) 230(4730):1132-1139); Yamamoto T., et al Nature 319, 230-234, 1986; Semba K., et al Proc. Natl. Acad. Sci. U.S.A. 82, 6497-6501, 1985; Swiercz J.M., et al J. Cell Biol. 165, 869-880, 2004; Kuhns J.J., et al J. Biol. Chem. 274, 36422-36427, 1999; Cho H.-S., et al Nature 421, 756-760, 2003; Ehsani A., et al (1993) Genomics 15, 426-429; WO2004048938 (Example 2); WO2004027049 (Fig 1I); WO2004009622; WO2003081210; WO2003089904 (Claim 9); WO2003016475 (Claim 1); US2003118592; WO2003008537 (Claim 1); WO2003055439 (Claim 29; Fig 1A-B); WO2003025228 (Claim 37; Fig 5C); WO200222636 (Example 13; Page 95-107); WO200212341 (Claim 68; Fig 7); WO200213847 (Page 71-74); WO200214503 (Page 114-117); WO200153463 (Claim 2; Page 41-46); WO200141787 (Page 15); WO200044899 (Claim 52; Fig 7); WO200020579 (Claim 3; Fig 2); US5869445 (Claim 3; Col 31-38); WO9630514 (Claim 2; Page 56-61); EP1439393 (Claim 7); WO2004043361 (Claim 7); WO2004022709; WO200100244 (Example 3; Fig 4); Accession: P04626; EMBL; M11767; AAA35808.1. EMBL; M11761; AAA35808.1

[00106] (18) NCA (CEACAM6, Genbank accession no. M18728); Barnett T., et al Genomics 3, 59-66, 1988; Tawaragi Y., et al Biochem. Biophys. Res. Commun. 150, 89-96, 1988; Strausberg R.L., et al Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903, 2002; WO2004063709; EP1439393 (Claim 7); WO2004044178 (Example 4); WO2004031238; WO2003042661 (Claim 12); WO200278524 (Example 2); WO200286443 (Claim 27; Page 427); WO200260317 (Claim 2); Accession: P40199; Q14920; EMBL; M29541; AAA59915.1. EMBL; M18728

[00107] (19) MDP (DPEP1, Genbank accession no. BC017023); Proc. Natl. Acad. Sci. U.S.A. 99 (26):16899-16903 (2002)); WO2003016475 (Claim 1); WO200264798 (Claim 33; Page 85-87); JP05003790 (Fig 6-8); WO9946284 (Fig 9); Cross-references: MIM:179780;

AAH17023.1; BC017023_1

[00108] (20) IL20Rα (IL20Ra, ZCYTOR7, Genbank accession no. AF184971); Clark H.F., et al Genome Res. 13, 2265-2270, 2003; Mungall A.J., et al Nature 425, 805-811, 2003; Blumberg H., et al Cell 104, 9-19, 2001; Dumoutier L., et al J. Immunol. 167, 3545-3549, 2001; Parrish-Novak J., et al J. Biol. Chem. 277, 47517-47523, 2002; Pletnev S., et al (2003) Biochemistry 42:12617-12624; Sheikh F., et al (2004) J. Immunol. 172, 2006-2010; EP1394274 (Example 11); US2004005320 (Example 5); WO2003029262 (Page 74-75); WO2003002717 (Claim 2; Page 63); WO200222153 (Page 45-47); US2002042366 (Page 20-21); WO200146261 (Page 57-59); WO200146232 (Page 63-65); WO9837193 (Claim 1; Page 55-59); Accession: Q9UHF4; Q6UWA9; Q96SH8; EMBL; AF184971; AAF01320.1.

[00109] (21) Brevican (BCAN, BEHAB, Genbank accession no. AF229053); Gary S.C., et al Gene 256, 139-147, 2000; Clark H.F., et al Genome Res. 13, 2265-2270, 2003; Strausberg R.L., et al Proc. Natl. Acad. Sci. U.S.A. 99, 16899-16903, 2002; US2003186372 (Claim 11); US2003186373 (Claim 11); US2003119131 (Claim 1; Fig 52); US2003119122 (Claim 1; Fig 52); US2003119126 (Claim 1); US2003119121 (Claim 1; Fig 52); US2003119129 (Claim 1); US2003119130 (Claim 1); US2003119128 (Claim 1; Fig 52); US2003119125 (Claim 1); WO2003016475 (Claim 1); WO200202634 (Claim 1)

[00110] (22) EphB2R (DRT, ERK, Hek5, EPHT3, Tyro5, Genbank accession no. NM_004442); Chan,J. and Watt, V.M., Oncogene 6 (6), 1057-1061 (1991) Oncogene 10 (5):897-905 (1995), Annu. Rev. Neurosci. 21:309-345 (1998), Int. Rev. Cytol. 196:177-244 (2000)); WO2003042661 (Claim 12); WO200053216 (Claim 1; Page 41); WO2004065576 (Claim 1); WO2004020583 (Claim 9); WO2003004529 (Page 128-132); WO200053216 (Claim 1; Page 42); Cross-references: MIM:600997; NP_004433.2; NM_004442_1

[00111] (23) ASLG659 (B7h, Genbank accession no. AX092328); US20040101899 (Claim 2); WO2003104399 (Claim 11); WO2004000221 (Fig 3); US2003165504 (Claim 1); US2003124140 (Example 2); US2003065143 (Fig 60); WO2002102235 (Claim 13; Page 299); US2003091580 (Example 2); WO200210187 (Claim 6; Fig 10); WO200194641 (Claim 12; Fig 7b); WO200202624 (Claim 13; Fig 1A-1B); US2002034749 (Claim 54; Page 45-46); WO200206317 (Example 2; Page 320-321, Claim 34; Page 321-322); WO200271928 (Page 468-469); WO200202587 (Example 1; Fig 1); WO200140269 (Example 3; Pages 190-192); WO200036107 (Example 2; Page 205-207); WO2004053079 (Claim 12); WO2003004989 (Claim 1); WO200271928 (Page 233-234, 452-453); WO 0116318

[00112] (24) PSCA (Prostate stem cell antigen precursor, Genbank accession no.

AJ297436); Reiter R.E., et al Proc. Natl. Acad. Sci. U.S.A. 95, 1735-1740, 1998; Gu Z., et al Oncogene 19, 1288-1296, 2000; Biochem. Biophys. Res. Commun. (2000) 275(3):783-788; WO2004022709; EP1394274 (Example 11); US2004018553 (Claim 17); WO2003008537 (Claim 1); WO200281646 (Claim 1; Page 164); WO2003003906 (Claim 10; Page 288); WO200140309 (Example 1; Fig 17); US2001055751 (Example 1; Fig 1b); WO200032752 (Claim 18; Fig 1); WO9851805 (Claim 17; Page 97); WO9851824 (Claim 10; Page 94); WO9840403 (Claim 2; Fig 1B); Accession: O43653; EMBL; AF043498; AAC39607.1

[00113] (25) GEDA (Genbank accession No. AY260763); AAP14954 lipoma HMGIC fusion-partner-like protein /pid=AAP14954.1 - Homo sapiens (human); WO2003054152 (Claim 20); WO2003000842 (Claim 1); WO2003023013 (Example 3, Claim 20); US2003194704 (Claim 45); Cross-references: GI:30102449; AAP14954.1; AY260763_1

[00114] (26) BAFF-R (B cell -activating factor receptor, BLyS receptor 3, BR3, Genbank accession No. AF116456); BAFF receptor /pid=NP_443177.1 - Homo sapiens: Thompson, J.S., et al Science 293 (5537), 2108-2111 (2001); WO2004058309; WO2004011611; WO2003045422 (Example; Page 32-33); WO2003014294 (Claim 35; Fig 6B); WO2003035846 (Claim 70; Page 615-616); WO200294852 (Col 136-137); WO200238766 (Claim 3; Page 133); WO200224909 (Example 3; Fig 3); Cross-references: MIM:606269; NP_443177.1; NM_052945_1; AF132600

[00115] (27) CD22 (B-cell receptor CD22-B isoform, BL-CAM, Lyb-8, Lyb8, SIGLEC-2, FLJ22814, Genbank accession No. AK026467); Wilson et al (1991) J. Exp. Med. 173:137-146; WO2003072036 (Claim 1; Fig 1); Cross-references: MIM:107266; NP_001762.1; NM_001771_1

[00116] (28) CD79a (CD79A, CD79α, immunoglobulin-associated alpha, a B cell-specific protein that covalently interacts with Ig beta (CD79B) and forms a complex on the surface with Ig M molecules, transduces a signal involved in B-cell differentiation), pI: 4.84, MW: 25028 TM: 2 [P] Gene Chromosome: 19q13.2, Genbank accession No. NP_001774.10); WO2003088808, US20030228319; WO2003062401 (claim 9); US2002150573 (claim 4, pages 13-14); WO9958658 (claim 13, Fig 16); WO9207574 (Fig 1); US5644033; Ha et al (1992) J. Immunol. 148(5):1526-1531; Mueller et al (1992) Eur. J. Biochem. 22:1621-1625; Hashimoto et al (1994) Immunogenetics 40(4):287-295; Preud'homme et al (1992) Clin. Exp. Immunol. 90(1):141-146; Yu et al (1992) J. Immunol. 148(2) 633-637; Sakaguchi et al (1988) EMBO J. 7(11):3457-3464

[00117] (29) CXCR5 (Burkitt's lymphoma receptor 1, a G protein-coupled receptor

that is activated by the CXCL13 chemokine, functions in lymphocyte migration and humoral defense, plays a role in HIV-2 infection and perhaps development of AIDS, lymphoma, myeloma, and leukemia); 372 aa, pI: 8.54 MW: 41959 TM: 7 [P] Gene Chromosome: 11q23.3, Genbank accession No. NP_001707.1); WO2004040000; WO2004015426; US2003105292 (Example 2); US6555339 (Example 2); WO200261087 (Fig 1); WO200157188 (Claim 20, page 269); WO200172830 (pages 12-13); WO200022129 (Example 1, pages 152-153, Example 2, pages 254-256); WO9928468 (claim 1, page 38); US5440021 (Example 2, col 49-52); WO9428931 (pages 56-58); WO9217497 (claim 7, Fig 5); Dobner et al (1992) Eur. J. Immunol. 22:2795-2799; Barella et al (1995) Biochem. J. 309:773-779

[00118] (30) HLA-DOB (Beta subunit of MHC class II molecule (Ia antigen) that binds peptides and presents them to CD4+ T lymphocytes); 273 aa, pI: 6.56, MW: 30820.TM: 1 [P] Gene Chromosome: 6p21.3, Genbank accession No. NP_002111.1); Tonnelle et al (1985) EMBO J. 4(11):2839-2847; Jonsson et al (1989) Immunogenetics 29(6):411-413; Beck et al (1992) J. Mol. Biol. 228:433-441; Strausberg et al (2002) Proc. Natl. Acad. Sci USA 99:16899-16903; Servenius et al (1987) J. Biol. Chem. 262:8759-8766; Beck et al (1996) J. Mol. Biol. 255:1-13; Naruse et al (2002) Tissue Antigens 59:512-519; WO9958658 (claim 13, Fig 15); US6153408 (Col 35-38); US5976551 (col 168-170); US6011146 (col 145-146); Kasahara et al (1989) Immunogenetics 30(1):66-68; Larhammar et al (1985) J. Biol. Chem. 260(26):14111-14119

[00119] (31) P2X5 (Purinergic receptor P2X ligand-gated ion channel 5, an ion channel gated by extracellular ATP, may be involved in synaptic transmission and neurogenesis, deficiency may contribute to the pathophysiology of idiopathic detrusor instability); 422 aa), pI: 7.63, MW: 47206 TM: 1 [P] Gene Chromosome: 17p13.3, Genbank accession No. NP_002552.2); Le et al (1997) FEBS Lett. 418(1-2):195-199; WO2004047749; WO2003072035 (claim 10); Touchman et al (2000) Genome Res. 10:165-173; WO200222660 (claim 20); WO2003093444 (claim 1); WO2003087768 (claim 1); WO2003029277 (page 82)

[00120] (32) CD72 (B-cell differentiation antigen CD72, Lyb-2); 359 aa, pI: 8.66, MW: 40225, TM: 1 [P] Gene Chromosome: 9p13.3, Genbank accession No. NP_001773.1); WO2004042346 (claim 65); WO2003026493 (pages 51-52, 57-58); WO200075655 (pages 105-106); Von Hoegen et al (1990) J. Immunol. 144(12):4870-4877; Strausberg et al (2002) Proc. Natl. Acad. Sci USA 99:16899-16903.

[00121] (33) LY64 (Lymphocyte antigen 64 (RP105), type I membrane protein of the

leucine rich repeat (LRR) family, regulates B-cell activation and apoptosis, loss of function is associated with increased disease activity in patients with systemic lupus erythematosis); 661 aa, pI: 6.20, MW: 74147 TM: 1 [P] Gene Chromosome: 5q12, Genbank accession No. NP_005573.1); US2002193567; WO9707198 (claim 11, pages 39-42); Miura et al (1996) Genomics 38(3):299-304; Miura et al (1998) Blood 92:2815-2822; WO2003083047; WO9744452 (claim 8, pages 57-61); WO200012130 (pages 24-26)

[00122] (34) FcRH1 (Fc receptor-like protein 1, a putative receptor for the immunoglobulin Fc domain that contains C2 type Ig-like and ITAM domains, may have a role in B-lymphocyte differentiation); 429 aa, pI: 5.28, MW: 46925 TM: 1 [P] Gene Chromosome: 1q21-1q22, Genbank accession No. NP_443170.1); WO2003077836; WO200138490 (claim 6, Fig 18E-1-18-E-2); Davis et al (2001) Proc. Natl. Acad. Sci USA 98(17):9772-9777; WO2003089624 (claim 8); EP1347046 (claim 1); WO2003089624 (claim 7)

[00123] (35) IRTA2 (Immunoglobulin superfamily receptor translocation associated 2, a putative immunoreceptor with possible roles in B cell development and lymphomagenesis; deregulation of the gene by translocation occurs in some B cell malignancies); 977 aa, pI: 6.88, MW: 106468, TM: 1 [P] Gene Chromosome: 1q21, Genbank accession No. Human:AF343662, AF343663, AF343664, AF343665, AF369794, AF397453, AK090423, AK090475, AL834187, AY358085; Mouse:AK089756, AY158090, AY506558; NP_112571.1; WO2003024392 (claim 2, Fig 97); Nakayama et al (2000) Biochem. Biophys. Res. Commun. 277(1):124-127; WO2003077836; WO200138490 (claim 3, Fig 18B-1-18B-2)

[00124] (36) TENB2 (TMEFF2, tomoregulin, TPEF, HPP1, TR, putative transmembrane proteoglycan, related to the EGF/heregulin family of growth factors and follistatin); 374 aa, NCBI Accession: AAD55776, AAF91397, AAG49451, NCBI RefSeq: NP_057276; NCBI Gene: 23671; OMIM: 605734; SwissProt Q9UIK5; Genbank accession No. AF179274; AY358907, CAF85723, CQ782436; WO2004074320; JP2004113151; WO2003042661; WO2003009814; EP1295944 (pages 69-70); WO200230268 (page 329); WO200190304; US2004249130; US2004022727; WO2004063355; US2004197325; US2003232350; US2004005563; US2003124579; Horie et al (2000) Genomics 67:146-152; Uchida et al (1999) Biochem. Biophys. Res. Commun. 266:593-602; Liang et al (2000) Cancer Res. 60:4907-12; Glynne-Jones et al (2001) Int J Cancer. Oct 15; 94(2):178-84.

[00125] The parent antibody may also be a fusion protein comprising an albumin-binding peptide (ABP) sequence (Dennis et al. (2002) "Albumin Binding As A General

Strategy For Improving The Pharmacokinetics Of Proteins" J Biol Chem. 277:35035-35043; WO 01/45746). Antibodies of the invention include fusion proteins with ABP sequences taught by: (i) Dennis et al (2002) J Biol Chem. 277:35035-35043 at Tables III and IV, page 35038; (ii) US 20040001827 at [0076]; and (iii) WO 01/45746 at pages 12-13, and all of which are incorporated herein by reference.

[00126] MUTAGENESIS

[00127] DNA encoding an amino acid sequence variant of the starting polypeptide is prepared by a variety of methods known in the art. These methods include, but are not limited to, preparation by site-directed (or oligonucleotide-mediated) mutagenesis, PCR mutagenesis, and cassette mutagenesis of an earlier prepared DNA encoding the polypeptide. Variants of recombinant antibodies may be constructed also by restriction fragment manipulation or by overlap extension PCR with synthetic oligonucleotides. Mutagenic primers encode the cysteine codon replacement(s). Standard mutagenesis techniques can be employed to generate DNA encoding such mutant cysteine engineered antibodies. General guidance can be found in Sambrook et al Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989; and Ausubel et al Current Protocols in Molecular Biology, Greene Publishing and Wiley-Interscience, New York, N.Y., 1993.

[00128] Site-directed mutagenesis is one method for preparing substitution variants, i.e. mutant proteins. This technique is well known in the art (see for example, Carter (1985) et al Nucleic Acids Res. 13:4431-4443; Ho et al (1989) Gene (Amst.) 77:51-59; and Kunkel et al (1987) Proc. Natl. Acad. Sci. USA 82:488). Briefly, in carrying out site-directed mutagenesis of DNA, the starting DNA is altered by first hybridizing an oligonucleotide encoding the desired mutation to a single strand of such starting DNA. After hybridization, a DNA polymerase is used to synthesize an entire second strand, using the hybridized oligonucleotide as a primer, and using the single strand of the starting DNA as a template. Thus, the oligonucleotide encoding the desired mutation is incorporated in the resulting double-stranded DNA. Site-directed mutagenesis may be carried out within the gene expressing the protein to be mutagenized in an expression plasmid and the resulting plasmid may be sequenced to confirm the introduction of the desired cysteine replacement mutations (Liu et al (1998) J. Biol. Chem. 273:20252-20260). Site-directed of protocols and formats, including those commercially available, e.g. QuikChange® Multi Site-Directed Mutagenesis Kit (Stratagene, La Jolla, CA).

[00129] PCR mutagenesis is also suitable for making amino acid sequence variants of the starting polypeptide. See Higuchi, (1990) in PCR Protocols, pp.177-183, Academic Press; Ito et al (1991) Gene 102:67-70; Bernhard et al (1994) Bioconjugate Chem. 5:126-132; and Vallette et al (1989) Nuc. Acids Res. 17:723-733. Briefly, when small amounts of template DNA are used as starting material in a PCR, primers that differ slightly in sequence from the corresponding region in a template DNA can be used to generate relatively large quantities of a specific DNA fragment that differs from the template sequence only at the positions where the primers differ from the template.

[00130] Another method for preparing variants, cassette mutagenesis, is based on the technique described by Wells et al (1985) Gene 34:315-323. The starting material is the plasmid (or other vector) comprising the starting polypeptide DNA to be mutated. The codon(s) in the starting DNA to be mutated are identified. There must be a unique restriction endonuclease site on each side of the identified mutation site(s). If no such restriction sites exist, they may be generated using the above described oligonucleotide-mediated mutagenesis method to introduce them at appropriate locations in the starting polypeptide DNA. The plasmid DNA is cut at these sites to linearize it. A double-stranded oligonucleotide encoding the sequence of the DNA between the restriction sites but containing the desired mutation(s) is synthesized using standard procedures, wherein the two strands of the oligonucleotide are synthesized separately and then hybridized together using standard techniques. Oligonucleotides are prepared by the phosphoramidite synthesis method (US 4415732; US 4458066; Beaucage, S. and Iyer, R. (1992) "Advances in the synthesis of oligonucleotides by the phosphoramidite approach", Tetrahedron 48:2223-2311). This double-stranded oligonucleotide is referred to as the cassette. This cassette is designed to have 5' and 3' ends that are compatible with the ends of the linearized plasmid, such that it can be directly ligated to the plasmid. This plasmid now contains the mutated DNA sequence. Mutant DNA containing the encoded cysteine replacements can be confirmed by DNA sequencing.

[00131] Single mutations are also generated by oligonucleotide directed mutagenesis using double stranded plasmid DNA as template by PCR based mutagenesis (Sambrook and Russel, (2001) Molecular Cloning: A Laboratory Manual, 3rd edition; Zoller et al (1983) Methods Enzymol. 100:468-500; Zoller, M.J. and Smith, M. (1982) Nucl. Acids Res. 10:6487-6500).

[00132] In the present invention, hu4D5Fabv8 displayed on M13 phage (Gerstner et al (2002) "Sequence Plasticity In The Antigen-Binding Site Of A Therapeutic Anti-HER2

Antibody", J Mol Biol. 321:851-62) was used for experiments as a model system. Cysteine mutations were introduced in hu4D5Fabv8-phage, hu4D5Fabv8, and ABP-hu4D5Fabv8 constructs. The hu4D5-ThioFab-Phage preps were carried out using the polyethylene glycol (PEG) precipitation method as described earlier (Lowman, Henry B. (1998) Methods in Molecular Biology (Totowa, New Jersey) 87 (Combinatorial Peptide Library Protocols) 249-264).

[00133] PHESELECTOR ASSAY

[00134] The PHESELECTOR (Phage ELISA for Selection of Reactive Thiols) assay allows for detection of reactive cysteine groups in antibodies in an ELISA phage format. The process of coating the protein (e.g. antibody) of interest on well surfaces, followed incubation with phage particles and then HRP labeled secondary antibody with absorbance detection is detailed in Example 2. Mutant proteins displayed on phage may be screened in a rapid, robust, and high-throughput manner. Libraries of cysteine engineered antibodies can be produced and subjected to binding selection using the same approach to identify appropriately reactive sites of free Cys incorporation from random protein-phage libraries of antibodies or other proteins. This technique includes reacting cysteine mutant proteins displayed on phage with an affinity reagent or reporter group which is also thiol-reactive. Figure 8 illustrates the PHESELECTOR Assay by a schematic representation depicting the binding of Fab or ThioFab to HER2 (top) and biotinylated ThioFab to streptavidin (bottom).

[00135] PROTEIN EXPRESSION AND PURIFICATION

[00136] DNA encoding the cysteine engineered antibodies is readily isolated and sequenced using conventional procedures (*e.g.*, by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells serve as a source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as *E. coli* cells, simian COS cells, Chinese Hamster Ovary (CHO) cells, or other mammalian host cells, such as myeloma cells (US 5807715; US 2005/0048572; US 2004/0229310) that do not otherwise produce the antibody protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The yields of hu4D5Fabv8 cysteine engineered antibodies were similar to wild type hu4D5Fabv8. Review articles on recombinant expression in bacteria of DNA encoding the antibody include Skerra et al (1993) Curr. Opinion in Immunol. 5:256-262 and Plückthun (1992) Immunol. Revs. 130:151-188.

[00137] After design and selection, cysteine engineered antibodies, e.g. ThioFabs, with highly reactive unpaired Cys residues, may be produced by: (i) expression in a bacterial, e.g. *E. coli*, system or a mammalian cell culture system (WO 01/00245), e.g. Chinese Hamster Ovary cells (CHO); and (ii) purification using common protein purification techniques (Lowman et al (1991) J. Biol. Chem. 266(17):10982-10988).

[00138] ThioFabs were expressed upon induction in 34B8, a non-suppressor E. *coli* strain (Baca et al (1997) Journal Biological Chemistry 272(16):10678-84). See Example 3a. The harvested cell pellet was resuspended in PBS (phosphate buffered saline), total cell lysis was performed by passing through a microfluidizer and the ThioFabs were purified by affinity chromatography with protein G SEPHAROSE™ (Amersham). ThioFabs were conjugated with biotin-PEO-maleimide as described above and the biotinylated-ThioFabs were further purified by Superdex-200™ (Amersham) gel filtration chromatography, which eliminated the free biotin-PEO-maleimide and the oligomeric fraction of ThioFabs.

