ANTIBODIES COMPRISING CHIMERIC CONSTANT DOMAINS

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit under 35 U.S.C. § 119(e) of U.S. Provisional Application No. 61/759,578, filed 1 February 2013, which application is herein incorporated by reference.

SEQUENCE LISTING

[0002] This application incorporates by reference the Sequence Listing submitted in Computer Readable Form as file 8550PCT_ST25.txt created on January 29, 2014 (43,512 bytes).

FIELD OF THE INVENTION

[0003] The present invention concerns antibodies or antigen-binding proteins engineered with recombinant polypeptides comprising a chimeric constant region, more specifically including a chimeric hinge region in the heavy chain constant region. The present invention relates to antibodies and antigen-binding proteins comprising such recombinant polypeptides that reduce effector functions and provide an advantage for use in therapy.

BACKGROUND OF THE INVENTION

[0004] Immunoglobulins of the IgG class are attractive as therapeutic agents. IgGs exists as four subclasses in humans, IgG1, IgG2, IgG3, and IgG4. The heavy chain constant (C_H) region of IgG comprises three domains, C_H1, C_H2, C_H3, where C_H1 and C_H2 are linked by a hinge. Although the role of each subclass appears to vary between species, it is known that the heavy chain constant domain is responsible for various biological effector functions. The human IgG subclasses mediate a plethora of cellular immune responses through their interaction with Fcγ receptors (FcγRs), such as cell killing, complement activation, phagocytosis and opsonization. In an attempt to understand and manipulate the effects of IgG subclass binding to FcγRs, researchers have made various mutations to the constant domains of IgGs and studied the resulting IgG/FcγR interaction (see e.g. Canfield and Morrison *J Exp Med* 73, 1483-1491 (1991); Chappel, M.S., et al. *JBC* 268(33), 25124-31 (1993); and Armour, K. L., et al. *Eur J Immunol* 29, 2613-24 (1999)).

[0005] Fc dependent cytotoxic activity of human IgG antibodies requires binding of the Fc region of the antibody (which consists of at least a functional CH2 and CH3 domain) to an FcγR on the surface of an effector cell, such as a natural killer cell, an activated macrophage

or the like. Complement-mediated lysis can also be triggered by the interaction of the Fc region with various complement components. With regard to FcγR binding, it has been suggested that several amino acid residues in the hinge region and in the C_H2 domain of the antibody are important (see Sarmay, G, et al. *Mol Immunol* 29, 633-9 (1992); Greenwood, J et al., *Eur. J. Immunol*, 23(5), 1098 (1993), Morgan, A. et al, *Immunology*, 86, 319 (1995), Stevenson, GT, *Chemical Immunology*, 65, 57-72 (1997)). Glycosylation of a site (N297) in the CH2 domain and variations in the composition of its carbohydrates also strongly affect the IgG/FcγR interaction (Stevenson, GT, *Chemical Immunology*, 65, 57-72 (1997); Sibéril et al *Immunol Ltrs* 106, 111–118 (2006)).

[0006] For certain antibody therapies, it may be advantageous to engineer the Fc receptor binding properties so as to activate all, some, or none of the available effector mechanisms, without affecting the antibody's pharmacokinetic properties. The desired combination of therapeutic properties may not be available in the natural antibody repertoire. The design of antibodies with reduced effector function should be efficacious for example when the therapeutic objective is not to kill a target cell, but to block or activate a cell surface molecule on its surface without triggering cytotoxicity. Another setting in which reduced binding to Fc receptors could be desirable is when the antibody is bispecific, and its desired therapeutic properties arise from the different binding specificities. For example, a common usage of bispecific antibodies is to combine a tumor targeting specificity with a T cell activating specificity in order to trigger tumor-specific T cell killing. In this case, if the Fc portion binds to an Fc receptor, then potentially that could trigger undesirable killing of cells bearing Fc receptors by T cells, or killing of T cells by Fc receptor-bearing cells such as natural killer cells or macrophages.

[0007] Thus, there exists a need for improved biological therapies, such as antibodies with desirable properties for use in such therapies. Applicants have discovered that recombinant proteins containing substituted or otherwise modified antibody heavy chains, including recombinant antibodies and recombinant receptor-Fc fusion proteins, have altered Fc receptor binding activity, which reduce the risk of unwanted side effects, and thus provide improved therapeutic effect.

SUMMARY OF THE INVENTION

[0008] The antibodies, antigen-binding proteins and Fc-fusion proteins that are disclosed herein are engineered to have reduced binding to Fc receptors.

[0009] One aspect of the invention provides a recombinant polypeptide comprising a chimeric Fc region, wherein the Fc region comprises a chimeric hinge comprising the amino acid sequence EPKSCDKTHTCPPCPAPPVA (SEQ ID NO: 8). The invention also provides a recombinant polypeptide comprising a chimeric Fc region, wherein the Fc region comprises a chimeric hinge comprising the amino acid sequence ESKYGPPCPPCPAPPVA (SEQ ID NO: 9).

[0010] Another aspect of the invention provides a recombinant polypeptide comprising a chimeric Fc region, wherein the Fc region comprises a chimeric hinge comprising the amino acid sequence EPKSCDKTHTCPPCPAPPVA (SEQ ID NO: 8) linked to an IgG4 CH2 region. Still another aspect of the invention provides a recombinant polypeptide comprising a chimeric Fc region, wherein the Fc region comprises a chimeric hinge comprising the amino acid sequence ESKYGPPCPPCPAPPVA (SEQ ID NO: 9) linked to an IgG4 CH2 region.

[0011] In some embodiments, the recombinant polypeptide comprises a chimeric Fc region, wherein the Fc region comprises an IgG1 or IgG4 CH3 region, or a variant thereof. In other embodiments, the recombinant polypeptide comprises a chimeric Fc region, wherein the Fc region binds to FcγRIIA. In other aspects the recombinant polypeptide comprises a chimeric Fc region, wherein the Fc region binds to FcγRIIA and FcγRIIB.

[0012] In other embodiments, the invention provides a recombinant polypeptide comprising a chimeric Fc region, wherein the Fc region comprises chimeric hinge comprising an amino acid sequence EPKSCDKTHTCPPCPAPPVA (SEQ ID NO: 8) and the recombinant polypeptide binds to FcγRIIA.

[0013] In still other aspects, the invention provides a recombinant polypeptide comprising a chimeric Fc region, wherein the Fc region comprises a chimeric hinge comprising an amino acid sequence ESKYGPPCPPCPAPPVA (SEQ ID NO: 9) and the recombinant polypeptide binds to FcγRIIA.

[0014] A further aspect of the invention provides a recombinant polypeptide comprising a heavy chain constant (CH) region comprising, from N-terminus to C-terminus, a CH1 domain, a chimeric hinge, a CH2 domain, and a CH3 domain wherein the CH1 domain comprises a human IgG1 CH1 or a human IgG4 CH1 having at least the amino acid sequence DKKV or DKRV from positions 212 to 215 (EU numbering), the chimeric hinge comprises a human IgG1 or a human IgG4 upper hinge amino acid sequence from positions 216 to 227 (EU numbering) and a human IgG2 lower hinge amino acid sequence

PCPAPPVA (SEQ ID NO: 3) from positions 228 to 236 (EU numbering), the CH2 domain comprises a human IgG4 CH2 domain amino acid sequence from positions 237 to 340 (EU numbering), and the CH3 domain comprises a human IgG1 or a human IgG4 CH3 domain sequence from positions 341 to 447 (EU numbering), or a variant thereof.

[0015] Some embodiments of the invention provide a recombinant polypeptide wherein the CH1 domain comprises a human IgG1 CH1 amino acid sequence (SEQ ID NO: 43), and the chimeric hinge comprises the amino acid sequence EPKSCDKTHTCPPCPAPPVA (SEQ ID NO: 8). Still another embodiment of the invention provides a recombinant polypeptide wherein the CH1 domain comprises a human IgG4 CH1 amino acid sequence (SEQ ID NO: 44), and the chimeric hinge comprises the amino acid sequence ESKYGPPCPPCPAPPVA (SEQ ID NO: 9).

[0016] Another embodiment of the invention provides a recombinant polypeptide wherein the CH1 domain comprises the amino acid sequence DKKV (SEQ ID NO: 4), and the chimeric hinge comprises the amino acid sequence EPKSCDKTHTCPPCPAPPVA (SEQ ID NO: 8). Still another embodiment of the invention provides a recombinant polypeptide wherein the CH1 domain comprises the amino acid sequence DKRV (SEQ ID NO: 5), and the chimeric hinge comprises the amino acid sequence ESKYGPPCPPCPAPPVA (SEQ ID NO: 9). In another aspect, the CH1 domain comprises a variant of SEQ ID NO: 43 or 44.

