CL AND/OR CH1 MUTATED ANTIBODIES FOR DRUG CONJUGATION

FIELD OF THE INVENTION

The present invention relates to antibodies which include a modified constant region so as to permit conjugation of the antibody to a payload such as a radionuclide, a polymer, a cytotoxic agent or a drug moiety. Preferably the conjugated antibodies yield a desired payload to antibody ratio. Aspects of the invention relate to payload-antibody conjugates.

BACKGROUND TO THE INVENTION

Antibody-drug conjugates (ADCs) are a class of targeted therapies which combine the specificity of antibodies with the cytotoxicity of cytotoxic therapeutics. ADCs are primarily considered candidates for the treatment of various cancers. ADCs comprise an antibody linked to a therapeutic drug.

One problem with development of ADCs is the conjugation technology used; if drugs are conjugated non-selectively to cysteine or lysine residues in the antibody, then this can result in a heterogeneous mixture of ADCs. This approach leads to suboptimal safety and efficacy properties and makes optimization of the biological, physical and pharmacological properties of an ADC challenging. In particular, heterogeneity can be a problem with respect to the distribution of cytotoxins (that is, site of attachment), and the loading of cytotoxins (that is, number of drug molecules per antibody).

Heterogeneity presents safety concerns since high drug / antibody ratio (DAR) species can have poor binding to their target and increase risks of off-target toxicity. Low drug loading species are less active (DAR 1) or inactive (DAR 0). As the number of drugs per mAb decreases, the pharmacokinetic properties of the ADC improves (Hamblett, Clin. Cancer Res. 2004, 10, 7063-7070). Furthermore, heterogeneity of ADCs leads to challenges associated with consistent manufacturing and analytical testing.

Site-selective conjugation (SSC) would presumably improve ADCs' safety and efficacy, and thus, results in higher ADC quality. Junutula et al Nature Biotech 2008 report that same activity is achieved with half ADC dose in a SSC-ADC compared to control. Thus, ADC homogeneity will improve Therapeutic Index (TI is the ratio between

maximum tolerated dose and effective dose. (TI = TD50/ED50)). Furthermore, higher DAR homogeneity would result in:

- Simpler product characterization for regulatory filings, better defined product specifications and
- Reduced off-target or bystander toxicity
- Potentially more controlled pharmacology (fewer species to reckon on)
- Potentially reduce dosage requirements (per gram) to achieve similar pharmacological effect – - Reduced potential incidence of side-effects (e.g. immunogenicity, toxicity, etc.)
- Reduced costs due to higher conjugation yields and reduced dosage (required amount of ADC to be administered)

However, simply making antibodies with modified residues may result in unforeseen effects, such as changes to antibody aggregation propensity, solubility, or efficacy. The present applicants therefore developed a rational screening process to determine which residues may be modified. In selected embodiments, the modification achieves an antibody suitable for conjugation to a payload (such as a drug) to give a DAR of around 2.

SUMMARY OF THE INVENTION

According to a first aspect of the invention, there is provided an antibody, or a fragment or derivative thereof, having a variable region which binds a target molecule, and a constant region, wherein the constant region comprises one or more mutations introducing a site specific conjugation site selected so as to permit conjugation of the antibody, fragment, or derivative to a payload, wherein the one or more mutations include a mutation at light chain position 180 (positional numbering).

The antibody may comprise two introduced site specific conjugation sites.

In preferred embodiments, the wild type residue at position 180 is T. The mutated residue at position 180 is preferably selected from cysteine, lysine, glutamine, or a non-natural amino acid, and is most preferably cysteine.

In certain embodiments, the antibody may further comprise one or more mutations selected from light chain (LC) S208, LC S171, LC S182, LC A184, LC V191, LC S202, LC S203, LC T206, heavy chain (HC) S160, HC T190, HC S443, HC S447, HC S139, HC S168, HC V170, HC V176, HC T200, HC S445 according to a positional numbering convention. Preferred mutations are at one or more positions selected from residues 206 (light chain), 160, 190, 443, and 447 (heavy chain) (positional numbering). The mutated residues are preferably independently selected from cysteine, lysine, glutamine, or a non-natural amino acid, and is most preferably cysteine. For example, the modification of antibodies with non-natural amino acids is described in WO2013/185115.

According to a further aspect of the invention, there is provided an antibody, or a fragment or derivative thereof, having a variable region which binds a target molecule, and a constant region, wherein the constant region comprises one or more mutations introducing a site specific conjugation site selected so as to permit conjugation of the antibody, fragment, or derivative to a payload, wherein the antibody comprises the amino acid sequence of SEQ ID No 33; where X is selected from C, K, Q, or a non-natural amino acid. The antibody may further comprise one or more amino acid sequences selected from the group consisting of SEQ ID No 22-32 and SEQ ID No 34-40; where each X is independently selected from C, K ,Q, or a non-natural amino acid, and is most preferably cysteine..

According to a second aspect of the invention, there is provided an antibody, or a fragment or derivative thereof, having a variable region which binds a target molecule, and a constant region, wherein the constant region comprises one or more mutations introducing a site specific conjugation site selected so as to permit conjugation of the antibody, fragment, or derivative to a payload, wherein the one or more mutations include a mutation at light chain position 208 (positional numbering).

The antibody may comprise two introduced site specific conjugation sites.

In preferred embodiments, the wild type residue at position 208 is S. The mutated residue at position 208 is preferably selected from cysteine, lysine, glutamine, or a non-natural amino acid, and is most preferably cysteine.

In certain embodiments, the antibody may further comprise one or more mutations selected from light chain (LC) T180, LC S171, LC S182, LC A184, LC V191, LC S202, LC S203, LC T206, heavy chain (HC) S160, HC T190, HC S443, HC S447, HC S139, HC S168, HC V170, HC V176, HC T200, HC S445 according to a positional numbering convention. Preferred mutations are at one or more positions selected from residues 180, 206 (light chain), 160, 190, 443, and 447 (heavy chain) (positional numbering). The mutated residues are preferably independently selected from cysteine, lysine, glutamine, or a non-natural amino acid, and is most preferably cysteine. For example, the modification of antibodies with non-natural amino acids is described in WO2013/185115.

According to a further aspect of the invention, there is provided an antibody, or a fragment or derivative thereof, having a variable region which binds a target molecule, and a constant region, wherein the constant region comprises one or more mutations introducing a site specific conjugation site selected so as to permit conjugation of the antibody, fragment, or derivative to a payload, wherein the antibody comprises the amino acid sequence of SEQ ID No 40; where X is selected from C, K, Q, or a non-natural amino acid. The antibody may further comprise one or more amino acid sequences selected from the group consisting of SEQ ID No 22-39; where each X is independently selected from C, K ,Q, or a non-natural amino acid, and is most preferably cysteine.

The invention further provides an isolated or engineered antibody, or a fragment or derivative thereof, having a variable region which binds a target molecule, and a constant region, wherein the constant region comprises one or more mutations introducing a site specific conjugation site by:

a) substituting a residue selected from the group consisting of light chain (LC) T180, LC S208, LC S171, LC S182, LC A184, LC V191, LC S202, LC S203, LC T206, heavy chain (HC) S160, HC T190, HC S443, HC S447, HC S139, HC S168, HC V170, HC V176, HC T200, HC S445 according to a positional numbering convention
with a cysteine residue, a lysine residue, a glutamine residue or a non-natural amino acid; or

b) introducing a cysteine substitution at a residue selected from the group consisting of LC T180C, LC S208C, LC S171C, LC S182C, LC A184C, LC V191C, LC

S202C, LC S203C, LC T206C, HC S160C, HC T190C, HC S443C, HC S447C, HC S139C, HC S168C, HC V170C, HC V176C, HC T200C, HC S445C according to a positional numbering convention; or

c) comprising at least one amino acid sequence selected from the group consisting of: SEQ ID No 22 to 40, wherein X is a cysteine residue, a lysine residue, a glutamine residue or a non-natural amino acid; or

d) comprising at least one amino acid sequence selected from the group consisting of: SEQ ID No 22 to 40, wherein X is a cysteine residue.

The invention still further provides an antibody, or a fragment or derivative thereof, having a variable region which binds a target molecule, and a constant region, wherein the constant region comprises one or more mutations introducing a site specific conjugation site selected so as to permit conjugation of the antibody, fragment, or derivative to a payload, wherein the antibody includes a light chain constant region comprising the amino acid sequence of residues 109-214 of SEQ ID No 14.

The invention also provides an antibody, or a fragment or derivative thereof, having a variable region which binds a target molecule, and a constant region, wherein the constant region comprises one or more mutations introducing a site specific conjugation site selected so as to permit conjugation of the antibody, fragment, or derivative to a payload, wherein the antibody includes a light chain constant region comprising the amino acid sequence of residues 109-214 of SEQ ID No 21.

The following features may apply to all aspects of the invention. The antibody is preferably selected from the group comprising IgG1, IgG2, IgG3, and IgG4. The light chain may either be kappa or lambda light chain, the light chain constant region either C kappa (Ck) or C lambda (Cλ). The constant region may comprise at least a portion of an IgG1 constant region, preferably one or more, preferably all, of the Ck , CH1 and CH3 domains of the IgG1 constant region. The antibody may be selected from the group consisting of Fabs, bi specific antibody fragments (tandem scFv-Fc, scFv-Fc knobs-into-holes, scFv-Fc-scFv, F(ab')2, Fab-scFv, (Fab'scFv)2, scDiabody-Fc, or scDiabody-CH3), IgG-based bispecific antibodies (Hybrid hybridoma, Knobs-into-holes with common light chain, Two-in-one IgG, Dual V domain IgG, IgG-scFv, scFv-IgG, IgG-V, V-IgG), minibody, tribi-minibody, nanobodies, and di-diabody. The antibody may be human, humanised, or chimeric.

Preferred antibodies are selected from Abciximab; Rituximab; Basiliximab ;Daclizumab; Palivizumab; Infliximab; Trastuzumab; Alemtuzumab; Adalimumab; Efalizumab; Cetuximab; Ibritumomab; Omalizumab; Bevacizumab; Ranibizumab; Golimumab; Canakinumab; Ustekinumab; Tocilizumab; Ofatumumab; Belimumab; Ipilimumab; Brentuximab; Pertuzumab; Raxibacumab; Vedolizumab; Ramucirumab; Obinutuzumab; Siltuximab; Secukinumab; Dinutuximab.

The antibody may lack one or more Fc effector functions; may lack ADCC activity; or may have increased ADCC activity.

A further aspect of the invention provides an antibody, or a fragment or derivative thereof, having a variable region which binds a target molecule, and a constant region, wherein the constant region comprises one or more mutations introducing a site specific conjugation site selected so as to permit conjugation of the antibody, fragment, or derivative to a payload, wherein the antibody includes a light chain comprising the amino acid sequence of SEQ ID No 14. The antibody may include a heavy chain comprising an amino acid sequence selected from SEQ ID No 2 to SEQ ID No 12.

In another aspect of the invention provides an antibody, or a fragment or derivative thereof, having a variable region which binds a target molecule, and a constant region, wherein the constant region comprises one or more mutations introducing a site specific conjugation site selected so as to permit conjugation of the antibody, fragment, or derivative to a payload, wherein the antibody includes a light chain comprising the amino acid sequence of SEQ ID No 21. The antibody may include a heavy chain comprising an amino acid sequence selected from SEQ ID No 2 to SEQ ID No 12.