[00139] MASS SPECTROSCOPY ANALYSIS

[00140] Liquid chromatography electrospray ionization mass spectrometric (LC-ESI-MS) analysis was employed for the accurate molecular weight determination of biotin conjugated Fab (Cole, R.B. Electro Spray Ionization Mass Spectrometry: Fundamentals, Instrumentation And Applications. (1997) Wiley, New York). The amino acid sequence of biotinylated hu4D5Fabv8 (A121C) peptide was determined by tryptic digestion followed by LC-ESI-Tandem MS analysis (Table 4, Example 3b).

[00141] The antibody Fab fragment hu4D5Fabv8 contains about 445 amino acid residues, including 10 Cys residues (five on the light and five on the heavy chain). The high-resolution structure of the humanized 4D5 variable fragment (Fv4D5) has been established, see: Eigenbrot et al "X-Ray Structures Of The Antigen-Binding Domains From Three Variants Of Humanized Anti-P185her2 Antibody 4D5 And Comparison With Molecular Modeling" (1993) J Mol Biol. 229:969-995). All the Cys residues are present in the form of disulfide bonds, therefore these residues do not have any reactive thiol groups to conjugate with drug-maleimide (unless treated with a reducing agent). Hence, the newly engineered Cys residue, can remain unpaired, and able to react with, i.e. conjugate to, an electrophilic linker reagent or drug-linker intermediate, such as a drug-maleimide. Figure 1A shows a three-dimensional representation of the hu4D5Fabv8 antibody fragment derived by X-ray crystal coordinates. The structure positions of the engineered Cys residues of the heavy and light chains are numbered according to a sequential numbering system. This sequential numbering

system is correlated to the Kabat numbering system (Kabat et al., (1991) Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD) for the 4d5v7fabH variant of trastuzumab according to Figure 1B which shows the sequential numbering scheme (top row), starting at the N-terminus, differs from the Kabat numbering scheme (bottom row) by insertions noted by a,b,c. Using the Kabat numbering system, the actual linear amino acid sequence may contain fewer or additional amino acids corresponding to a shortening of, or insertion into, a FR or CDR of the variable domain. The cysteine engineered heavy chain variant sites are identified by the sequential numbering and Kabat numbering schemes in the following chart:

4D5Fab Heavy chain variants	Sequential Numbering	Kabat Numbering
A40C	Ala-40	Ala-40
A88C	Ala-88	Ala-84
S119C	Ser-119	Ser-112
S120C	Ser-120	Ser-113
A121C	Ala-121	Ala-114
S122C	Ser-122	Ser-115
A175C	Ala-175	Ala-168

[00142] M13 phagemid-Cys mutant Fabs (Figures 3A and 3B) can be rapidly screened compared to Fab proteins. Phagemid-ThioFab binding to antigen and to streptavidin can be tested by coating HER2 and streptavidin, respectively, onto ELISA plates followed by probing with anti-Fab-HRP (Horse radish peroxidase) as described in Example 2 and depicted in Figure 8. This method allowed simultaneous monitoring of the effect on the antigen binding and the reactivity of the thiol group by the engineered Cys residue/conjugated biotin molecule. Also, the method can be applied to screen the reactive thiol groups for any protein displayed on M13 phage. Conjugated or unconjugated phagemid-ThioFabs are purified by simple PEG precipitation.

[00143] The antigen-binding fragment of humanized 4D5 (hu4D5Fab) is well expressed in *E. Coli* and has been displayed on bacteriophage (Garrard et al (1993) Gene 128:103-109). The antibody Fab fragment hu4D5Fabv8 was displayed on M13 phage as a model system in the ELISA based assay to probe thiol reactivity. Figure 8 is a graphical representation of the PHESELECTOR assay, depicting binding of a biotinylated ThioFab phage and an anti-phage HRP antibody to HER2 (top) and Streptavidin (bottom). Five amino acid residues (L-Ala43, H-Ala40, H-Ser119, H-Ala121 and H-Ser122) were initially selected from crystal structure information as remote from the antigen binding surface (Eigenbrot et

al. (1993) J Mol Biol. 229:969-995). The Protein Database X-ray crystal structure was designated as 1FVC. Cys residues were engineered at these positions by site directed mutagenesis. ThioFab-phage preparations were isolated and reacted with the biotinylation reagent.

[00144] Biotin conjugated and unconjugated variants were tested for HER2 and streptavidin binding using an ELISA based PHESELECTOR assay (Figure 8, Example 2) with an HRP (horseradish peroxidase)-conjugated anti-phage antibody. The interaction of non-biotinylated phage-hu4D5Fabv8 (Figure 2A) and biotinylated phage-hu4D5Fabv8 (Figure 2B) with BSA (open box), HER2 (grey box) or streptavidin (solid box) were monitored through anti-M13-horseradish peroxidase (HRP) antibody by developing a standard HRP reaction and measuring absorbance at 450 nm. The absorbance produced by turnover of a colorimetric substrate was measured at 450 nm. The reactivity of ThioFab with HER2 measures antigen binding. The reactivity of ThioFab with streptavidin measures the extent of biotinylation. The reactivity of ThioFab with BSA is a negative control for nonspecific interaction. As seen in Figure 2A, all the ThioFab-phage variants have similar binding to HER2 compared to that of wild type hu4D5Fabv8-phage. Furthermore, conjugation with biotin did not interfere in the ThioFab binding to HER2 (Figure 2B).

[00145] Surprisingly and unexpectedly, the ThioFabs-phage samples showed varying levels of streptavidin binding activity. From all the tested phage-ThioFabs, the A121C cysteine engineered antibody exhibited maximal thiol reactivity. Even though wild type hu4D5Fabv8-phage was incubated with the same amounts of biotin-maleimide, these phage had little streptavidin binding indicating that preexisting cysteine residues (involved in disulfide bond formation) from the hu4D5Fabv8 and M13 phage coat proteins did not interfere with the site-specific conjugation of biotin-maleimide. These results demonstrate that the phage ELISA assay can be used successfully to screen reactive thiol groups on the Fab surface.

[00146] The PHESELECTOR assay allows screening of reactive thiol groups in antibodies. Identification of the A121C variant by this method is exemplary. The entire Fab molecule may be effectively searched to identify more ThioFab variants with reactive thiol groups. A parameter, fractional surface accessibility, was employed to identify and quantitate the accessibility of solvent to the amino acid residues in a polypeptide. The surface accessibility can be expressed as the surface area ($Å^2$) that can be contacted by a solvent molecule, e.g. water. The occupied space of water is approximated as a 1.4 Å radius sphere. Software is freely available or licensable (Secretary to CCP4, Daresbury Laboratory,

Warrington, WA4 4AD, United Kingdom, Fax: (+44) 1925 603825, or by internet: www.ccp4.ac.uk/dist/html/INDEX.html) as the CCP4 Suite of crystallography programs which employ algorithms to calculate the surface accessibility of each amino acid of a protein with known x-ray crystallography derived coordinates ("The CCP4 Suite: Programs for Protein Crystallography" (1994) Acta. Cryst. D50:760-763). Two exemplary software modules that perform surface accessibility calculations are "AREAIMOL" and "SURFACE", based on the algorithms of B.Lee and F.M.Richards (1971) J.Mol.Biol. 55:379-400. AREAIMOL defines the solvent accessible surface of a protein as the locus of the centre of a probe sphere (representing a solvent molecule) as it rolls over the Van der Waals surface of the protein. AREAIMOL calculates the solvent accessible surface area by generating surface points on an extended sphere about each atom (at a distance from the atom centre equal to the sum of the atom and probe radii), and eliminating those that lie within equivalent spheres associated with neighboring atoms. AREAIMOL finds the solvent accessible area of atoms in a PDB coordinate file, and summarizes the accessible area by residue, by chain and for the whole molecule. Accessible areas (or area differences) for individual atoms can be written to a pseudo-PDB output file. AREAIMOL assumes a single radius for each element, and only recognizes a limited number of different elements. Unknown atom types (i.e. those not in AREAIMOL's internal database) will be assigned the default radius of 1.8 Å. The list of recognized atoms is:

Atom	Atomic no.	Van der Waals rad. (Å)
C	6	1.80
N	7	1.65
O	8	1.60
Mg	12	1.60
S	16	1.85
P	15	1.90
Cl	17	1.80
Co	27	1.80

[00147] AREAIMOL and SURFACE report absolute accessibilities, i.e. the number of square Angstroms (Å). Fractional surface accessibility is calculated by reference to a standard state relevant for an amino acid within a polypeptide. The reference state is tripeptide Gly-X-Gly, where X is the amino acid of interest, and the reference state should be an 'extended' conformation, i.e. like those in beta-strands. The extended conformation maximizes the accessibility of X. A calculated accessible area is divided by the accessible

area in a Gly-X-Gly tripeptide reference state and reports the quotient, which is the fractional accessibility. Percent accessibility is fractional accessibility multiplied by 100.

[00148] Another exemplary algorithm for calculating surface accessibility is based on the SOLV module of the program xsae (Broger, C., F. Hoffman-LaRoche, Basel) which calculates fractional accessibility of an amino acid residue to a water sphere based on the X-ray coordinates of the polypeptide.

[00149] The fractional surface accessibility for every amino acid in hu4D5Fabv7 was calculated using the crystal structure information (Eigenbrot et al. (1993) J Mol Biol. 229:969-995; US 7521541). The following two criteria were applied to identify the residues of hu4D5Fabv8 that can be engineered to replace with Cys residues:

[00150] 1. Amino acid residues that are completely buried are eliminated, i.e. less than 10% fractional surface accessibility. There are 134 (light chain) and 151 (heavy chain) residues of hu4D5Fabv8 that are more than 10% accessible (fractional surface accessibility). The top ten most accessible Ser, Ala and Val residues were selected due to their close structural similarity to Cys over other amino acids, introducing only minimal structural constraints in the antibody by newly engineered Cys. Other cysteine replacement sites can also be screened, and may be useful for conjugation.

[00151] 2. Residues are sorted based on their role in functional and structural interactions of Fab. The residues which are not involved in antigen interactions and distant from the existing disulfide bonds were further selected. The newly engineered Cys residues should be distinct from, and not interfere with, antigen binding nor mispair with cysteines involved in disulfide bond formation.

[00152] Thiol reactivity may be generalized to any antibody where substitution of amino acids with reactive cysteine amino acids may be made within the ranges in the light chain selected from: L-10 to L-20; L-38 to L-48; L-105 to L-115; L-139 to L-149; L-163 to L-173; and within the ranges in the heavy chain selected from: H-35 to H-45; H-83 to H-93; H-114 to H-127; and H-170 to H-184, and in the Fc region within the ranges selected from H-268 to H-291; H-319 to H-344; H-370 to H-380; and H-395 to H-405.

[00153] Thiol reactivity may also be generalized to certain domains of an antibody, such as the light chain constant domain (CL) and heavy chain constant domains, CH1, CH2 and CH3. Cysteine replacements resulting in thiol reactivity values of about 0.8 and higher may be made in the heavy chain constant domains α, δ, ε, γ, and μ of intact antibodies: IgA, IgD, IgE, IgG, and IgM, respectively, including the IgG subclasses: IgG1, IgG2, IgG3, IgG4, IgA, and IgA2.

[00154] It is evident from the crystal structure data that the selected 10 Cys mutants are far away from the antigen-combining site, such as the interface with HER2 in this case. These mutants can be tested experimentally for indirect effects on functional interactions. The thiol reactivities of all the Cys Fab variants were measured and calculated as described in Examples 1 and 2, and presented in Table 1. The residues L-V15C, L-V110C, H-A88C and H-A121C have reactive and stable thiol groups (Figures 3A and 3B). Mutants V15C, V110C, A144C, S168C are light chain Cys variants. Mutants A88C, A121C, A175C, S179C are heavy chain Cys variants. It was surprising and unexpected that the sites with high fractional surface accessibility did not have the highest thiol reactivity as calculated by the PHESELECTOR assay (Table 1). In other words, fractional surface accessibility (Figure 1A) did not correlate with thiol reactivity (Table 1). In fact, the Cys residues engineered at the sites with moderate surface accessibility of 20% to 80% (Figure 4A), or partially exposed sites, like Ala or Val residues, exhibited better thiol reactivity, i.e. >0.6, (Figure 3B, Table 1) than the Cys introduced at Ser residues, thus necessitating the use of PHESELECTOR assay in the screening of thiol reactive sites since the crystal structure information alone is not sufficient to select these sites (Figure 3B and 4A).

[00155] Thiol reactivity data is shown in Figures 3A and 3B for amino acid residues of 4D5 ThioFab Cys mutants: (3A) non-biotinylated (control) and (3B) biotinylated phage-ThioFabs. Reactive thiol groups on antibody/Fab surface were identified by PHESELECTOR assay analyses for the interaction of non-biotinylated phage-hu4D5Fabv8 (3A) and biotinylated phage-hu4D5Fabv8 (3B) with BSA (open box), HER2 (grey box) or streptavidin (solid box). The assay was carried out as described in Example 2. Light chain variants are on the left side and heavy chain variants are on the right side. The binding of non-biotinylated 4D5 ThioFab Cys mutants is low as expected, but strong binding to HER2 is retained. The ratio of binding to streptavidin and to HER2 of the biotinylated 4D5 ThioFab Cys mutants gives the thiol reactivity values in Table 1. Background absorbance at 450 nm or small amounts of non-specific protein binding of the biotinylated 4D5 ThioFab Cys mutants to BSA is also evident in Figure 3B. Fractional Surface Accessibility values of the selected amino acid residues that were replaced with a Cys residue are shown in Figure 4A. Fractional surface accessibility was calculated from the available hu4D5Fabv7 structure (Eigenbrot et al. (1993) J Mol Biol. 229:969-995). The conformational parameters of the hu4D5Fabv7 and hu4D5Fabv8 structures are highly consistent and allow for determination of any correlation between fractional surface accessibility calculations of hu4D5Fabv7 and thiol reactivity of hu4D5Fabv8 cysteine mutants. The measured thiol reactivity of phage ThioFab

Cys residues introduced at partially exposed residues (Ala or Val) have better thiol reactivity compared to the ones introduced at Ser residues (Table 1). It can be seen from the ThioFab Cys mutants of Table 1 that there is little or no correlation between thio reactivity values and fractional surface accessibility.

[00156] Amino acids at positions L-15, L-43, L-110, L-144, L-168, H-40, H-88, H-119, H-121, H-122, H-175, and H-179 of an antibody may generally be mutated (replaced) with free cysteine amino acids. Ranges within about 5 amino acid residues on each side of these positions may also be replaced with free cysteine acids, i.e. L-10 to L-20; L-38 to L-48; L-105 to L-115; L-139 to L-149; L-163 to L-173; H-35 to H-45; H-83 to H-93; H-114 to H-127; and H-170 to H-184, as well as the ranges in the Fc region selected from H-268 to H-291; H-319 to H-344; H-370 to H-380; and H-395 to H-405, to yield the cysteine engineered antibodies of the invention.

Table 1. Thiol reactivity of phage-ThioFabs

Phage-ThioFab construct	Thiol Reactivity*	Fractional Surface Accessibility (%)
hu4D5Fabv8-wt	0.125	-
L-V15C	0.934	52.46
L-A43C	0.385	26.80
L-V110C	0.850	44.84
L-A144C	0.373	23.65
L-S168C	0.514	79.68
H-A40C	0.450	21.97
H-A88C	0.914	51.60
H-S119C	0.680	18.88
H-A121C	0.925	33.05
H-S122C	0.720	72.87
H-A175C	0.19	23.80
H-S179C	0.446	99.48

L = light chain, H = heavy chain, A = alanine, S = serine, V = valine, C = cysteine

* Thiol reactivity is measured as the ratio of $OD_{450\ nm}$ for streptavidin binding to $OD_{450\ nm}$ for HER2 (antibody) binding (Example 2). Thiol reactivity value of 1 indicates complete biotinylation of the cysteine thiol.

[00157] Two Cys variants from light chain (L-V15C and L-V110C) and two from heavy chain (H-A88C and H-A121C) were selected for further analysis as these variants

showed the highest thiol reactivity (Table 1).

[00158] Unlike phage purification, Fab preparation may require 2-3 days, depending on the scale of production. During this time, thiol groups may lose reactivity due to oxidation. To probe the stability of thiol groups on hu4D5Fabv8-phage, stability of the thiol reactivity of phage-thioFabs was measured (Figure 4B). After ThioFab-phage purification, on day 1, day 2 and day 4, all the samples were conjugated with biotin-PEO-maleimide and probed with phage ELISA assay (PHESELECTOR) to test HER2 and streptavidin binding. L-V15C, L-V110C, H-A88C and H-A121C retain significant amounts of thiol reactivity compared to other ThioFab variants (Figure 4B).

[00159] LABELLED CYSTEINE ENGINEERED ANTIBODIES

[00160] The cysteine engineered antibodies of the invention may be conjugated with any label moiety which can be covalently attached to the antibody through a reactive cysteine thiol group (Singh et al (2002) Anal. Biochem. 304:147-15; Harlow E. and Lane, D. (1999) Using Antibodies: A Laboratory Manual, Cold Springs Harbor Laboratory Press, Cold Spring Harbor, NY; Lundblad R.L. (1991) Chemical Reagents for Protein Modification, 2nd ed. CRC Press, Boca Raton, FL). The attached label may function to: (i) provide a detectable signal; (ii) interact with a second label to modify the detectable signal provided by the first or second label, e.g. to give FRET (fluorescence resonance energy transfer); (iii) stabilize interactions or increase affinity of binding, with antigen or ligand; (iv) affect mobility, e.g. electrophoretic mobility or cell-permeability, by charge, hydrophobicity, shape, or other physical parameters, or (v) provide a capture moiety, to modulate ligand affinity, antibody/antigen binding, or ionic complexation.

[00161] Labelled cysteine engineered antibodies may be useful in diagnostic assays, *e.g.,* for detecting expression of an antigen of interest in specific cells, tissues, or serum. For diagnostic applications, the antibody will typically be labeled with a detectable moiety. Numerous labels are available which can be generally grouped into the following categories:

[00162] (a) Radioisotopes (radionuclides), such as ^{3}H, ^{11}C, ^{14}C, ^{18}F, ^{32}P, ^{35}S, ^{64}Cu, ^{68}Ga, ^{86}Y, ^{89}Zr, ^{99}Tc, ^{111}In, ^{123}I, ^{124}I, ^{125}I, ^{131}I, ^{133}Xe, ^{177}Lu, ^{211}At, or ^{213}Bi. Radioisotope labelled antibodies are useful in receptor targeted imaging experiments. The antibody can be labeled with ligand reagents that bind, chelate or otherwise complex a radioisotope metal where the reagent is reactive with the engineered cysteine thiol of the antibody, using the techniques described in *Current Protocols in Immunology*, (1991) Volumes 1 and 2, Coligen et al, Ed. Wiley-Interscience, New York, NY, Pubs.. Chelating ligands which may complex a

metal ion include DOTA, DOTP, DOTMA, DTPA and TETA (Macrocyclics, Dallas, TX). Radionuclides can be targetted via complexation with the antibody-drug conjugates of the invention (Wu et al (2005) Nature Biotechnology 23(9):1137-1146). DOTA-maleimide reagents react with the free cysteine amino acids of the cysteine engineered antibodies and provide a metal complexing ligand on the antibody (Lewis et al (1998) Bioconj. Chem. 9:72-86). Chelating linker labelling reagents such as DOTA-NHS (1,4,7,10-tetraazacyclododecane-1,4,7,10-tetraacetic acid mono (*N*-hydroxysuccinimide ester) are commercially available (Macrocyclics, Dallas, TX). Receptor target imaging with radionuclide labelled antibodies can provide a marker of pathway activation by detection and quantitation of progressive accumulation of antibodies in tumor tissue (Albert et al (1998) Bioorg. Med. Chem. Lett. 8:1207-1210).

[00163] Metal-chelate complexes suitable as antibody labels for imaging experiments (US 2010/0111856; US 5342606; US 5428155; US 5316757; US 5480990; US 5462725; US 5428139; US 5385893; US 5739294; US 5750660; US 5834456; Hnatowich et al (1983) J. Immunol. Methods 65:147-157; Meares et al (1984) Anal. Biochem. 142:68-78; Mirzadeh et al (1990) Bioconjugate Chem. 1:59-65; Meares et al (1990) J. Cancer1990, Suppl. 10:21-26; Izard et al (1992) Bioconjugate Chem. 3:346-350; Nikula et al (1995) Nucl. Med. Biol. 22:387-90; Camera et al (1993) Nucl. Med. Biol. 20:955-62; Kukis et al (1998) J. Nucl. Med. 39:2105-2110; Verel et al (2003) J. Nucl. Med. 44:1663-1670; Camera et al (1994) J. Nucl. Med. 21:640-646; Ruegg et al (1990) Cancer Res. 50:4221-4226; Verel et al (2003) J. Nucl. Med. 44:1663-1670; Lee et al (2001) Cancer Res. 61:4474-4482; Mitchell, et al (2003) J. Nucl. Med. 44:1105-1112; Kobayashi et al (1999) Bioconjugate Chem. 10:103-111; Miederer et al (2004) J. Nucl. Med. 45:129-137; DeNardo et al (1998) Clinical Cancer Research 4:2483-90; Blend et al (2003) Cancer Biotherapy & Radiopharmaceuticals 18:355-363; Nikula et al (1999) J. Nucl. Med. 40:166-76; Kobayashi et al (1998) J. Nucl. Med. 39:829-36; Mardirossian et al (1993) Nucl. Med. Biol. 20:65-74; Roselli et al (1999) Cancer Biotherapy & Radiopharmaceuticals, 14:209-20).

[00164] (b) Fluorescent labels such as rare earth chelates (europium chelates), fluorescein types including FITC, 5-carboxyfluorescein, 6-carboxy fluorescein; rhodamine types including TAMRA; dansyl; Lissamine; cyanines; phycoerythrins; Texas Red; and analogs thereof. The fluorescent labels can be conjugated to antibodies using the techniques disclosed in *Current Protocols in Immunology*, *supra*, for example. Fluorescent dyes and fluorescent label reagents include those which are commercially available from Invitrogen/Molecular Probes (Eugene, OR) and Pierce Biotechnology, Inc. (Rockford, IL).

[00165] Detection labels such as fluorescent dyes and chemiluminescent dyes (Briggs et al (1997) "Synthesis of Functionalised Fluorescent Dyes and Their Coupling to Amines and Amino Acids," J. Chem. Soc., Perkin-Trans. 1:1051-1058) provide a detectable signal and are generally applicable for labelling antibodies, preferably with the following properties: (i) the labelled antibody should produce a very high signal with low background so that small quantities of antibodies can be sensitively detected in both cell-free and cell-based assays; and (ii) the labelled antibody should be photostable so that the fluorescent signal may be observed, monitored and recorded without significant photo bleaching. For applications involving cell surface binding of labelled antibody to membranes or cell surfaces, especially live cells, the labels preferably (iii) have good water-solubility to achieve effective conjugate concentration and detection sensitivity and (iv) are non-toxic to living cells so as not to disrupt the normal metabolic processes of the cells or cause premature cell death.