[0017] Another embodiment of the invention provides a recombinant polypeptide wherein the CH2 domain comprises the amino acid sequence SEQ ID NO: 10. Yet another embodiment of the invention provides a recombinant polypeptide wherein the CH3 domain comprises the amino acid sequence SEQ ID NO: 11 or SEQ ID NO: 12. In another aspect, the CH3 domain comprises SEQ ID NO: 41 or 42.

[0018] An aspect of the invention provides a recombinant polypeptide, wherein the polypeptide comprises N'-VD1-$X1_n$-Y1-Y2-X2-X3-C', wherein:

N' is the N-terminus and C' is the C-terminus of the polypeptide,

VD1 is an amino acid sequence comprising an antigen-binding domain,

X1 is an amino acid sequence comprising a domain selected from the group consisting of an IgG1 CH1 domain or a variant thereof, an IgG4 CH1 domain or a variant thereof, and at least positions 212-215 (EU numbering) of an IgG1 or IgG4 CH1 domain,

Y1 comprises an amino acid sequence from positions 216-227 (EU numbering) of an IgG1 or IgG4 hinge region,

Y2 comprises the human IgG2 lower hinge region amino acid sequence PCPAPPVA (SEQ ID NO: 3) from positions 228 to 236 (EU numbering),

X2 is an amino acid sequence comprising an IgG4 CH2 domain, or a variant thereof, and

X3 is an amino acid sequence comprising an IgG1 CH3 domain or an IgG4 CH3 domain, or a variant thereof; wherein n = 0 or 1.

[0019] In some embodiments of the invention, n = 1. In yet another embodiment of the invention, X1 comprises the amino acid sequence DKKV (SEQ ID NO: 4), and Y1-Y2 comprises a chimeric hinge consisting of the amino acid sequence EPKSCDKTHTCPPCPAPPVA (SEQ ID NO: 8). In still another embodiment of the invention, X1 comprises the amino acid sequence DKRV (SEQ ID NO: 5), and Y1-Y2 comprises a chimeric hinge consisting of the amino acid sequence ESKYGPPCPPCPAPPVA (SEQ ID NO: 9). In one more embodiment, X1 comprises SEQ ID NO 43 or SEQ ID NO: 44. In another aspect of the invention, X2 comprises SEQ ID NO: 10. In another embodiment of the invention, X3 comprises SEQ ID NO: 11 or SEQ ID NO: 12. In yet another embodiment, X3 comprises SEQ ID NO: 41 or SEQ ID NO: 42.

[0020] Another aspect of the invention provides a recombinant polypeptide wherein the heavy chain constant region (CH) region comprises an amino acid sequence at least 99% identical to any one of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 37 or SEQ ID NO: 38.

[0021] In some embodiments, n = 0 and Y1-Y2 comprises a chimeric hinge having the amino acid sequence EPKSCDKTHTCPPCPAPPVA (SEQ ID NO: 8). In other embodiments, n = 0 and Y1-Y2 comprises a chimeric hinge having the amino acid sequence ESKYGPPCPPCPAPPVA (SEQ ID NO: 9).

[0022] In another embodiment of the invention, the recombinant polypeptide is an antigen-binding protein. In another embodiment, the recombinant polypeptide is a Fc-fusion protein, such as a receptor-Fc fusion protein. In yet another embodiment of the invention, the recombinant polypeptide is an antibody.

[0023] A further aspect of the invention provides a recombinant polypeptide, antigen-binding protein, Fc-fusion protein or antibody that exhibits decreased effector functions when compared to a corresponding recombinant polypeptide, antigen-binding protein, Fc-fusion protein or antibody comprising the wild-type IgG1 or IgG4 heavy chain constant region, at a concentration of at least 10 nM. The invention thus provides a recombinant polypeptide, antigen-binding protein, Fc-fusion protein or antibody having decreased binding, cytotoxic activity, and cellular proliferation.

[0024] The invention further provides a recombinant polypeptide, antigen-binding protein, Fc-fusion protein or antibody that exhibits cytotoxic activity of less than about 50%, at a concentration of at least 10 nM or at least 100 nM. The invention also provides a recombinant polypeptide, antigen-binding protein, Fc-fusion protein or antibody that exhibits

cytotoxic activity of less than about 40%, or less than about 30%, or less than about 20%, or less than about 10%, or less than about 5%, or even undetectable, at a concentration of at least 10 nM or at least 100 nM.

[0025] In other embodiments, the recombinant polypeptide, antigen-binding protein, Fc-fusion protein or antibody exhibits CDC activity of less than about 50% cytotoxicity, or less than

[0026] 40%, 30%, 20%, 10%, or 5%, 4%, 3%, 2%, or even 0% or undetectable cytotoxicity, as measured in an *in vitro* or *ex vivo* cell killing assay. In certain embodiments, CDC activity is less than 50%, 40%, 30%, 20%, 10%, or 5%, 4%, 3%, 2%, or even 0% or undetectable, at a concentration of 100 nM. In more embodiments, the recombinant polypeptide, antigen-binding protein, Fc-fusion protein or antibody exhibits ADCC activity of less than about 50% cytotoxicity, or less than cytotoxicity 40%, 30%, 20%, 10%, or 5%, 4%, 3%, 2%, or even 0% or undetectable cytotoxicity, as measured in an *in vitro* or *ex vivo* cell killing assay. In certain embodiments, ADCC activity is less than 50%, 40%, 30%, 20%, 10%, or 5%, 4%, 3%, 2%, or even 0% or undetectable ADCC activity, at a concentration of 100 nM.

[0027] In still other embodiments, the recombinant polypeptide, antigen-binding protein, Fc-fusion protein or antibody exhibits ADCP activity of less than about 50% ADCP activity, or less than 40%, 30%, 20%, 10%, or 5%, 4%, 3%, 2%, or even 0% or undetectable ADCP activity, as measured in an *in vitro* or *ex vivo* cellular phagocytosis assay. In certain embodiments, ADCP activity is less than 50%, 40%, 30%, 20%, 10%, or 5%, 4%, 3%, 2%, or even 0% or undetectable ADCP activity, at a concentration of 100 nM.

[0028] The invention further provides a recombinant polypeptide wherein the cytotoxic activity is at least about 10-fold less than the cytotoxic activity of a corresponding polypeptide comprising a wild-type IgG1 or wild-type IgG4 heavy chain constant region. The invention also provides a recombinant polypeptide wherein the cytotoxic activity is at least about 10-fold less, about 20-filed less, about 50-fold less, or about 100-fold less, or about 1000-fold less than the cytotoxic activity of a corresponding polypeptide comprising a wild-type IgG1 or wild-type IgG4 heavy chain constant region.

[0029] An aspect of the invention provides a composition comprising the recombinant polypeptide.

[0030] Another aspect of the invention provides a nucleic acid molecule encoding any one of the recombinant polypeptides of the invention. The invention further provides a nucleic acid molecule encoding a recombinant polypeptide of the invention, wherein the recombinant polypeptide comprises an amino acid sequence selected from the group consisting of SEQ

ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 38 and SEQ ID NO: 37.

[0031] The invention further provides a nucleic acid molecule comprising a nucleotide sequence having greater than 99% sequence identity to SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 32, or SEQ ID NO: 33. The invention also provides a nucleic acid molecule comprising a nucleotide sequence having greater than 99% sequence identity to SEQ ID NO: 36 or SEQ ID NO: 35.

[0032] The invention also provides a nucleic acid molecule comprising a nucleotide sequence selected the group consisting of SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 36 and SEQ ID NO: 35.

[0033] An aspect of the invention provides a vector comprising any one of the nucleic acid molecules of the invention. The invention further provides a vector wherein the nucleic acid molecule of the invention is operatively linked to an expression control sequence suitable for expression in a host cell. The invention also provides a vector of the invention wherein the expression control sequence comprises a promoter selected from the group consisting of SV40, CMV, CMV-IE, CMV-MIE, UbC, RSV, SL3-3, MMTV, Ubi and HIV LTR. The invention further provides a vector of the invention wherein the promoter is a CMV-MIE/TetO or CMV-MIE/Arc hybrid promoter. The invention also provides a vector of the invention comprising one or more selectable marker genes selected from the group consisting of bla, bls, BSD, bsr, Sh ble, hpt, tetR, tetM, npt, kanR and pac.

[0034] Another aspect of the invention provides a cell comprising a nucleic acid of the invention. The invention further provides a cell comprising a vector of the invention.

[0035] The invention further provides a cell comprising a nucleic acid of the invention, wherein the nucleic acid is integrated into the genome of the cell. The invention also provides a cell comprising a nucleic acid encoding a protein expression enhancer. The invention still further provides a cell comprising a nucleic acid encoding an XBP polypeptide.

[0036] In an embodiment of the invention, the cell is a eukaryotic cell. In an embodiment of the invention, the cell is an animal cell. In an embodiment of the invention, the cell is a mammalian cell. In another embodiment of the invention, the cell is a CHO cell. In an embodiment of the invention, the cell is a CHO-K1 cell.