The invention further provides an immunoconjugate comprising an antibody according to any of the preceding aspects of the invention, a payload, and a linker joining the payload to the antibody. The linker may be selected from 6-maleimidocaproyl (MC), maleimidopropanoyl (MP), valine-citrulline (val-cit), alanine-phenylalanine (ala-phe), p-aminobenzyloxycarbonyl (PAB), N-Succinimidyl 4-(2-pyridylthio) pentanoate (SPP), N-succinimidyl 4-(N-maleimidomethyl) cyclohexane-1 carboxylate (SMCC), N-Succinimidyl, (4-iodo-acetyl) aminobenzoate (SIAB), and 6-maleimidocaproyl-valine-citrulline-p-aminobenyloxycarbonyl (MC-vc-PAB); or is a branched linker which

comprises a peptide chain and is derived from o-hydroxy p-amino benzylic alcohol, wherein the peptide chain is connected to the phenyl ring via the p-amino group, the payload is connected to the phenyl ring via the benzylic alcohol moiety, and the antibody is connected to the phenyl ring via the o-hydroxy group.

The payload may be selected from the group consisting of a radionuclide, a chemotherapeutic agent, a cytotoxic agent, a microbial toxin, a plant toxin, a polymer, a carbohydrate, a cytokine, a fluorescent label, a luminescent label, an enzyme-substrate label, an enzyme, a peptide, a peptidomimetic, a nucleotide, an siRNA, a microRNA, an RNA mimetic, and an aptamer. A preferred polymer is a PEG molecule. Other preferred payloads include 90Y, 131I, 67Cu, 177Lu, 213Bi, 211At, dolastatin, vedotin, monomethyl auristatin F, maytansinoids including DM1 and DM4, duocarmycin analogs, calicheamicin, pyrrolobenzodiazepines, centanamycin, irinotecan, and doxorubicin, Pseudomonas exotoxin A, Diphtheria toxin, ricin, polyethylene glycol, hydroxyethyl starch, and a mannosyl residue. The payload may be a microtubule disrupting agent, or a DNA modifying agent.

The invention further provides a pharmaceutical composition comprising an antibody or an immunoconjugate according to any of the above aspects, and a pharmaceutically acceptable diluent, carrier or excipient.

Also provided is a method for generating an immunoconjugate, the method comprising conjugating an antibody according to any of the above aspects to a payload.

A process for preparing an antibody may comprise:
(i) mutagenizing a nucleic acid sequence of a parent antibody by replacing one or more amino acid residues with a mutant residue to encode the antibody;
(ii) expressing the mutant antibody; and
(iii) isolating the mutant antibody.

The antibody may be expressed in a prokaryotic (such as E.coli or Bacillus) or an eukaryotic cell (such as yeast (Pichia, Saccharomyces, Hansenula, Yarrowia) or mammalian cells (CHO cells, NSO cells, SP2/ 0 cells, 293 cells) or insect cells (SF9 cells).

The process may further comprise:

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

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

Other aspects of the invention provide an antibody, or a fragment or derivative thereof, having a variable region which binds a target molecule, and a constant region, wherein the constant region comprises one or more mutations introducing a site specific conjugation site selected so as to permit conjugation of the antibody, fragment, or derivative to a payload, such that from 85% to 110% of site specific conjugation sites per antibody are conjugated to a payload. In a preferred embodiment at least 90%, at least 95%, or at least 100% of site specific conjugation sites per antibody are conjugated to a payload.In a preferred embodiment, the antibody comprises two site specific conjugation sites (ie, one on either the heavy or light chain, and two such chains per antibody). For such an antibody, 85-110% conjugation yields a drug-antibody ratio (DAR) of from 1.7-2.2. In certain embodiments, the DAR is preferably from 1.8-2.1, more preferably from 1.9-2.1, and most preferably around 2.0.

In another preferred embodiment, the antibody comprises four site specific conjugation sites (ie, one on the heavy and one on the light chain, or two on the heavy and none on the light chain, or none on the heavy and two on the light chain, and two such chains per antibody). For such an antibody, 85-110% conjugation yields a drug-antibody ratio (DAR) of from 2x(1.7-2.2) i.e. 3.4 – 4.4. In certain embodiments, the DAR is preferably from 2x1.8-2.1, i.e. 3.6 – 4.2, more preferably from 2x 1.9-2.1 i.e. 3.8-4.2, and most preferably around 2x2.0 i.e. 4.

The antibody, fragment, or derivative may be conjugated directly or indirectly to the payload; indirect conjugation may take place via a linker. The antibody may further comprise a linker. Suitable linkers include maleimide linkers, which permit conjugation to a payload via succinimide conjugation. The linker may be cleavable, or non-cleavable. Other suitable linkers are disclosed in international patent application WO2012/113847, which describes a branched linker which comprises a peptide chain and is derived from o-hydroxy p-amino benzylic alcohol, wherein the peptide chain is connected to the phenyl ring via the p-amino group, the drug is connected to the phenyl

ring via the benzylic alcohol moiety, and the antibody is connected to the phenyl ring via the o-hydroxy group.

The constant region preferably comprises at least a portion of an IgG IgA, IgD, IgE, or IgM constant region, more preferably a human IgG constant region. In preferred embodiments, the constant region is a full length IgG constant region, although in other embodiments truncated constant regions or light or heavy chain only constant regions may be used. For example, the constant region may comprise one or more, preferably all, of the Ck, CH1 and CH3 domains of the IgG constant region. A preferred IgG is IgG1, other IgG include IgG2, IgG3, and IgG4.

By "antibody" is meant any antigen-binding immunoglobulin molecule. The antibody is preferably a complete mammalian antibody (comprising two heavy chains and two light chains, each of which includes a constant region and a variable region), but other forms of antibody and derivative may be used. For example, Fabs, bi specific antibody fragments (tandem scFv-Fc, scFv-Fc knobs-into-holes, scFv-Fc-scFv, $F(ab')_2$, Fab-scFv, $(Fab'scFv)_2$, scDiabody-Fc, or scDiabody-C_H3), IgG-based bispecific antibodies (Hybrid hybridoma, Knobs-into-holes with common light chain, Two-in-one IgG, Dual V domain IgG, IgG-scFv, scFv-IgG, IgG-V, V-IgG), minibody, tribi-minibody, nanobodies, di-diabody.

The antibody may be human, or humanised, or chimeric.

The one or more mutations preferably comprise mutation from a non-cysteine amino acid to a cysteine amino acid. Preferably the non-cysteine amino acid is selected from serine, valine, threonine, or alanine; more preferably serine or threonine. Alternatively, the mutation may be to lysine, glutamine, or a non-natural amino acid.

In preferred embodiments, the one or more mutations is selected from S160C, T190C, S443C, S447C (on the heavy chain), T180C, or T206C (on the light chain). The numbering recited herein is positional numbering based on the full length trastuzumab sequence. Other numbering conventions are summarised in the below table:

ADC Substitution	Strands, turns and	IMGT unique	CH1 / CL(kappa)

(positional numbering)	loops for C-DOMAINs	numbering for C-DOMAINs	IGHG1 amino acid translation	IMGT exon numbering	Eu numbering	Kabat numbering
H:S160C	**C-strand**	**40**	S	40	157	**156**
H:T190C	**E-strand**	**90**	T	70	187	**192**
H:S443C	**G-strand**	**120**	S	100	440	**471**
H:S447C	**G-strand**	**124**	S	104	444	**475**
L:T180C	**E-strand**	**90**	T	73	180	**180**
L:T206C	**G-strand**	**118**	T	99	206	**206**

Preferred antibodies include the light chain T180 mutation. This may be the sole mutation, or may be combined with any of the other mutations disclosed herein.

Preferred antibodies comprise combinations of 2 mutations which are selected from the group of

LC T180 in combination with LC S208,
LC T180 in combination with LC S171,
LC T180 in combination with LC S182,
LC T180 in combination with LC A184,
LC T180 in combination with LC V191,
LC T180 in combination with LC S202,
LC T180 in combination with LC S203,
LC T180 in combination with LC T206,
LC T180 in combination with HC S160,
LC T180 in combination with HC T190
LC T180 in combination with HC S443,
LC T180 in combination with HC S447,
LC T180 in combination with HC S139,
LC T180 in combination with HC S168,
LC T180 in combination with HC V170,
LC T180 in combination with HC V176,
LC T180 in combination with HC T200,
LC T180 in combination with HC S445.

The mutations are preferably mutations to cysteine, lysine, glutamine, or a non-natural amino acid.

Further preferred antibodies comprise combinations of 2 mutations selected from the group of

LC T180C in combination with LC S208C,
LC T180C in combination with LC S171C,
LC T180C in combination with LC S182C,
LC T180C in combination with LC A184C,
LC T180C in combination with LC V191C,
LC T180C in combination with LC S202C,
LC T180C in combination with LC S203C,
LC T180C in combination with LC T206C,
LC T180C in combination with HC S160C,
LC T180C in combination with HC T190C,
LC T180C in combination with HC S443C,
LC T180C in combination with HC S447C,
LC T180C in combination with HC S139C,
LC T180C in combination with HC S168C,
LC T180C in combination with HC V170C,
LC T180C in combination with HC V176C,
LC T180C in combination with HC T200C,
LC T180C in combination with HC S445C.

Most preferred antibodies comprise LC T180C in combination with HC S160C.

Other preferred antibodies comprise combinations of the 2 amino acid sequences selected from the group of:

SEQ ID No. 33 and SEQ ID No. 22,
SEQ ID No. 33 and SEQ ID No. 23,
SEQ ID No. 33 and SEQ ID No. 24,
SEQ ID No. 33 and SEQ ID No. 25,
SEQ ID No. 33 and SEQ ID No. 26,
SEQ ID No. 33 and SEQ ID No. 27,
SEQ ID No. 33 and SEQ ID No. 28,
SEQ ID No. 33 and SEQ ID No. 29,

SEQ ID No. 33 and SEQ ID No. 30,
SEQ ID No. 33 and SEQ ID No. 31,
SEQ ID No. 33 and SEQ ID No. 32,
SEQ ID No. 33 and SEQ ID No. 34,
SEQ ID No. 33 and SEQ ID No. 35,
SEQ ID No. 33 and SEQ ID No. 36,
SEQ ID No. 33 and SEQ ID No. 37,
SEQ ID No. 33 and SEQ ID No. 38,
SEQ ID No. 33 and SEQ ID No. 39,
SEQ ID No. 33 and SEQ ID No. 40.

In preferred antibodies, X is cysteine. Alternatively, X may be independently selected from lysine, glutamine, cysteine, or a non-natural amino acid, and is most preferably cysteine.

Most preferred antibodies comprise SEQ ID No. 33 and SEQ ID No. 23.

Additional mutations which may be combined with any of the aspects disclosed herein include:

Engineered Cysteine (Kabat)	Cys (Positional No.)	Sequence	SEQ ID No:
Heavy chain			
S134C	S139	FPLAPSSKST**X**GGTAALGCLV	22
S156C	S160	KDYFPEPVTV**X**WNSGALTSGV	23
S168C	S168	TVSWNSGALT**X**GVHTFPAVLQ	24
V171C	V170	SWNSGALTSG**X**HTFPAVLQSS	25
V177C	V176	LTSGVHTFPA**X**LQSSGLYSLS	26
T192C	T190	SGLYSLSSVV**X**VPSSSLGTQT	27
T205C	T200	TVPSSSLGTQ**X**YICNVNHKPS	28
S471C	S443	EALHNHYTQK**X**LSLSPGK	29
S473C	S445	EALHNHYTQKSL**X**LSPGK	30
S475C	S447	EALHNHYTQKSLSL**X**PGK	31
Light chain			
S171C	S171	ESVTEQDSKD**X**TYSLSSTLTL	32
T180C	T180	DSTYSLSSTL**X**LSKADYEKHK	33
S182C	S182	TYSLSSTLTL**X**KADYEKHKVY	34
A184C	A184	SLSSTLTLSK**X**DYEKHKVYAC	35
V191C	V191	LSKADYEKHK**X**YACEVTHQGL	36
S202C	S202	YACEVTHQGL**X**SPVTKSFNRG	37
S203C	S203	ACEVTHQGLS**X**PVTKSFNRGE	38

T206C	T206	VTHQGLSSPV**X**KSFNRGEC	39
S208C	S208	VTHQGLSSPVTK**X**FNRGEC	40

In the above table, the mutated residues are indicated as X. X is preferably cysteine, but other mutant residues may be used, in particular lysine, glutamine, or a non-natural amino acid. Note that V191 may be L191 in certain parent antibodies, in particular Kappa allotypes Km1 and Km2; where reference is made herein to V191 mutations, then unless the context requires otherwise this is understood to refer also to L191 mutations.