[00166] (c) Various enzyme-substrate labels are available or disclosed (US 4275149). The enzyme generally catalyzes a chemical alteration of a chromogenic substrate that can be measured using various techniques. For example, the enzyme may catalyze a color change in a substrate, which can be measured spectrophotometrically. Alternatively, the enzyme may alter the fluorescence or chemiluminescence of the substrate. Techniques for quantifying a change in fluorescence are described above. The chemiluminescent substrate becomes electronically excited by a chemical reaction and may then emit light which can be measured (using a chemiluminometer, for example) or donates energy to a fluorescent acceptor. Examples of enzymatic labels include luciferases (*e.g.,* firefly luciferase and bacterial luciferase; US 4737456), luciferin, 2,3-dihydrophthalazinediones, malate dehydrogenase, urease, peroxidase such as horseradish peroxidase (HRP), alkaline phosphatase (AP), β-galactosidase, glucoamylase, lysozyme, saccharide oxidases (*e.g.,* glucose oxidase, galactose oxidase, and glucose-6-phosphate dehydrogenase), heterocyclic oxidases (such as uricase and xanthine oxidase), lactoperoxidase, microperoxidase, and the like. Techniques for conjugating enzymes to antibodies are described in O'Sullivan et al (1981) "Methods for the Preparation of Enzyme-Antibody Conjugates for use in Enzyme Immunoassay", in *Methods in Enzym.* (ed J. Langone & H. Van Vunakis), Academic Press, New York, 73:147-166.

[00167] Examples of enzyme-substrate combinations (US 4275149; US 4318980) include, for example:

[00168] (i) Horseradish peroxidase (HRP) with hydrogen peroxidase as a

substrate, wherein the hydrogen peroxidase oxidizes a dye precursor (e.g., orthophenylene diamine (OPD) or 3,3',5,5'-tetramethylbenzidine hydrochloride (TMB));

[00169] (ii) alkaline phosphatase (AP) with para-nitrophenyl phosphate as chromogenic substrate; and

[00170] (iii) β-D-galactosidase (β-D-Gal) with a chromogenic substrate (*e.g.*, p-nitrophenyl-β-D-galactosidase) or fluorogenic substrate 4-methylumbelliferyl-β-D-galactosidase.

[00171] A label may be indirectly conjugated with a cysteine engineered antibody. For example, the antibody can be conjugated with biotin and any of the three broad categories of labels mentioned above can be conjugated with avidin or streptavidin, or vice versa. Biotin binds selectively to streptavidin and thus, the label can be conjugated with the antibody in this indirect manner. Alternatively, to achieve indirect conjugation of the label with the polypeptide variant, the polypeptide variant is conjugated with a small hapten (e.g., digoxin) and one of the different types of labels mentioned above is conjugated with an anti-hapten polypeptide variant (*e.g.*, anti-digoxin antibody). Thus, indirect conjugation of the label with the polypeptide variant can be achieved (Hermanson, G. (1996) in *Bioconjugate Techniques* Academic Press, San Diego).

[00172] The polypeptide variant of the present invention may be employed in any known assay method, such as ELISA, competitive binding assays, direct and indirect sandwich assays, and immunoprecipitation assays (Zola, (1987) *Monoclonal Antibodies: A Manual of Techniques*, pp.147-158, CRC Press, Inc.).

[00173] A detection label may be useful for localizing, visualizing, and quantitating a binding or recognition event. The labelled antibodies of the invention can detect cell-surface receptors. Another use for detectably labelled antibodies is a method of bead-based immunocapture comprising conjugating a bead with a fluorescent labelled antibody and detecting a fluorescence signal upon binding of a ligand. Similar binding detection methodologies utilize the surface plasmon resonance (SPR) effect to measure and detect antibody-antigen interactions.

[00174] Labelled cysteine engineered antibodies of the invention are useful as imaging biomarkers and probes by the various methods and techniques of biomedical and molecular imaging such as: (i) MRI (magnetic resonance imaging); (ii) MicroCT (computerized tomography); (iii) SPECT (single photon emission computed tomography); (iv) PET (positron emission tomography) Tinianow, J. et al (2010) Nuclear Medicine and Biology,

37(3):289-297; Chen et al (2004) Bioconjugate Chem. 15:41-49; US 2010/0111856 (v) bioluminescence; (vi) fluorescence; and (vii) ultrasound. Immunoscintigraphy is an imaging procedure in which antibodies labeled with radioactive substances are administered to an animal or human patient and a picture is taken of sites in the body where the antibody localizes (US 6528624). Imaging biomarkers may be objectively measured and evaluated as an indicator of normal biological processes, pathogenic processes, or pharmacological responses to a therapeutic intervention. Biomarkers may be of several types: Type 0 are natural history markers of a disease and correlate longitudinally with known clinical indices, e.g. MRI assessment of synovial inflammation in rheumatoid arthritis; Type I markers capture the effect of an intervention in accordance with a mechanism-of-action, even though the mechanism may not be associated with clinical outcome; Type II markers function as surrogate endpoints where the change in, or signal from, the biomarker predicts a clinical benefit to "validate" the targeted response, such as measured bone erosion in rheumatoid arthritis by CT. Imaging biomarkers thus can provide pharmacodynamic (PD) therapeutic information about: (i) expression of a target protein, (ii) binding of a therapeutic to the target protein, i.e. selectivity, and (iii) clearance and half-life pharmacokinetic data. Advantages of *in vivo* imaging biomarkers relative to lab-based biomarkers include: non-invasive treatment, quantifiable, whole body assessment, repetitive dosing and assessment, i.e. multiple time points, and potentially transferable effects from preclinical (small animal) to clinical (human) results. For some applications, bioimaging supplants or minimizes the number of animal experiments in preclinical studies.

[00175] Peptide labelling methods are well known. See Haugland, 2003, *Molecular Probes Handbook of Fluorescent Probes and Research Chemicals*, Molecular Probes, Inc.; Brinkley, 1992, Bioconjugate Chem. 3:2; Garman, (1997) *Non-Radioactive Labelling: A Practical Approach*, Academic Press, London; Means (1990) Bioconjugate Chem. 1:2; Glazer et al (1975) *Chemical Modification of Proteins. Laboratory Techniques in Biochemistry and Molecular Biology* (T. S. Work and E. Work, Eds.) American Elsevier Publishing Co., New York; Lundblad, R. L. and Noyes, C. M. (1984) *Chemical Reagents for Protein Modification*, Vols. I and II, CRC Press, New York; Pfleiderer, G. (1985) "Chemical Modification of Proteins", *Modern Methods in Protein Chemistry*, H. Tschesche, Ed., Walter DeGryter, Berlin and New York; and Wong (1991) *Chemistry of Protein Conjugation and Cross-linking*, CRC Press, Boca Raton, Fla.); De Leon-Rodriguez et al (2004) Chem.Eur. J. 10:1149-1155; Lewis et al (2001) Bioconjugate Chem. 12:320-324; Li et al (2002) Bioconjugate Chem. 13:110-115; Mier et al (2005) Bioconjugate Chem. 16:240-237.

[00176] Peptides and proteins labelled with two moieties, a fluorescent reporter and quencher in sufficient proximity undergo fluorescence resonance energy transfer (FRET). Reporter groups are typically fluorescent dyes that are excited by light at a certain wavelength and transfer energy to an acceptor, or quencher, group, with the appropriate Stokes shift for emission at maximal brightness. Fluorescent dyes include molecules with extended aromaticity, such as fluorescein and rhodamine, and their derivatives. The fluorescent reporter may be partially or significantly quenched by the quencher moiety in an intact peptide. Upon cleavage of the peptide by a peptidase or protease, a detectable increase in fluorescence may be measured (Knight, C. (1995) "Fluorimetric Assays of Proteolytic Enzymes", Methods in Enzymology, Academic Press, 248:18-34).

[00177] The labelled antibodies of the invention may also be used as an affinity purification agent. In this process, the labelled antibody is immobilized on a solid phase such a Sephadex resin or filter paper, using methods well known in the art. The immobilized antibody is contacted with a sample containing the antigen to be purified, and thereafter the support is washed with a suitable solvent that will remove substantially all the material in the sample except the antigen to be purified, which is bound to the immobilized polypeptide variant. Finally, the support is washed with another suitable solvent, such as glycine buffer at pH 5.0 that will release the antigen from the polypeptide variant.

[00178] Labelling reagents typically bear reactive functionality which may react (i) directly with a cysteine thiol of a cysteine engineered antibody to form the labelled antibody, (ii) with a linker reagent to form a linker-label intermediate, or (iii) with a linker antibody to form the labelled antibody. Reactive functionality of labelling reagents include: maleimide, haloacetyl, iodoacetamide succinimidyl ester (e.g. NHS, N-hydroxysuccinimide), isothiocyanate, sulfonyl chloride, 2,6-dichlorotriazinyl, pentafluorophenyl ester, and phosphoramidite, although other functional groups can also be used.

[00179] CONJUGATION OF BIOTIN-MALEIMIDE TO THIOFABS

[00180] The above-described ThioFab properties were established in the presence of phage because fusion of the Fab to the phage coat protein could potentially alter Cys thiol accessibility or reactivity. Therefore, the ThioFab constructs were cloned into an expression vector under alkaline phosphatase promoter (Chang et al (1987) Gene 55:189-196) and the ThioFab expression was induced by growing *E. coli* cells in the phosphate-free medium. ThioFabs were purified on a Protein G SEPHAROSE™ column and analyzed on reducing and non-reducing SDS-PAGE gels. These analyses allow assessment of whether ThioFabs

retained their reactive thiol group or were rendered inactive by forming intramolecular or intermolecular disulfide bonds. ThioFabs L-V15C, L-V110C, H-A88C, and H-A121C were expressed and purified by Protein-G SEPHAROSE™ column chromatography (see methods sections for details). Purified proteins were analyzed on SDS-PAGE gel in reducing (with DTT) and non-reducing (without DTT) conditions. Other reducing agents such as BME (beta-mercaptoethanol) can used in the gel to cleave interchain disulfide groups. It is evident from SDS-PAGE gel analysis that the major (~90%) fraction of ThioFab is in the monomeric form, while wild type hu4D5Fabv8 is essentially in the monomeric form (47 kDa).

[00181] ThioFab (A121C) and wild type hu4D5Fabv8 were incubated with 100 fold excess of biotin-maleimide for 3 hours at room temperature and the biotinylated Fabs were loaded onto a Superdex-200™ gel filtration column. This purification step was useful in separating monomeric Fab from oligomeric Fab and also from excess free biotin-maleimide (or free cytotoxic drug).

[00182] Figure 5 shows validation of the properties of ThioFab variants in the absence of the phage context. The proteins without phage fusion, hu4D5Fabv8 and hu4D5Fabv8-A121C (ThioFab-A121C), were expressed and purified using protein-G agarose beads followed by incubation with 100 fold molar excess of biotin-maleimide. Streptavidin and HER2 binding of a biotinylated cys engineered ThioFab and a non-biotinylated wild type Fab was compared. The extent of biotin conjugation (interaction with streptavidin) and their binding ability to HER2 were monitored by ELISA analyses. Each Fab was tested at 2ng and 20ng.

[00183] Biotinylated A121C ThioFab retained comparable HER2 binding to that of wild type hu4D5Fabv8 (Figure 5). Wild type Fab and A121C-ThioFab were purified by gel filtration column chromatography. The two samples were tested for HER2 and streptavidin binding by ELISA using goat anti-Fab-HRP as secondary antibody. Both wild type (open box) and ThioFab (dotted box) have similar binding to HER2 but only ThioFab retained streptavidin binding. Only a background level of interaction with streptavidin was observed with non-biotinylated wild type hu4D5Fabv8 (Figure 5). Mass spectral (LC-ESI-MS) analysis of biotinylated-ThioFab (A121C) resulted in a major peak with 48294.5 daltons compared to the wild type hu4D5Fabv8 (47737 daltons). The 537.5 daltons difference between the two molecules exactly corresponds to a single biotin-maleimide conjugated to the ThioFab. Mass spec protein sequencing (LC-ESI-Tandem mass spec analysis) results further confirmed that the conjugated biotin molecule was at the newly engineered Cys residue (Table 8, Example 3b).

[00184] SITE SPECIFIC CONJUGATION OF BIOTIN-MALEIMIDE TO ALBUMIN BINDING PEPTIDE (ABP)-THIOFABS

[00185] Plasma-protein binding can be an effective means of improving the pharmacokinetic properties of short lived molecules. Albumin is the most abundant protein in plasma. Serum albumin binding peptides (ABP) can alter the pharmacodynamics of fused active domain proteins, including alteration of tissue uptake, penetration, and diffusion. These pharmacodynamic parameters can be modulated by specific selection of the appropriate serum albumin binding peptide sequence (US 20040001827). A series of albumin binding peptides were identified by phage display screening (Dennis et al. (2002) "Albumin Binding As A General Strategy For Improving The Pharmacokinetics Of Proteins" J Biol Chem. 277:35035-35043; WO 01/45746). Compounds of the invention include ABP sequences taught by: (i) Dennis et al (2002) J Biol Chem. 277:35035-35043 at Tables III and IV, page 35038; (ii) US 20040001827 at [0076]; and (iii) WO 01/45746 at pages 12-13, and all of which are incorporated herein by reference.

[00186] Albumin Binding (ABP)-Fabs were engineered by fusing an albumin binding peptide to the C-terminus of Fab heavy chain in 1:1 stoichiometric ratio (1 ABP / 1 Fab). It was shown that association of these ABP-Fabs with albumin increased their half life by more than 25 fold in rabbits and mice. The above described reactive Cys residues can therefore be introduced in these ABP-Fabs and used for site-specific conjugation with cytotoxic drugs followed by *in vivo* animal studies.

[00187] Exemplary albumin binding peptide sequences include, but are not limited to the amino acid sequences listed in SEQ ID NOS: 1-5:

CDKTHTGGGSQRLMEDICLPRWGCLWEDDF	SEQ ID NO:1
QRLMEDICLPRWGCLWEDDF	SEQ ID NO:2
QRLIEDICLPRWGCLWEDDF	SEQ ID NO:3
RLIEDICLPRWGCLWEDD	SEQ ID NO:4
DICLPRWGCLW	SEQ ID NO:5

[00188] The albumin binding peptide (ABP) sequences bind albumin from multiple species (mouse, rat, rabbit, bovine, rhesus, baboon, and human) with Kd (rabbit) = 0.3 μM. The albumin binding peptide does not compete with ligands known to bind albumin and has a half life (T½) in rabbit of 2.3 hr. ABP-ThioFab proteins were purified on BSA-SEPHAROSE™ followed by biotin-maleimide conjugation and purification on Superdex-S200 column chromatography as described in previous sections. Purified biotinylated

proteins were homogeneous and devoid of any oligomeric forms (Example 4).

[00189] Figure 6 shows the properties of Albumin Binding Peptide (ABP)-ThioFab variants. ELISA analyses were carried out to test the binding ability of ABP-hu4D5Fabv8-wt, ABP-hu4D5Fabv8-V110C and ABP-hu4D5Fabv8-A121C with rabbit albumin, streptavidin and HER2. Biotinylated ABP-ThioFabs are capable of binding to albumin and HER2 with similar affinity to that of wild type ABP-hu4D5Fabv8 as confirmed by ELISA (Figure 6) and BIAcore binding kinetics analysis (Table 2). An ELISA plate was coated with albumin, HER2 and SA as described. Binding of biotinylated ABP-ThioFabs to albumin, HER2 and SA was probed with anti-Fab HRP. Biotinylated ABP-ThioFabs were capable of binding to streptavidin compared to non biotinylated control ABP-hu4D5Fabv8-wt indicating that ABP-ThioFabs were conjugated with biotin maleimide like ThioFabs in a site specific manner as the same Cys mutants were used for both the variants (Figure 6).

Table 2. BIAcore kinetic analysis for HER2 and rabbit albumin binding to biotinylated ABP- hu4D5Fabv8 wild type and ThioFabs

Antibody	k_{on} ($M^{-1}s^{-1}$)	k_{off} (s^{-1})	K_d (nM)
HER2 binding			
wild type	4.57×10^5	4.19×10^{-5}	0.0917
V110C	4.18×10^5	4.05×10^{-5}	0.097
A121C	3.91×10^5	4.15×10^{-5}	0.106
Rabbit albumin binding			
wild type	1.66×10^5	0.0206	124
V110C	2.43×10^5	0.0331	136
A121C	1.70×10^5	0.0238	140

ABP = albumin binding peptide

[00190] Alternatively, an albumin-binding peptide may be linked to the antibody by covalent attachment through a linker moiety.

[00191] ENGINEERING OF ABP-THIOFABS WITH TWO FREE THIOL GROUPS PER FAB

[00192] The above results indicate that all four (L-V15C, L-V110C, H-A88C and H-A121C) thioFab (cysteine engineered Fab antibodies) variants have reactive thiol groups that can be used for site specific conjugation with a label reagent, linker reagent, or drug-linker intermediate. L-V15C can be expressed and purified but with relatively low yields. However the expression and purification yields of L-V110C, H-A88C and H-A121C variants were similar to that of hu4D5Fabv8. Therefore these mutants can be used for further analysis and recombined to get more than one thiol group per Fab. Towards this objective, one thiol group

on the light and one on heavy chain were constructed to obtain two thiol groups per Fab molecule (L-V110C/H-A88C and L-V110C/H-A121C). These two double Cys variants were expressed in an *E. coli* expression system and purified. The homogeneity of purified biotinylated ABP-ThioFabs was found to be similar to that of single Cys variants.

[00193] The effects of engineering two reactive Cys residues per Fab was investigated (Figure 7). The presence of a second biotin was tested by probing the binding of biotinylated ABP-ThioFab to SA using streptavidin-HRP (Figure 7). For HER2/Fab analysis, an ELISA plate was coated with HER2 and probed with anti-Fab HRP. For SA/Fab analysis, an ELISA plate was coated with SA and probed with anti-Fab HRP. For SA/SA analysis, an ELISA plate was coated with SA and probed with SA-HRP. Figure 7. ELISA analyses for the interaction of biotinylated ABP-hu4D5Fabv8 cys variants with HER2, streptavidin (SA). HER2/Fab, SA/Fab and SA/SA indicate that their interactions were monitored by anti-Fab-HRP, SA-HRP, respectively. SA/Fab monitors the presence of single biotin per Fab and more than one biotin per Fab is monitored by SA/SA analysis. Binding of HER2 with double cys mutants is similar to that of single Cys variants (Figure 7). However the extent of biotinylation on double Cys mutants was higher compared to single Cys variants due to more than one free thiol group per Fab molecule (Figure 7).

[00194] ENGINEERING OF THIO IgG VARIANTS OF TRASTUZUMAB

[00195] Cysteine was introduced into the full-length monoclonal antibody, trastuzumab (HERCEPTIN®, Genentech Inc.) at certain residues. The single cys mutants H-A88C, H-A121C and L-V110C of trastuzumab, and double cys mutants V110C-A121C and V110C-A121C of trastuzumab were expressed in CHO (Chinese Hamster Ovary) cells by transient fermentation in media containing 1 mM cysteine. The A88C mutant heavy chain sequence (450 aa) is SEQ ID NO:6. The A121C mutant heavy chain sequence (450 aa) is SEQ ID NO:7. The V110C mutant light chain sequence (214 aa) is SEQ ID NO:8.

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRY
ADSVKGRFTISADTSKNTAYLQMNSLRCEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSS
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE
MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
QQGNVFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO:6

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRY
ADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSS
CSTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE
MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
QQGNVFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO:7

DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPS
RFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTCAAPSVFIFPP
SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT
LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:8

[00196] According to one embodiment, the cysteine engineered thio-trastuzumab antibodies comprise one or more of the following variable region heavy chain sequences with a free cysteine amino acid (SEQ ID NOS: 9-16).

Mutant	Sequence	SEQ ID NO:
A40C	WVRQCPGKGL	SEQ ID NO:9
A88C	NSLRCEDTAV	SEQ ID NO:10
S119C	LVTVCSASTKGPS	SEQ ID NO:11
S120C	LVTVSCASTKGPS	SEQ ID NO:12
A121C	LVTVSSCSTKGPS	SEQ ID NO:13
S122C	LVTVSSACTKGPS	SEQ ID NO:14
A175C	HTFPCVLQSSGLYS	SEQ ID NO:15
S179C	HTFPAVLQCSGLYS	SEQ ID NO:16

[00197] According to another embodiment, the cysteine engineered thio-trastuzumab antibodies comprise one or more of the following variable region light chain sequences with a free cysteine amino acid (SEQ ID NOS: 17-27).

Mutant	Sequence	SEQ ID NO:
V15C	SLSASCGDRVT	SEQ ID NO:17
A43C	QKPGKCPKLLI	SEQ ID NO:18
V110C	EIKRTCAAPSV	SEQ ID NO:19
S114C	TCAAPCVFIFPP	SEQ ID NO:20
S121C	FIFPPCDEQLK	SEQ ID NO:21
S127C	DEQLKCGTASV	SEQ ID NO:22
A144C	FYPRECKVQWK	SEQ ID NO:23
A153C	WKVDNCLQSGN	SEQ ID NO:24
N158C	ALQSGCSQESV	SEQ ID NO:25
S168C	VTEQDCKDSTY	SEQ ID NO:26
V205C	GLSSPCTKSFN	SEQ ID NO:27

[00198] The resulting full-length, thio-trastuzumab IgG variants were assayed for thiol reactivity and HER2 binding activity. Figure 10A shows a cartoon depiction of biotinylated antibody binding to immobilized HER2 and HRP labeled secondary antibody for absorbance detection. Figure 10B shows binding measurements to immobilized HER2 with detection of absorbance at 450 nm of (left to right): non-biotinylated wild type trastuzumab (Wt), biotin-maleimide conjugated thio-trastuzumab variants V110C (single cys), A121C (single cys), and V110C-A121C (double cys). Each thio IgG variant and trastuzumab was tested at 1, 10, and 100 ng. The measurements show that biotinylated anti-HER2 ThioMabs retain HER2 binding activity.

[00199] Figure 11A shows a cartoon depiction of a biotinylated antibody binding to immobilized HER2 with binding of biotin to anti-IgG-HRP for absorbance detection. Figure 14B shows binding measurements with detection of absorbance at 450 nm of biotin-maleimide conjugated thio-trastuzumab variants and non-biotinylated wild type trastuzumab

in binding to streptavidin. From left to right: V110C (single cys), A121C (single cys), V110C/A121C (double cys), and trastuzumab. Each thio IgG trastuzumab variant and parent trastuzumab was tested at 1, 10, and 100 ng. The measurements show that the HER2 ThioMabs have high thiol reactivity.

[00200] Cysteine was introduced into the full-length 2H9 anti-EphB2R antibody at certain residues. The single cys mutant H-A121C of 2H9 was expressed in CHO (Chinese Hamster Ovary) cells by transient fermentation in media containing 1 mM cysteine. The A121C 2H9 mutant heavy chain sequence (450 aa) is SEQ ID NO:28.

EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYWMHWVRQAPGKGLEWVGFINPSTGYTDY
NQKFKDRFTISADTSKNTAYLQMNSLRAEDTAVYYCTRRPKIPRHANVFWGQGTLVTVSS
CSTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE
MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
QQGNVFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO:28

[00201] Cysteine engineered thio-2H9 antibodies comprise the following Fc constant region heavy chain sequences with a free cysteine amino acid (SEQ ID NOS: 29-38).