[0037] An aspect of the invention provides a method of making an antibody comprising a chimeric hinge region, said method comprising:

(a) transfecting a host cell with a nucleic acid molecule encoding the light chain of said antibody, said nucleic acid molecule comprising a nucleotide sequence encoding the V_L region of a selected antigen-specific antibody and a nucleotide sequence encoding the

constant C_L region of an Ig, wherein said nucleotide sequence encoding the V_L region of a selected antigen-specific antibody and said nucleotide sequence encoding the C_L region of an Ig are operably linked together; (b) transfecting the host cell of step (a) with a nucleic acid molecule encoding the heavy chain of said antibody, said nucleic acid molecule comprising a nucleotide sequence encoding the V_H region of a selected antigen-specific antibody and a nucleotide sequence encoding a constant C_H region of a human Ig, wherein the nucleotide sequence encoding the C_H region comprises the nucleotide sequence encoding SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 38 or SEQ ID NO: 37, wherein said nucleotide sequence encoding the V_H region of a selected antigen-specific antibody and said nucleotide sequence encoding the C_H region of said Ig are operably linked together; and (c) making said antibody by co-expressing the nucleic acid molecules of (a) and (b) in said host cell.

[0038] A method of making an antibody comprising a chimeric hinge region, said method comprising:

(a) transfecting a host cell with a nucleic acid molecule encoding the light chain of said antibody, said nucleic acid molecule comprising a nucleotide sequence encoding the VL region of a selected antigen-specific antibody and a nucleotide sequence encoding the constant CL region of an Ig, wherein said nucleotide sequence encoding the VL region of a selected antigen-specific antibody and said nucleotide sequence encoding the CL region of an Ig are operably linked together; (b) transfecting the host cell of step (a) with a nucleic acid molecule encoding the heavy chain of said antibody, said nucleic acid molecule comprising a nucleotide sequence encoding the VH region of a selected antigen-specific antibody and a nucleotide sequence encoding a constant CH region of a human Ig, wherein the nucleotide sequence encoding the CH region comprises the chimeric hinge nucleotide sequence encoding SEQ ID NO: 8 or SEQ ID NO: 9, wherein said nucleotide sequence encoding the VH region of a selected antigen-specific antibody and said nucleotide sequence encoding the CH region of said Ig are operably linked together; and (c) making said antibody by co-expressing the nucleic acid molecules of (a) and (b) in said host cell.

[0039] In another aspect of the invention, the method of making an antibody further comprises the steps of culturing the host cell of step (b) hereinabove, wherein the antibody is secreted into a cell culture medium; and isolating the antibody from the cell culture media.

[0040] An aspect of the invention provides a method of making a receptor-Fc fusion protein comprising a chimeric hinge region, said method comprising:

(a) transfecting a host cell with a nucleic acid molecule encoding said receptor-Fc fusion protein, said nucleic acid molecule comprising a nucleotide sequence encoding a receptor

protein, fused to a nucleotide sequence encoding a constant C_H region of a human Ig, wherein the nucleotide sequence encoding the C_H region comprises the nucleotide sequence encoding SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 38 or SEQ ID NO: 37, wherein said nucleotide sequence encoding the receptor protein and said nucleotide sequence encoding the C_H region of said Ig are operably linked together; and (b) making said receptor-Fc fusion protein by expressing the nucleic acid molecule of (a) in said host cell.

[0041] In another aspect of the invention, the method of making a receptor-Fc fusion comprises the steps of culturing the host cell of step (b) hereinabove, wherein the receptor-Fc fusion protein is secreted into a cell culture medium; and isolating the receptor-Fc fusion protein from the cell culture media.

[0042] An aspect of the invention provides a method of making a receptor-Fc fusion protein comprising a chimeric hinge region, said method comprising:

(a) transfecting a host cell with a nucleic acid molecule encoding said receptor-Fc fusion protein, said nucleic acid molecule comprising a nucleotide sequence encoding a receptor protein, fused to a nucleotide sequence encoding a constant CH region of a human Ig, wherein the nucleotide sequence encoding the CH region comprises the chimeric hinge nucleotide sequence encoding SEQ ID NO: 8 or SEQ ID NO: 9, wherein said nucleotide sequence encoding the receptor protein and said nucleotide sequence encoding the CH region of said Ig are operably linked together; and (b) making said receptor-Fc fusion protein by expressing the nucleic acid molecule of (a) in said host cell.

[0043] In other embodiments, the method of making an antibody comprises:

(a) producing a first cell culture comprising cells expressing a first heavy chain polypeptide of interest;

(b) producing a second cell culture comprising cells expressing a second heavy chain polypeptide of interest;

(c) combining the first and second cell culture, or the supernatants thereof; and

(d) recovering the first and second polypeptides in heterodimeric form;

wherein the heavy chains of the first and second heavy chain polypeptides each comprise an amino acid sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 38 and SEQ ID NO: 37. In the above methods, the first cell culture further comprises a first cognate light chain of interest and the second cell culture further comprises a second cognate light chain of interest, wherein the first and second cognate light chains are covalently bound to the first and second heavy chain polypeptides and are thus recovered. In other embodiments of the above methods, the

heavy chains of the first and second heavy chain polypeptides each comprise a chimeric hinge amino acid sequence selected from the group consisting of SEQ ID NO: 8 and SEQ ID NO: 9.

[0044] In other embodiments, the invention provides a method of making an antibody comprising a first single chain variable fragment-Fc (scFv-Fc) produced in a first cell culture, and a second scFv-Fc produced in a second cell culture, wherein the Fc of the first and second scFv-Fc each comprise an amino acid sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 38 and SEQ ID NO: 37, combining the first and second cell cultures or the supernatants thereof, and recovering or isolating the first and second scFv-Fc in heterodimeric form. In some embodiments, the first and second scFv-Fc are secreted into the cell culture medium (*e.g.* supernatant), and the method comprises combining the first and second cell culture media, and recovering or isolating the heterodimeric protein. In some embodiments of the above methods, the Fc of the first and second scFv-Fc each comprises a chimeric hinge amino acid sequence selected from the group consisting of SEQ ID NO: 8 and SEQ ID NO: 9.

[0045] In some embodiments of the invention, the host cell is selected from the group consisting of CHO, COS, retinal cell, Vero, CV1, 293, MDCK, HaK, BHK, HeLa, HepG2, WI38, MRC 5, Colo25, HB 8065, HL-60, Jurkat, Daudi, A431 (epidermal), CV-1, U937, 3T3, L cell, C127 cell, SP2/0, NS-0, MMT cell, tumor cell, a cell line derived from any of the aforementioned cells, and a PER.C6® cell.

[0046] Another aspect of the invention provides a bispecific antibody comprising:

(a) a first heavy chain comprising an antigen-binding domain capable of recognizing and binding to a first target antigen, (b) a second heavy chain comprising an antigen-binding domain capable of recognizing and binding to a second target antigen, and (c) a common light chain antigen-binding domain capable of recognizing and binding to the first or second target antigen, wherein the heavy chain of (a) or (b) or both (a) and (b) comprises the heavy chain constant region comprising the amino acid sequence of SEQ ID NO: 1, SEQ ID NO:2, SEQ ID NO: 30, or SEQ ID NO: 31, or wherein the heavy chain of (a) or (b) or both (a) and (b) comprises the chimeric hinge region comprising the amino acid sequence of SEQ ID NO: 8 or SEQ ID NO: 9.

[0047] A further aspect of the invention provides a bispecific antibody of the invention comprising:(a) a first heavy chain comprising a first heavy chain constant region comprising SEQ ID NO: 1, SEQ ID NO:2, SEQ ID NO: 30, or SEQ ID NO: 31, and (b) a second heavy chain comprising a second heavy chain constant region comprising SEQ ID NO: 38 or SEQ ID NO: 37.

[0048] These and other objects, along with advantages and features of the invention disclosed herein, will be made more apparent from the description, drawings, and claims that follow.

BRIEF DESCRIPTION OF DRAWINGS

[0049] FIG. 1 shows the corresponding amino acid numbering conventions for the hinge region of hIgG1, hIgG2 and hIgG4. Amino acid numbering is according to the most recently updated IMGT Scientific Chart (IMGT®, the international ImMunoGeneTics information system®, http://www.imgt.org/IMGTScientificChart/Numbering/Hu_IGHGnber.html (created: 17 May 2001, last updated:10 Jan 2013) and the EU index as reported in Kabat, E.A. et al. Sequences of Proteins of Immunological interest. 5th ed. US Department of Health and Human Services, NIH publication No. 91-3242 (1991). (wt = wild-type; - means no corresponding number was reported for the particular reference; -- means that no corresponding amino acid was reported in that position for the particular reference.)