Other preferred antibodies include the light chain T206 mutation in combination with one or more other mutations. In preferred embodiments, the light chain T206 mutation is combined with another mutation described herein. The following are preferred combinations of two mutations; antibodies according to the invention may comprise these mutations together with one or more additional mutations.

LC T206 in combination with LC S208,
LC T206 in combination with LC S171,
LC T206 in combination with LC S182,
LC T206 in combination with LC A184,
LC T206 in combination with LC V191,
LC T206 in combination with LC S202,
LC T206 in combination with LC S203,
LC T206 in combination with LC T180,
LC T206 in combination with HC S160,
LC T206 in combination with HC T190
LC T206 in combination with HC S443,
LC T206 in combination with HC S447,
LC T206 in combination with HC S139,
LC T206 in combination with HC S168,
LC T206 in combination with HC V170,
LC T206 in combination with HC V176,
LC T206 in combination with HC T200,
LC T206 in combination with HC S445.

Of which are preferred
LC T206 in combination with LC T180,

LC T206 in combination with HC S160,
LC T206 in combination with HC T190
LC T206 in combination with HC S443,
LC T206 in combination with HC S447,

Of which are most preferred
LC T206C in combination with LC T180C,
LC T206C in combination with HC S160C,
LC T206C in combination with HC T190C
LC T206C in combination with HC S443C,
LC T206C in combination with HC S447C.

Thus, preferred antibodies may comprise combinations of the amino acid sequence of SEQ ID No 39 together with an amino acid sequence selected from SEQ ID No 22 to 38 or 40. In preferred antibodies, X is cysteine. Alternatively, X may be independently selected from lysine, glutamine, cysteine, or a non-natural amino acid, and is most preferably cysteine.

Other preferred antibodies include the heavy chain S160 mutation in combination with one or more other mutations. In preferred embodiments, the heavy chain S160 mutation is combined with another mutation described herein. The following are preferred combinations of two mutations; antibodies according to the invention may comprise these mutations together with one or more additional mutations.
HC S160 in combination with LC S208,
HC S160 in combination with LC S171,
HC S160 in combination with LC S182,
HC S160 in combination with LC A184,
HC S160 in combination with LC V191,
HC S160 in combination with LC S202,
HC S160 in combination with LC S203,
HC S160 in combination with LC T180,
HC S160 in combination with LC T206,
HC S160 in combination with HC T190,
HC S160 in combination with HC S443,
HC S160 in combination with HC S447,

HC S160 in combination with HC S139,
HC S160 in combination with HC S168,
HC S160 in combination with HC V170,
HC S160 in combination with HC V176,
HC S160 in combination with HC T200,
HC S160 in combination with HC S445.

Of which are preferred
HC S160 in combination with LC T180,
HC S160 in combination with LC T206,
HC S160 in combination with HC T190,
HC S160 in combination with HC S443,
HC S160 in combination with HC S447,

Of which are most preferred
HC S160C in combination with LC T180C,
HC S160C in combination with LC T206C,
HC S160C in combination with HC T190C,
HC S160C in combination with HC S443C,
HC S160C in combination with HC S447C,

Thus, preferred antibodies may comprise combinations of the amino acid sequence of SEQ ID No 23 together with an amino acid sequence selected from SEQ ID No 22 or 24 to 40. In preferred antibodies, X is cysteine. Alternatively, X may be independently selected from lysine, glutamine, cysteine, or a non-natural amino acid, and is most preferably cysteine.

Other preferred antibodies include the heavy chain T190 mutation in combination with one or more other mutations. In preferred embodiments, the heavy chain T190 mutation is combined with another mutation described herein. The following are preferred combinations of two mutations; antibodies according to the invention may comprise these mutations together with one or more additional mutations.

HC T190 in combination with LC S208,
HC T190 in combination with LC S171,

HC T190 in combination with LC S182,
HC T190 in combination with LC A184,
HC T190 in combination with LC V191,
HC T190 in combination with LC S202,
HC T190 in combination with LC S203,
HC T190 in combination with LC T180,
HC T190 in combination with LC T206,
HC T190 in combination with HC S160,
HC T190 in combination with HC S443,
HC T190 in combination with HC S447,
HC T190 in combination with HC S139,
HC T190 in combination with HC S168,
HC T190 in combination with HC V170,
HC T190 in combination with HC V176,
HC T190 in combination with HC T200,
HC T190 in combination with HC S445.

Of which are preferred
HC T190 in combination with LC T180,
HC T190 in combination with LC T206,
HC T190 in combination with HC S160,
HC T190 in combination with HC S443,
HC T190 in combination with HC S447,

Of which are most preferred
HC T190C in combination with LC T180C,
HC T190C in combination with LC T206C,
HC T190C in combination with HC S160C,
HC T190C in combination with HC S443C,
HC T190C in combination with HC S447C.

Thus, preferred antibodies may comprise combinations of the amino acid sequence of SEQ ID No 27 together with an amino acid sequence selected from SEQ ID No 22 to 26 or 28 to 40. In preferred antibodies, X is cysteine. Alternatively, X may be

independently selected from lysine, glutamine, cysteine, or a non-natural amino acid, and is most preferably cysteine.

Other preferred antibodies include the heavy chain S443 mutation in combination with one or more other mutations. In preferred embodiments, the heavy chain S443 mutation is combined with another mutation described herein. The following are preferred combinations of two mutations; antibodies according to the invention may comprise these mutations together with one or more additional mutations.

HC S443 in combination with LC S208,
HC S443 in combination with LC S171,
HC S443 in combination with LC S182,
HC S443 in combination with LC A184,
HC S443 in combination with LC V191,
HC S443 in combination with LC S202,
HC S443 in combination with LC S203,
HC S443 in combination with LC T180,
HC S443 in combination with LC T206,
HC S443 in combination with HC S160,
HC S443 in combination with HC T190,
HC S443 in combination with HC S447,
HC S443 in combination with HC S139,
HC S443 in combination with HC S168,
HC S443 in combination with HC V170,
HC S443 in combination with HC V176,
HC S443 in combination with HC T200,
HC S443 in combination with HC S445.

Of which are preferred
HC S443 in combination with LC T180,
HC S443 in combination with LC T206,
HC S443 in combination with HC S160,
HC S443 in combination with HC T190,
HC S443 in combination with HC S447,

Of which are most preferred
HC S443C in combination with LC T180C,
HC S443C in combination with LC T206C,
HC S443C in combination with HC S160C,
HC S443C in combination with HC T190C,
HC S443C in combination with HC S447C.

Thus, preferred antibodies may comprise combinations of the amino acid sequence of SEQ ID No 29 together with an amino acid sequence selected from SEQ ID No 22 to 28 or 30 to 40. In preferred antibodies, X is cysteine. Alternatively, X may be independently selected from lysine, glutamine, cysteine, or a non-natural amino acid, and is most preferably cysteine.

Other preferred antibodies include the heavy chain S447 mutation in combination with one or more other mutations. In preferred embodiments, the heavy chain S447 mutation is combined with another mutation described herein. The following are preferred combinations of two mutations; antibodies according to the invention may comprise these mutations together with one or more additional mutations.

HC S447 in combination with LC S208,
HC S447 in combination with LC S171,
HC S447 in combination with LC S182,
HC S447 in combination with LC A184,
HC S447 in combination with LC V191,
HC S447 in combination with LC S202,
HC S447 in combination with LC S203,
HC S447 in combination with LC T180,
HC S447 in combination with LC T206,
HC S447 in combination with HC S160,
HC S447 in combination with HC T190,
HC S447 in combination with HC S443,
HC S447 in combination with HC S139,
HC S447 in combination with HC S168,
HC S447 in combination with HC V170,
HC S447 in combination with HC V176,

HC S447 in combination with HC T200,
HC S447 in combination with HC S445.

Of which are preferred
HC S447 in combination with LC T180,
HC S447 in combination with, LC T206,
HC S447 in combination with HC S160,
HC S447 in combination with HC T190,
HC S447 in combination with HC S443,

Of which are most preferred
HC S447C in combination with LC T180C,
HC S447C in combination with LC T206C,
HC S447C in combination with HC S160C,
HC S447C in combination with HC T190C,
HC S447C in combination with HC S443C.

Thus, preferred antibodies may comprise combinations of the amino acid sequence of SEQ ID No 31 together with an amino acid sequence selected from SEQ ID No 22 to 30 or 32 to 40. In preferred antibodies, X is cysteine. Alternatively, X may be independently selected from lysine, glutamine, cysteine, or a non-natural amino acid, and is most preferably cysteine.

Other preferred antibodies include the light chain S208 mutation in combination with one or more other mutations. In preferred embodiments, the light chain S208 mutation is combined with another mutation described herein. The following are preferred combinations of two mutations; antibodies according to the invention may comprise these mutations together with one or more additional mutations.

LC S208 in combination with LC S171,
LC S208 in combination with LC S182,
LC S208 in combination with LC A184,
LC S208 in combination with LC V191,
LC S208 in combination with LC S202,
LC S208 in combination with LC S203,

LC S208 in combination with LC T180,
LC S208 in combination with LC T206,
LC S208 in combination with HC S160,
LC S208 in combination with HC T190,
LC S208 in combination with HC S443,
LC S208 in combination with HC S447,
LC S208 in combination with HC S139,
LC S208 in combination with HC S168,
LC S208 in combination with HC V170,
LC S208 in combination with HC V176,
LC S208 in combination with HC T200,
LC S208 in combination with HC S445.

Of which are preferred
LC S208 in combination with LC T180,
LC S208 in combination with LC T206,
LC S208 in combination with HC S160,
LC S208 in combination with HC T190,
LC S208 in combination with HC S443,
LC S208 in combination with HC S447,

Of which are most preferred
LC S208C in combination with LC T180C,
LC S208C in combination with LC T206C,
LC S208C in combination with HC S160C,
LC S208C in combination with HC T190C,
LC S208C in combination with HC S443C,
LC S208C in combination with HC S447C.

Thus, preferred antibodies may comprise combinations of the amino acid sequence of SEQ ID No 40 together with an amino acid sequence selected from SEQ ID No 22 to 39. In preferred antibodies, X is cysteine. Alternatively, X may be independently selected from lysine, glutamine, cysteine, or a non-natural amino acid, and is most preferably cysteine.

Accordingly, preferred antibodies comprise combinations of the 2 amino acid sequences selected from the group of:

SEQ ID No. 40 and SEQ ID No. 22,
SEQ ID No. 40 and SEQ ID No. 23,
SEQ ID No. 40 and SEQ ID No. 24,
SEQ ID No. 40 and SEQ ID No. 25,
SEQ ID No. 40 and SEQ ID No. 26,
SEQ ID No. 40 and SEQ ID No. 27,
SEQ ID No. 40 and SEQ ID No. 28,
SEQ ID No. 40 and SEQ ID No. 29,
SEQ ID No. 40 and SEQ ID No. 30,
SEQ ID No. 40 and SEQ ID No. 31,
SEQ ID No. 40 and SEQ ID No. 32,
SEQ ID No. 40 and SEQ ID No. 33,
SEQ ID No. 40 and SEQ ID No. 34,
SEQ ID No. 40 and SEQ ID No. 35,
SEQ ID No. 40 and SEQ ID No. 36,
SEQ ID No. 40 and SEQ ID No. 37,
SEQ ID No. 40 and SEQ ID No. 38,
SEQ ID No. 40 and SEQ ID No. 39.