Mutant	Sequence	SEQ ID NO:
V273C	HEDPECKFNWYVDGVEVHNAKTKPR	SEQ ID NO:29
V279C	HEDPEVKFNWYCDGVEVHNAKTKPR	SEQ ID NO:30
V282C	HEDPEVKFNWYVDGCEVHNAKTKPR	SEQ ID NO:31
V284C	HEDPEVKFNWYVDGVECHNAKTKPR	SEQ ID NO:32
A287C	HEDPEVKFNWYVDGVEVHNCKTKPR	SEQ ID NO:33
S324C	YKCKVCNKALP	SEQ ID NO:34
S337C	IEKTICKAKGQPR	SEQ ID NO:35
A339C	IEKTISKCKGQPR	SEQ ID NO:36
S375C	KGFYPCDIAVE	SEQ ID NO:37
S400C	PPVLDCDGSFF	SEQ ID NO:38

[00202] Cysteine was introduced into the full-length 3A5 anti-MUC16 antibody at certain residues. The single cys mutant H-A121C of 3A5 was expressed in CHO (Chinese Hamster Ovary) cells by transient fermentation in media containing 1 mM cysteine. The A121C 3A5 mutant heavy chain sequence (446 aa) comprises SEQ ID NO:39.

DVQLQESGPGLVNPSQSLSLTCTVTGYSITNDYAWNWIRQFPGNKLEWMGYINYSGYTTY

NPSLKSRISITRDTSKNQFFLHLNSVTTEDTATYYCARWDGGLTYWGQGTLVTVSACSTK

GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS

LSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVF

LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR

VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKN

QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN

VFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO:39

[00203] Cysteine engineered thio-3A5 anti-MUC16 antibodies comprise the following variable region heavy chain sequences with a free cysteine amino acid (SEQ ID NOS: 40-44).

Mutant	Sequence	SEQ ID NO:
F45C	NWIRQCPGNK	SEQ ID NO:40
A90C	LNSCTTEDTAT	SEQ ID NO:41
A121C	GQGTLVTVSACSTKGPSVFPL	SEQ ID NO:42
A175C	HTFPCVLQSSGLYS	SEQ ID NO:43
V176C	HTFPACLQSSGLYS	SEQ ID NO:44

[00204] Cysteine engineered thio-3A5 anti-MUC16 antibodies comprise the following variable region light chain sequences with a free cysteine amino acid (SEQ ID NOS: 45-49).

Mutant	Sequence	SEQ ID NO:
L15C	FLSVSCGGRVT	SEQ ID NO:45
A43C	QKPGNCPRLLI	SEQ ID NO:46
V110C	EIKRTCAAPSV	SEQ ID NO:47
A144C	FYPRECKVQWK	SEQ ID NO:48
S168C	VTEQDCKDSTY	SEQ ID NO:49

[00205] ENGINEERING AND THIOL REACTIVITY OF 4D5 ANTI-HER2 THIOFABS

[00206] Cysteine was introduced into each position of the heavy chain and light chain of the anti-HER2 hu4D5Fabv8 Fab fragment antibody. All 440 of the heavy chain mutants and light chain mutants were prepared according to the methods described herein. Thiol reactivity was measured according to the PHESELECTOR assay. Heavy chain sequences are

numbered by the Sequential numbering system. Light chain sequences follow the Kabat numbering system. In the light chain, both Kabat and Sequential numbering denotes same numbers.

[00207] Heavy chain hu4D5Fabv8 mutants were selected for efficient binding to HER2 receptor protein (Figures 2 and 3) and thiol reactivity with the biotinylation reagent, Biotin-PEO-maleimide (Examples 1 and 2). Certain heavy chain mutants had limited or compromised binding to HER2 ECD because this is an important residue for antigen binding (HER2), located in CDRs in the variable region of the antibody-Fab. Some of the residues located in the constant domain of the Fabs also resulted in poor HER2 binding because these residues may contribute to structure and folding of Fab, thus resulting in poor 4D5-Fab display on M13-page (Junutula, J.R. et al. (2008) J. Immunol Methods, 332:41-52). Heavy chain hu4D5Fabv8 mutants with poor HER2 ECD binding included cysteine mutations at positions 1, 21, 31, 33-36, 38, 48-50, 59, 87, 95, 101, 104, 129, 131, 132, 136, 153, 155, 159, 166, 169, 170, 172, 197, 198, 202, 215, 219. Wild type cysteine variants 22, 96, 147, 203, 223 were measured. Other heavy chain mutants had limited thiol reactivity with the biotinylation reagent. The free cysteine amino acid residue is in the center with flanking residues in the sequences in the middle column of Table 3. The substituted amino acid and position in the heavy chain are designated in the left column. Heavy chain hu4D5Fabv8 mutants SEQ ID NOS: 50-98 of Table 3 have retained HER2 binding and thiol reactivity values of about 0.8 or higher, excluding wild type cysteine variants. Antibodies with SEQ ID NOS: 50-98 (Table 3) have demonstrated thiol reactivity and may be useful to form covalent attachments with a capture label, a detection label, a drug moiety, or a solid support. The heavy chain mutants of Table 3 may be conjugated as ThioFabs or ThioMabs for example as antibody-drug conjugates.

Table 3 Efficient binding, thiol-reactive heavy chain hu4D5Fabv8 mutants

HC-L4C	EVQCVESGG	SEQ ID NO: 50
HC-G8C	QLVESCGGLVQ	SEQ ID NO: 51
HC-G10C	VESGGCLVQPG	SEQ ID NO: 52
HC-L20C	GGSLRCSCAAS	SEQ ID NO: 53
HC-A23C	LRLSCCASGFN	SEQ ID NO: 54
HC-G26C	SCAASCFNIKD	SEQ ID NO: 55
HC-F27C	CAASGCNIKDT	SEQ ID NO: 56
HC-T32C	FNIKDCYIHWV	SEQ ID NO: 57
HC-Q39C	IHWVRCAPGKG	SEQ ID NO: 58
HC-P41C	WVRQACGKGLE	SEQ ID NO: 59

HC-K43C	RQAPGCGLEWV	SEQ ID NO: 60
HC-G44C	QAPGKCLEWVA	SEQ ID NO: 61
HC-W47C	GKGLECVARIY	SEQ ID NO: 62
HC-S63C	TRYADCVKGRF	SEQ ID NO: 63
HC-F68C	SVKGRCTISAD	SEQ ID NO: 64
HC-D73C	FTISACTSKNT	SEQ ID NO: 65
HC-K76C	SADTSCNTAYL	SEQ ID NO: 66
HC-T78C	DTSKNCAYLQM	SEQ ID NO: 67
HC-Y80C	SKNTACLQMNS	SEQ ID NO: 68
HC-L81C	KNTAYCQMNSL	SEQ ID NO: 69
HC-Q82C	NTAYLCMNSLR	SEQ ID NO: 70
HC-L86C	LQMNSCRAEDT	SEQ ID NO: 71
HC-A88C	MNSLRCEDTAV	SEQ ID NO: 72
HC-D90C	SLRAECTAVYY	SEQ ID NO: 73
HC-V93C	AEDTACYYCSR	SEQ ID NO: 74
HC-Y94C	EDTAVCYCSRW	SEQ ID NO: 75
HC-R98C	VYYCSCWGGDG	SEQ ID NO: 76
HC-G100C	YCSRWCGDGFY	SEQ ID NO: 77
HC-D108C	GFYAMCYWGQG	SEQ ID NO: 78
HC-G113C	DYWGQCTLVTV	SEQ ID NO: 79
HC-T117C	QGTLVCVSSAS	SEQ ID NO: 80
HC-A121C	VTVSSCSTKGP	SEQ ID NO: 81
HC-G125C	SASTKCPSVFP	SEQ ID NO: 82
HC-G141C	KSTSGCTAALG	SEQ ID NO: 83
HC-P154C	VKDYFCEPVTV	SEQ ID NO: 84
HC-N162C	VTVSWCSGALT	SEQ ID NO: 85
HC-S163C	TVSWNCGALTS	SEQ ID NO: 86
HC-G164C	VSWNSCALTSG	SEQ ID NO: 87
HC-S168C	SGALTCGVHTF	SEQ ID NO: 88
HC-F173C	SGVHTCPAVLQ	SEQ ID NO: 89
HC-T190C	LSSVVCVPSSS	SEQ ID NO: 90
HC-S194C	VTVPSCSLGTQ	SEQ ID NO: 91
HC-T200C	SLGTQCYICNV	SEQ ID NO: 92
HC-V205C	TYICNCNHKPS	SEQ ID NO: 93
HC-N211C	NHKPSCTKVDK	SEQ ID NO: 94
HC-T212C	HKPSNCKVDKK	SEQ ID NO: 95
HC-V214C	PSNTKCDKKVE	SEQ ID NO: 96
HC-K217C	TKVDKCVEPKS	SEQ ID NO: 97
HC-T226C	KSCDKCH	SEQ ID NO: 98

[00208] Light chain hu4D5Fabv8 mutants were selected for efficient binding to HER2 receptor protein (Figures 2 and 3) and thiol reactivity with the biotinylation reagent, Biotin-PEO-maleimide (Examples 1 and 2). Certain light chain mutants had limited or

compromised binding to HER2 because this is an important residue for antigen binding (HER2), located in CDRs in the variable region of the antibody-Fab. Some of the residues located in constant domain of Fab also resulted in poor HER2 binding because these residues may contribute to structure and folding of Fab, thus resulting in poor 4D5-Fab display on M13-page (Junutula, J.R. et al. (2008) J. Immunol Methods, 332:41-52). Light chain hu4D5Fabv8 mutants with poor binding to HER2 included cysteine mutants at positions 4, 29-32, 35, 36, 50, 82, 86, 89-91, 113, 115, 117, 120, 126, 128, 139, 141, 146, 148, 179, 186, 192, 202. Wild type cysteine variants 23, 134, 194, 214 were measured. Other light chain mutants had limited thiol reactivity with the biotinylation reagent. The free cysteine amino acid residue is in the center with flanking residues in the sequences in the middle column of Table 4. The substituted amino acid and position in the light chain are designated in the left column. Light chain hu4D5Fabv8 mutants SEQ ID NOS: 99-147 of Table 4 have retained HER2 binding and thiol reactivity values of about 0.8 or higher, excluding wild type cysteine variants. Antibodies with SEQ ID NOS: 99-147 (Table 4) have demonstrated thiol reactivity and may be useful to form covalent attachments with a capture label, a detection label, a drug moiety, or a solid support. The light chain mutants of Table 4 may be conjugated as ThioFabs or ThioMabs for example as antibody-drug conjugates.

Table 4 Efficient binding, thiol-reactive light chain hu4D5Fabv8 mutants

LC-S9C	MTQSPCSLSAS	SEQ ID NO: 99
LC-L46C	GKAPKCLIYSA	SEQ ID NO: 100
LC-Y49C	PKLLICSASFL	SEQ ID NO: 101
LC-F53C	IYSASCLYSGV	SEQ ID NO: 102
LC-T72C	SGTDFCLTISS	SEQ ID NO: 103
LC-L73C	GTDFTCTISSL	SEQ ID NO: 104
LC-T74C	TDFTLCISSLQ	SEQ ID NO: 105
LC-I75C	DFTLTCSSLQP	SEQ ID NO: 106
LC-S77C	TLTISCLQPED	SEQ ID NO: 107
LC-Q79C	TISSLCPEDFA	SEQ ID NO: 108
LC-P80C	ISSLQCEDFAT	SEQ ID NO: 109
LC-Y92C	YCQQHCTTPPT	SEQ ID NO: 110
LC-P95C	QHYTTCPTFGQ	SEQ ID NO: 111
LC-G99C	TPPTFCQGTKV	SEQ ID NO: 112
LC-G101C	PTFGQCTKVEI	SEQ ID NO: 113
LC-K103C	FGQGTCVEIKR	SEQ ID NO: 114
LC-E105C	QGTKVCIKRTV	SEQ ID NO: 115
LC-V110C	EIKRTCAAPSV	SEQ ID NO: 116
LC-A112C	KRTVACPSVFI	SEQ ID NO: 117

LC-S114C	TVAAPCVFIFP	SEQ ID NO: 118
LC-F116C	AAPSVCIFPPS	SEQ ID NO: 119
LC-F118C	PSVFICPPSDE	SEQ ID NO: 120
LC-S121C	FIFPPCDEQLK	SEQ ID NO: 121
LC-L125C	PSDEQCKSGTA	SEQ ID NO: 122
LC-S127C	DEQLKCGTASV	SEQ ID NO: 123
LC-T129C	QLKSGCASVVC	SEQ ID NO: 124
LC-A130C	LKSGTCSVVCL	SEQ ID NO: 125
LC-S131C	KSGTACVVCLL	SEQ ID NO: 126
LC-N137C	VVCLLCNFYPR	SEQ ID NO: 127
LC-N138C	VCLLNCFYPRE	SEQ ID NO: 128
LC-Y140C	LLNNFCPREAK	SEQ ID NO: 129
LC-R142C	NNFYPCEAKVQ	SEQ ID NO: 130
LC-A144C	FYPRECKVQWK	SEQ ID NO: 131
LC-Q147C	REAKVCWKVDN	SEQ ID NO: 132
LC-K149C	AKVQWCVDNAL	SEQ ID NO: 133
LC-D151C	VQWKVCNALQS	SEQ ID NO: 134
LC-Q155C	VDNALCSGNSQ	SEQ ID NO: 135
LC-Q160C	QSGNSCESVTE	SEQ ID NO: 136
LC-A184C	LTLSKCDYEKH	SEQ ID NO: 137
LC-D185C	TLSKACYEKHK	SEQ ID NO: 138
LC-K188C	KADYECHKVYA	SEQ ID NO: 139
LC-T197C	YACEVCHQGLS	SEQ ID NO: 140
LC-G200C	EVTHQCLSSPV	SEQ ID NO: 141
LC-L201C	VTHQGCSSPVT	SEQ ID NO: 142
LC-S203C	HQGLSCPVTKS	SEQ ID NO: 143
LC-P204C	QGLSSCVTKSF	SEQ ID NO: 144
LC-V205C	GLSSPCTKSFN	SEQ ID NO: 145
LC-T206C	LSSPVCKSFNR	SEQ ID NO: 146
LC-K207C	SSPVTCSFNRG	SEQ ID NO: 147

[00209] THIOL REACTIVITY OF THIOMABS

[00210] The thiol reactivity of full length, IgG cysteine engineered antibodies (ThioMabs) was measured by biotinylation and streptavidin binding (US 7521541). A western blot assay was set up to screen the ThioMab that is specifically conjugated with biotin-maleimide. In this assay, the antibodies are analyzed on reducing SDS-PAGE and the presence of Biotin is specifically probed by incubating with streptavidin-HRP. As seen from figure 18, the streptavidin-HRP interaction is either observed in heavy chain or light chain depending on which engineered cys variant is being used and no interaction is seen with wild type, indicating that ThioMab variants specifically conjugated the biotin at engineered Cys

residue. Figure 18 shows denaturing gel analysis of reduced, biotinylated Thio-IgG variants after capture on immobilized anti-IgG-HRP (top gel) and streptavidin-HRP (bottom gel). Lane 1: 3A5 H-A121C. Lane 2: 3A5 L-V110C. Lane 3: 2H9 H-A121C. Lane 4: 2H9 L-V110C. Lane 5: anti-EphB2R 2H9 parent, wild type. Each mutant (lanes 1-4) was captured by anti-IgG with HRP detection (top) indicating that selectivity and affinity were retained. Capture by immobilized streptavidin with HRP detection (bottom) confirmed the location of biotin on heavy and light chains. The location of cysteine mutation on the cysteine engineered antibodies in lanes 1 and 3 is the heavy chain. The location of cysteine mutation on the cysteine engineered antibodies in lanes 2 and 4 is the light chain. The cysteine mutation site undergoes conjugation with the biotin-maleimide reagent.

[00211] Analysis of the ThioMab cysteine engineered antibodies of Figure 18 and a 2H9 V15C variant by LC/MS gave quantitative indication of thiol reactivity (Table 5).

Table 5 LC/MS quantitation of biotinylation of ThioMabs - Thiol reactivity

ThioMab variant	number of biotin per ThioMab
2H9 wt	0.0
2H9 L-V15C	0.6
2H9 L-V110C	0.5
2H9 H-A121C	2.0
3A5 L-V110C	1.0
3A5 H-A121C	2.0

[00212] Cysteine engineering was conducted in the constant domain, i.e. Fc region, of IgG antibodies. A variety of amino acid sites were converted to cysteine sites and the expressed mutants, i.e. cysteine engineered antibodies, were assessed for their thiol reactivity. Biotinylated 2H9 ThioMab Fc variants were assessed for thiol reactivity by HRP quantitation by capture on immobilized streptavidin in an ELISA assay (Figure 19). An ELISA assay was established to rapidly screen the Cys residues with reactive Thiol groups. As depicted in Figure 19 schematic diagram, the streptavidin-biotin interaction is monitored by probing with anti-IgG-HRP followed by measuring absorbance at 450 nm. These results confirmed 2H9-ThioFc variants V282C, A287C, A339C, S375C and S400C had moderate to highest Thiol reactivity. The extent of biotin conjugation of 2H9 ThioMab Fc variants was quantitated by LS/MS analysis as reported in Table 6. The LS/MS analysis confirmed that the A282C, S375C and S400C variants had 100% biotin conjugation and V284C and A339C had 50% conjugation, indicating the presence of a reactive cysteine thiol group. The other ThioFc variants, and the parent, wild type 2H9, had either very little biotinylation or none.

Table 6 LC/MS quantitation of biotinylation of 2H9 Fc ThioMabs

2H9 ThioMab Fc variant	% biotinylation
V273C	0
V279C	31
V282C	100
V284C	50
A287C	0
S324C	71
S337C	0
A339C	54
S375C	100
S400C	100
(wild type 2H9)	0

[00213] THIOL REACTIVITY OF THIO-4D5 FAB LIGHT CHAIN VARIANTS

[00214] Screening of a variety of cysteine engineered light chain variant Fabs of the antiErbB2 antibody 4D5 gave a number of variants with a thiol reactivity value of 0.6 and higher (Table 7), as measured by the PHESELECTOR assay of Figure 8. The thiol reactivity values of Table 7 are normalized to the heavy chain 4D5 ThioFab variant (HC-A121C) which is set at 100%, assuming complete biotinylation of HC-A121C variant, and represented as per cent values.

Table 7 Thiol reactivity per cent values of 4D5 ThioFab light chain variants

4D5 ThioFab variant	Thiol reactivity value (%)
V15C	100
V110C	95
S114C	78
S121C	75
S127C	75
A153C	82
N158C	77
V205C	78
(HC-A121C)	100
(4D5 wild type)	25

[00215] ANTIBODY-DRUG CONJUGATES

[00216] The cysteine engineered antibodies of the invention may be conjugated with any therapeutic agent, i.e. drug moiety, which can be covalently attached to the antibody through a reactive cysteine thiol group.

[00217] An exemplary embodiment of an antibody-drug conjugate (ADC) compound comprises a cysteine engineered antibody (Ab), and a drug moiety (D) wherein the antibody has one or more free cysteine amino acids, and the antibody is attached through the one or more free cysteine amino acids by a linker moiety (L) to D; the composition having Formula I:

$$Ab-(L-D)_p \qquad I$$

[00218] where p is 1, 2, 3, or 4. The number of drug moieties which may be conjugated via a thiol reactive linker moiety to an antibody molecule is limited by the number of cysteine residues which are introduced by the methods described herein. Exemplary ADC of Formula **I** therefore comprise antibodies which have 1, 2, 3, or 4 engineered cysteine amino acids.

[00219] Another exemplary embodiment of an antibody-drug conjugate compound (ADC) comprises a cysteine engineered antibody (Ab), an albumin-binding peptide (ABP) and a drug moiety (D) wherein the antibody is attached to the drug moiety by a linker moiety (L) and the antibody is attached to the albumin-binding peptide by an amide bond or a second linker moiety; the composition having Formula Ia:

$$ABP-Ab-(L-D)_p \qquad Ia$$

[00220] where p is 1, 2, 3, or 4.

[00221] The ADC compounds of the invention include those with utility for anticancer activity. In particular, the compounds include a cysteine-engineered antibody conjugated, i.e. covalently attached by a linker, to a drug moiety, i.e. toxin. When the drug is not conjugated to an antibody, the drug has a cytotoxic or cytostatic effect. The biological activity of the drug moiety is thus modulated by conjugation to an antibody. The antibody-drug conjugates (ADC) of the invention selectively deliver an effective dose of a cytotoxic agent to tumor tissue whereby greater selectivity, i.e. a lower efficacious dose, may be achieved.

[00222] DRUG MOIETIES

[00223] The drug moiety (D) of the antibody-drug conjugates (ADC) includes any

compound, moiety or group which has a cytotoxic or cytostatic effect. Drug moieties include: (i) chemotherapeutic agents, which may function as microtubulin inhibitors, mitosis inhibitors, topoisomerase inhibitors, or DNA intercalators; (ii) protein toxins, which may function enzymatically; and (iii) radioisotopes.

[00224] Exemplary drug moieties include, but are not limited to, a maytansinoid, an auristatin, a dolastatin, a trichothecene, CC1065, a calicheamicin and other enediyne antibiotics, a taxane, an anthracycline, and stereoisomers, isosteres, analogs or derivatives thereof.

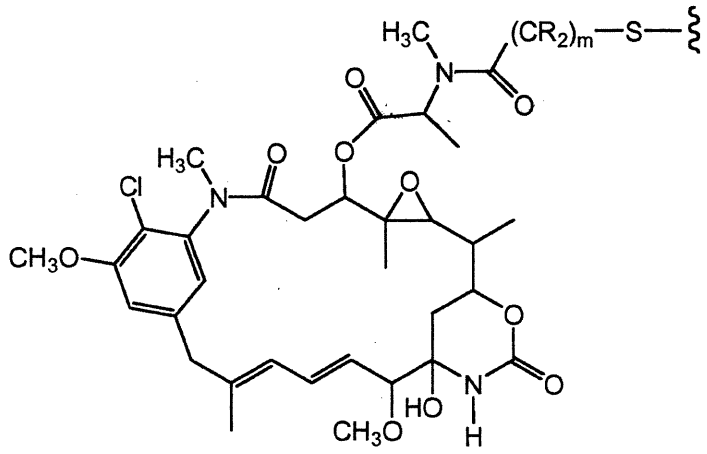
[00225] Maytansine compounds suitable for use as maytansinoid drug moieties are well known in the art, and can be isolated from natural sources according to known methods, produced using genetic engineering techniques (see Yu et al (2002) PROC. NAT. ACAD. SCI. (USA) 99:7968-7973), or maytansinol and maytansinol analogues prepared synthetically according to known methods.

[00226] 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 ansamytocin P2); C-20-hydroxy (or C-20-demethyl) +/-C-19-dechloro (US Pat. Nos. 4361650 and 4307016) (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

[00227] Exemplary maytansinoid drug moieties also include those having modifications such as: C-9-SH (US 4424219) (prepared by the reaction of maytansinol with H_2S or P_2S_5); C-14-alkoxymethyl(demethoxy/CH_2 OR)(US 4331598); C-14-hydroxymethyl or acyloxymethyl (CH_2OH or CH_2OAc) (US 4450254) (prepared from Nocardia); C-15-hydroxy/acyloxy (US 4364866) (prepared by the conversion of maytansinol by Streptomyces); C-15-methoxy (US Pat. Nos. 4313946 and 4315929) (isolated from Trewia nudlflora); C-18-N-demethyl (US Pat. Nos. 4362663 and 4322348) (prepared by the demethylation of maytansinol by Streptomyces); and 4,5-deoxy (US 4371533) (prepared by the titanium trichloride/LAH reduction of maytansinol). Many positions on maytansine compounds are known to be useful as the linkage position, depending upon the type of link. For example, for forming an ester linkage, the C-3 position having a hydroxyl group, the C-14 position modified with hydroxymethyl, the C-15 position modified with a hydroxyl group and the C-20 position having a hydroxyl group are all suitable.