[0050] FIG. 2 illustrates hinge amino acids used in the construction of chimeric hinge regions and the corresponding amino acid conventions.

[0051] FIG. 3. Amino acid sequence of the human IgG1 heavy chain constant region including CH1, hinge, CH2 and CH3 domains as described as IGHG1 in UniProtKB/Swiss-Prot Accn. No. P01857 (SEQ ID NO:13).

[0052] FIG. 4. Amino acid sequence of the human IgG2 heavy chain constant region including CH1, hinge, CH2 and CH3 domains as described as IGHG2 in UniProtKB/Swiss-Prot Accn. No. P01859 (SEQ ID NO:14).

[0053] . FIG. 5. Amino acid sequence of the human IgG4 heavy chain constant region including CH1, hinge, CH2 and CH3 domains as described as IGHG4 in UniProtKB/Swiss-Prot Accn. No. P01861 (SEQ ID NO:15).

[0054] FIG. 6. Single-parameter histograms showing antibody binding (% of Max) to antigen on Jurkat cells in a fluorescent binding assay. FIG 6A: Background fluorescence was measured for control assays, *i.e.* Jurkat cells incubated with secondary antibody only (sec) and unstained Jurkat cells. FIG 6B: Comparison of Jurkat cell binding to antibody containing a chimeric hinge heavy chain constant region (Ab 1 = sIgG4) vs. binding to antibody containing a corresponding antigen-binding domain and a wild-type (wt) IgG4 constant region (Control Ab 2). FIG 6C: Comparison of Jurkat cell binding to antibody containing a chimeric hinge heavy chain constant region (Ab 2 = sIgG1) vs. binding to antibody containing a corresponding antigen-binding domain and a wild-type (wt) IgG1 heavy chain constant region (Control Ab 1).

[0055] FIG. 7. Dose-response curve depicting chimeric hinge antibody ability to bind U937 cells. Half-maximal concentration (EC_{50}) values with respect to binding (mean fluorescence intensity) are given. (Control antibody 1 = wt IgG1 C_H; Antibody 2 = sIgG1; Control Ab 2 = wt IgG4 C_H; and Antibody 1 = sIgG4.)

[0056] FIG. 8. Dose-response curve depicting chimeric hinge antibody lack of cytotoxicity with respect to U937 cells in the presence of activated PBMCs (T cells). Half-maximal concentration (EC_{50}) values with respect to % cytotoxicity are reflected. (Control antibody 1 = wt IgG1 C_H; Antibody 1 = sIgG4; Control Ab 2 = wt IgG4 C_H; and Antibody 2 = sIgG1; Control Ab 3 = wt IgG1 C_H.)

[0057] FIG. 9. Dose-response curve depicting the half-maximal concentration (EC_{50}) with respect to cell viability in a PBMC proliferation assay. (Control antibody 1 = wt IgG1 C_H; Antibody 1 = sIgG4; Control Ab 2 = wt IgG4 C_H; Antibody 2 = sIgG1; Control Ab 3 = wt IgG1 C_H; and Control Ab 4 = non-specific Ab with wt IgG1 C_H).

[0058] FIG 10. Dose-response curves depicting lack of CDC activity with respect to Daudi (FIG 10A) and Raji (FIG. 10B) cells in the presence of antibodies having wild-type or chimeric hinge C_H regions. (Control antibody 5 = Bispecific Ab with wt IgG1 C_H; Antibody 3 = sIgG1*; Antibody 4 = sIgG1*; IgG1 Isotype Control = nonspecific Ab with wt IgG1 C_H.)

[0059] FIG 11. Dose-response curves depicting lack of ADCC activity with respect to Daudi (FIG 11A) and Raji (FIG. 11B) cells in the presence of antibodies having wild-type or chimeric hinge C_H regions. (Control antibody 5 = Bispecific Ab with wt IgG1 C_H; Antibody 3 = sIgG1*; Antibody 4 = sIgG1*; IgG1 Isotype Control = nonspecific Ab with wt IgG1 C_H.)

DETAILED DESCRIPTION OF THE INVENTION

[0060] It is to be understood that this invention is not limited to particular methods, and experimental conditions described, as such methods and conditions may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting, since the scope of the present invention is defined by the claims.

[0061] As used in this specification and the appended claims, the singular forms “a”, “an”, and “the” include plural references unless the context clearly dictates otherwise. Thus for example, a reference to “a method” includes one or more methods, and/or steps of the type described herein and/or which will become apparent to those persons skilled in the art upon reading this disclosure.

[0062] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this

invention belongs. Although any methods and materials similar or equivalent to those described herein can be used in the practice of the present invention, particular methods and materials are now described. All publications mentioned herein are incorporated herein by reference in their entirety.

[0063] The term "immunoglobulin" refers to a class of structurally related glycoproteins consisting of two pairs of polypeptide chains, one pair of light (L) chains and one pair of heavy (H) chains, which may all four be inter-connected by disulfide bonds. The structure of immunoglobulins has been well characterized. See for instance Fundamental Immunology Ch. 7 (Paul, W., ed., 2nd ed. Raven Press, N. Y. (1989)). Briefly, each heavy chain typically comprises a heavy chain variable region (abbreviated herein as V_H or VH) and a heavy chain constant region (C_H or CH). The “heavy chain constant region”, as used herein, typically comprises three domains, C_H1, C_H2, and C_H3, whereas the C_H1 and C_H2 domains are linked by a hinge, or a functional fragment thereof. Each light chain typically comprises a light chain variable region (abbreviated herein as V_L or VL) and a light chain constant region. There are two types of light chains in humans, and other mammals: kappa (κ) chain and lambda (λ) chain. The light chain constant region typically comprises one domain (C_L). The V_H and V_L regions may be further subdivided into regions of hypervariability (or hypervariable regions which may be hypervariable in sequence and/or form of structurally defined loops), also termed complementarity determining regions (CDRs), interspersed with regions that are more conserved, termed framework regions (FRs). Each V_H and V_L is typically composed of three CDRs and four FRs, arranged from amino-terminus (N-terminus) to carboxy-terminus (C-terminus) in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4 (see also Chothia and Lesk *J. Mol. Biol.* 196, 901-917 (1987)). Typically, the numbering of amino acid residues in this region is according to IMGT, Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD. (1991), or by the EU numbering system of Kabat (also known as “EU numbering” or “EU index”), *e.g.*, as in Kabat, E.A. et al. Sequences of Proteins of Immunological interest. 5th ed. US Department of Health and Human Services, NIH publication No. 91-3242 (1991).

[0064] The term "antibody" (Ab) as used herein, refers to an immunoglobulin molecule, or a derivative thereof, which has the ability to specifically bind to an antigen. The variable regions of the heavy and light chains of the immunoglobulin molecule contain a binding domain that interacts with an antigen as outlined above under “immunoglobulin”. An antibody may also be a bispecific antibody, diabody, or similar molecule (see for instance *PNAS USA* 90(14), 6444-8 (1993) for a description of diabodies). Further, it has been shown that the antigen-binding function of an antibody may be performed by fragments of a full-length

antibody, *i.e.* “antigen-binding fragments” or “antigen-binding proteins”. As with full antibody molecules, antigen-binding proteins may be monospecific or multispecific (*e.g.*, bispecific). Examples of binding molecules or fragments encompassed within the term "antibody" include, but are not limited to (i) a Fab' or Fab fragment, a monovalent fragment consisting of the V_L, V_H, C_L and C_H1 domains, or a monovalent antibody as described in the international patent publication number WO2007059782; (ii) $F(ab')_2$ fragments, bivalent fragments comprising two Fab fragments linked by a disulfide bridge at the hinge region; (iii) a Fd fragment consisting essentially of the V_H and C_H1 domains; (iv) a Fv fragment consisting essentially of a V_L and V_H domains, (v) a dAb fragment (Ward et al., *Nature* 341, 544-546 (1989)), which consists essentially of a V_H domain and also called domain antibodies (Holt et al; *Trends Biotechnol*. 2003 Nov;21(11):484-90); (vi) camelid or nanobodies (Revets et al; *Expert Opin Biol Ther*. 2005 Jan;5 (1):111-24) and (vii) an isolated complementarity determining region (CDR).

[0065] The term "human antibody", as used herein, is intended to include antibodies having variable and constant regions derived from human germline immunoglobulin sequences. The human antibodies of the invention may include amino acid residues not encoded by human germline immunoglobulin sequences (*e.g.*, mutations introduced by random or site- specific mutagenesis *in vitro* or during gene rearrangement or by somatic mutation *in vivo*).

[0066] A multispecific antigen-binding fragment of an antibody (*e.g.*, a bispecific antibody) will typically comprise at least two different variable domains, wherein each variable domain is capable of specifically binding to a separate antigen or to a different epitope on the same antigen. Any multispecific antibody format, including bispecific antibody formats disclosed herein, may be adapted for use in the context of an antigen-binding fragment of an antibody of the present invention using routine techniques available in the art.