In preferred antibodies, X is cysteine. Alternatively, X may be independently selected from lysine, glutamine, cysteine, or a non-natural amino acid, and is most preferably cysteine.

Other preferred antibodies include the light chain S171 mutation in combination with one or more other mutations. In preferred embodiments, the light chain S171 mutation is combined with another mutation described herein. The following are preferred combinations of two mutations; antibodies according to the invention may comprise these mutations together with one or more additional mutations.

LC S171 in combination with LC S208,
LC S171 in combination with LC S182,
LC S171 in combination with LC A184,
LC S171 in combination with LC V191,

LC S171 in combination with LC S202,
LC S171 in combination with LC S203,
LC S171 in combination with LC T180,
LC S171 in combination with LC T206,
LC S171 in combination with HC S160,
LC S171 in combination with HC T190,
LC S171 in combination with HC S443,
LC S171 in combination with HC S447,
LC S171 in combination with HC S139,
LC S171 in combination with HC S168,
LC S171 in combination with HC V170,
LC S171 in combination with HC V176,
LC S171 in combination with HC T200,
LC S171 in combination with HC S445.

Of which are preferred
LC S171 in combination with LC T180,
LC S171 in combination with LC T206,
LC S171 in combination with HC S160,
LC S171 in combination with HC T190,
LC S171 in combination with HC S443,
LC S171 in combination with HC S447,

Of which are most preferred
LC S171C in combination with LC T180C,
LC S171C in combination with LC T206C,
LC S171C in combination with HC S160C,
LC S171C in combination with HC T190C,
LC S171C in combination with HC S443C,
LC S171C in combination with HC S447C.

Thus, preferred antibodies may comprise combinations of the amino acid sequence of SEQ ID No 32 together with an amino acid sequence selected from SEQ ID No 22 to 31 or 33 to 40. In preferred antibodies, X is cysteine. Alternatively, X may be

independently selected from lysine, glutamine, cysteine, or a non-natural amino acid, and is most preferably cysteine.

Other preferred antibodies include the light chain S182 mutation in combination with one or more other mutations. In preferred embodiments, the light chain S182 mutation is combined with another mutation described herein. The following are preferred combinations of two mutations; antibodies according to the invention may comprise these mutations together with one or more additional mutations.

LC S182 in combination with LC S208,
LC S182 in combination with LC S171,
LC S182 in combination with LC A184,
LC S182 in combination with LC V191,
LC S182 in combination with LC S202,
LC S182 in combination with LC S203,
LC S182 in combination with LC T180,
LC S182 in combination with LC T206,
LC S182 in combination with HC S160,
LC S182 in combination with HC T190,
LC S182 in combination with HC S443,
LC S182 in combination with HC S447,
LC S182 in combination with HC S139,
LC S182 in combination with HC S168,
LC S182 in combination with HC V170,
LC S182 in combination with HC V176,
LC S182 in combination with HC T200,
LC S182 in combination with HC S445.

Of which are preferred
LC S182 in combination with LC T180,
LC S182 in combination with LC T206,
LC S182 in combination with HC S160,
LC S182 in combination with HC T190,
LC S182 in combination with HC S443,
LC S182 in combination with HC S447,

Of which are most preferred
LC S182C in combination with LC T180C,
LC S182C in combination with LC T206C,
LC S182C in combination with HC S160C,
LC S182C in combination with HC T190C,
LC S182C in combination with HC S443C,
LC S182C in combination with HC S447C.

Thus, preferred antibodies may comprise combinations of the amino acid sequence of SEQ ID No 34 together with an amino acid sequence selected from SEQ ID No 22 to 33 or 35 to 40. In preferred antibodies, X is cysteine. Alternatively, X may be independently selected from lysine, glutamine, cysteine, or a non-natural amino acid, and is most preferably cysteine.

Other preferred antibodies include the light chain A184 mutation in combination with one or more other mutations. In preferred embodiments, the light chain A184 mutation is combined with another mutation described herein. The following are preferred combinations of two mutations; antibodies according to the invention may comprise these mutations together with one or more additional mutations.

LC A184 in combination with LC S208,
LC A184 in combination with LC S171,
LC A184 in combination with LC S182,
LC A184 in combination with LC V191,
LC A184 in combination with LC S202,
LC A184 in combination with LC S203,
LC A184 in combination with LC T180,
LC A184 in combination with LC T206,
LC A184 in combination with HC S160,
LC A184 in combination with HC T190,
LC A184 in combination with HC S443,
LC A184 in combination with HC S447,
LC A184 in combination with HC S139,
LC A184 in combination with HC S168,

LC A184 in combination with HC V170,
LC A184 in combination with HC V176,
LC A184 in combination with HC T200,
LC A184 in combination with HC S445.

Of which are preferred
LC A184 in combination with LC T180,
LC A184 in combination with LC T206,
LC A184 in combination with HC S160,
LC A184 in combination with HC T190,
LC A184 in combination with HC S443,
LC A184 in combination with HC S447,

Of which are most preferred
LC A184C in combination with LC T180C,
LC A184C in combination with LC T206C,
LC A184C in combination with HC S160C,
LC A184C in combination with HC T190C,
LC A184C in combination with HC S443C,
LC A184C in combination with HC S447C.

Thus, preferred antibodies may comprise combinations of the amino acid sequence of SEQ ID No 35 together with an amino acid sequence selected from SEQ ID No 22 to 34 or 36 to 40. In preferred antibodies, X is cysteine. Alternatively, X may be independently selected from lysine, glutamine, cysteine, or a non-natural amino acid, and is most preferably cysteine.

Other preferred antibodies include the light chain V191 mutation in combination with one or more other mutations. In preferred embodiments, the light chain V191 mutation is combined with another mutation described herein. The following are preferred combinations of two mutations; antibodies according to the invention may comprise these mutations together with one or more additional mutations.

LC V191 in combination with LC S208,
LC V191 in combination with LC S171,

LC V191 in combination with LC S182,
LC V191 in combination with LC A184,
LC V191 in combination with LC S202,
LC V191 in combination with LC S203,
LC V191 in combination with LC T180,
LC V191 in combination with LC T206,
LC V191 in combination with HC S160,
LC V191 in combination with HC T190,
LC V191 in combination with HC S443,
LC V191 in combination with HC S447,
LC V191 in combination with HC S139,
LC V191 in combination with HC S168,
LC V191 in combination with HC V170,
LC V191 in combination with HC V176,
LC V191 in combination with HC T200,
LC V191 in combination with HC S445.

Of which are preferred
LC V191 in combination with LC T180,
LC V191 in combination with LC T206,
LC V191 in combination with HC S160,
LC V191 in combination with HC T190,
LC V191 in combination with HC S443,
LC V191 in combination with HC S447,

Of which are most preferred
LC V191C in combination with LC T180C,
LC V191C in combination with LC T206C,
LC V191C in combination with HC S160C,
LC V191C in combination with HC T190C,
LC V191C in combination with HC S443C,
LC V191C in combination with HC S447C.

Thus, preferred antibodies may comprise combinations of the amino acid sequence of SEQ ID No 36 together with an amino acid sequence selected from SEQ ID No 22 to

35 or 37 to 40. In preferred antibodies, X is cysteine. Alternatively, X may be independently selected from lysine, glutamine, cysteine, or a non-natural amino acid, and is most preferably cysteine.

Other preferred antibodies include the light chain S202 mutation in combination with one or more other mutations. In preferred embodiments, the light chain S202 mutation is combined with another mutation described herein. The following are preferred combinations of two mutations; antibodies according to the invention may comprise these mutations together with one or more additional mutations.

LC S202 in combination with LC S208,
LC S202 in combination with LC S171,
LC S202 in combination with LC S182,
LC S202 in combination with LC A184,
LC S202 in combination with LC V191,
LC S202 in combination with LC S203,
LC S202 in combination with LC T180,
LC S202 in combination with LC T206,
LC S202 in combination with HC S160,
LC S202 in combination with HC T190,
LC S202 in combination with HC S443,
LC S202 in combination with HC S447,
LC S202 in combination with HC S139,
LC S202 in combination with HC S168,
LC S202 in combination with HC V170,
LC S202 in combination with HC V176,
LC S202 in combination with HC T200,
LC S202 in combination with HC S445.

Of which are preferred
LC S202 in combination with LC T180,
LC S202 in combination with LC T206,
LC S202 in combination with HC S160,
LC S202 in combination with HC T190,
LC S202 in combination with HC S443,

LC S202 in combination with HC S447,

Of which are most preferred
LC S202C in combination with LC T180C,
LC S202C in combination with LC T206C,
LC S202C in combination with HC S160C,
LC S202C in combination with HC T190C,
LC S202C in combination with HC S443C,
LC S202C in combination with HC S447C.

Thus, preferred antibodies may comprise combinations of the amino acid sequence of SEQ ID No 37 together with an amino acid sequence selected from SEQ ID No 22 to 36 or 38 to 40. In preferred antibodies, X is cysteine. Alternatively, X may be independently selected from lysine, glutamine, cysteine, or a non-natural amino acid, and is most preferably cysteine.

Other preferred antibodies include the light chain S203 mutation in combination with one or more other mutations. In preferred embodiments, the light chain S203 mutation is combined with another mutation described herein. The following are preferred combinations of two mutations; antibodies according to the invention may comprise these mutations together with one or more additional mutations.

LC S203 in combination with LC S208,
LC S203 in combination with LC S171,
LC S203 in combination with LC S182,
LC S203 in combination with LC A184,
LC S203 in combination with LC V191,
LC S203 in combination with LC S202,
LC S203 in combination with LC T180,
LC S203 in combination with LC T206,
LC S203 in combination with HC S160,
LC S203 in combination with HC T190,
LC S203 in combination with HC S443,
LC S203 in combination with HC S447,
LC S203 in combination with HC S139,

LC S203 in combination with HC S168,
LC S203 in combination with HC V170,
LC S203 in combination with HC V176,
LC S203 in combination with HC T200,
LC S203 in combination with HC S445.

Of which are preferred
LC S203 in combination with LC T180,
LC S203 in combination with LC T206,
LC S203 in combination with HC S160,
LC S203 in combination with HC T190,
LC S203 in combination with HC S443,
LC S203 in combination with HC S447,

Of which are most preferred
LC S203C in combination with LC T180C,
LC S203C in combination with LC T206C,
LC S203C in combination with HC S160C,
LC S203C in combination with HC T190C,
LC S203C in combination with HC S443C,
LC S203C in combination with HC S447C.

Thus, preferred antibodies may comprise combinations of the amino acid sequence of SEQ ID No 38 together with an amino acid sequence selected from SEQ ID No 22 to 37 or 39 to 40. In preferred antibodies, X is cysteine. Alternatively, X may be independently selected from lysine, glutamine, cysteine, or a non-natural amino acid, and is most preferably cysteine..

Other preferred antibodies include the heavy chain S139 mutation in combination with one or more other mutations. In preferred embodiments, the heavy chain S139 mutation is combined with another mutation described herein. The following are preferred combinations of two mutations; antibodies according to the invention may comprise these mutations together with one or more additional mutations.

HC S139 in combination with LC S208,

HC S139 in combination with LC S171,
HC S139 in combination with LC S182,
HC S139 in combination with LC A184,
HC S139 in combination with LC V191,
HC S139 in combination with LC S202,
HC S139 in combination with LC S203,
HC S139 in combination with LC T180,
HC S139 in combination with LC T206,
HC S139 in combination with HC S160,
HC S139 in combination with HC T190,
HC S139 in combination with HC S443,
HC S139 in combination with HC S447,
HC S139 in combination with HC S168,
HC S139 in combination with HC V170,
HC S139 in combination with HC V176,
HC S139 in combination with HC T200,
HC S139 in combination with HC S445.