[00228] The drug moiety (D) of the antibody-drug conjugates (ADC) of Formula **I**

include maytansinoids having the structure:



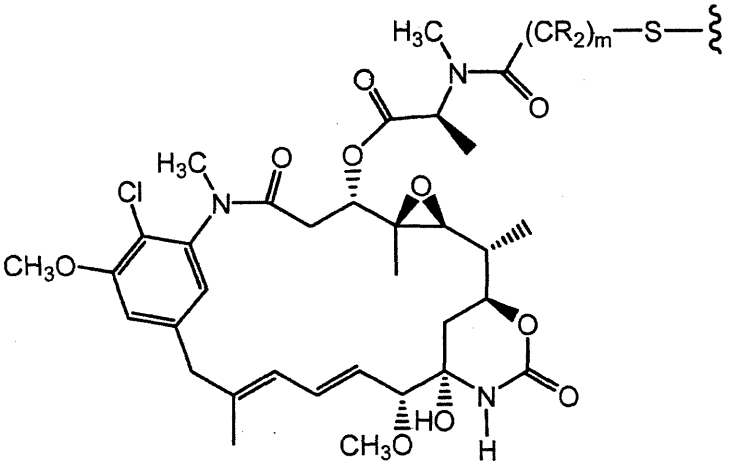
[00229] where the wavy line indicates the covalent attachment of the sulfur atom of D to a linker (L) of an antibody-drug conjugate (ADC). R may independently be H or a C_1–C_6 alkyl selected from methyl, ethyl, 1-propyl, 2-propyl, 1-butyl, 2-methyl-1-propyl, 2-butyl, 2-methyl-2-propyl, 1-pentyl, 2-pentyl, 3-pentyl, 2-methyl-2-butyl, 3-methyl-2-butyl, 3-methyl-1-butyl, 2-methyl-1-butyl, 1-hexyl, 2-hexyl, 3-hexyl, 2-methyl-2-pentyl, 3-methyl-2-pentyl, 4-methyl-2-pentyl, 3-methyl-3-pentyl, 2-methyl-3-pentyl, 2,3-dimethyl-2-butyl, and 3,3-dimethyl-2-butyl. The alkylene chain attaching the amide group to the sulfur atom may be methanyl, ethanyl, or propyl, i.e. m is 1, 2, or 3.

[00230] Maytansine compounds inhibit cell proliferation by inhibiting the formation of microtubules during mitosis through inhibition of polymerization of the microtubulin protein, tubulin (Remillard et al (1975) Science 189:1002-1005). Maytansine and maytansinoids are highly cytotoxic but their clinical use in cancer therapy has been greatly limited by their severe systemic side-effects primarily attributed to their poor selectivity for tumors. Clinical trials with maytansine had been discontinued due to serious adverse effects on the central nervous system and gastrointestinal system (Issel et al (1978) Can. Treatment. Rev. 5:199-207).

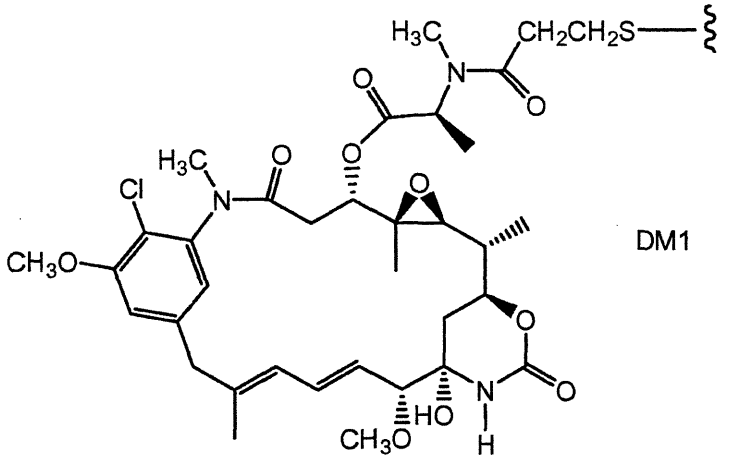
[00231] Maytansinoid drug moieties are attractive drug moieties in antibody-drug conjugates because they are: (i) relatively accessible to prepare by fermentation or chemical modification, derivatization of fermentation products, (ii) amenable to derivatization with functional groups suitable for conjugation through the non-disulfide linkers to antibodies, (iii) stable in plasma, and (iv) effective against a variety of tumor cell lines (US 2005/0169933; WO 2005/037992; US 5208020).

[00232] As with other drug moieties, all stereoisomers of the maytansinoid drug moiety are contemplated for the compounds of the invention, i.e. any combination of R and S

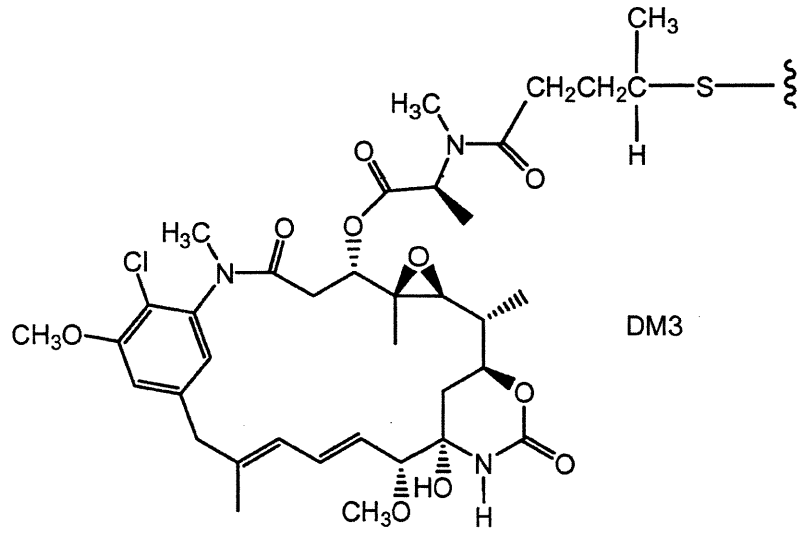
configurations at the chiral carbons of D. In one embodiment, the maytansinoid drug moiety (D) will have the following stereochemistry:



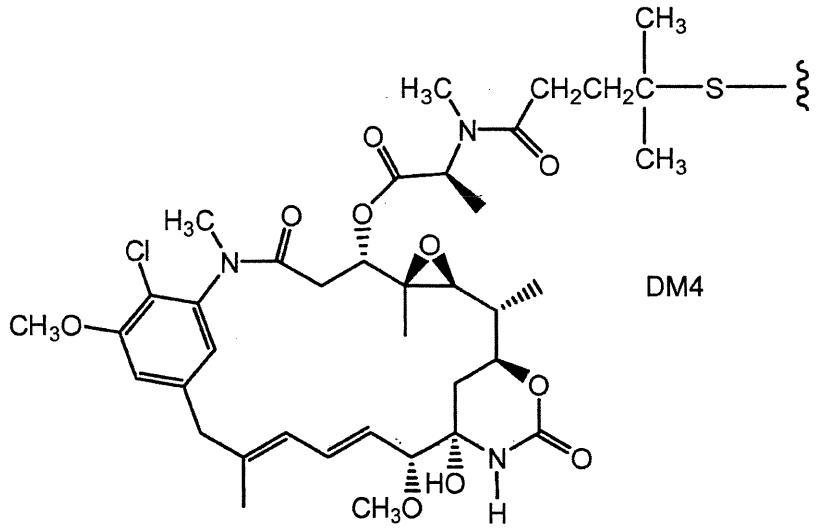
[00233] Exemplary embodiments of maytansinoid drug moieties include: DM1, $(CR_2)_m = CH_2CH_2$; DM3, $(CR_2)_m = CH_2CH_2CH(CH_3)$; and DM4, $(CR_2)_m = CH_2CH_2C(CH_3)_2$, having the structures:



DM1



DM3



DM4

[00234] The linker may be attached to the maytansinoid molecule at various positions, depending on the type of the link. For example, an ester linkage may be formed by reaction with a hydroxyl group using conventional coupling techniques. The reaction may occur at the C-3 position having a hydroxyl group, the C-14 position modified with hydroxymethyl, the C-15 position modified with a hydroxyl group, and the C-20 position having a hydroxyl group. In a preferred embodiment, the linkage is formed at the C-3 position of maytansinol or a maytansinol analogue.

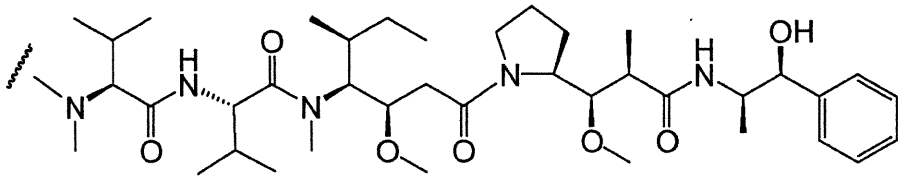
[00235] The drug moiety (D) of the antibody-drug conjugates (ADC) of Formula **I** also include dolastatins and their peptidic analogs and derivatives, the auristatins (US Patent Nos. 5635483; 5780588). Dolastatins and auristatins have been shown to interfere with microtubule dynamics, GTP hydrolysis, and nuclear and cellular division (Woyke et al (2001) Antimicrob. Agents and Chemother. 45(12):3580-3584) and have anticancer (US 5663149)

and antifungal activity (Pettit et al (1998) Antimicrob. Agents Chemother. 42:2961-2965). Various forms of a dolastatin or auristatin drug moiety may be covalently attached to an antibody through the N (amino) terminus or the C (carboxyl) terminus of the peptidic drug moiety (WO 02/088172; Doronina et al (2003) Nature Biotechnology 21(7):778-784; Francisco et al (2003) Blood 102(4):1458-1465).

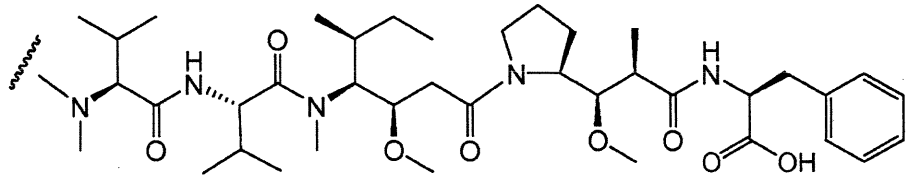
[00236] Drug moieties include dolastatins, auristatins (US 5635483; US 5780588; US 5767237; US 6124431), and analogs and derivatives thereof. Dolastatins and auristatins have been shown to interfere with microtubule dynamics, GTP hydrolysis, and nuclear and cellular division (Woyke et al (2001) Antimicrob. Agents and Chemother. 45(12):3580-3584) and have anticancer (US 5663149) 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).

[00237] Exemplary auristatin embodiments include the N-terminus linked monomethylauristatin drug moieties DE and DF, disclosed in US 7498298 and US 7659241, the disclosure of each which is expressly incorporated by reference in their entirety.

[00238] The drug moiety (D) of the antibody-drug conjugates (ADC) of Formula **I** include the monomethylauristatin drug moieties MMAE and MMAF linked through the N-terminus to the antibody, and having the structures:



MMAE



MMAF

[00239] 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. Schröder and K. Lübke, "The Peptides", volume 1, pp 76-136, 1965, Academic Press) that is well known in

the field of peptide chemistry.

[00240] The drug moiety includes calicheamicin, and analogs and derivatives thereof. 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 US 5712374; US 5714586; US 5739116; US 5767285; US 5770701, US 5770710; US 5773001; US 5877296. 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).

[00241] Protein toxins include: diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from Pseudomonas aeruginosa), ricin A chain (Vitetta et al (1987) Science, 238:1098), 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 (WO 93/21232).

[00242] Therapeutic radioisotopes include: ^{32}P, ^{33}P, ^{90}Y, ^{125}I, ^{131}I, ^{131}In, ^{153}Sm, ^{186}Re, ^{188}Re, ^{211}At, ^{212}Bi, ^{212}Pb, and radioactive isotopes of Lu.

[00243] The radioisotope or other labels may be incorporated in the conjugate in known ways (Fraker et al (1978) Biochem. Biophys. Res. Commun. 80: 49-57; "Monoclonal Antibodies in Immunoscintigraphy" Chatal, CRC Press 1989). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of a radionuclide to the antibody (WO 94/11026).

[00244] LINKERS

[00245] A "Linker" (L) is a bifunctional or multifunctional moiety which can be used to link one or more Drug moieties (D) and an antibody unit (Ab) to form antibody-drug conjugates (ADC) of Formula I. Antibody-drug conjugates (ADC) can be conveniently prepared using a Linker having reactive functionality for binding to the Drug and to the Antibody. A cysteine thiol of a cysteine engineered antibody (Ab) can form a bond with a functional group of a linker reagent, a drug moiety or drug-linker intermediate.

[00246] In one aspect, a Linker has a reactive site which has an electrophilic group that is reactive to a nucleophilic cysteine present on an antibody. The cysteine thiol of the antibody is reactive with an electrophilic group on a Linker and forms a covalent bond to a Linker. Useful electrophilic groups include, but are not limited to, maleimide and haloacetamide groups.

[00247] Cysteine engineered antibodies react with linker reagents or drug-linker intermediates, with electrophilic functional groups such as maleimide or α-halo carbonyl, according to the conjugation method at page 766 of Klussman, et al (2004), Bioconjugate Chemistry 15(4):765-773, and according to the protocol of Example 4.

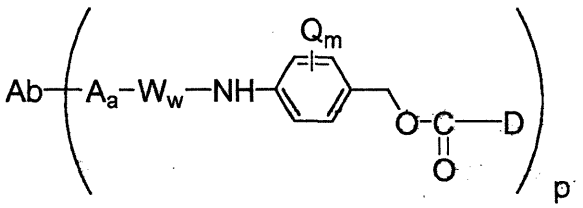
[00248] In yet another embodiment, the reactive group of a linker reagent or drug-linker intermediate contains a thiol-reactive functional group that can form a bond with a free cysteine thiol of an antibody. Examples of thiol-reaction functional groups include, but are not limited to, maleimide, α-haloacetyl, activated esters such as succinimide esters, 4-nitrophenyl esters, pentafluorophenyl esters, tetrafluorophenyl esters, anhydrides, acid chlorides, sulfonyl chlorides, isocyanates and isothiocyanates.

[00249] In another embodiment, the linker may be a dendritic type linker for covalent attachment of more than one drug moiety through a branching, multifunctional linker moiety to an antibody (Sun et al (2002) Bioorganic & Medicinal Chemistry Letters 12:2213-2215; Sun et al (2003) Bioorganic & Medicinal Chemistry 11:1761-1768; King (2002) Tetrahedron Letters 43:1987-1990). Dendritic linkers can increase the molar ratio of drug to antibody, i.e. loading, which is related to the potency of the ADC. Thus, where a cysteine engineered antibody bears only one reactive cysteine thiol group, a multitude of drug moieties may be attached through a dendritic linker.

[00250] The linker may comprise amino acid residues which links the antibody (Ab) to the drug moiety (D) of the cysteine engineered antibody-drug conjugate (ADC) of the invention. The amino acid residues may form a dipeptide, tripeptide, tetrapeptide, pentapeptide, hexapeptide, heptapeptide, octapeptide, nonapeptide, decapeptide, undecapeptide or dodecapeptide unit. Amino acid residues include those occurring naturally, as well as minor amino acids and non-naturally occurring amino acid analogs, such as citrulline.

[00251] Useful amino acid residue units can be designed and optimized in their selectivity for enzymatic cleavage by a particular enzymes, for example, a tumor-associated protease to liberate an active drug moiety. In one embodiment, an amino acid residue unit, such as valine-citrulline (vc or val-cit), is that whose cleavage is catalyzed by cathepsin B, C and D, or a plasmin protease.

[00252] A linker unit may be of the self-immolative type such as a p-aminobenzylcarbamoyl (PAB) unit where the ADC has the exemplary structure:

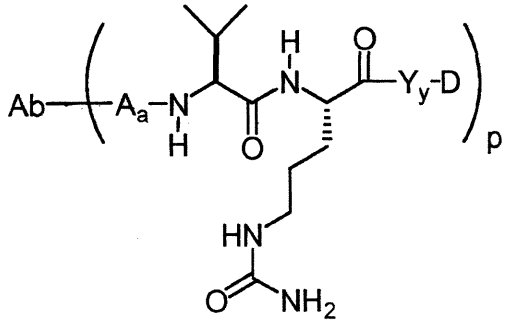


[00253] wherein Q is -C_1-C_8 alkyl, -O-(C_1-C_8 alkyl), -halogen, -nitro or -cyano; m is an integer ranging from 0-4; and p ranges from 1 to 4.

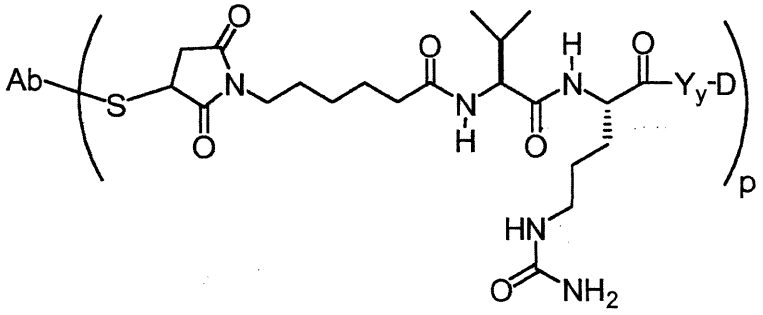
[00254] Other examples of self-immolative spacers include, but are not limited to, aromatic compounds that are electronically similar to the PAB group such as 2-aminoimidazol-5-methanol derivatives (US 7375078; Hay et al. (1999) Bioorg. Med. Chem. Lett. 9:2237) and ortho or para-aminobenzylacetals. Spacers 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 glycine (Kingsbury et al (1984) J. Med. Chem. 27:1447) are also examples of self-immolative spacer useful in ADCs.

[00255] In another embodiment, linker L may be a dendritic type linker for covalent attachment of more than one drug moiety through a branching, multifunctional linker moiety to an antibody (Sun et al (2002) Bioorganic & Medicinal Chemistry Letters 12:2213-2215; Sun et al (2003) Bioorganic & Medicinal Chemistry 11:1761-1768). Dendritic linkers can increase the molar ratio of drug to antibody, i.e. loading, which is related to the potency of the ADC. Thus, where a cysteine engineered antibody bears only one reactive cysteine thiol group, a multitude of drug moieties may be attached through a dendritic linker (WO 2004/01993; Szalai et al (2003) J. Amer. Chem. Soc. 125:15688-15689; Shamis et al (2004) J. Amer. Chem. Soc. 126:1726-1731; Amir et al (2003) Angew. Chem. Int. Ed. 42:4494-4499).

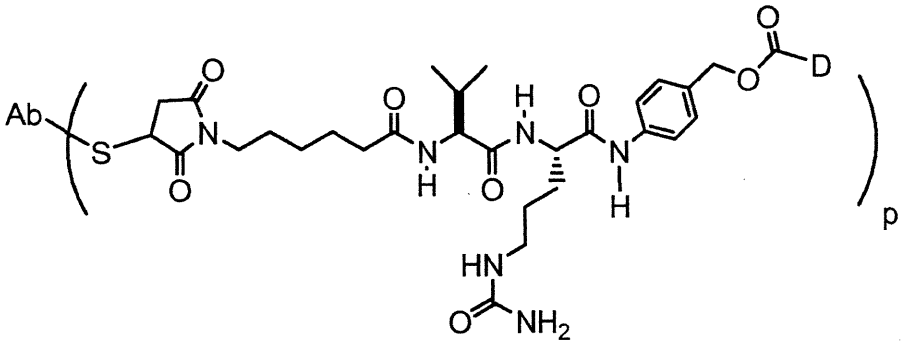
[00256] Embodiments of the Formula Ia antibody-drug conjugate compounds include (val-cit), (MC-val-cit), and (MC-val-cit-PAB):



val-cit

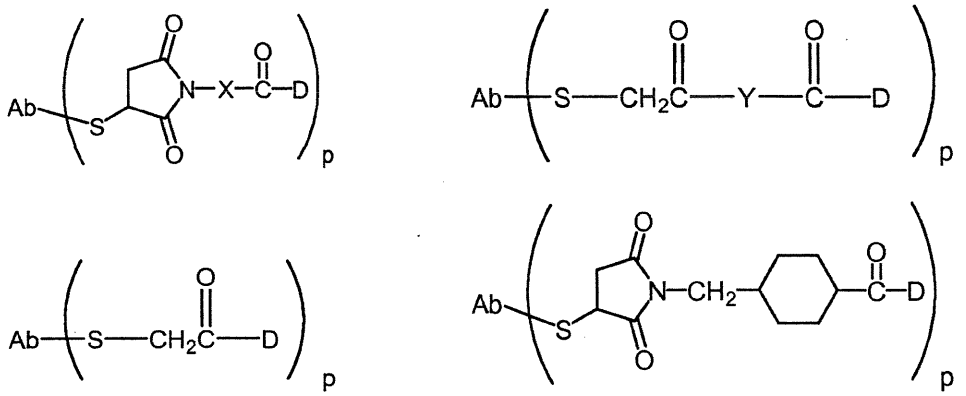


MC-val-cit

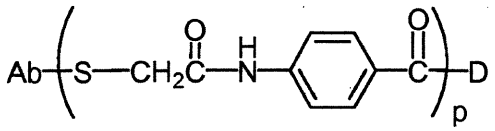


MC-val-cit-PAB

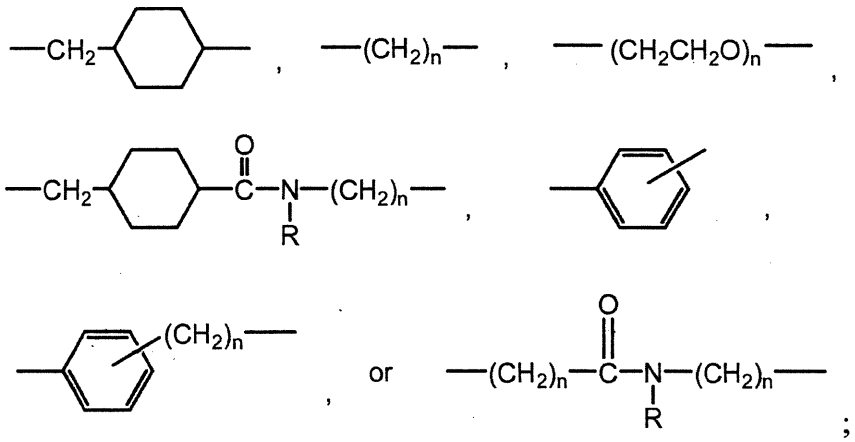
[00257] Other exemplary embodiments of the Formula **Ia** antibody-drug conjugate compounds include the structures:



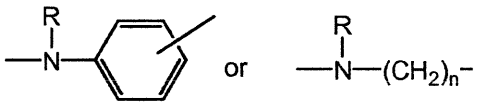
XIVd



[00258] where X is:



Y is:



[00259] and R is independently H or C_1–C_6 alkyl; and n is 1 to 12.