[0067] Furthermore, although the two domains of the Fv fragment, V_L and V_H, are coded for by separate genes, they may be joined, using recombinant methods, by a synthetic linker that enables them to be made as a single protein chain in which the V_L and V_H regions pair to form monovalent molecules (known as single chain antibodies or single chain Fv (scFv), see for instance Bird et al., *Science* 242, 423-426 (1988) and Huston et al., *PNAS USA* 85, 5879-5883 (1988)). Such single chain antibodies are encompassed within the term “antibody” unless otherwise noted or clearly indicated by context. Although such polypeptides are generally included within the meaning of antibody, they collectively, and each independently, are unique features of the present invention, exhibiting different biological properties and utility. These and other antibody fragments and recombinant polypeptides that are useful in the context of the present invention are discussed further

herein. It also should be understood that the term antibody, unless specified otherwise, also includes polyclonal antibodies, monoclonal antibodies (mAbs), antibody-like polypeptides, such as chimeric antibodies and humanized antibodies, and any antibody fragments retaining the ability to specifically bind to the antigen (antigen-binding fragments or molecules) provided by any known technique, such as enzymatic cleavage, peptide synthesis, and recombinant techniques. An antibody as generated can possess any Ig isotype or combination thereof. Any scFv may be fused to the heavy chain constant regions of the invention by known techniques.

[0068] Other exemplary bispecific formats that can be used in the context of the present invention include, without limitation, e.g., scFv-based bispecific formats, IgG-scFv fusions, dual variable domain (DVD)-Ig, Quadroma, knobs-into-holes, common light chain (e.g., common light chain with knobs-into-holes, etc.), CrossMab, CrossFab, (SEED)body, dual acting Fab (DAF)-IgG, and Mab2 bispecific formats (see, e.g., Klein et al. 2012, mAbs 4:6, 1-11, and references cited therein, for a review of the foregoing formats). Bispecific antibodies can also be constructed using peptide/nucleic acid conjugation, e.g., wherein unnatural amino acids with orthogonal chemical reactivity are used to generate site-specific antibody-oligonucleotide conjugates which then self-assemble into multimeric complexes with defined composition, valency and geometry. (See, e.g., Kazane et al. 2013, J. Am. Chem. Soc. 9;135(1):340-6 [Epub: Dec. 21, 2012]).

[0069] Further exemplary multispecific formats can be used in the context of the present invention include, without limitation, e.g., involving a first antigen-binding domain that specifically binds a target molecule, and a second antigen-binding domain that specifically binds an internalizing effector protein, wherein such second antigen-binding domains are capable of activating and internalizing the effector protein, e.g. a receptor. (See U.S. Application Publication. No. 2013/0243775A1, published on September 19, 2013, which is incorporated by reference.)

[0070] Recombinant proteins may be produced by standard molecular biology techniques well known to the skilled artisan (see e.g., Sambrook, J., E. F. Fritsch And T. Maniatis. Molecular Cloning: A Laboratory Manual, Second Edition, Vols 1, 2, and 3, 1989; Current Protocols in Molecular Biology, Eds. Ausubel et al., Greene Publ. Assoc., Wiley Interscience, NY).

[0071] The phrase “complementarity determining regions” or the term "CDR," includes an amino acid sequence encoded by a nucleic acid sequence of an organism's immunoglobulin (Ig) genes. CDRs are regions of hypervariability that are normally (*i.e.*, in the context of a wild-type animal) interspersed within the more conserved framework regions (FRs) in a

variable region of a light chain or a heavy chain of *e.g.,* an antibody or a T cell receptor (TCR). A CDR can be encoded by, for example, a germline sequence or a rearranged or unrearranged sequence, and, for example, by a naive or a mature B cell or a T cell. In some circumstances (*e.g.,* for a CDR3), CDRs can be encoded by two or more sequences (*e.g.,* germline sequences) that are not contiguous (*e.g.,* in an unrearranged nucleic acid sequence) but are contiguous in a B cell nucleic acid sequence, *e.g.*, as the result of splicing or connecting the sequences (*e.g.,* V-D-J recombination to form a heavy chain CDR3).

[0072] The term “antigen-binding domain”, as used herein, is the amino acid sequence of a heavy chain or light chain capable of selectively recognizing and binding to antigen with a K_D at least in the micromolar range. The antigen-binding domain of the invention includes at least one CDR.

[0073] The phrase "variable domain" includes an amino acid sequence of an immunoglobulin light or heavy chain (modified as desired) that comprises the following amino acid regions, in sequence from N-terminal to C-terminal (unless otherwise indicated): FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4. A "variable domain" includes an amino acid sequence capable of folding into a canonical domain (VH or VL) having a dual beta sheet structure wherein the beta sheets are connected by a disulfide bond between a residue of a first beta sheet and a second beta sheet.

[0074] The phrase “heavy chain” or “immunoglobulin (Ig) heavy chain”, as used herein, includes Ig heavy chain constant region sequence from any organism, and unless otherwise specified includes a heavy chain variable domain. Heavy chain variable domains include three heavy chain CDRs and four FR regions, unless otherwise specified. Fragments of heavy chain variable domains include CDRs, or both CDRs and FRs. A typical heavy chain constant region has, following the variable domain (from N-terminal to C-terminal), a CH1 domain, a hinge, a CH2 domain, and a CH3 domain. A functional fragment of a heavy chain in an antigen-binding protein includes a fragment that is capable of specifically recognizing an antigen (*e.g.,* recognizing the antigen with a K_D in the micromolar, nanomolar, or picomolar range), that is capable of being expressed in and secreted from a cell, and that comprises at least one CDR. For the purposes of this invention, a functional fragment of a heavy chain constant region includes at least an Fc domain or fragment thereof.

[0075] The phrase “Fc-containing protein” includes antibodies, bispecific antibodies, antibody-binding fragments, trap molecules and other receptor-Fc fusion proteins, and other binding proteins that comprise at least a functional portion of an immunoglobulin CH2 and CH3 region, such as ligand-Fc fusion proteins. A "functional portion" refers to a CH2 and CH3 region that can bind an Fc receptor *e.g.*, an FcγR, (namely FcγRI (CD64), FcγRIIa

(CD32a), FcγRIIb (CD32b), FcγRIIIa (CD16a), or FcγRIIIb (CD16b)) or FcRn, (the neonatal Fc receptor, which confers to antibodies their extended half-life). If the CH2 and CH3 region contains deletions, substitutions, and/or insertions or other modifications that render it unable to bind any Fc receptor, then the CH2 and CH3 region is considered to be non-functional. As such, when diminishing or eliminating certain effector functions is desired, any Fc-containing protein may be engineered to comprise a chimeric heavy chain constant region or fragment as described herein.

[0076] The phrase "Fc-fusion proteins", and specifically "receptor-Fc fusion proteins" includes recombinant proteins engineered to contain a functional Fc fragment as described herein. For example a "receptor-Fc fusion protein" includes a chimeric protein comprising an amino acid sequence of a receptor protein fused to an amino acid sequence of an Fc domain of Ig. Examples of receptor proteins used in fusion proteins are known in the art (see *e.g.* Klinkert, et al. *J Neuroimmunol.* 72(2):163-8 (1997); Milligan, G., et al. *Curr Pharm Des.* 10(17):1989-2001 (2004); and Schwache D, and Müller-Newen G, *Eur J Cell Biol.* 91(6-7):428-34 (2012), doi: 10.1016/j.ejcb.2011.07.008. Epub 2011 Sep 29).

[0077] In the context of the present invention, receptor-Fc fusion proteins are encoded by a nucleotide sequence encoding a receptor protein fused to a nucleotide sequence of a chimeric heavy chain constant region as described herein. In some embodiments, the nucleotide sequence of the receptor protein encodes for the ligand-binding domain or the extracellular domain of the receptor. In other embodiments, the nucleotide sequence of the receptor protein encodes for the extracellular domain of the receptor and the transmembrane domain of the receptor. Receptor-Fc fusion proteins are also exemplified in US20090137416 A1.

[0078] Flow cytometry-based autologous secretion trap (FASTR) methods that utilize the hFcγRI allow rapid isolation of high expression clones expressing or secreting an antibody or receptor-Fc fusion protein of the invention. (See, *e.g.,* US20090137416 A1, which is herein incorporated by reference.) Such high expression clones may be employed to isolate cells expressing proteins comprising a chimeric heavy chain constant region of the invention. FASTR methods may be utilized to directly screen and isolate cells expressing any recombinant polypeptide, antigen-binding protein, antibody, or Fc fusion protein of the invention.