Of which are preferred
HC S139 in combination with LC T180,
HC S139 in combination with LC T206,
HC S139 in combination with HC S160,
HC S139 in combination with HC T190,
HC S139 in combination with HC S443,
HC S139 in combination with HC S447,

Of which are most preferred
HC S139C in combination with LC T180C,
HC S139C in combination with LC T206C,
HC S139C in combination with HC S160C,
HC S139C in combination with HC T190C,
HC S139C in combination with HC S443C,
HC S139C in combination with HC S447C.

Thus, preferred antibodies may comprise combinations of the amino acid sequence of SEQ ID No 22 together with an amino acid sequence selected from SEQ ID No 23 to 40. In preferred antibodies, X is cysteine. Alternatively, X may be independently selected from lysine, glutamine, cysteine, or a non-natural amino acid, and is most preferably cysteine.

Other preferred antibodies include the heavy chain S168 mutation in combination with one or more other mutations. In preferred embodiments, the heavy chain S168 mutation is combined with another mutation described herein. The following are preferred combinations of two mutations; antibodies according to the invention may comprise these mutations together with one or more additional mutations.

HC S168 in combination with LC S208,
HC S168 in combination with LC S171,
HC S168 in combination with LC S182,
HC S168 in combination with LC A184,
HC S168 in combination with LC V191,
HC S168 in combination with LC S202,
HC S168 in combination with LC S203,
HC S168 in combination with LC T180,
HC S168 in combination with LC T206,
HC S168 in combination with HC S160,
HC S168 in combination with HC T190,
HC S168 in combination with HC S443,
HC S168 in combination with HC S447,
HC S168 in combination with HC S139,
HC S168 in combination with HC V170,
HC S168 in combination with HC V176,
HC S168 in combination with HC T200,
HC S168 in combination with HC S445.

Of which are preferred
HC S168 in combination with LC T180,
HC S168 in combination with LC T206,
HC S168 in combination with HC S160,

HC S168 in combination with HC T190,
HC S168 in combination with HC S443,
HC S168 in combination with HC S447,

Of which are most preferred
HC S168C in combination with LC T180C,
HC S168C in combination with LC T206C,
HC S168C in combination with HC S160C,
HC S168C in combination with HC T190C,
HC S168C in combination with HC S443C,
HC S168C in combination with HC S447C.

Thus, preferred antibodies may comprise combinations of the amino acid sequence of SEQ ID No 24 together with an amino acid sequence selected from SEQ ID No 22, 23, or 25 to 40. In preferred antibodies, X is cysteine. Alternatively, X may be independently selected from lysine, glutamine, cysteine, or a non-natural amino acid, and is most preferably cysteine.

Other preferred antibodies include the heavy chain V170 mutation in combination with one or more other mutations. In preferred embodiments, the heavy chain V170 mutation is combined with another mutation described herein. The following are preferred combinations of two mutations; antibodies according to the invention may comprise these mutations together with one or more additional mutations.

HC V170 in combination with LC S208,
HC V170 in combination with LC S171,
HC V170 in combination with LC S182,
HC V170 in combination with LC A184,
HC V170 in combination with LC V191,
HC V170 in combination with LC S202,
HC V170 in combination with LC S203,
HC V170 in combination with LC T180,
HC V170 in combination with LC T206,
HC V170 in combination with HC S160,
HC V170 in combination with HC T190,

HC V170 in combination with HC S443,
HC V170 in combination with HC S447,
HC V170 in combination with HC S139,
HC V170 in combination with HC S168,
HC V170 in combination with HC V176,
HC V170 in combination with HC T200,
HC V170 in combination with HC S445.

Of which are preferred
HC V170 in combination with LC T180,
HC V170 in combination with LC T206,
HC V170 in combination with HC S160,
HC V170 in combination with HC T190,
HC V170 in combination with HC S443,
HC V170 in combination with HC S447,

Of which are most preferred
HC V170C in combination with LC T180C,
HC V170C in combination with LC T206C,
HC V170C in combination with HC S160C,
HC V170C in combination with HC T190C,
HC V170C in combination with HC S443C,
HC V170C in combination with HC S447C.

Thus, preferred antibodies may comprise combinations of the amino acid sequence of SEQ ID No 25 together with an amino acid sequence selected from SEQ ID No 22 to 24 or 26 to 40. In preferred antibodies, X is cysteine. Alternatively, X may be independently selected from lysine, glutamine, cysteine, or a non-natural amino acid, and is most preferably cysteine.

Other preferred antibodies include the heavy chain V176 mutation in combination with one or more other mutations. In preferred embodiments, the heavy chain V176 mutation is combined with another mutation described herein. The following are preferred combinations of two mutations; antibodies according to the invention may comprise these mutations together with one or more additional mutations.

HC V176 in combination with LC S208,
HC V176 in combination with LC S171,
HC V176 in combination with LC S182,
HC V176 in combination with LC A184,
HC V176 in combination with LC V191,
HC V176 in combination with LC S202,
HC V176 in combination with LC S203,
HC V176 in combination with LC T180,
HC V176 in combination with LC T206,
HC V176 in combination with HC S160,
HC V176 in combination with HC T190,
HC V176 in combination with HC S443,
HC V176 in combination with HC S447,
HC V176 in combination with HC S139,
HC V176 in combination with HC S168,
HC V176 in combination with HC V170,
HC V176 in combination with HC T200,
HC V176 in combination with HC S445.

Of which are preferred
HC V176 in combination with LC T180,
HC V176 in combination with LC T206,
HC V176 in combination with HC S160,
HC V176 in combination with HC T190,
HC V176 in combination with HC S443,
HC V176 in combination with HC S447,

Of which are most preferred
HC V176C in combination with LC T180C,
HC V176C in combination with LC T206C,
HC V176C in combination with HC S160C,
HC V176C in combination with HC T190C,
HC V176C in combination with HC S443C,
HC V176C in combination with HC S447C.

Thus, preferred antibodies may comprise combinations of the amino acid sequence of SEQ ID No 26 together with an amino acid sequence selected from SEQ ID No 22 to 25 or 27 to 40. In preferred antibodies, X is cysteine. Alternatively, X may be independently selected from lysine, glutamine, cysteine, or a non-natural amino acid, and is most preferably cysteine.

Other preferred antibodies include the heavy chain T200 mutation in combination with one or more other mutations. In preferred embodiments, the heavy chain T200 mutation is combined with another mutation described herein. The following are preferred combinations of two mutations; antibodies according to the invention may comprise these mutations together with one or more additional mutations.

HC T200 in combination with LC S208,
HC T200 in combination with LC S171,
HC T200 in combination with LC S182,
HC T200 in combination with LC A184,
HC T200 in combination with LC V191,
HC T200 in combination with LC S202,
HC T200 in combination with LC S203,
HC T200 in combination with LC T180,
HC T200 in combination with LC T206,
HC T200 in combination with HC S160,
HC T200 in combination with HC T190,
HC T200 in combination with HC S443,
HC T200 in combination with HC S447,
HC T200 in combination with HC S139,
HC T200 in combination with HC S168,
HC T200 in combination with HC V170,
HC T200 in combination with HC V176,
HC T200 in combination with HC S445.

Of which are preferred
HC T200 in combination with LC T180,
HC T200 in combination with LC T206,

HC T200 in combination with HC S160,
HC T200 in combination with HC T190,
HC T200 in combination with HC S443,
HC T200 in combination with HC S447,

Of which are most preferred
HC T200C in combination with LC T180C,
HC T200C in combination with LC T206C,
HC T200C in combination with HC S160C,
HC T200C in combination with HC T190C,
HC T200C in combination with HC S443C,
HC T200C in combination with HC S447C.

Thus, preferred antibodies may comprise combinations of the amino acid sequence of SEQ ID No 28 together with an amino acid sequence selected from SEQ ID No 22 to 27 or 29 to 40. In preferred antibodies, X is cysteine. Alternatively, X may be independently selected from lysine, glutamine, cysteine, or a non-natural amino acid, and is most preferably cysteine.

Other preferred antibodies include the heavy chain S445 mutation in combination with one or more other mutations. In preferred embodiments, the heavy chain S445 mutation is combined with another mutation described herein. The following are preferred combinations of two mutations; antibodies according to the invention may comprise these mutations together with one or more additional mutations.

HC S445 in combination with LC S208,
HC S445 in combination with LC S171,
HC S445 in combination with LC S182,
HC S445 in combination with LC A184,
HC S445 in combination with LC V191,
HC S445 in combination with LC S202,
HC S445 in combination with LC S203,
HC S445 in combination with LC T180,
HC S445 in combination with LC T206,
HC S445 in combination with HC S160,

HC S445 in combination with HC T190,
HC S445 in combination with HC S443,
HC S445 in combination with HC S447,
HC S445 in combination with HC S139,
HC S445 in combination with HC S168,
HC S445 in combination with HC V170,
HC S445 in combination with HC V176,
HC S445 in combination with HC T200.

Of which are preferred
HC S445 in combination with LC T180,
HC S445 in combination with LC T206,
HC S445 in combination with HC S160,
HC S445 in combination with HC T190,
HC S445 in combination with HC S443,
HC S445 in combination with HC S447,

Of which are most preferred
HC S445C in combination with LC T180C,
HC S445C in combination with LC T206C,
HC S445C in combination with HC S160C,
HC S445C in combination with HC T190C,
HC S445C in combination with HC S443C,
HC S445C in combination with HC S447C.

Thus, preferred antibodies may comprise combinations of the amino acid sequence of SEQ ID No 30 together with an amino acid sequence selected from SEQ ID No 22 to 29 or 31 to 40. In preferred antibodies, X is cysteine. Alternatively, X may be independently selected from lysine, glutamine, cysteine, or a non-natural amino acid, and is most preferably cysteine.

The antibody may be selected from Abciximab; Rituximab; Basiliximab ;Daclizumab; Palivizumab; Infliximab; Trastuzumab; Alemtuzumab; Adalimumab; Efalizumab; Cetuximab; Ibritumomab; Omalizumab; Bevacizumab; Ranibizumab; Golimumab; Canakinumab; Ustekinumab; Tocilizumab; Ofatumumab; Belimumab; Ipilimumab;

Brentuximab; Pertuzumab; Raxibacumab; Vedolizumab; Ramucirumab; Obinutuzumab; Siltuximab; Secukinumab; Dinutuximab.

The invention further provides an antibody having a light chain comprising or consisting of the amino acid sequence of SEQ ID NO 1, and a heavy chain comprising or consisting of an amino acid sequence selected from any of SEQ ID NO 3 to 12. Alternatively the antibody has a light chain comprising or consisting of an amino acid sequence selected from SEQ ID NO 13 to 21, and a heavy chain comprising or consisting of the amino acid sequence of SEQ ID NO 2. The antibody preferably has two light chains and two heavy chains.

Also provided is an antibody having a variable region providing binding specificity to a target, and a constant region, wherein the constant region comprises a light chain constant region having the amino acid sequence of residues 109 to 214 of SEQ ID NO 1, and a heavy chain constant region having the amino acid sequence of residues 121 to 450 of a sequence selected from SEQ ID NO 3 to 12. Alternatively, the constant region comprises a light chain constant region having the amino acid sequence of residues 109 to 214 of SEQ ID NO 13 to 21, and a heavy chain constant region having the amino acid sequence of residues 121 to 450 of SEQ ID NO 2. Preferably, the antibody comprises a light chain constant region having the amino acid sequence of residues 109 to 214 of SEQ ID NO 14, and a heavy chain constant region having the amino acid sequence of residues 121 to 450 of SEQ ID NO 2; or the antibody comprises a light chain constant region having the amino acid sequence of residues 109 to 214 of SEQ ID NO 14, and a heavy chain constant region having the amino acid sequence of residues 121 to 450 of SEQ ID NO 4; or the antibody comprises a light chain constant region having the amino acid sequence of residues 109 to 214 of SEQ ID NO 21, and a heavy chain constant region having the amino acid sequence of residues 121 to 450 of SEQ ID NO 2.