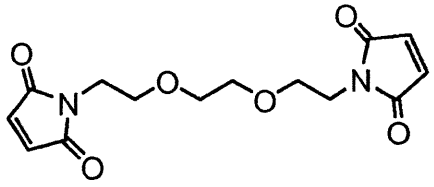
[00260] In another embodiment, a Linker has a reactive functional group which has a nucleophilic group that is reactive to an electrophilic group present on an antibody. Useful electrophilic groups on an antibody include, but are not limited to, aldehyde and ketone carbonyl groups. The heteroatom of a nucleophilic group of a Linker can react with an electrophilic group on an antibody and form a covalent bond to an antibody unit. Useful nucleophilic groups on a Linker include, but are not limited to, hydrazide, oxime, amino, hydrazine, thiosemicarbazone, hydrazine carboxylate, and arylhydrazide. The electrophilic group on an antibody provides a convenient site for attachment to a Linker.

[00261] Typically, peptide-type Linkers 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 (E. Schröder and K. Lübke (1965) "The Peptides", volume 1, pp 76-136, Academic Press) which is well known in the field of peptide chemistry.

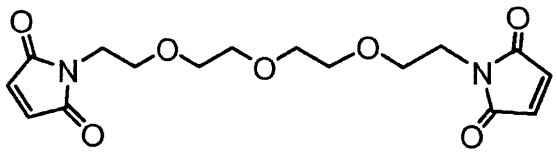
[00262] In another embodiment, the Linker may be substituted with groups which modulated solubility or reactivity. For example, a charged substituent such as sulfonate ($-SO_3^-$) or ammonium, may increase water solubility of the reagent and facilitate the coupling reaction of the linker reagent with the antibody or the drug moiety, or facilitate the coupling

reaction of Ab-L (antibody-linker intermediate) with D, or D-L (drug-linker intermediate) with Ab, depending on the synthetic route employed to prepare the ADC.

[00263] The compounds of the invention expressly contemplate, but are not limited to, ADC prepared with linker reagents: BMPEO, BMPS, EMCS, GMBS, HBVS, LC-SMCC, MBS, MPBH, SBAP, SIA, SIAB, SMCC, SMPB, SMPH, sulfo-EMCS, sulfo-GMBS, sulfo-KMUS, sulfo-MBS, sulfo-SIAB, sulfo-SMCC, and sulfo-SMPB, and SVSB (succinimidyl-(4-vinylsulfone)benzoate), and including bis-maleimide reagents: DTME, BMB, BMDB, BMH, BMOE, $BM(PEO)_3$, and $BM(PEO)_4$, which are commercially available from Pierce Biotechnology, Inc., Customer Service Department, P.O. Box 117, Rockford, IL. 61105 U.S.A, 1-800-874-3723, International +815-968-0747. See pages 467-498, 2003-2004 Applications Handbook and Catalog. Bis-maleimide reagents allow the attachment of the thiol group of a cysteine engineered antibody to a thiol-containing drug moiety, label, or linker intermediate, in a sequential or concurrent fashion. Other functional groups besides maleimide, which are reactive with a thiol group of a cysteine engineered antibody, drug moiety, label, or linker intermediate include iodoacetamide, bromoacetamide, vinyl pyridine, disulfide, pyridyl disulfide, isocyanate, and isothiocyanate.



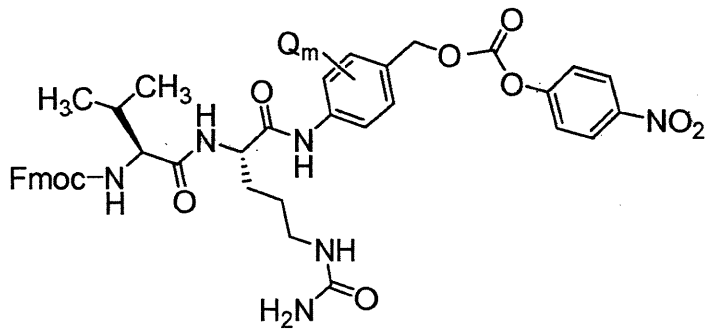
$BM(PEO)_2$



$BM(PEO)_3$

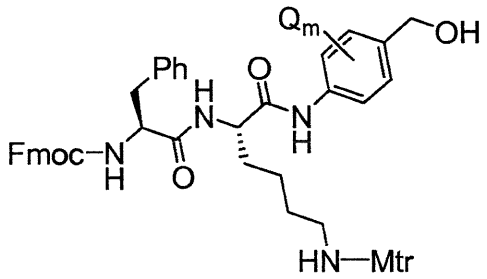
[00264] Useful linker reagents can also be obtained via other commercial sources, such as Molecular Biosciences Inc.(Boulder, CO), or synthesized in accordance with procedures described in Toki et al (2002) J. Org. Chem. 67:1866-1872; Walker, M.A. (1995) J. Org. Chem. 60:5352-5355; Frisch et al (1996) Bioconjugate Chem. 7:180-186; US 6214345; WO 02/088172; US 2003130189; US2003096743; WO 03/026577; WO 03/043583; and WO 04/032828.

[00265] An exemplary valine-citrulline (val-cit or vc) dipeptide linker reagent having a maleimide Stretcher and a para-aminobenzylcarbamoyl (PAB) self-immolative Spacer has the structure:



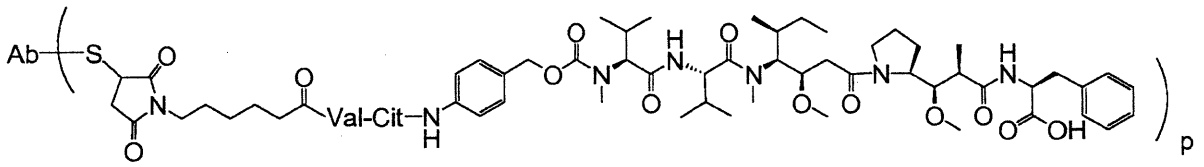
[00266] where Q is -C_1-C_8 alkyl, -O-(C_1-C_8 alkyl), -halogen, -nitro or -cyano; and m is an integer ranging from 0-4.

[00267] An exemplary phe-lys(Mtr) dipeptide linker reagent having a maleimide Stretcher unit and a p-aminobenzyl self-immolative Spacer unit can be prepared according to Dubowchik, et al. (1997) Tetrahedron Letters, 38:5257-60, and has the structure:

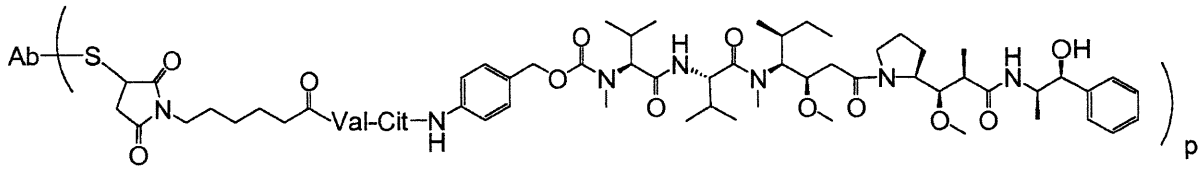


[00268] where Mtr is mono-4-methoxytrityl, Q is -C_1-C_8 alkyl, -O-(C_1-C_8 alkyl), -halogen, -nitro or -cyano; and m is an integer ranging from 0-4.

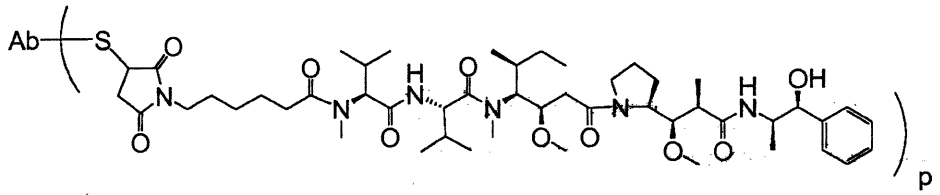
[00269] Exemplary antibody-drug conjugate compounds of the invention include:



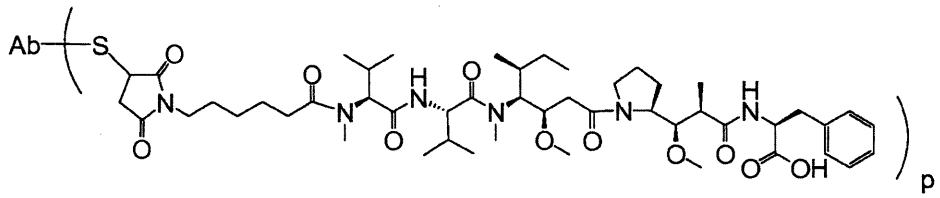
Ab-MC-vc-PAB-MMAF



Ab-MC-vc-PAB-MMAE

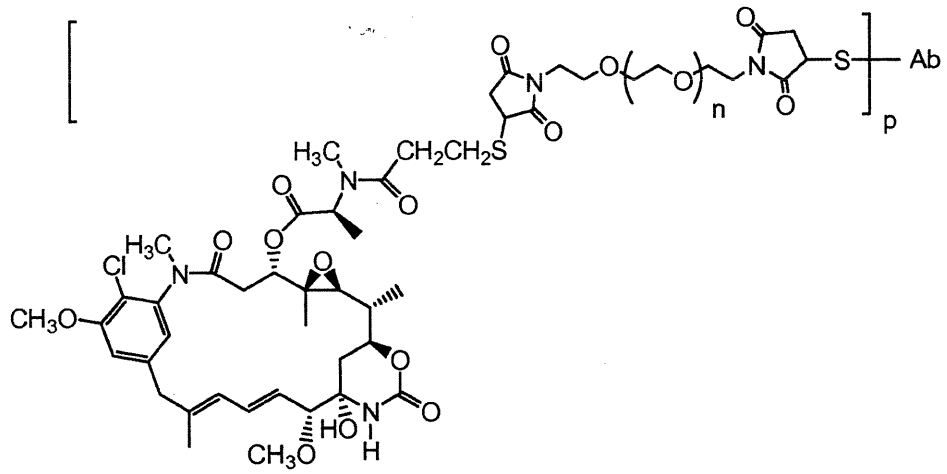


Ab-MC-MMAE



Ab-MC-MMAF

[00270] where Val is valine; Cit is citrulline; p is 1, 2, 3, or 4; and Ab is a cysteine engineered antibody. Other exemplary antibody drug conjugates where maytansinoid drug moiety DM1 is linked through a BMPEO linker to a thiol group of trastuzumab have the structure:



[00271] where Ab is a cysteine engineered antibody; n is 0, 1, or 2; and p is 1, 2, 3, or 4.

[00272] PREPARATION OF ANTIBODY-DRUG CONJUGATES

[00273] The ADC of Formula **I** may be prepared by several routes, employing organic chemistry reactions, conditions, and reagents known to those skilled in the art, including: (1) reaction of a cysteine group of a cysteine engineered antibody with a linker reagent, to form antibody-linker intermediate Ab-L, via a covalent bond, followed by reaction with an activated drug moiety D; and (2) reaction of a nucleophilic group of a drug moiety with a linker reagent, to form drug-linker intermediate D-L, via a covalent bond, followed by reaction with a cysteine group of a cysteine engineered antibody. Conjugation methods (1) and (2) may be employed with a variety of cysteine engineered antibodies, drug moieties, and

linkers to prepare the antibody-drug conjugates of Formula **I**.

[00274] Antibody cysteine thiol groups are nucleophilic and capable of reacting to form covalent bonds with electrophilic groups on linker reagents and drug-linker intermediates including: (i) active esters such as NHS esters, HOBt esters, haloformates, and acid halides; (ii) alkyl and benzyl halides, such as haloacetamides; (iii) aldehydes, ketones, carboxyl, and maleimide groups; and (iv) disulfides, including pyridyl disulfides, via sulfide exchange. Nucleophilic groups on a drug moiety include, but are not limited to: amine, thiol, hydroxyl, hydrazide, oxime, hydrazine, thiosemicarbazone, hydrazine carboxylate, and arylhydrazide groups capable of reacting to form covalent bonds with electrophilic groups on linker moieties and linker reagents.

[00275] Maytansine may, for example, be converted to May-$SSCH_3$, which can be reduced to the free thiol, May-SH, and reacted with a modified antibody (Chari et al (1992) Cancer Research 52:127-131) to generate a maytansinoid-antibody immunoconjugate with a disulfide linker. Antibody-maytansinoid conjugates with disulfide linkers have been reported (WO 04/016801; US 6884874; US 2004/039176 A1; WO 03/068144; US 2004/001838 A1; US Patent Nos. 6441163, 5208020, 5416064; WO 01/024763). The disulfide linker SPP is constructed with linker reagent N-succinimidyl 4-(2-pyridylthio) pentanoate.

[00276] Under certain conditions, the cysteine engineered antibodies may be made reactive for conjugation with linker reagents by treatment with a reducing agent such as DTT (Cleland's reagent, dithiothreitol) or TCEP (tris(2-carboxyethyl)phosphine hydrochloride; Getz et al (1999) Anal. Biochem. Vol 273:73-80; Soltec Ventures, Beverly, MA). Full length, cysteine engineered monoclonal antibodies (ThioMabs) expressed in CHO cells were reduced with about a 50 fold excess of TCEP for 3 hrs at 37 °C to reduce disulfide bonds which may form between the newly introduced cysteine residues and the cysteine present in the culture media. The reduced ThioMab was diluted and loaded onto HiTrap S column in 10 mM sodium acetate, pH 5, and eluted with PBS containing 0.3M sodium chloride. Disulfide bonds were reestablished between cysteine residues present in the parent Mab with dilute (200 nM) aqueous copper sulfate ($CuSO_4$) at room temperature, overnight. Other oxidants, i.e. oxidizing agents, and oxidizing conditions, which are known in the art may be used. Ambient air oxidation is also effective. This mild, partial reoxidation step forms intrachain disulfides efficiently with high fidelity. An approximate 10 fold excess of drug-linker intermediate, e.g. $BM(PEO)_4$-DM1 was added, mixed, and let stand for about an hour at room temperature to effect conjugation and form the ThioMab antibody-drug conjugate. The conjugation mixture was gel filtered and loaded and eluted through a HiTrap S column to

remove excess drug-linker intermediate and other impurities.

[00277] Figure 11 shows the general process to prepare a cysteine engineered antibody expressed from cell culture for conjugation. Cysteine adducts, presumably along with various interchain disulfide bonds, are reductively cleaved to give a reduced form of the antibody. The interchain disulfide bonds between paired cysteine residues are reformed under partial oxidation conditions, such as exposure to ambient oxygen. The newly introduced, engineered, and unpaired cysteine residues remain available for reaction with linker reagents or drug-linker intermediates to form the antibody conjugates of the invention. The ThioMabs expressed in mammalian cell lines result in externally conjugated Cys adduct to an engineered Cys through –S-S- bond formation. Hence the purified ThioMabs have to be treated with reduction and oxidation procedures as described in Example 11 to produce reactive ThioMabs. These ThioMabs are used to conjugate with maleimide containing cytotoxic drugs, fluorophores, and other labels.

[00278] A variety of ThioFab and ThioMab antibody-drug conjugates were prepared (Examples 4-8). Cysteine mutant hu4D5Fabv8 (V110C) was conjugated with the maytansinoid drug moiety DM1 with a bis-maleimido linker reagent BMPEO to form hu4D5Fabv8 (V110C) -BMPEO-DM1 (Example 8).

[00279] IN VITRO CELL PROLIFERATION ASSAYS

[00280] Generally, the cytotoxic or cytostatic activity of an antibody-drug conjugate (ADC) is measured by: exposing mammalian cells having receptor proteins, e.g. HER2, to the antibody of the ADC 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 were used to measure viability (proliferation), cytotoxicity, and induction of apoptosis (caspase activation) of the ADC of the invention.

[00281] The *in vitro* potency of antibody-drug conjugates was measured by a cell proliferation assay (Figures 10 and 11, Example 9). The CellTiter-Glo® Luminescent Cell Viability Assay is a commercially available (Promega Corp., Madison, WI), homogeneous assay method based on the recombinant expression of *Coleoptera* luciferase (US Patent Nos. 5583024; 5674713 and 5700670). This cell proliferation assay determines the number of viable cells in culture based on quantitation of the ATP present, an indicator of metabolically active cells (Crouch et al (1993) J. Immunol. Meth. 160:81-88; US 6602677). The CellTiter-Glo® Assay was conducted in 96 well format, making it amenable to automated high-throughput screening (HTS) (Cree et al (1995) AntiCancer Drugs 6:398-404). The homogeneous assay procedure involves adding the single reagent (CellTiter-Glo® Reagent)

directly to cells cultured in serum-supplemented medium. Cell washing, removal of medium and multiple pipetting steps are not required. The system detects as few as 15 cells/well in a 384-well format in 10 minutes after adding reagent and mixing. The cells may be treated continuously with ADC, or they may be treated and separated from ADC. Generally, cells treated briefly, i.e. 3 hours, showed the same potency effects as continuously treated cells.

[00282] The homogeneous "add-mix-measure" format results in cell lysis and generation of a luminescent signal proportional to the amount of ATP present. The amount of ATP is directly proportional to the number of cells present in culture. The CellTiter-Glo® Assay generates a "glow-type" luminescent signal, produced by the luciferase reaction, which has a half-life generally greater than five hours, depending on cell type and medium used. Viable cells are reflected in relative luminescence units (RLU). The substrate, Beetle Luciferin, is oxidatively decarboxylated by recombinant firefly luciferase with concomitant conversion of ATP to AMP and generation of photons.

[00283] IN VIVO EFFICACY

[00284] The *in vivo* efficacy of two albumin binding peptide-DM1 (maytansinoid)-antibody-drug conjugates (ADC) of the invention is measured by a high expressing HER2 transgenic explant mouse model (Figure 12, Example 10). An allograft is propagated from the Fo5 mmtv transgenic mouse which does not respond to, or responds poorly to, HERCEPTIN® therapy. Subjects were treated once with ABP-rhuFab4D5-cys(light chain)-DM1; ABP-rhuFab4D5-cys(heavy chain)-DM1; and placebo PBS buffer control (Vehicle) and monitored over 3 weeks to measure the time to tumor doubling, log cell kill, and tumor shrinkage.

[00285] ADMINISTRATION OF ANTIBODY-DRUG CONJUGATES

[00286] The antibody-drug conjugates (ADC) of the invention may be administered by any route appropriate to the condition to be treated. The ADC will typically be administered parenterally, i.e. infusion, subcutaneous, intramuscular, intravenous, intradermal, intrathecal and epidural.

[00287] PHARMACEUTICAL FORMULATIONS

[00288] Pharmaceutical formulations of therapeutic antibody-drug conjugates (ADC) of the invention are typically prepared for parenteral administration, i.e. bolus, intravenous, intratumor injection with a pharmaceutically acceptable parenteral vehicle and in a unit dosage injectable form. An antibody-drug conjugate (ADC) having the desired degree of purity is optionally mixed with pharmaceutically acceptable diluents, carriers, excipients or

stabilizers (Remington's Pharmaceutical Sciences (1980) 16th edition, Osol, A. Ed.), in the form of a lyophilized formulation or an aqueous solution.

[00289] ANTIBODY-DRUG CONJUGATE TREATMENTS

[00290] It is contemplated that the antibody-drug conjugates (ADC) of the present invention may be used to treat various diseases or disorders, e.g. characterized by the overexpression of a tumor antigen. Exemplary conditions or hyperproliferative disorders include benign or malignant tumors; leukemia and lymphoid malignancies. Others include neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, epithelial, stromal, blastocoelic, inflammatory, angiogenic and immunologic, including autoimmune, disorders.

[00291] Generally, the disease or disorder to be treated is a hyperproliferative disease such as cancer. Examples of cancer to be treated herein include, but are not limited to, carcinoma, lymphoma, blastoma, sarcoma, and leukemia or lymphoid malignancies. More particular examples of such cancers include squamous cell cancer (e.g. epithelial squamous cell cancer), lung cancer including small-cell lung cancer, non-small cell lung cancer, adenocarcinoma of the lung and squamous carcinoma of the lung, cancer of the peritoneum, hepatocellular cancer, gastric or stomach cancer including gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, hepatoma, breast cancer, colon cancer, rectal cancer, colorectal cancer, endometrial or uterine carcinoma, salivary gland carcinoma, kidney or renal cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma, anal carcinoma, penile carcinoma, as well as head and neck cancer.

[00292] Autoimmune diseases for which the ADC compounds may be used in treatment include rheumatologic disorders (such as, for example, rheumatoid arthritis, Sjögren's syndrome, scleroderma, lupus such as SLE and lupus nephritis, polymyositis/dermatomyositis, cryoglobulinemia, anti-phospholipid antibody syndrome, and psoriatic arthritis), osteoarthritis, autoimmune gastrointestinal and liver disorders (such as, for example, inflammatory bowel diseases (e.g., ulcerative colitis and Crohn's disease), autoimmune gastritis and pernicious anemia, autoimmune hepatitis, primary biliary cirrhosis, primary sclerosing cholangitis, and celiac disease), vasculitis (such as, for example, ANCA-associated vasculitis, including Churg-Strauss vasculitis, Wegener's granulomatosis, and polyarteriitis), autoimmune neurological disorders (such as, for example, multiple sclerosis, opsoclonus myoclonus syndrome, myasthenia gravis, neuromyelitis optica, Parkinson's disease, Alzheimer's disease, and autoimmune polyneuropathies), renal disorders (such as, for example, glomerulonephritis, Goodpasture's syndrome, and Berger's disease),

autoimmune dermatologic disorders (such as, for example, psoriasis, urticaria, hives, pemphigus vulgaris, bullous pemphigoid, and cutaneous lupus erythematosus), hematologic disorders (such as, for example, thrombocytopenic purpura, thrombotic thrombocytopenic purpura, post-transfusion purpura, and autoimmune hemolytic anemia), atherosclerosis, uveitis, autoimmune hearing diseases (such as, for example, inner ear disease and hearing loss), Behcet's disease, Raynaud's syndrome, organ transplant, and autoimmune endocrine disorders (such as, for example, diabetic-related autoimmune diseases such as insulin-dependent diabetes mellitus (IDDM), Addison's disease, and autoimmune thyroid disease (*e.g.*, Graves' disease and thyroiditis)). More preferred such diseases include, for example, rheumatoid arthritis, ulcerative colitis, ANCA-associated vasculitis, lupus, multiple sclerosis, Sjögren's syndrome, Graves' disease, IDDM, pernicious anemia, thyroiditis, and glomerulonephritis.

[00293] For the prevention or treatment of disease, the appropriate dosage of an ADC will depend on the type of disease to be treated, as defined above, the severity and course of the disease, whether the molecule is administered for preventive or therapeutic purposes, previous therapy, the patient's clinical history and response to the antibody, and the discretion of the attending physician. The molecule is suitably administered to the patient at one time or over a series of treatments. Depending on the type and severity of the disease, about 1 μg/kg to 15 mg/kg (e.g. 0.1-20 mg/kg) of molecule is an initial candidate dosage for administration to the patient, whether, for example, by one or more separate administrations, or by continuous infusion. A typical daily dosage might range from about 1 μg/kg to 100 mg/kg or more, depending on the factors mentioned above. An exemplary dosage of ADC to be administered to a patient is in the range of about 0.1 to about 10 mg/kg of patient weight.

[00294] For repeated administrations over several days or longer, depending on the condition, the treatment is sustained until a desired suppression of disease symptoms occurs. An exemplary dosing regimen comprises administering an initial loading dose of about 4 mg/kg, followed by a weekly maintenance dose of about 2 mg/kg of an anti-ErbB2 antibody. Other dosage regimens may be useful. The progress of this therapy is easily monitored by conventional techniques and assays.