[0079] The phrase "light chain" includes an immunoglobulin light chain constant region sequence from any organism, and unless otherwise specified includes human kappa and lambda light chains. Light chain variable (VL) domains typically include three light chain CDRs and four framework (FR) regions. Generally (*i.e.* in the context of a wild-type animal),

a full-length light chain includes, from amino terminus to carboxyl terminus, a VL domain that includes FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4, and a light chain constant domain.

[0080] The polypeptides of the invention comprise amino acid sequences that are derived from an immunoglobulin domain. A polypeptide or amino acid sequence “derived from” a designated protein refers to the origin of the polypeptide.

[0081] The term “hinge”, as used herein, is intended to include the region of consecutive amino acid residues that connect the C-terminus of the C_H1 to the N-terminus of the C_H2 domain of an immunoglobulin. Several amino acids of the N-terminus of the C_H2 domain, which are coded by the C_H2 exon, are also considered part of the “lower hinge”. Without being bound by any one theory, amino acids of the hinge region of IgG1, IgG2 and IgG4 have been characterized as comprising 12-15 consecutive amino acids encoded by a distinct hinge exon, and several N-terminal amino acids of the C_H2 domain (encoded by the C_H2 exon) (Brekke, O.H., et al. *Immunology Today* 16(2):85-90 (1995)). On the other hand, IgG3 comprises a hinge region consisting of four segments: one upper segment resembling the hinge region of IgG1, and 3 segments that are identical amino acid repeats unique to IgG3.

[0082] In the present disclosure for the convenience of the practitioner of the invention, amino acids of the hinge region for human IgG1, IgG2 and IgG4 have been identified herein by the EU numbering system of Kabat (Kabat, E.A. et al., Sequences of Proteins of Immunological interest. 5th ed. US Department of Health and Human Services, NIH publication No. 91-3242 (1991)), also known as “EU numbering” or the “EU index”, as updated according to the IMGT® Scientific Chart, IMGT®, the international ImMunoGeneTics information system®, http://www.imgt.org/IMGTScientificChart/Numbering/Hu_IGHGnber.html, created: 17 May 2001, last updated:10 Jan 2013.

[0083] Correspondence between EU numbering for human IgG1, IgG2 and IgG4 hinge amino acids and IMGT unique domain numbering, IMGT exon numbering, and Kabat numbering conventions (see also Kabat, E.A. et al., 1991, *supra*) are described in Figure 1 and as follows:

[0084] Table 1: IgG1 hinge numbering

IgG1 (IGHG1) amino acids [SwissProt P01857]	IMGT *Unique Numbering for* ***the HINGE*** [a]	IMGT Exon Numbering [a]	EU Numbering	Kabat Numbering
(E)	1	1	216	226
P	2	2	217	227
K	3	3	218	228
S	4	4	219	232[a] [229][b]
C	5	5	220	233[a] [230][b]
D	6	6	221	234[a] [232][b]
K	7	7	222	235
T	8	8	223	236
H	9	9	224	237
T	10	10	225	238
C	11	11	226	239
P	12	12	227	240
P	13	13	228	241
C	14	14	229	242
P	15	15	230	243

[0085] Table 2: IgG1 C-domain hinge numbering

IgG1 (IGHG1) amino acids [SwissProt P01857]	IMGT *Unique Numbering for* ***C-domains*** [a]	IMGT Exon Numbering [a]	EU Numbering	Kabat Numbering
(A)	1.6	1	231	244
P	1.5	2	232	245
E	1.4	3	233	246
L	1.3	4	234	247
L	1.2	5	235	248
G	1.1	6	236	249

[0086] Table 3: IgG2 hinge numbering

IgG2 (IGHG2) amino acids [SwissProt P01859]	IMGT *Unique Numbering for* ***the HINGE*** [a]	IMGT Exon Numbering [a]	EU Numbering	Kabat Numbering
(E)	1	1	216	226
R	2	2	217	227
K	3	3	218	228
C	4	4	219[a] (221)[b]	232
C	5	5	220[a] (-)[b]	233
V	6	6	222	235
E	7	7	224	237
C	8	8	226	239
P	9	9	227	240
P	10	10	228	241
C	11	11	229	242
P	12	12	230	243

[0087] Table 4: IgG2 C-domain hinge numbering

IgG2 (IGHG2) amino acids [SwissProt P01859]	EU numbering	Kabat numbering
(A)	231	244
P	232	245
P	233	246
V	234	247
A	235	248
--	236	249

[0088] Table 5: IgG4 hinge numbering

IgG4 (IGHG4) amino acids [SwissProt P01861]	IMGT *Unique Numbering for* ***the HINGE*** [a]	IMGT Exon Numbering [a]	EU Numbering	Kabat Numbering
(E)	1	1	216	226
S	2	2	217	227
K	3	3	218	228
Y	4	4	- [a] (219)[b]	229
G	5	5	- [a] (220)[b]	230
P	6	6	224	237
P	7	7	225	238
C	8	8	226	239
P	9	9	227	240
S	10	10	228	241
C	11	11	229	242
P	12	12	230	243

[0089] Table 6: IgG4 C-domain hinge numbering

IgG4 (IGHG4) amino acids [SwissProt P01861]	EU Numbering	Kabat Numbering
(A)	231	244
P	232	245
E	233	246
F	234	247
L	235	248
G	236	249

Amino acids resulting from exon splicing are shown in parentheses.

- means no corresponding number reported

-- means no corresponding amino acid in this position

[a] numbering according to the last updated IMGT Scientific Chart

[b] numbering according to EU index as reported in Kabat, EA, et al. 1991

See also, *e.g.*, Lefranc, M.-P. et al., *Devel Comp Immunol*, 29, 185-203 (2005); and Edelman, G.M. et al. *PNAS USA*, 63:78-85 (1969).

[0090] For the purposes of this disclosure, an “upper hinge” region is intended to include amino acid residues from positions 216 to 227 according to EU numbering (amino acid residues from positions 226 to 240 according to Kabat numbering) (see also Figure 2). A “lower hinge” region is intended to include amino acid residues from positions 228 to 236 according to EU numbering (amino acid residues from positions 241 to 249 according to Kabat numbering) (see also Figure 2).

[0091] The term “chimeric”, as used herein, means composed of parts of different origin. The phrase “chimeric protein” includes a first amino acid protein linked to a second amino acid protein that is not normally linked in nature. The amino acid sequences may normally exist as separate proteins or in a different arrangement on the same protein, and are brought together in a fusion polypeptide in a new arrangement. Chimeric proteins may be created by various methods known in the art, *e.g.* by chemical synthesis or by creating a polynucleotide that encodes for amino acids of the chimeric protein in the desired arrangement. Exemplary chimeric proteins include the chimeric hinge sequences connecting heavy chain domains of IgG, and the fusion proteins engineered to make the human antibodies, antigen-binding proteins and receptor-Fc fusion proteins of the present invention.

[0092] The chimeric proteins disclosed herein were designed to minimize the creation of immunogenic epitopes in the junctions, *e.g.* compared to a wild-type IgG Fc region or domain. The engineered proteins of the invention therefore have reduced immunogenicity, and display reduced binding to Fc receptors, as well as reduced to no effector functions.

[0093] The term “chimeric hinge”, as used herein, is intended to include a chimeric protein comprising a first amino acid sequence derived from the hinge region of one Ig molecule and a second amino acid sequence derived from the hinge region of a different class or subclass of Ig molecule. Exemplary chimeric hinges of the present invention comprise a first amino acid sequence, or an “upper hinge” sequence, derived from a human IgG1 or human IgG4 hinge region, and a second amino acid sequence, or a “lower hinge” sequence, derived from a human IgG2 hinge region. In certain embodiments, the first or “upper hinge” sequence comprises amino acid residues from positions 216 to 227 according to EU numbering. In some embodiments, the second or “lower hinge” sequence comprises amino acid residues from positions 228 to 236 according to EU numbering.

[0094] The term "humanized antibody", as used herein, is intended to include antibodies in which CDR sequences are derived from the germline of another mammalian species, such as a mouse, and have been grafted onto human framework sequences. Humanized monoclonal antibodies may be generated by a hybridoma which includes a B lymphocyte

cell obtained from a transgenic or transchromosomal nonhuman animal, such as a transgenic mouse, having a genome comprising a human heavy chain transgene and a light chain transgene, fused to an immortalized cell. For example, when non-human antibodies are prepared with respect to a particular antigen, the variable regions can be “reshaped” or “humanized” by grafting CDRs derived from nonhuman antibody on the FRs present in the human antibody to be modified. Application of this approach has been reported by Sato, K. et al. *Cancer Research* 53:851-856 (1993); Riechmann, L., et al., *Nature* 332:323-327 (1988); Verhoeyen, M., et al., *Science* 239:1534-1536 (1988); Kettleborough, C. A., et al., *Protein Engineering* 4:773-3783 (1991); Maeda, H., et al., *Human Antibodies Hybridoma* 2:124-134 (1991); Gorman, S. D., et al., *Proc Natl Acad Sci USA* 88:4181-4185 (1991); Tempest, P. R., et al., *Bio/Technology* 9:266-271 (1991); Co, M. S., et al., *Proc Natl Acad Sci USA* 88:2869-2873 (1991); Carter, P., et al., *Proc Natl Acad Sci USA* 89:4285-4289 (1992); and Co, M. S. et al., *J Immunol* 148:1149-1154 (1992). In some embodiments, humanized antibodies preserve all CDR sequences (for example, a humanized mouse antibody which contains all six CDRs from the mouse antibodies). In other embodiments, humanized antibodies have one or more CDRs (one, two, three, four, five, or six) which are altered with respect to the original antibody, which are also termed one or more CDRs "derived from" one or more CDRs from the original antibody. Humanized antibodies may refer to chimeric molecules prepared using recombinant techniques.