Also provided is an antibody-drug conjugate (ADC), comprising an antibody according to the first aspect of the invention, conjugated to a payload, preferably a drug payload, such that the DAR is from 1.7-2.2 in case of one mutation on either heavy or light chain and a DAR of 3.4 – 4.4 in case of 2 mutations in light or heavy chain or one in light and one in heavy chain.

The drug payload may be a microtubule disrupting agent, or a DNA modifying agent. Examples of suitable drug payloads include dolastatin, vedotin, monomethyl auristatin F, maytansinoids including DM1 and DM4, duocarmycin analogs, calicheamicin, pyrrolobenzodiazepines, duocarmycin, centanamycin, irinotecan, and doxorubicin. Other drug payloads may be used.

A yet further aspect of the invention provides an antibody or an ADC as herein described, for use as a therapeutic. The invention also provides a pharmaceutical composition comprising an antibody or an ADC as herein described. A further aspect of the invention provides a method for generating an ADC, the method comprising conjugating an antibody as herein described to a drug payload.

Another aspect of the invention provides a method for improving a selected characteristic of a parent antibody after conjugation of the antibody to a payload, wherein the improvement is selected from a reduction in loss of monomers , reduction in antibody fragmentation, and/or reduction in antibody aggregation after conjugation, wherein the method comprises preparing a modified antibody having the amino acid sequence of the parent antibody with one or more substitutions in residues selected from HC T200, HC V170, HC V176, HC T190, HC S139, HC S160, HC S168, HC S443 HC S445, HC S447, LC S171C, LC T180, LC T206, LC V191, LC S202, LC S203 or or LC S208. The substitution is preferably cysteine, but other mutant residues may be used, in particular lysine, glutamine, or a non-natural amino acid.

Definitions

The following terms used herein are given the following definitions:

By “fragment” is meant a portion of the full size antibody which retains the specific binding properties of the antibody. By “derivative” is meant a modified antibody or antibody fragment having one or more changes to the peptide sequence, and/or bearing one or more functional groups or one or more moieties bound thereto, which retains the specific binding properties of the antibody. A “derivative” may include post-translationally modified antibodies.

By “positional numbering”, “sequential numbering” and similar terms is meant the numbering of the amino acid sequence of the peptide in which the first residue at the N

terminus is designated residue number 1, and subsequent residues are sequentially numbered residue 2, 3, 4.. etc. This is contrasted with Kabat or EU numbering systems for antibodies.

By "site specific conjugation sites" are meant amino acid residues within an antibody which are specifically modified in order to permit conjugation of a payload.

By "wild type" is meant an unmodified, naturally occurring, peptide or nucleic acid sequence.

By "parent antibody" is meant an antibody which is used as the basis for preparing modified antibodies.

By "non-natural amino acid" is meant to an amino acid that is not a proteinogenic amino acid, or a post-translationally modified variant thereof. In particular, the term refers to an amino acid that is not one of the 20 common amino acids.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 shows levels of expression of candidate antibodies in 25 ml CHOK1SV cultures.

Figure 2 shows results of SEC-HPLC analysis for % monomer of conjugated and unconjugated variant antibodies, and % aggregation and fragmentation for conjugated variants.

Figure 3 shows extent of biotin-maleimide conjugation to light chains of antibody variants. Open bars represent unconjugated product, striped bars represent products with a single conjugated payload, and solid bars represent products with two conjugated payloads.

Figure 4 shows extent of biotin-maleimide conjugation to heavy chains of antibody variants. Open bars represent unconjugated product, striped bars represent products with a single conjugated payload, and solid bars represent products with two conjugated payloads.

Figure 5 shows calculated drug antibody ratio for the antibody variants of figures 3 and 4.

Figure 6 shows percentage biotin decrease over time for the subset of antibody variants.

Figure 7 shows calculated drug to antibody ratio of some of the selected variants conjugated to MMAE.

Figure 8 shows the decrease in cell viability for different cell lines that have been exposed to different concentrations of the selected ADC over a period of 72h. PBS = phosphate buffered saline; vc-MMAE = valine-citrulline-MMAE.

DETAILED DESCRIPTION OF THE INVENTION

The present inventors have developed a process for rational design of modified antibodies to allow selection of antibodies having desired properties for production of antibodies conjugated to payloads such as for example ADCs (ADC variants). The design process incorporates in silico and in vitro screening steps. Thus, the antibodies of the present invention share a number of properties, as will be seen.

To incorporate residues for site specific conjugation, it was decided to replace native residues with another residue such as cysteine residues in selected positions of antibody structures. Candidate variants were analysed (in silico and in vitro) for desirable properties including titre and aggregation, and optionally immunogenicity (in silico only). As an initial proof of concept, Herceptin (trastuzumab) was chosen as a model antibody, and conjugation optimization and analysis carried out with biotin maleimide.

Criteria for selecting mutation sites included:

- Residues to be mutated to cysteine (cys) must have similar physicochemical properties or be a small non-hydrophobic non-charged residue (ser, val, thr, ala)
- Residues amenable to be mutated to cysteine must be in constant regions of either light chain (Cκ, Cλ,) or heavy chain (CH1, CH2 or CH3) of an antibody or a fragment thereof.

- In cases where a modified antibody or scaffold is used, introduced cys should be at a distance >5Å from any target-binding interface or domain to minimise risk of interfering with biological activity of the molecule.
- Mutations to cys should not create intra-chain hydrogen bonds leading to the alteration of the local environment and the properties of the protein
- Mutations to cys must not be placed in the interfaces between chains or domains of the antibody (or scaffold). As a general rule modifications should be at a distance >5Å from residues involved in either chain-chain or domain-domain interfaces.
- Mutations to cys should be at a distance >5Å from any antibody native cys and should not interfere with the Fc glycosylation site (i.e. should be placed at a distance >5Å from residue Asn295 where glycosylation occurs)
- Mutations to cys should not increase the chemical degradation risk / should not introduce undesired post translational modifications

Screening of the trastuzumab sequence was then carried out to identify suitable sites for mutation to another residue such as e.g.cysteine.

The unmodified light chain sequence is:

DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSG
SRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:1)

The unmodified heavy chain sequence is:

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSV
KGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSSASTKGPSV
FPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI
SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK (SEQ ID NO: 2)

Ser, Thr, Val, and Ala residues in CH1, CH3, and CL were explored. This gave a number of candidates:

Light: SER171, VAL191, SER208, SER182, THR180, THR206, ALA184, SER203, SER202

Heavy: VAL170, VAL176, THR190, SER445, SER443, SER139, SER160, SER447, THR200, SER168.

These mutations were then analysed for desirable properties. Solvent accessibility surface modelling was carried out in silico. Discovery Studio (Accelrys Software Inc., Discovery Studio Modeling Environment, Release 4.0, San Diego: Accelrys Software Inc., 2013.) was used to calculate the Side Chain Solvent Accessibility Surface of the chosen residues. Solvent accessibility should be greater than 15% (> 15%), or greater than 17% (> 17%) to facilitate 'conjugability' of the molecule. The percentage side chain solvent accessibility surface is calculated as 100 times the side chain solvent accessibility divided by the side chain solvent accessibility of the fully exposed amino acid residue calculated using the extended Ala-X-Ala tripeptide, where X is the residue of interest. Side chains with solvent accessibility ratios of equal to or less than 15% (<= 15%) or equal to or less than 17% (<= 17%) are considered buried and not taken into account. The results of the SAS modelling are shown below:

Variant LC	**% SAS**	**Variant HC**	**% SAS**
SER171	5.45	VAL170	17.74
VAL191	48.069	VAL176	25.179
SER208	48.585	THR190	27.548
SER182	67.216	SER445	33.961
THR180	67.518	SER443	46.173
THR206	75.247	SER139	53.401
ALA184	116.94	SER160	61.951
SER203	122.689	SER447	72.323
SER202	136.452	THR200	91.354
		SER168	133.127

Aggregation propensity modelling was also carried out in silico. Aggregation propensity should not be significantly increased by the introduction of the intended engineered

Cys of any of these (potential) ADC variants. This propensity will be calculated based on a Z score comparison of the reference molecule and any of the (potential) ADC variants described above to the distribution of values for a reference set of the smallest functional domain of the antibody or protein where the mutation to Cys is introduced. A mean and standard deviation is determined for the reference set. The Z-score is then calculated by subtracting the reference mean from the target proteins score and dividing by the standard deviation. The result is a zero (0) centred score where positive values indicated that the target is more aggregation prone (in this case) than the mean. Targets with a Z-score within (-1, 1) are within the standard deviation of the score within the reference set. The AggreSolve™ in silico platform (Lonza, Basel, Switzerland) comprises a collection of algorithms which, based on sequence and structural parameters, can calculate predictors that reflect the aggregation propensity of a given polypeptide. Such predictors reflect global and local (residue-specific) aggregation propensities as well as local flexibility and stability.

Antibody Name	**Z-score**	**Difference (Variant – WT)**
Trastuzumab Heavy Chain (H)	0.36	
H:S160C	0.02	-0.34
H:T190C	0.36	0.00
H:S443C	0.19	-0.17
H:S447C	0.19	-0.17
Trastuzumab Light Chain (L)	3.09	
L:T180C	2.85	-0.24
L:T206C	3.10	0.01
Trastuzumab Heavy Chain constant domain 1 (CH1)	0.77	
CH1:S160C	0.17	-0.60
CH1:T190C	0.80	0.04
Trastuzumab Heavy Chain constant domain 3 (CH3)	-0.07	
CH3:S443C	-0.33	-0.26
CH3:S447C	-0.36	-0.29
Trastuzumab Light Chain constant domain (CL)	1.95	
CL:T180C	1.66	-0.29
CL:T206C	1.98	0.03

The AggreSolve Z-score has been calculated for the full length Trastuzumab heavy and light chain, as well as for the CH1, CH3, and CL domains in which the ADC substitutions are located (the minimal functional domains).

The boundaries for the CH1, CH3 and CL domains are as per the IMGT definition in M. P. Lefranc, C. Pommie, Q. Kaas, E. Duprat, N. Bosc, D. Guiraudou, C. Jean, M. Ruiz, I. Da Piedade, M. Rouard, E. Foulquier, V. Thouvenin, and G. Lefranc. IMGT unique numbering for immunoglobulin and T cell receptor constant domains and Ig superfamily C-like domains. Developmental and comparative immunology 29 (3), 2005.

Following these in silico selection steps, in vitro tests were carried out on the variants to determine protein yield (in vitro), aggregation / fragmentation, and binding kinetics.

- Protein yield, as estimated by product titre in supernatant and after protein A purification must be at least 70% or higher of the parental molecule
- The percentage of monomer lost after conjugation measured through Size Exclusion Chromatography HPLC) is preferably ≤ 35%, more preferably ≤5%, ≤10%, ≤15%, ≤20%, ≤25%, or ≤30%.
- Percentage aggregation of the conjugated molecule is preferably <5%, <10%, <15%, or <20%.
- Percentage fragmentation of the conjugated antibody antibody is preferably <5%, <10%, <15%, <20%, <25%, <30%, <32%, <35% or <40%.
- The Constant of Dissociation (KD) of the conjugated variants must be equal to or less than 2 (≤2) orders of magnitude than the reference standard KD of an unmutated or parent antibody. For the antibodies described herein the reference standard is herceptin (trastuzumab), although it will be appreciated that where a different parent antibody is used, then that parent may be used as a reference standard.

Systems for cloning and expression of antibodies in a variety of different host cells are well known. Suitable host cells include bacteria, mammalian cells, yeast and baculovirus systems. Mammalian cell lines available in the art for expression of a heterologous polypeptide include Chinese hamster ovary cells, HeLa cells, baby hamster kidney cells, NSO mouse melanoma cells and many others. A common, preferred bacterial host for small immunoglobulin molecules is E. coli. The expression of immunoglobulins, such as antibodies and antibody fragments, in

prokaryotic cells such as E. coli is well established in the art. Expression in eukaryotic cells in culture is also available to those skilled in the art as an option for production of a immunoglobulin. Immunoglobulins, such as antibodies and antibody fragments, may also be expressed in cell-free systems.