[00295] LABELLED ANTIBODY IMAGING METHODS

[00296] In another embodiment of the invention, cysteine engineered antibodies may be labelled through the cysteine thiol with radionuclides, fluorescent dyes, bioluminescence-triggering substrate moieties, chemiluminescence-triggering substrate moieties, enzymes, and

other detection labels for imaging experiments with diagnostic, pharmacodynamic, and therapeutic applications. Generally, the labelled cysteine engineered antibody, i.e. "biomarker" or "probe", is administered by injection, perfusion, or oral ingestion to a living organism, e.g. human, rodent, or other small animal, a perfused organ, or tissue sample. The distribution of the probe is detected over a time course and represented by an image.

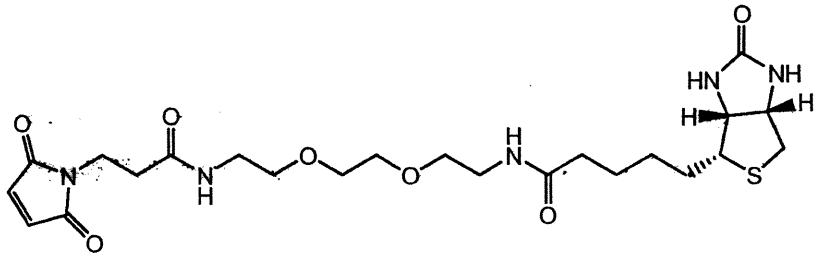
[00297] ARTICLES OF MANUFACTURE

[00298] In another embodiment of the invention, an article of manufacture, or "kit", containing materials useful for the treatment of the disorders described above is provided. The article of manufacture comprises a container and a label or package insert on or associated with the container. Suitable containers include, for example, bottles, vials, syringes, blister pack, etc. The containers may be formed from a variety of materials such as glass or plastic. The container holds an antibody-drug conjugate (ADC) composition which is effective for treating the condition and may have a sterile access port (for example the container may be an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection needle). At least one active agent in the composition is an ADC. The label or package insert indicates that the composition is used for treating the condition of choice, such as cancer. Alternatively, or additionally, the article of manufacture may further comprise a second (or third) container comprising a pharmaceutically-acceptable buffer, such as bacteriostatic water for injection (BWFI), phosphate-buffered saline, Ringer's solution and dextrose solution. It may further include other materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, needles, and syringes.

[00299] EXAMPLES

[00300] Example 1 - Preparation of Biotinylated ThioFab Phage

[00301] ThioFab-phage (5×10^{12} phage particles) were reacted with 150 fold excess of biotin-PEO-maleimide ((+)-biotinyl-3-maleimidopropionamidyl-3,6-dioxaoctanediamine, Oda et al (2001) Nature Biotechnology 19:379-382, Pierce Biotechnology, Inc.) for 3 hours at room temperature. Excess biotin-PEO-maleimide was removed from biotin-conjugated phage by repeated PEG precipitations (3-4 times). Other commercially available biotinylation reagents with electrophilic groups which are reactive with cysteine thiol groups may be used, including Biotin-BMCC, PEO-Iodoacetyl Biotin, Iodoacetyl-LC-Biotin, and Biotin-HPDP (Pierce Biotechnology, Inc.), and N^{α}-(3- maleimidylpropionyl)biocytin (MPB, Molecular Probes, Eugene, OR). Other commercial sources for biotinylation, bifunctional and multifunctional linker reagents include Molecular Probes, Eugene, OR, and Sigma, St. Louis, MO.



Biotin-PEO-maleimide

[00302] Example 2 - PHESELECTOR Assay

[00303] Bovine serum albumin (BSA), erbB2 extracellular domain (HER2) and streptavidin (100 µl of 2 µg/ml) were separately coated on Maxisorp 96 well plates. After blocking with 0.5% Tween-20 (in PBS), biotinylated and non-biotinylated hu4D5Fabv8-ThioFab-Phage ($2x10^{10}$ phage particles) were incubated for 1 hour at room temperature followed by incubation with horseradish peroxidase (HRP) labeled secondary antibody (anti-M13 phage coat protein, pVIII protein antibody). Figure 8 illustrates the PHESELECTOR Assay by a schematic representation depicting the binding of Fab or ThioFab to HER2 (top) and biotinylated ThioFab to streptavidin (bottom).

[00304] Standard HRP reaction was carried out and the absorbance was measured at 450 nm. Thiol reactivity was measured by calculating the ratio between OD_{450} for streptavidin/OD_{450} for HER2. A thiol reactivity value of 1 indicates complete biotinylation of the cysteine thiol. In the case of Fab protein binding measurements, hu4D5Fabv8 (2-20 ng) was used followed by incubation with HRP labeled goat polyclonal anti-Fab antibodies.

[00305] Example 3a - Expression and Purification of ThioFabs

[00306] ThioFabs were expressed upon induction in 34B8, a non-suppressor *E. coli* strain (Baca et al (1997) Journal Biological Chemistry 272(16):10678-84). The harvested cell pellet was resuspended in PBS (phosphate buffered saline), total cell lysis was performed by passing through a microfluidizer and the ThioFabs were purified by affinity chromatography with protein G SEPHAROSE™ (Amersham).

[00307] ThioFabs L-V15C, L-V110C, H-A88C, and H-A121C were expressed and purified by Protein-G SEPHAROSE™ column chromatography. Oligomeric-Fab was present in fractions 26 to 30, and most of the monomeric form was in fractions 31-34. Fractions consisting of the monomeric form were pooled and analyzed by SDS-PAGE along with wild type hu4D5Fabv8and analyzed on SDS-PAGE gel in reducing (with DTT or BME) and non-reducing (without DTT or BME) conditions. Gel filtration fractions of A121C-ThioFab were analyzed on non-reducing SDS-PAGE.

[00308] ThioFabs were conjugated with biotin-PEO-maleimide as described above and the biotinylated-ThioFabs were further purified by Superdex-200™ (Amersham) gel filtration chromatography, which eliminated the free biotin-PEO-maleimide and the oligomeric fraction of ThioFabs. Wild type hu4D5Fabv8 and hu4D5Fabv8 A121C-ThioFab (0.5 mg in quantity) were each and separately incubated with 100 fold molar excess of biotin-PEO-maleimide for 3 hours at room temperature and loaded onto a Superdex-200 gel filtration column to separate free biotin as well as oligomeric Fabs from the monomeric form.

[00309] Example 3b - Analysis of ThioFabs

[00310] Enzymatic digest fragments of biotinylated hu4D5Fabv8 (A121C) ThioFab and wild type hu4D5Fabv8 were analyzed by liquid chromatography electrospray ionization mass spectroscopy (LS-ESI-MS) The difference between the 48294.5 primary mass of biotinylated hu4D5Fabv8 (A121C) and the 47737.0 primary mass of wild type hu4D5Fabv8 was 557.5 mass units. This fragment indicates the presence of a single biotin-PEO-maleimide moiety ($C_{23}H_{36}N_5O_7S_2$). Table 8 shows assignment of the fragmentation values which confirms the sequence.

Table 8. LC-ESI-Mass spec analysis of biotinylated hu4D5Fabv8 ThioFab A121C after tryptic digestion

Amino acid	**b Fragment**	**y Fragment**
A (Alanine)	72	
M (Methionine)	203	2505
D (Aspartic acid)	318	2374
Y (Tyrosine)	481	2259
W (Tryptophan)	667	2096
G (Glycine)	724	1910
Q (glutamine)	852	1853
G (Glycine)	909	1725
T (Threonine)	1010	1668
L (Leucine)	1123	1567
V (Valine)	1222	1454
T (Threonine)	1323	1355
V (Valine)	1422	1254
S (Serine)	1509	1155
S (Serine)	1596	1068
C (Cysteine) + biotin	**2242**	**981**
S (Serine)	2329	335
T (Threonine)	2430	248
K (Lysine)		175

[00311] Before and after Superdex-200 gel filtration, SDS-PAGE gel analyses, with and without reduction by DTT or BME, of biotinylated ABP- hu4D5Fabv8-A121C, biotinylated ABP- hu4D5Fabv8-V110C, biotinylated double Cys ABP-hu4D5Fabv8-(V110C-A88C), and biotinylated double Cys ABP-hu4D5Fabv8-(V110C-A121C) were conducted.

[00312] Mass spectroscopy analysis (MS/MS) of of hu4D5Fabv8-(V110C)-BMPEO-DM1 (after Superdex-200 gel filtration purification): Fab+1 51607.5, Fab 50515.5. This data shows 91.2% conjugation. MS/MS analysis of hu4D5Fabv8-(V110C)-BMPEO-DM1 (reduced): LC 23447.2, LC+1 24537.3, HC (Fab) 27072.5. This data shows that all DM1 conjugation is on the light chain of the Fab.

[00313] Example 4 - Preparation of ABP-hu4D5Fabv8-(V110C)-MC-MMAE by conjugation of ABP-hu4D5Fabv8-(V110C) and MC-MMAE

[00314] The drug linker reagent, maleimidocaproyl-monomethyl auristatin E (MMAE), i.e. MC-MMAE, dissolved in DMSO, is diluted in acetonitrile and water at known concentration, and added to chilled ABP-hu4D5Fabv8-(V110C) ThioFab in phosphate buffered saline (PBS) according to US 7521541, US 7659241, and US 7498298. After about one hour, an excess of maleimide is added to quench the reaction and cap any unreacted antibody thiol groups. The reaction mixture is concentrated by centrifugal ultrafiltration and ABP-hu4D5Fabv8-(V110C)-MC-MMAE is purified and desalted by elution through G25 resin in PBS, filtered through 0.2 μm filters under sterile conditions, and frozen for storage.

[00315] Example 5 - Preparation of ABP-hu4D5Fabv8-(LC V110C)-MC-MMAF by conjugation of ABP-hu4D5Fabv8-(LC V110C) and MC-MMAF

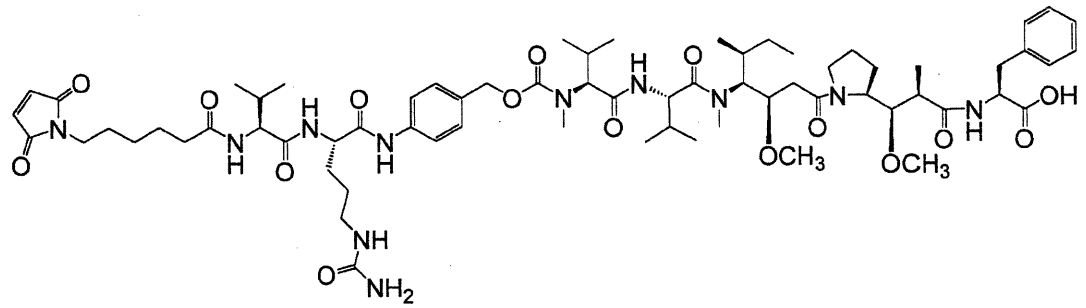
[00316] ABP-hu4D5Fabv8-(LC V110C)-MC-MMAF is prepared by conjugation of ABP-hu4D5Fabv8-(LC V110C) ThioFab and MC-MMAF following the procedure of Example 4.

[00317] Example 6 - Preparation of ABP-HC A121C-ThioFab -MC- val-cit-PAB-MMAE by conjugation of ABP-HC A121C-ThioFab and MC-val-cit-PAB-MMAE

[00318] ABP-hu4D5Fabv8-(HC A121C)-MC-val-cit-PAB-MMAE is prepared by conjugation of ABP-hu4D5Fabv8-(HC A121C) and MC-val-cit-PAB-MMAE following the procedure of Example 4.

[00319] Example 7 - Preparation of ABP-HC A121C-ThioFab -MC- val-cit-PAB-MMAF by conjugation of ABP-HC A121C-ThioFab and MC-val-cit-PAB-MMAF

[00320] ABP-hu4D5Fabv8-(HC A121C)-MC-val-cit-PAB-MMAF is prepared by conjugation of ABP-hu4D5Fabv8-(HC A121C) and MC-val-cit-PAB-MMAF following the procedure of Example 4.



MC-val-cit-PAB-MMAF

[00321] Example 8 - Preparation of hu4D5Fabv8-(LC V110C) ThioFab-BMPEO-DM1

[00322] The free cysteine on hu4D5Fabv8-(V110C) ThioFab was modified by the bis-maleimido reagent BM(PEO)3 (Pierce Chemical), leaving an unreacted maleimido group on the surface of the antibody. This was accomplished by dissolving BM(PEO)4 in a 50% ethanol/water mixture to a concentration of 10 mM and adding a tenfold molar excess of BM(PEO)3 to a solution containing hu4D5Fabv8-(V110C) ThioFab in phosphate buffered saline at a concentration of approximately 1.6 mg/ml (10 micromolar) and allowing it to react for 1 hour. Excess BM(PEO)3 was removed by gel filtration (HiTrap column, Pharmacia) in 30 mM citrate, pH 6 with 150 mM NaCl buffer. An approximate 10 fold molar excess DM1 dissolved in dimethyl acetamide (DMA) was added to the hu4D5Fabv8-(LC V110C) ThioFab-BMPEO intermediate. Dimethylformamide (DMF) may also be employed to dissolve the drug moiety reagent. The reaction mixture was allowed to react overnight before gel filtration or dialysis into PBS to remove unreacted drug. Gel filtration on S200 columns in PBS was used to remove high molecular weight aggregates and furnish purified hu4D5Fabv8-(LC V110C) ThioFab-BMPEO-DM1.

[00323] By the same protocol, hu4D5Fabv8 (HC A121C) ThioFab-BMPEO-DM1 was prepared.

[00324] Example 9 - In vitro cell proliferation assay

[00325] Efficacy of ADC were measured by a cell proliferation assay employing the following protocol (CellTiter Glo Luminiscent Cell Viability Assay, Promega Corp. Technical Bulletin TB288; Mendoza et al (2002) Cancer Res. 62:5485-5488):

1. An aliquot of 100 μl of cell culture containing about 10^4 cells (SKBR-3, BT474, MCF7 or MDA-MB-468) in medium was deposited in each well of a 96-well, opaque-walled plate.
2. Control wells were prepared containing medium and without cells.
3. ADC was added to the experimental wells and incubated for 3-5 days.
4. The plates were equilibrated to room temperature for approximately 30 minutes.
5. A volume of CellTiter-Glo Reagent equal to the volume of cell culture medium present in each well was added.
6. The contents were mixed for 2 minutes on an orbital shaker to induce cell lysis.
7. The plate was incubated at room temperature for 10 minutes to stabilize the luminescence signal.
8. Luminescence was recorded and reported in graphs as RLU = relative luminescence units.

[00326] Certain cells are seeded at 1000-2000/well (PC3 lines) or 2000-3000/well (OVCAR-3) in a 96-well plate, 50 uL/well. After one (PC3) or two (OVCAR-3) days, ADC are added in 50 μL volumes to final concentration of 9000, 3000, 1000, 333, 111, 37, 12.4, 4.1, or 1.4 ng/mL, with "no ADC" control wells receiving medium alone. Conditions are in duplicate or triplicate After 3 (PC3) or 4-5 (OVCAR-3) days, 100 μL/well Cell TiterGlo II is added (luciferase-based assay; proliferation measured by ATP levels) and cell counts are determined using a luminometer. Data are plotted as the mean of luminescence for each set of replicates, with standard deviation error bars. The protocol is a modification of the CellTiter Glo Luminiscent Cell Viability Assay (Promega):

1. Plate 1000 cells/ well of PC3/Muc16 , PC3/ neo (in 50 μL/well) of media. Ovcar3 cells should be plated at 2000 cells/ well (in 50 μL) of their media. (recipes below) Allow cells to attach overnight.

2. ADC is serially diluted 1:3 in media beginning at at working concentration 18 μg/ml (this results in a final concentration of 9 μg/ml). 50 μL of diluted ADC is added to the 50 μL of cells and media already in the well.

3. Incubate 72-96 hrs (the standard is 72 hours, but watch the 0 ug/mL concentration to stop assay when the cells are 85-95% confluent).

4. Add 100 μL/well of Promega Cell Titer Glo reagent, shake 3 min. and read on luminometer

Media: PC3/ neo and PC3/MUC16 grow in 50/50/10%FBS/glutamine/250 μg/mL G-418 OVCAR-3 grow in RPMI/20%FBS/glutamine

[00327] Example 10 - Tumor growth inhibition, in vivo efficacy in high expressing HER2 transgenic explant mice

[00328] Animals suitable for transgenic experiments can be obtained from standard commercial sources such as Taconic (Germantown, N.Y.). Many strains are suitable, but FVB female mice are preferred because of their higher susceptibility to tumor formation. FVB males were used for mating and vasectomized CD.1 studs were used to stimulate pseudopregnancy. Vasectomized mice can be obtained from any commercial supplier. Founders were bred with either FVB mice or with 129/BL6 x FVB p53 heterozygous mice. The mice with heterozygosity at p53 allele were used to potentially increase tumor formation. However, this has proven unnecessary. Therefore, some F1 tumors are of mixed strain. Founder tumors are FVB only. Six founders were obtained with some developing tumors without having litters.

[00329] Animals having tumors (allograft propagated from Fo5 mmtv transgenic mice) were treated with a single or multiple dose by IV injection of ADC. Tumor volume was assessed at various time points after injection.

[00330] Tumors arise readily in transgenic mice that express a mutationally activated form of neu, the rat homolog of HER2, but the HER2 that is overexpressed in human breast cancers is not mutated and tumor formation is much less robust in transgenic mice that overexpress nonmutated HER2 (Webster et al (1994) Semin. Cancer Biol. 5:69-76).

[00331] To improve tumor formation with nonmutated HER2, transgenic mice were produced using a HER2 cDNA plasmid in which an upstream ATG was deleted in order to prevent initiation of translation at such upstream ATG codons, which would otherwise reduce the frequency of translation initiation from the downstream authentic initiation codon of HER2 (for example, see Child et al (1999) J. Biol. Chem. 274: 24335-24341). Additionally, a chimeric intron was added to the 5' end, which should also enhance the level of expression as reported earlier (Neuberger and Williams (1988) Nucleic Acids Res. 16:6713; Buchman and Berg (1988) Mol. Cell. Biol. 8:4395; Brinster et al (1988) Proc. Natl. Acad. Sci. USA 85:836). The chimeric intron was derived from a Promega vector, Pci-neo mammalian expression vector (bp 890-1022). The cDNA 3'-end is flanked by human growth hormone exons 4 and 5, and polyadenylation sequences. Moreover, FVB mice were used because this strain is more susceptible to tumor development. The promoter from MMTV-LTR was used to ensure tissue-specific HER2 expression in the mammary gland. Animals were fed the AIN 76A diet in order to increase susceptibility to tumor formation (Rao et al (1997) Breast Cancer Res. and Treatment 45:149-158).

[00332] Example 11 - Reduction/Oxidation of ThioMabs for Conjugation

[00333] Full length, cysteine engineered monoclonal antibodies (ThioMabs) expressed in CHO cells were reduced with about a 50 fold excess of TCEP (tris(2-carboxyethyl)phosphine hydrochloride; Getz et al (1999) Anal. Biochem. Vol 273:73-80; Soltec Ventures, Beverly, MA) for 3 hrs at 37 °C. The reduced ThioMab (Figure 11) was diluted and loaded onto a HiTrap S column in 10 mM sodium acetate, pH 5, and eluted with PBS containing 0.3M sodium chloride. The eluted reduced ThioMab was treated with 200 nM aqueous copper sulfate ($CuSO_4$) at room temperature, overnight. Dehydroascorbic acid (DHAA) and ambient air oxidation are also effective oxidants.

[00334] Example 12 - Conjugation of ThioMabs

[00335] The reoxidized ThioMabs from Example 11, including thio-trastuzumab (HC A121C), thio-2H9 (A121C), and thio-3A5 (A121C), were combined with a 10 fold excess of

drug-linker intermediate, $BM(PEO)_3$-DM1, mixed, and let stand for about an hour at room temperature to effect conjugation and form the ThioMab antibody-drug conjugates, including thio-trastuzumab (HC A121C)-BMPEO-DM1, thio-2H9 (HC A121C)-BMPEO-DM1, and thio-3A5 (HC A121C)-BMPEO-DM1. The conjugation mixture was gel filtered, or loaded and eluted through a HiTrap S column to remove excess drug-linker intermediate and other impurities.

[00336] The present invention is not to be limited in scope by the specific embodiments disclosed in the examples which are intended as illustrations of a few aspects of the invention and any embodiments that are functionally equivalent are within the scope of this invention. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art and are intended to fall within the scope of the appended claims.

[00337] All patents, patent applications, and references cited throughout the specification are expressly incorporated by reference in their entirety and for all purposes.

We claim:

1. An isolated cysteine engineered antibody comprising a free cysteine amino acid and a sequence in the heavy chain selected from SEQ ID NOS 50-98 or a sequence in the light chain selected from SEQ ID NOS 99-147 wherein a cysteine in the sequence is the free cysteine amino acid.

2. The isolated cysteine engineered antibody of claim 1 prepared by a process comprising:

(i) mutagenizing a nucleic acid sequence of a parent antibody by replacing one or more amino acid residues by cysteine to encode the cysteine engineered antibody;

(ii) expressing the cysteine engineered antibody; and

(iii) isolating the cysteine engineered antibody.

3. The cysteine engineered antibody of claim 2 wherein mutagenizing comprises site-directed mutagenesis.

4. The cysteine engineered antibody of claim 2 wherein the cysteine engineered antibody is expressed on a viral particle selected from a phage or a phagemid particle.

5. The cysteine engineered antibody of claim 2 further comprising:

(i) reacting the cysteine engineered antibody with a thiol-reactive affinity reagent to generate an affinity labelled, cysteine engineered antibody; and

(ii) measuring the binding of the affinity labelled, cysteine engineered antibody to a capture media.

6. The cysteine engineered antibody of claim 5 wherein the thiol-reactive affinity reagent comprises a biotin moiety.

7. The cysteine engineered antibody of claim 5 wherein the thiol-reactive reagent comprises a maleimide moiety.

8. The cysteine engineered antibody of claim 5 wherein the capture media comprises streptavidin.

9. The cysteine engineered antibody of claim 1 wherein the cysteine engineered

antibody is a fusion protein comprising the albumin-binding peptide (ABP).

10. The cysteine engineered antibody of claim 9 wherein the ABP comprises a sequence selected from SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, and SEQ ID NO: 5.

11. The cysteine engineered antibody of claim 1 wherein the cysteine engineered antibody is selected from a monoclonal antibody, an antibody fragment, a bispecific antibody, a chimeric antibody, a human antibody, and a humanized antibody.