[0095] In another embodiment, chimeric antibodies comprising human variable regions linked to murine constant regions, such as those produced by cell lines generated by a VELOCIMMUNE mouse, are humanized by replacing the murine constant region for a human constant region comprising SEQ ID NO: 1, SEQ ID NO:2, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 38 or SEQ ID NO:37.

[0096] The terms "monoclonal antibody" or "monoclonal antibody composition" as used herein refer to a preparation of antibody molecules of single molecular composition. A monoclonal antibody composition displays a single binding specificity and affinity for a particular epitope. Accordingly, the term "mouse or murine monoclonal antibody" refers to antibodies displaying a single binding specificity which have variable and constant regions derived from murine or mouse germline immunoglobulin sequences.

[0097] As used herein, the term "binding" in the context of the binding of an antibody, Ig, antibody-binding fragment, or Fc-containing protein to either, *e.g.,* a predetermined antigen or to a FcR, typically refers to an interaction or association between a minimum of two entities, or molecular structures, such as an antibody-antigen interaction, or an Fc-containing

protein to an FcγR (wherein the Fc-containing protein is an antibody, Ig, antibody-binding fragment, or Fc-fusion protein, *e.g.* receptor-Fc fusion).

[0098] For instance, binding affinity typically corresponds to a K_D value of about 10^{-7} M or less, such as about 10^{-8} M or less, such as about 10^{-9} M or less when determined by, for instance, surface plasmon resonance (SPR) technology in a BIAcore 3000 instrument using the antigen or FcR as the ligand and the antibody, Ig, antibody-binding fragment, or Fc-containing protein as the analyte (or antiligand). Accordingly, the antibody or other binding protein binds to the predetermined antigen or receptor with an affinity corresponding to a K_D value that is at least ten-fold lower, such as at least 100 fold lower, for instance at least 1,000 fold lower, such as at least 10,000 fold lower, for instance at least 100,000 fold lower than its affinity for binding to a non-specific antigen (e.g., BSA, casein).

[0099] The term "K_D" (M), as used herein, refers to the dissociation equilibrium constant of a particular antibody-antigen interaction, or the dissociation equilibrium constant of an antibody, Ig, antibody-binding fragment, or Fc-containing protein to an FcγR. There is an inverse relationship between K_D and binding affinity, therefore the smaller the K_D value, the higher the affinity. Thus, the term “lower affinity” relates to a lower ability to form an interaction and therefore a larger K_D value.

[00100] The term "k_d" (sec $^{-1}$ or 1/s), as used herein, refers to the dissociation rate constant of a particular antibody-antigen interaction, or the dissociation rate constant of an antibody, Ig, antibody-binding fragment, or Fc-containing protein to an FcγR. Said value is also referred to as the k_{off} value.

[00101] The term "k_a" (M^{-1} x sec^{-1} or 1/M), as used herein, refers to the association rate constant of a particular antibody-antigen interaction, or the association rate constant of an antibody, Ig, antibody-binding fragment, or Fc-containing protein to an FcγR.

[00102] The term "K_A" (M^{-1} or 1/M), as used herein, refers to the association equilibrium constant of a particular antibody-antigen interaction, or the association equilibrium constant of an antibody, Ig, antibody-binding fragment, or Fc-containing protein to an FcγR. The association equilibrium constant is obtained by dividing the k_a by the k_d.

[00103] The term “EC_{50}” or “EC50”, as used herein, refers to the half maximal effective concentration, which includes the concentration of an antibody which induces a response halfway between the baseline and maximum after a specified exposure time. The EC_{50} essentially represents the concentration of an antibody where 50% of its maximal effect is observed. Thus, reduced binding is observed with an increased EC_{50}, or half maximal effective concentration value.

[00104] In one embodiment, decreased binding can be defined as an increased EC_{50} antibody concentration which enables binding to the half-maximal amount of target cells.

[00105] In some embodiments, decreased cytotoxic activity can be defined as an increased EC_{50} antibody concentration which enables lysis of the half-maximal amount of target cells.

[00106] In other embodiments, decreased proliferation can be defined as an increased EC_{50} antibody concentration which enables proliferation of the half-maximal amount of target cells.

[00107] The phrase "bispecific antibody" as used herein includes antibodies that are specific for different epitopes of one target polypeptide or may contain antigen-binding domains specific for more than one target polypeptide. See, *e.g.,* Tutt et al. (1991*) J. Immunol*. 147:60-69. For example, the human antibodies can be linked to or co-expressed with another functional molecule, *e.g.,* another peptide or protein. For example, an antibody or fragment thereof can be functionally linked (e.g., by chemical coupling, genetic fusion, noncovalent association or otherwise) to one or more other molecular entities, such as another antibody or antibody fragment, to produce a bispecific or a multispecific antibody with a second binding specificity. As such, bispecific antibody also includes two antibodies of different specificity.

[00108] Another strategy, for example using a common light chain, may be employed as described in US Patent Application Publication No. 20100331527A1, wherein two antibodies of different specificity use the same light chain. In certain embodiments, the heavy chain of at least one of the Ig heavy chains in a bispecific antibody is modified to comprise a chimeric heavy chain constant region comprising a recombinant polypeptide of the invention. In some embodiments, at least one of the heavy chains is modified in the CH3 domain resulting in a differential affinity for the bispecific antibody for an affinity reagent, such as Protein A, for ease of isolation. In another embodiment, at least one of the heavy chains in such bispecific antibody comprises an amino acid modification at i) 95R or ii) 95R and 96F in the IMGT numbering system (95R and 96F correspond to 435R and 436F in the EU numbering system), for example SEQ ID NO: 37 and SEQ ID NO: 38. (*See* US20100331527A1, the contents of which are herein incorporated by reference.) A multispecific antigen-binding fragment of an antibody will typically comprise at least two different variable domains, wherein each variable domain is capable of specifically binding to a separate antigen or to a different epitope on the same antigen. Any multispecific antibody format may be adapted for use in the context of an antigen-binding protein or antibody of the present invention using routine techniques available in the art.

[00109] As used herein, "isotype" refers to the immunoglobulin class (for instance, IgG1, IgG2, IgG3, IgG4, IgD, IgA, IgE, or IgM) that is encoded by heavy chain constant region genes.

[00110] The term "epitope" means an antigenic determinant capable of specific binding to an antibody. Epitopes usually consist of surface groupings of molecules such as amino acids or sugar side chains and usually have specific three dimensional structural characteristics, as well as specific charge characteristics. Conformational and nonconformational epitopes are distinguished in that the binding to the former, but not the latter, is lost in the presence of denaturing solvents. The epitope may comprise amino acid residues directly involved in the binding (also called immunodominant component of the epitope) and other amino acid residues, which are not directly involved in the binding, such as amino acid residues which are effectively blocked by the specific antigen binding peptide (in other words, the amino acid residue is within the footprint of the specific antigen binding peptide).

[00111] As used herein, a humanized antibody is "derived from" a particular germline sequence if the antibody is obtained from a system using human immunoglobulin sequences, for instance by immunizing a transgenic mouse carrying human immunoglobulin genes or by screening a human immunoglobulin gene library, and wherein the selected human antibody V domain sequence is at least 90%, such as at least 95%, for instance at least 96%, such as at least 97%, for instance at least 98%, or such as at least 99% identical in amino acid V domain sequence to the amino acid sequence encoded by the germline immunoglobulin gene.

[00112] Typically, outside the heavy chain CDR3, a human antibody derived from a particular human germline sequence will display no more than 20 amino acid differences, e.g. no more than 10 amino acid differences, such as no more than 9, 8, 7, 6 or 5, for instance no more than 4, 3, 2, or 1 amino acid difference from the amino acid sequence encoded by the germline immunoglobulin gene.