Suitable vectors for the expression of immunoglobulins can be chosen or constructed, containing appropriate regulatory sequences, including promoter sequences, terminator sequences, polyadenylation sequences, enhancer sequences, marker genes and other sequences as appropriate. Vectors may be plasmids, viral e.g. 'phage, or phagemid, as appropriate. For further details see, for example, Molecular Cloning: a Laboratory Manual: 2nd edition, Sambrook et al., 1989, Cold Spring Harbor Laboratory Press. Many known techniques and protocols for manipulation of nucleic acid, for example in preparation of nucleic acid constructs, mutagenesis, sequencing, introduction of DNA into cells and gene expression, and analysis of proteins, are described in detail in Current Protocols in Molecular Biology, Second Edition, Ausubel et al. eds., John Wiley & Sons, 1992. Nucleic acid encoding a variant immunoglobulin or a CH1 , VH and/or VL domain thereof may be contained in a host cell.

Variant antibodies were generated as described for example in WO2011021009A1. In detail: DNA encoding the antibody variants as described herein were chemically synthesized and cloned into a suitable mammalian expression vector. For transient expression experiments heavy and light chain were cloned into separate expression vectors. For generation of cell lines stably expressing a variant antibody heavy and light chains were cloned into one single expression vector. Each expression vector comprises a DNA encoding a signal sequence upstream of the heavy chain and the light chain coding regions to enable secretion of the heavy and light chain from the mammalian cells.

For transient expression, CHOK1SV cells were transfected using for example Lipofectamine with the expression vectors encoding the variants as described herein. For example in case of variants comprising at least one mutation in the light chain, an expression vector comprising said mutation(s) was co-transfected with a vector encoding the unmodified heavy chain; in case of variants comprising at least one mutation in the heavy chain, an expression vector comprising said mutation(s) was co-transfected with a vector encoding the unmodified light chain.72h post-transfection,

supernatants were harvested form the transfected cells, centrifuged and stored at 4°C prior to purification.

For Large scale production CHOK1SV cells are transfected as described above with a single vector comprising modified or unmodified light and heavy chain. Either pools of stably transfected cell are used for further experiments or a clonal selection is performed. Supernatants of such stable transfected cells expressing a variant of the present invention was harvested and stored at 4°C prior to purification.

Cell culture supernatants were Protein A purified using HiTrap columns (GE) and stored at 4°C prior to concentration and buffer exchange. Samples were concentrated by centrifugation at 2000g 15-20min. Material was buffer exchanged 4-5 times using formulation buffer (50mM Phosphate, 100mM NaCl, pH7.4). Once buffer exchanged, samples were diluted in formulation buffer to an appropriate working concentration.

Protein yield assessment (*in vitro*)

The antibody or antibody variant yield is estimated by product titre in supernatant and after protein A purification (e.g. through sandwich ELISA, with absorbance at 280nm, or via HPLC protein A quantification).

Fig 1 shows levels of expression of each candidate antibody in 25 ml CHOK1SV cultures. All variants show similar levels of expression.

Conjugation

Conjugation was carried out with biotin-maleimide conjugation to free thiol groups by standard techniques Junutula J R *et al*, Nature Biotechnology 2008, 8, 925-932; Jeffrey S C *et al*, Bioconjugate Chem. 2013, 24, 1256-1263..

For conjugation to a toxin engineered antibodies are e.g reduced with a tris(2-carboxyethyl)phosphine (12.5 eq.) for 2 h at 35 °C and pH 7.7. The mixture is buffer exchanged into 50 mM Tris, 5 mM EDTA, pH 7.7. Dehydroascorbic acid (15 eq.) is added and the oxidation reaction allowed to proceed for 3 h at 24 °C. N,N-dimethylacetamide is added to reach a concentration of typically between 1 and 5%.

Maleimidocaproyl-valine-citrulline-p-aminobenzyloxycarbonyl-monomethylauristatin E (5 eq.) is added and the conjugation reaction allowed to proceed for 1 h at 22 °C. The reaction is quenched by addition of N-acetyl-cysteine (5 eq.). Following 0.5 h incubation at 22 °C, the mixture is buffered exchanged into 1x PBS.

Aggregation propensity / fragmentation assessment (*in vitro*)

Before and after conjugation the percentage of monomer lost due to antibody aggregation and/or fragmentation was measured quantitatively using Size Exclusion Chromatography HPLC (SEC-HPLC) and qualitatively using SDS PAGE. For the latter, each variant antibody was treated with beta mercaptoethanol, or given no treatment, and size fractionated on a SDS PAGE. There was no apparent aggregation or fragmentation of the variants visible.

Results from SEC-HPLC analysis of conjugated and unconjugated samples are shown in Fig 2, using samples at 1 mg/ml on a Zorbax-250GF column. Surprisingly some of the antibodies of the invention such as for example HC S139C, HC V170C, HC S160C, HC T200C, LC V191C, LC T206C, and LC T180C showed less monomer lost, and/or decreased amount of antibody aggregation or fragmentation compared with the parent / unmutated antibody.

Binding kinetics assessment (*in vitro*)

Binding kinetics of the variants were also analysed using a quartz crystal microbalance. ERB2/HER2 Fc chimaera were immobilized to carboxyl chip, and three different concentrations of each variant (conjugated and not conjugated) were tested. The table below summarises the Kd for each variant:

	K_D (nM)	
Reference	**Not Conjugated**	**Conjugated**
Herceptin	3.0	1.63
Variant	**Not Conjugated**	**Conjugated**
LCHerS208C	-	-
HCHerS443C	4.36	31.13

LCHerS202C	12.22	0.72
HCHerT200C	3.52	12.91
HCHerV170C	3.43	2.90
HCHerS447C	3.17	1.34
LCHerV191C	4.94	3.56
HCHerS445C	1.27	1.74
HCHerS168C	18.11	1.55
HCHerT190C	1.26	2.28
HCHerS139C	3.56	2.44
LCHerT206C	9.41	19.91
LCHerT180C	5.19	1.46
HCHerS160C	9.76	1.50
LCHerS182C	5.28	0.008
LCHerA184C	1.25	1.04
LCHerS203C	-	-

Drug to Antibody Ratio (DAR) assessment (*in vitro*)

Finally, the DAR was determined for each of the variants, by liquid chromatography-electrospray ionization-tandem mass spectrometry (LC-ESI-MS/MS or LC-ESI-MS). The DAR values for the different variants must be >1.7 and <2.2, as there are two site specific conjugation sites per antibody.

For determining the DAR samples at 1 mg/ml were treated with PNGaseF. Reduced and not-reduced samples were analysed, by RP chromatography, electrospray, and mass spectrometry.

The extent of biotin-maleimide conjugation to light and heavy chains of the variants is shown in Figs 3 and 4 respectively, with the calculated DAR for each variant being shown in Fig 5.

Conjugation and de-conjugation assessment (*in vitro*)

When stability of the ADC is analysed in vitro, the percentage average loss of conjugated molecule over a period of 8 days should be <39%.

Six preferred variants were selected, and each of the preferred six variants was then further analysed. Conjugate stability (levels of deconjugation) was determined for four different concentrations (150ng/ml; 300ng/ml; 1000ng/ml and 2000ng/ml) of each of the final variants in human serum at 37 deg C for 8 days. Samples were taken on days 0, 2, 4, and 8, and analysed by ELISA.

The percentage biotin decrease over 8 days is shown in Fig 6.

Each of the final six variants was then ranked for desirable characteristics (purity, DAR, deconjugation, and positive environment), and given a score from 6 (=best) to 1 (=worst). The scores were then totalled, to give an overall score from 4 to 24. This gives an indication of the desirability of each antibody for further development. The scores are shown in the table below.

	Purity		DAR		% Deconjugation		Positive Environment		Total
HCHerS443C	60.83	1	2.00	6	29	6	LYS	6	19
HCHerS447C	66.94	2	2.09	4	40	1		2	9
HCHerT190C	77.19	3	1.77	2	37	3		2	10
LCHerT206C	82.7	5	2.13	3	40	1	LYS	6	15
LCHerT180C	84.58	6	1.76	1	32	5		2	14
HCHerS160C	81.03	4	1.96	5	32	5		2	16

Although the antibody variants can be ranked in this way, as each of the final six has been through the initial selection process, they can all be said to have desirable characteristics for development as an ADC. In particular, not every antibody will make it through subsequent drug development processes and in vivo testing, so it is beneficial to be able to generate a selection of candidates. Furthermore, other variants not selected for the final six, such as the remaining variants disclosed herein, may also have beneficial properties and so may be considered useful for further investigation.

The six final variants were: four heavy chain (S160C, T190C, S443C, S447C), and two light chain (T180C, or T206C) variants. As a result of the sequential method of

selection all final variants can be expected to share a number of specific properties (or design criteria): Stability; low aggregation; low chemical degradation risk; low undesired post translational modifications; structural stability preserved; productivity; suitability for being conjugated; and biological activity.

5

The values for each tested variant are shown in the table below; the six final selected variants are highlighted.

	Prot A HPLC	SEC HPLC	K_D (nM)		LC MS Light Chain			LC MS Heavy Chain				DAR
	mg/L	% Monomer conj. Ab	NOT CONJUGATED	CONJUGATED	Unmodified	+1 Conjugate	+2 Conjugates	Unmodified	+1 Conjugate	+2 Conjugates	+3 Conjugates	
Herceptin	55.13	78.53	3.02	1.63	100%	0%	0%	100%	0%	0%	0%	0.00%
LCHerS208C	48.11	54.06	-	-	-	-	-	-	-	-	-	-
HCHerS443C	54.96	60.83	4.36	31.13	89%	11%	0%	11%	89%	0%	0%	2.00%
LCHerS202C	55.00	69.00	12.22	0.72	32%	60%	7%	95%	5%	0%	0%	1.60%
HCHerT200C	58.83	94.94	3.52	12.91	100%	0%	0%	100%	0%	0%	0%	0.00%
HCHerV170C	55.42	93.54	3.43	2.90	100%	0%	0%	100%	0%	0%	0%	0.00%
HCHerS447C	49.11	66.94	3.17	1.34	81%	19%	0%	15%	85%	0%	0%	2.09%
LCHerV191C	56.37	95.73	4.94	3.56	100%	0%	0%	100%	0%	0%	0%	0.00%
HCHerS445C	57.93	77.22	1.27	1.74	78%	22%	0%	22%	35%	34%	8%	3.01%
HCHerS168C	57.68	78.01	18.11	1.55	93%	7%	0%	39%	61%	0%	0%	1.36%
HCHerT190C	46.22	77.19	1.26	2.28	94%	6%	0%	18%	82%	0%	0%	1.77%
HCHerS139C	60.58	80.27	3.56	2.44	84%	16%	0%	22%	52%	22%	4%	2.47%
LCHerT206C	53.83	82.70	9.41	19.91	4%	88%	8%	97%	3%	0%	0%	2.13%
LCHerT180C	46.87	84.58	5.19	1.46	16%	81%	4%	100%	0%	0%	0%	1.76%
HCHerS160C	55.47	81.03	9.76	1.50	95%	5%	0%	7%	93%	0%	0%	1.96%
LCHerS182C	51.18	73.15	5.28	8x10-3	38%	62%	0%	100%	0%	0%	0%	1.25%
LCHerA184C	60.11	80.20	1.25	1.04	86%	14%	0%	100%	0%	0%	0%	0.28%
LCHerS203C	53.61	58.22	-	-	-	-	-	-	-	-	-	-

Subsequently the final six variants were conjugated to Monomethyl Auristatin E (MMAE) by standard techniques. The conjugation method follows broadly methods described above. The DAR for the selected variants was determined as described above. An example of the results is shown in figure 7. Cond 1-3 represent minor variants in the conjugation procedure with parameters varied to try to optimise the DAR; the reduction time and temperature for antibodies prior to conjugation were varied in each of conditions 1-3:

Condition 1: reduction at 35°C for 2h (as described above)

Condition 2: reduction at 25°C for 2h

Condition 3: reduction at 35°C for 1h.