12. The cysteine engineered antibody of claim 11 wherein the antibody fragment is a Fab fragment.

13. The cysteine engineered antibody of claim 11 wherein the cysteine engineered antibody is an anti-HER2 antibody.

14. The cysteine engineered antibody of claim 1 wherein the cysteine engineered antibody binds to one or more of receptors (1)-(36):

(1) BMPR1B (bone morphogenetic protein receptor-type IB);

(2) E16 (LAT1, SLC7A5);

(3) STEAP1 (six transmembrane epithelial antigen of prostate);

(4) 0772P (CA125, MUC16);

(5) MPF (MPF, MSLN, SMR, megakaryocyte potentiating factor, mesothelin);

(6) Napi3b (NAPI-3B, NPTIIb, SLC34A2, solute carrier family 34 (sodium phosphate), member 2, type II sodium-dependent phosphate transporter 3b);

(7) Sema 5b (FLJ10372, KIAA1445, Mm.42015, SEMA5B, SEMAG, Semaphorin 5b Hlog, sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5B);

(8) PSCA hlg (2700050C12Rik, C530008O16Rik, RIKEN cDNA 2700050C12, RIKEN cDNA 2700050C12 gene);

(9) ETBR (Endothelin type B receptor);

(10) MSG783 (RNF124, hypothetical protein FLJ20315);

(11) STEAP2 (HGNC_8639, IPCA-1, PCANAP1, STAMP1, STEAP2, STMP, prostate cancer associated gene 1, prostate cancer associated protein 1, six transmembrane epithelial antigen of prostate 2, six transmembrane prostate protein);

(12) TrpM4 (BR22450, FLJ20041, TRPM4, TRPM4B, transient receptor potential cation channel, subfamily M, member 4);

(13) CRIPTO (CR, CR1, CRGF, CRIPTO, TDGF1, teratocarcinoma-derived growth factor);

(14) CD21 (CR2 (Complement receptor 2) or C3DR (C3d/Epstein Barr virus receptor) or Hs.73792);

(15) CD79b (CD79B, CD79β, IGb (immunoglobulin-associated beta), B29);

(16) FcRH2 (IFGP4, IRTA4, SPAP1A (SH2 domain containing phosphatase anchor protein 1a), SPAP1B, SPAP1C);

(17) HER2;

(18) NCA;

(19) MDP;

(20) IL20Rα;

(21) Brevican;

(22) EphB2R;

(23) ASLG659;

(24) PSCA;

(25) GEDA;

(26) BAFF-R (B cell -activating factor receptor, BLyS receptor 3, BR3;

(27) CD22 (B-cell receptor CD22-B isoform);

(28) CD79a (CD79A, CD79α, immunoglobulin-associated alpha, a B cell-specific protein);

(29) CXCR5 (Burkitt's lymphoma receptor 1, a G protein-coupled receptor);

(30) HLA-DOB (Beta subunit of MHC class II molecule (Ia antigen);

(31) P2X5 (Purinergic receptor P2X ligand-gated ion channel 5);

(32) CD72 (B-cell differentiation antigen CD72, Lyb-2);

(33) LY64 (Lymphocyte antigen 64 (RP105), type I membrane protein of the leucine rich repeat (LRR) family);

(34) FcRH1 (Fc receptor-like protein 1);

(35) IRTA2 (Immunoglobulin superfamily receptor translocation associated 2); and

(36) TENB2 (putative transmembrane proteoglycan).

15. The cysteine engineered antibody of claim 1 wherein the antibody is covalently attached to a capture label, a detection label, a drug moiety, or a solid support.

16. The cysteine engineered antibody of claim 15 wherein the antibody is covalently attached to a biotin capture label.

17. The cysteine engineered antibody of claim 15 wherein the antibody is covalently attached to a fluorescent dye detection label.

18. The cysteine engineered antibody of claim 17 wherein the fluorescent dye is selected from a fluorescein type, a rhodamine type, dansyl, Lissamine, a cyanine, a phycoerythrin, Texas Red, and an analog thereof.

19. The cysteine engineered antibody of claim 15 wherein the antibody is covalently attached to a radionuclide detection label selected from ^{3}H, ^{11}C, ^{14}C, ^{18}F, ^{32}P, ^{35}S, ^{64}Cu, ^{68}Ga, ^{86}Y, ^{89}Zr, ^{99}Tc, ^{111}In, ^{123}I, ^{124}I, ^{125}I, ^{131}I, ^{133}Xe, ^{177}Lu, ^{211}At, and ^{213}Bi.

20. The cysteine engineered antibody of claim 15 wherein the antibody is covalently attached to a detection label by a chelating ligand.

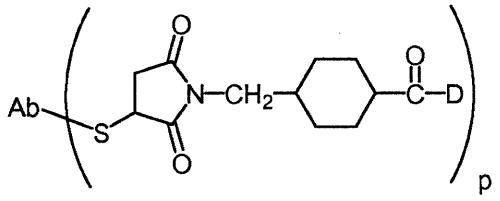
21. The cysteine engineered antibody of claim 20 wherein the chelating ligand is selected from DOTA, DOTP, DOTMA, DTPA and TETA.

22. The cysteine engineered antibody of claim 15 wherein the antibody is covalently attached to a drug moiety selected from a maytansinoid, an auristatin, a dolastatin, a trichothecene, CC1065, a calicheamicin, enediyne antibiotics, a taxane, and an anthracycline to form an antibody-drug conjugate having Formula I:

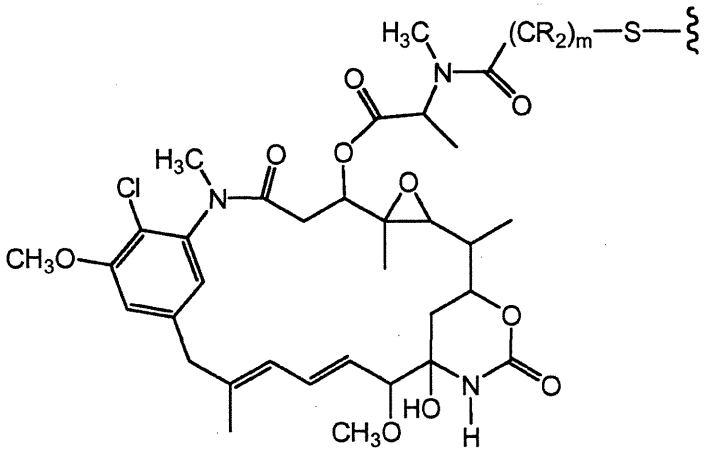
$$Ab\text{–}(L\text{–}D)_p \qquad \text{I}$$

where Ab is the antibody, L is a linker, D is the drug moiety, and p is 1, 2, 3, or 4.

23. The cysteine engineered antibody of claim 22 wherein the antibody-drug conjugate has the structure:



24. The cysteine engineered antibody of claim 22 wherein D is a maytansinoid having the structure:

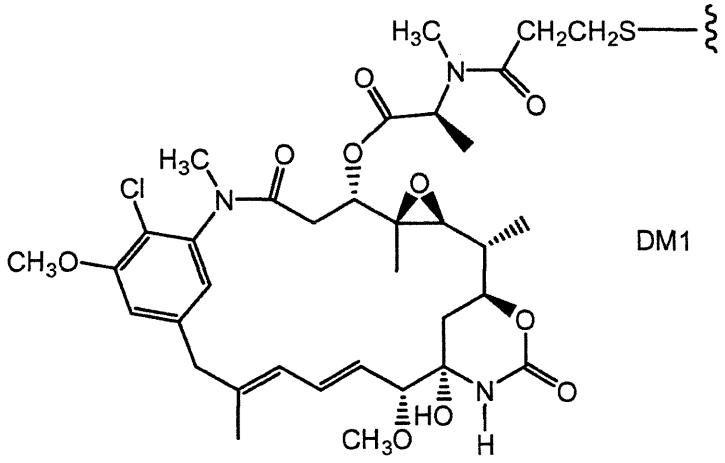


wherein the wavy line indicates the covalent attachment of the sulfur atom of D to the linker;

R is independently selected from H, methyl, ethyl, 1-propyl, 2-propyl, 1-butyl, 2-methyl-1-propyl, 2-butyl, 2-methyl-2-propyl, 1-pentyl, 2-pentyl, 3-pentyl, 2-methyl-2-butyl, 3-methyl-2-butyl, 3-methyl-1-butyl, 2-methyl-1-butyl, 1-hexyl, 2-hexyl, 3-hexyl, 2-methyl-2-pentyl, 3-methyl-2-pentyl, 4-methyl-2-pentyl, 3-methyl-3-pentyl, 2-methyl-3-pentyl, 2,3-dimethyl-2-butyl, and 3,3-dimethyl-2-butyl; and

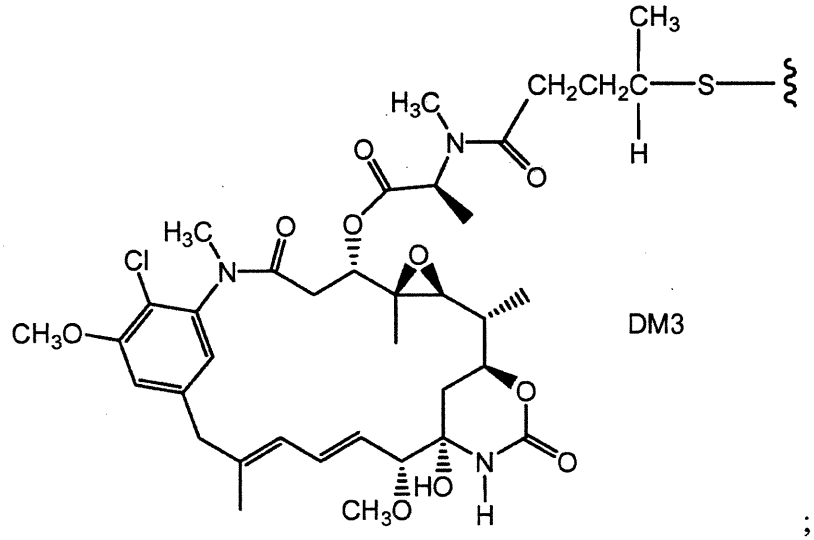
m is 1, 2, or 3.

25. The cysteine engineered antibody of claim 24 wherein D is selected from the structures:



DM1

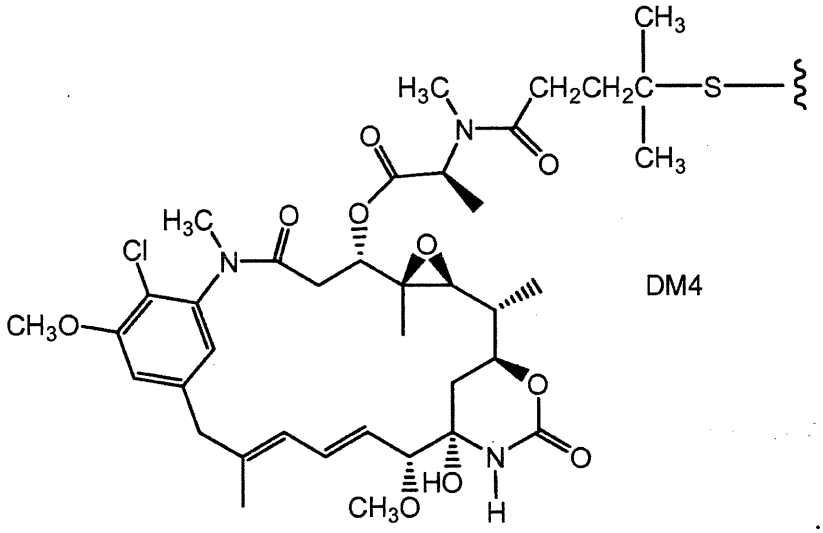
;



DM3

;

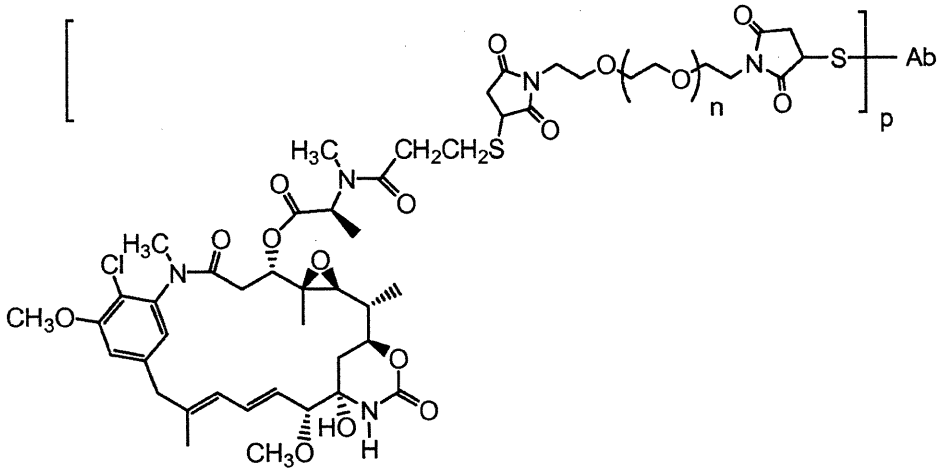
and



DM4

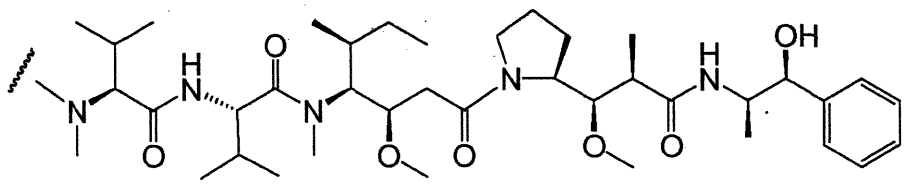
.

26. The cysteine engineered antibody of claim 25 having the structure:

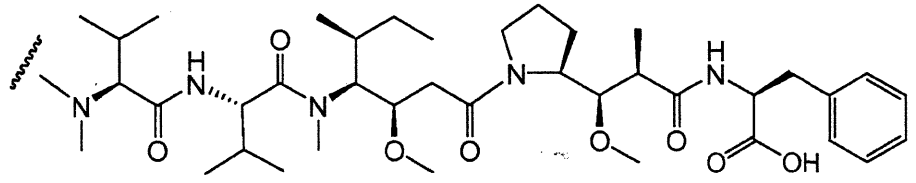


wherein n is 0, 1, or 2.

27. The cysteine engineered antibody of claim 22 wherein D is a monomethylauristatin drug moiety MMAE or MMAF having the structures:

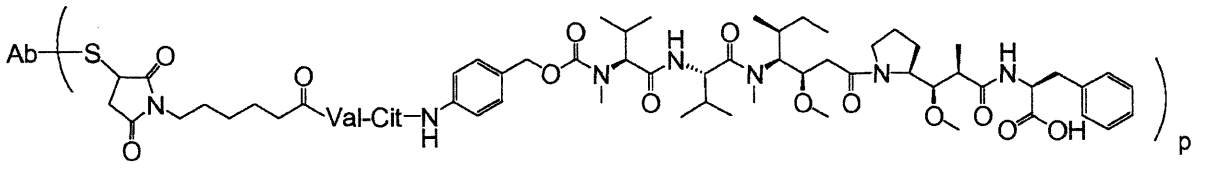


MMAE

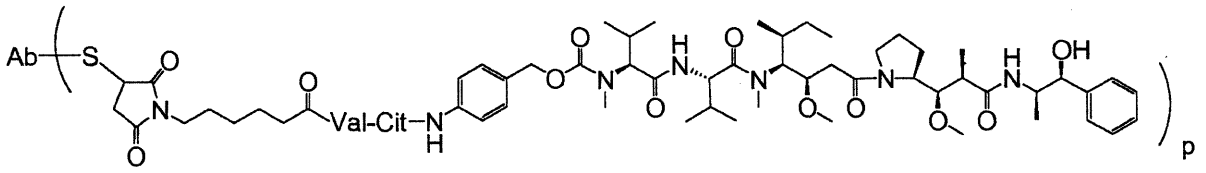


MMAF .

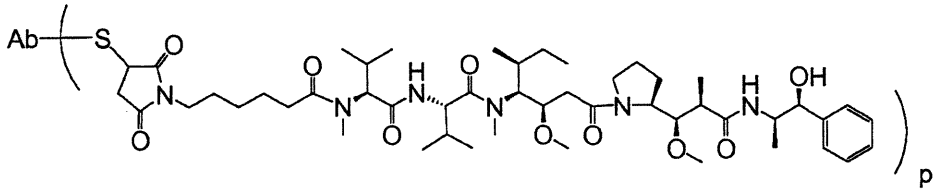
28. The cysteine engineered antibody of claim 27 wherein the antibody-drug conjugate is selected from the structures:



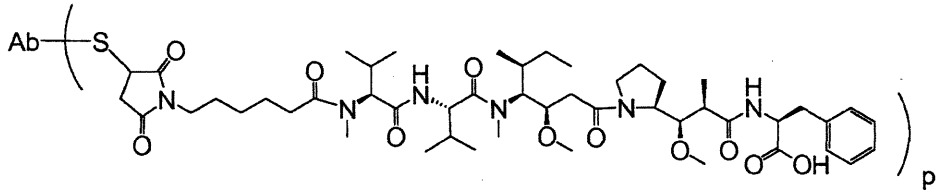
Ab-MC-vc-PAB-MMAF



Ab-MC-vc-PAB-MMAE



Ab-MC-MMAE



where Val is valine; Cit is citrulline; and p is 1, 2, 3, or 4.

Sequence Listing

<110> GENENTECH, INC.
Bhakta, Sunil
Junutula, Jagath Reddy

<120> CYSTEINE ENGINEERED ANTIBODIES AND CONJUGATES

<130> P4444R1-WO

<141> 2011-06-07

<150> US 61/352,728
<151> 2010-06-08

<160> 147

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Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp Glu Asp Asp Phe
20 25 30

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<211> 20
<212> PRT
<213> Artificial sequence

<220>
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Gln Arg Leu Met Glu Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu
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Trp Glu Asp Asp Phe
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<210> 3
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<212> PRT
<213> Artificial sequence

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<223> chemically synthesized

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Trp Glu Asp Asp Phe
20

<210> 4
<211> 18

<212> PRT
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Arg Leu Ile Glu Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp
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Glu Asp Asp

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<212> PRT
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Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys
20 25 30

Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
35 40 45

Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr
50 55 60

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser
65 70 75

Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Cys Glu Asp
80 85 90

Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr
95 100 105

Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
110 115 120

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
125 130 135

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
140 145 150

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Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
                155                 160                 165

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                170                 175                 180

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
                185                 190                 195

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
                200                 205                 210

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
                215                 220                 225

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
                230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
                260                 265                 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
                275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
                290                 295                 300

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
                305                 310                 315

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
                320                 325                 330

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
                335                 340                 345

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
                350                 355                 360

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                365                 370                 375

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
                380                 385                 390

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
                395                 400                 405

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                410                 415                 420

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
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His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys
             20                  25                  30

Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
             35                  40                  45

Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr
             50                  55                  60

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser
             65                  70                  75

Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
             80                  85                  90

Thr Ala Val Tyr Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr
             95                 100                 105

Ala Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
            110                 115                 120

Cys Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
            125                 130                 135

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
            140                 145                 150

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
            155                 160                 165

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
            170                 175                 180

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            185                 190                 195

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
            200                 205                 210

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
            215                 220                 225

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
            230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            260                 265                 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
            275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
            290                 295                 300
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Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
305 310 315

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
320 325 330

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
335 340 345

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
350 355 360

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
365 370 375

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
380 385 390

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
395 400 405

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
410 415 420

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
425 430 435

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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1 5 10 15

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn
20 25 30

Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
35 40 45

Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser
50 55 60

Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile
65 70 75

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
80 85 90

His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu
95 100 105

Ile Lys Arg Thr Cys Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
110 115 120

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Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
                125                 130                 135

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
                140                 145                 150

Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
                155                 160                 165

Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
                170                 175                 180

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu
                185                 190                 195

Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn
                200                 205                 210

Arg Gly Glu Cys
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  1   5   10

<210> 12
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1 5 10

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Leu Val Thr Val Ser Ser Cys Ser Thr Lys Gly Pro Ser
1 5 10

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<400> 14
Leu Val Thr Val Ser Ser Ala Cys Thr Lys Gly Pro Ser
1 5 10

<210> 15
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1 5 10

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1 5 10

<210> 20
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Thr Cys Ala Ala Pro Cys Val Phe Ile Phe Pro Pro
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Phe Ile Phe Pro Pro Cys Asp Glu Gln Leu Lys
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<211> 11
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Phe Tyr Pro Arg Glu Cys Lys Val Gln Trp Lys
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Ser Tyr Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
             35                  40                  45

Glu Trp Val Gly Phe Ile Asn Pro Ser Thr Gly Tyr Thr Asp Tyr
             50                  55                  60

Asn Gln Lys Phe Lys Asp Arg Phe Thr Ile Ser Ala Asp Thr Ser
             65                  70                  75

Lys Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
             80                  85                  90

Thr Ala Val Tyr Tyr Cys Thr Arg Arg Pro Lys Ile Pro Arg His
             95                 100                 105

Ala Asn Val Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
            110                 115                 120

Cys Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
            125                 130                 135

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
            140                 145                 150

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
            155                 160                 165

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
            170                 175                 180

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
            185                 190                 195

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
            200                 205                 210

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
            215                 220                 225

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
            230                 235                 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            260                 265                 270

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
            275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
            290                 295                 300

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
            305                 310                 315
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 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
                 320                 325                 330

 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
                 335                 340                 345

 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
                 350                 355                 360

 Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
                 365                 370                 375

 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
                 380                 385                 390

 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
                 395                 400                 405

 Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                 410                 415                 420

 Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
                 425                 430                 435

 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                 440                 445                 450

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 Glu Val His Asn Ala Lys Thr Lys Pro Arg
                 20                  25

<210> 30
<211> 25
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 Glu Val His Asn Ala Lys Thr Lys Pro Arg
                 20                  25

<210> 31
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1 5 10 15

Glu Val His Asn Ala Lys Thr Lys Pro Arg
20 25

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1 5 10 15

Glu Cys His Asn Ala Lys Thr Lys Pro Arg
20 25

<210> 33
<211> 25
<212> PRT
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<220>
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His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
1 5 10 15

Glu Val His Asn Cys Lys Thr Lys Pro Arg
20 25

<210> 34
<211> 11
<212> PRT
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<210> 35
<211> 13
<212> PRT
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1 5 10

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1 5 10

<210> 38
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<212> PRT
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1 5 10

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Gln Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr
20 25 30

Asn Asp Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys
35 40 45

Leu Glu Trp Met Gly Tyr Ile Asn Tyr Ser Gly Tyr Thr Thr Tyr
50 55 60

Asn Pro Ser Leu Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser
65 70 75

Lys Asn Gln Phe Phe Leu His Leu Asn Ser Val Thr Thr Glu Asp
80 85 90

Thr Ala Thr Tyr Tyr Cys Ala Arg Trp Asp Gly Gly Leu Thr Tyr
95 100 105

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Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Cys Ser Thr Lys
                110                 115                 120

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
                125                 130                 135

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
                140                 145                 150

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                155                 160                 165

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
                170                 175                 180

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
                185                 190                 195

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
                200                 205                 210

Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
                215                 220                 225

Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
                230                 235                 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
                260                 265                 270

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
                275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
                290                 295                 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
                305                 310                 315

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                320                 325                 330

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
                335                 340                 345

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
                350                 355                 360

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
                365                 370                 375

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                380                 385                 390

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
                395                 400                 405

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
                410                 415                 420
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Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
425 430 435

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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1 5 10

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1 5 10 15

Pro Ser Val Phe Pro Leu
20

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<211> 14
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<220>
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<400> 43
His Thr Phe Pro Cys Val Leu Gln Ser Ser Gly Leu Tyr Ser
1 5 10

<210> 44
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<220>
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<400> 44
His Thr Phe Pro Ala Cys Leu Gln Ser Ser Gly Leu Tyr Ser
1 5 10

<210> 45
<211> 11
<212> PRT
<213> Artificial sequence

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<400> 45
Phe Leu Ser Val Ser Cys Gly Gly Arg Val Thr
1 5 10

<210> 46
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<212> PRT
<213> Artificial sequence

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Gln Lys Pro Gly Asn Cys Pro Arg Leu Leu Ile
1 5 10

<210> 47
<211> 11
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<400> 47
Glu Ile Lys Arg Thr Cys Ala Ala Pro Ser Val
1 5 10

<210> 48
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Phe Tyr Pro Arg Glu Cys Lys Val Gln Trp Lys
1 5 10

<210> 49
<211> 11
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<220>
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Val Thr Glu Gln Asp Cys Lys Asp Ser Thr Tyr
1 5 10

<210> 50
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Glu Val Gln Cys Val Glu Ser Gly Gly
1 5

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1 5 10

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1 5 10

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<212> PRT
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