A double mutant (DM) combining LC T180C and HC S160C was also tested to determine aggregation propensity and DAR data, using the same techniques as described above. The results are shown in the following tables:

DM Aggregation data from the transient transfections

using size-exclusion chromatography SEC

Species	**Relative % by SEC**	
	Before conjugation	**After conjugation**
Purity, main peak	95.4	96.1
High molecular weight forms	3.0	3.0
Low molecular weight forms	1.6	0.9

DM DAR Data from the transient transfections

using PLRP HPLC

or ESI-MS methods

Variant	**PLRP**	**Intact mass**
DM	3.77	3.97

In vitro toxicity tests

After MMAE conjugation the ADC variants were tested for in vitro cytotoxicity. The analysis was carried out by standard techniques (Andreotti, P.E. et al. Cancer Res

1995.55, 5276–82; Gerhardt, R.T. et al. Am. J. Obstet. Gynecol 1991 165, 245–55). The cells chosen for the assay were based on Neve R.M. et al. Cancer Cell 2006 10, 515-527.

Assay schematics:

Day 1: Seed three 96-well plates each of SKBR3 cells (5k/well) in media (McCoy5A + 10%FBS + 1XPen/Strep), BT474 cells (8k/well) in media (DMEM/F12 + 10%FBS + 1XPen/Strep), and MCF7 cells (4k/well) in media (RPMI + 10%FBS + 1XPen/Strep). Incubate in 37°C humidified CO2 incubator for 18hrs.

Day 2: Prepare ADC variants sample dilutions. Make the initial 667nM working stocks of these samples in RPMI media with 10% FBS. Then prepare 1/3 serial dilution from 667nM to 11pM in media. Add 5ul of the dilution into each well of ~100ul cells. Final sample concentrations range from 33.3nM to 0.56pM (as 1/3 serial dilutions). Incubate at 37°C in a humidified CO2 incubator for 72hrs.

Day 4: Evaluate the plates under a microscope

Day 5: Determine cell viability using Cell-Titer Glo reagent:

–Aspirate the media from the 96-well plate.

–Add 100ul of Cell-Titer Glo reagent (Promega Inc.) in each well. Incubate at room temperature for 10min.

– Determine luminescence using Tecan Ultra plate reader.

–Analyze andplot data either as Percent Viability vs. Concentration (nM), or as random luminesce.

An example of the results is shown in figure 8. As can be seen in Figure 8, ADC variants HC S443C and LC T180C reduce the viability of SKBR3 cells and BT474 cells by 50% at very low concentrations, whereas these ADC variants do not show an effect over 72 hours in less responsive cells like MCF7.

The full sequences of the variant chain of each of the variants described herein are shown below. These show only the variant chain; the other chain will be the same as the unmodified trastuzumab sequence (that is, SEQ ID No 1 (LC) or 2 (HC)).

Heavy chains:

>HCherS139C (SEQ ID No 3)
EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWV
ARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYC
SRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTCGGTAA
LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLSLSPGK

>HCherS160C (SEQ ID No 4)
EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWV
ARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYC
SRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAA
LGCLVKDYFPEPVTVCWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLSLSPGK

>HCherS168C (SEQ ID No 5)
EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWV
ARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYC
SRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAA
LGCLVKDYFPEPVTVSWNSGALTCGVHTFPAVLQSSGLYSLSSVVTVP
SSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLSLSPGK

>HCherV170C (SEQ ID No 6)
EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWV
ARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYC
SRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAA
LGCLVKDYFPEPVTVSWNSGALTSGCHTFPAVLQSSGLYSLSSVVTVP
SSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW

ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLSLSPGK

>HCherV176C (SEQ ID No 7)
EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWV
ARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYC
SRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAA
LGCLVKDYFPEPVTVSWNSGALTSGVHTFPACLQSSGLYSLSSVVTVP
SSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLSLSPGK

>HCherT190C (SEQ ID No 8)
EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWV
ARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYC
SRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAA
LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVCVP
SSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLSLSPGK

>HCherT200C (SEQ ID No 9)
EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWV
ARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYC
SRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAA
LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSSLGTQCYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLSLSPGK

>HCherS443C (SEQ ID No 10)
EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWV
ARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYC
SRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAA
LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKCLSLSPGK

>HCherS445C (SEQ ID No 11)
EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWV
ARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYC
SRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAA
LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLCLSPGK

>HCherS447C (SEQ ID No 12)
EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWV
ARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYC
SRWGGDGFYAMDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAA
LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH
NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLSLCPGK

Light chains:

>LCherS171C (SEQ ID No 13)
DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLI
YSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPP
TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA
KVQWKVDNALQSGNSQESVTEQDSKDCTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

>LCherT180C (SEQ ID No 14)
DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLI
YSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPP
TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA
KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLCLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

>LCherS182C (SEQ ID No 15)
DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLI
YSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPP
TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA
KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLCKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

>LCherA184C (SEQ ID No 16)

DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLI
YSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPP
TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA
KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKCDYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

>LCherV191C (SEQ ID No 17)
DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLI
YSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPP
TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA
KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKCY
ACEVTHQGLSSPVTKSFNRGEC

>LCherS202C (SEQ ID No 18)
DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLI
YSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPP
TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA
KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLCSPVTKSFNRGEC

>LCherS203C (SEQ ID No 19)
DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLI
YSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPP
TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA
KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSCPVTKSFNRGEC

>LCherT206C (SEQ ID No 20)
DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLI
YSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPP
TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA
KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVCKSFNRGEC

>LCherS208C (SEQ ID No 21)
DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLI
YSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPP
TFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREA
KVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKCFNRGEC

It will be appreciated that a similar selection and screening process may be used to develop other variant antibodies, not only those based on trastuzumab, and further that it may be expected that variants of these other antibodies having the same constant region mutations as identified herein would also be expected to have similar desirable properties.

CLAIMS:

1. An antibody or a fragment thereof, having a variable region which binds a target molecule, and a constant region, wherein the light chain is a kappa light chain, and wherein the constant region comprises one or more mutations introducing a site specific conjugation site selected so as to permit conjugation of the antibody, or fragment to a payload, wherein the light chain comprises the amino acid sequence of SEQ ID NO: 40, where X is C; the heavy chain comprises one or more amino acid sequence selected from SEQ ID NOs: 23, 24, 25, 26, 27, or 28, where each X is C.

2. The antibody of claim 1, wherein the antibody is selected from IgG1, IgG2, IgG3, and IgG4.

3. The antibody of any preceding claim wherein the constant region comprises at least a portion of an IgG1 constant region.

4. The antibody of claim 3 wherein the constant region comprises one or more of the Ck, CH1 and CH3 domains of the IgG1 constant region.

5. The antibody of any preceding claim wherein the antibody is selected from the group consisting of Fabs, bi specific antibody fragments (tandem scFv-Fc, scFv-Fc knobs-into-holes, scFv-Fc-scFv, F(ab')2, Fab-scFv, (Fab'scFv)2, scDiabody-Fc, or scDiabody-CH3), IgG-based bispecific antibodies (Hybrid hybridoma, Knobs-into-holes with common light chain, Two-in-one IgG, Dual V domain IgG, IgG-scFv, scFv-IgG, IgG-V, V-IgG), minibody, and tribi-minibody.

6. The antibody of any preceding claim wherein the antibody is human, humanised, or chimeric.

7. The antibody of any preceding claim comprising one or more mutations introducing a site specific conjugation site selected so as to permit conjugation of the antibody, wherein the antibody is selected from Abciximab; Rituximab; Basiliximab ;Daclizumab; Palivizumab; Infliximab; Trastuzumab; Alemtuzumab; Adalimumab; Efalizumab; Cetuximab; Ibritumomab; Omalizumab; Bevacizumab; Ranibizumab; Golimumab; Canakinumab; Ustekinumab; Tocilizumab; Ofatumumab; Belimumab; Ipilimumab; Brentuximab; Pertuzumab; Raxibacumab; Vedolizumab; Ramucirumab; Obinutuzumab; Siltuximab; Secukinumab; Dinutuximab.

8. The antibody of any preceding claim which lacks one or more Fc effector functions.

9. The antibody of claim 8 which lacks ADCC activity.

10. The antibody of any of claims 1 to 9 which has increased ADCC activity.

11. The antibody of any preceding claim further comprising a linker.

12. An immunoconjugate comprising an antibody according to any of claims 1 to 11, a payload, and a linker joining the payload to the antibody.

13. The antibody of claim 11, or the immunoconjugate of claim 12, wherein the linker is selected from 6-maleimidocaproyl (MC), maleimidopropanoyl (MP), valine-citrulline (val-cit), alanine-phenylalanine (ala-phe), p-aminobenzyloxycarbonyl (PAB), N-Succinimidyl 4-(2-pyridylthio) pentanoate (SPP), N-succinimidyl 4-(N-maleimidomethyl) cyclohexane-1 carboxylate (SMCC), N-Succinimidyl, (4-iodo-acetyl) aminobenzoate (SIAB), SPDB, hydrazone, maleimidocaproyl and 6-maleimidocaproyl-valine-citrulline-p-aminobenyloxycarbonyl (MC-vc-PAB); or is a branched linker which comprises a peptide chain and is derived from o- hydroxy p-amino benzylic alcohol, wherein the peptide chain is connected to the phenyl ring via the p-amino group, the payload is connected to the phenyl ring via the benzylic alcohol moiety, and the antibody is connected to the phenyl ring via the o-hydroxy group.

14. The immunoconjugate of claim 12 or 13, wherein the payload is selected from the group consisting of a radionuclide, a chemotherapeutic agent, a cytotoxic agent, a microbial toxin, a plant toxin, a polymer, a carbohydrate, a cytokine, a fluorescent label, a luminescent label, an enzyme-substrate label, an enzyme, a peptide, a peptidomimetic, a nucleotide, an siRNA, a microRNA, an RNA mimetic, and an aptamer.

15. The immunoconjugate of claim 14 wherein the payload is selected from the group consisting of 90Y, 131I, 67Cu, 177Lu, 213Bi, 211At, dolastatin, vedotin, monomethyl auristatin F(MMAF), monomethyl auristatin E (MMAE);maytansinoids including DM1 and DM4, duocarmycin, duocarmycin analogs, calicheamicin, pyrrolobenzodiazepines (PBD), centanamycin, irinotecan, and doxorubicin, alpha-amanitin, melatonin, membrane disrupting peptide, Pseudomonas exotoxin A, Diphtheria toxin, ricin, polyethylene glycol, hydroxyethyl starch, and a mannosyl residue.

16. The immunoconjugate of claim 12 or 13, wherein the payload is a microtubule disrupting agent, or a DNA modifying agent.

17. A pharmaceutical composition comprising an antibody or an immunoconjugate according to any preceding claim, and a pharmaceutically acceptable diluent, carrier or excipient.

18. A method for generating an immunoconjugate, the method comprising conjugating an antibody according to any of claims 1 to 11 to a payload.

19. An isolated or recombinant polynucleotide encoding the antibody of any of claims 1-10.

20. A vector comprising the polynucleotide of claim 19.

21. The vector of claim 20 further comprising an inducible promoter operably linked to the polynucleotide.

22. A host cell comprising the vector of claim 20 or claim 21.

23. A method of producing an antibody comprising:

(a) providing a culture medium comprising the host cell of claim 22; and

(b) placing the culture medium in conditions under which the antibody is expressed, and optionally (c) isolating the antibody.