[00113] The term "transgenic non-human animal" refers to a non-human animal having a genome comprising one or more human heavy and/or light chain transgenes or transchromosomes (either integrated or non-integrated into the animal's natural genomic DNA) and which is capable of expressing fully human antibodies. Mice that express antibodies that are fully human, or partly human and partly mouse, have previously been reported. For example, a transgenic mouse can have a human light chain transgene and either a human heavy chain transgene or human heavy chain transchromosome, such that the mouse produces human antibody when immunized with target antigen and/or cells

expressing the target antigen. The human heavy chain transgene may be integrated into the chromosomal DNA of the mouse, as is the case for transgenic mice, for instance HuMAb mice, such as HCo7 or HCol2 mice, or the human heavy chain transgene may be maintained extrachromosomally, as is the case for transchromosomal KM mice as described in WO02/43478. Such transgenic and transchromosomal mice (collectively referred to herein as "transgenic mice") are capable of producing multiple isotypes of human monoclonal antibodies to a given antigen (such as IgG, IgA, IgM, IgD and/or IgE) by undergoing V-D-J recombination and isotype switching.

[00114] VELOCIMMUNE® genetically engineered mice comprise a replacement of unrearranged V(D)J gene segments at endogenous mouse loci with human V(D)J gene segments. VELOCIMMUNE® mice express chimeric antibodies having human variable domains and mouse constant domains (see, e.g., U.S. Pat. No. 7,605,237). Most other reports concern mice that express fully human antibodies from fully human transgenes in mice that have disabled endogenous immunoglobulin loci.

[00115] The VELOCIMMUNE® mouse includes, in part, having a genome comprising human variable regions operably linked to endogenous mouse constant region loci such that the mouse produces antibodies comprising a human heavy chain variable region and a mouse heavy chain constant region in response to antigenic stimulation. The DNA encoding the variable regions of the heavy chains of the antibodies can be isolated and operably linked to DNA encoding the human heavy chain constant regions of the invention. The DNA can then be expressed in a cell capable of expressing the fully human heavy chain of the antibody.

[00116] A transgenic, nonhuman animal can also be used for production of antibodies against a specific antigen by introducing into the animal genes encoding such specific antibody, for example by operatively linking the genes to a gene which is expressed in the milk of the animal.

[00117] The phrase “effector functions”, as used herein, is intended to include the functional capabilities imparted by an Fc-containing protein upon binding to an FcγR. Without being bound to any one theory, formation of an Fc/FcγR complex recruits a variety of effector cells to sites of bound antigen, typically resulting in diverse signaling events within the cells and important subsequent immune responses.

[00118] An "effectorless polypeptide" refers to a recombinant polypeptide, antigen-binding protein or antibody which has altered or reduced effector function as compared to a corresponding recombinant polypeptide, antigen-binding protein or antibody comprising a wild-type heavy chain constant region of the IgG1 or IgG4 isotype. In some embodiments,

the effector function that is reduced or altered is a cytotoxic effector function, *e.g.,* cytotoxicity, complement-dependent cytotoxicity (CDC), antibody-dependent cytotoxicity (ADCC), or antibody-dependent cellular phagocytosis (ADCP). In one embodiment, the effector function that is reduced or altered is complement-dependent cytotoxicity. In another embodiment, the effector function that is reduced or altered is antibody-dependent cytotoxicity. In other embodiments, the effector function that is reduced or altered is cellular proliferation.

[00119] Several antibody effector functions are mediated at least in part by Fc receptors (FcRs), which bind the Fc region of an antibody in the constant domain (specifically, the C_H2 and C_H3 domain) of a typical immunoglobulin. There are a number of Fc receptors which are specific for the different classes of immunoglobulins, *i.e*. IgG, IgE, IgA, IgM, and IgD. The human IgG Fc receptor family is divided into three groups: FcγRI (CD64), which is capable of binding IgG with high affinity, FcγRII (CD32) and FcγRIII (CD16) both of which are low affinity receptors. Each FcγR subclass is encoded by two or three genes, and alternative RNA splicing leads to multiple transcripts, hence, a broad diversity in FcγR isoforms exists (*e.g.* FcγRIA (CD64; FCGR1A), FcγRIB (CD64; FCRG1B), FcγRIIA (CD32; FCGR2A), FcγRIIB (CD32; FCGR2B), FcγRIIC (CD32; FCGR2C), FcγRIIIA (CD16a; FCGR3A), and FcγRIIIB (CD16b; FCGR3B)). Additionally, the FcRn, or neonatal Fc receptor (also known as the Fc receptor transporter, alpha, or FCGRT) is capable of transferring IgG antibodies from mother to fetus across the placenta. Furthermore, Fc receptors are expressed on a variety of cells, including, *e.g.,* B cells, monocytes, dendritic cells, neutrophils, and certain lymphocytes. For example, U937 cells, a human monocyte cell line, express both FcγRI and FcγRIIA (see *e.g.*, Jones, et al. *J Immunol* 135(5):3348-53 (1985); and Brooks, et al. *J Exp Med* 170:1369-85 (October 1989)).

[00120] Binding of an Ig Fc to its receptor brings these effector cells to sites of the bound antigen, resulting ultimately in a variety of signaling and immune responses, including B cell activation, inflammatory responses, cytotoxic responses, and phagocytic responses. As such, reduced or altered binding of an Ig Fc to its receptor may result in reduced effector functions.

[00121] Alternatively, increased "effector functions" such as cytotoxicity, complement-dependent cytotoxicity ("CDC"), antibody-dependent cytotoxicity ("ADCC") and abnormal antibody production, may be unwanted side effects associated with certain therapeutic antibodies.

[00122] The phrase “antibody-dependent cellular cytotoxicity”, “Antibody-dependent cell-dependent cytotoxicity”, or “ADCC” means an activity to damage a target cell when an

Fcγ receptor-bearing cell (an immune cell or the like) binds to an Fc portion of a specific antibody through the Fcγ receptor, when the specific antibody has attached to a cell-surface antigen of the target cell. Thus, ADCC is a mechanism by which Fc receptor-positive effector cells can lyse target cells that have adherent antigen-specific molecule. The ADCC activity can be evaluated by a number of well-known methods, including measuring the fluorescent intensity using a fluorescent dye such as calcein AM (Wako Pure Chemical Industries, Ltd., 349-07201). When this approach is employed, the cytotoxic activity (%) can be calculated, using the obtained values, according to the equation: (A-C)/(B-C)x100, wherein A is a fluorescent value in each sample, B is an average fluorescent value of the cells lysed and released into a medium with Nonidet P-40 having a final concentration of 1%, and C is an average fluorescent value when only the medium was added.

[00123] The phrase ”antibody-dependent cellular phagocytosis” or ”ADCP”, as used herein, relates to effector function that eliminates (or kills) a target cell by engulfing the target cell rather than inducing cytolysis. ADCP may be an important *in vivo* mechanism for killing tumor cells. ADCP can be measured by two-color fluorescence flow cytometry methods, for example methods utilizing, *e.g.* PKH2 (green fluorescent dye) and phycoerythrin-conjugated (red) monoclonal antibodies against different cell surface proteins to differentiate the test cells, thus determining phagocytic activity and rate of phagocytosis. Therapeutic strategies that selectively activate FcγRIIa relative to FcγRIIb may enhance macrophage phagocytic activity (Richards, JO, et al. 2008 *Mol Cancer Ther* 7(8):2517-27).

[00124] The phrase “complement-directed cytotoxicity” or “CDC”, as used herein, includes a cytotoxic activity by the complement system. The CDC activity is measured by well-known methods, for example the target cells, antibody, and complement solution (such as baby rabbit complement (Cedarlane Technologies) are incubated and are allowed to react, according to standard protocols (NIAID Manual of Tissue Typing Techniques 1979-1980, Edited by J.G. Ray, NIH Publication No. NIH-83-545.) The cytotoxic activity can be calculated in the same manner as the measurement of the ADCC activity. The cytotoxic activity can also be measured using a fluorescent dye (such as calcein) or radioactive dyes similarly to the above with respect to ADCC.

[00125] The phrase “cytotoxicity” or “direct cytotoxicity” includes any cytotoxic activity including that which is independent of NK cells. Cytotoxicity may be measured by techniques well known in the art, for example, determining cell lysis or cell death, *i.e.* apoptosis. Direct cell lysis, or cell killing, can be evaluated by a number of well-known methods, including measuring the fluorescent intensity using calcein and calculating an average fluorescent value in a similar fashion as described with respect to ADCC hereinabove. Alternatively, a

cytotoxic molecule, such as an antibody, is effective in an apoptosis assay by activating a genetic program of controlled cell death. Apoptosis is characterized by well defined cytological and molecular events including a change in the refractive index of the cell, cytoplasmic shrinkage, nuclear condensation and cleavage of DNA into regularly sized fragments. Cells that are undergoing apoptosis shut down metabolism, lose membrane integrity and form membrane blebs. The apoptotic activity is measured using standard methods of determining dying and/or dead cells. In order to measure apoptosis, cytotoxicity assays can be employed. These assays may be radioactive or non-radioactive assays that measure increases in plasma membrane permeability, since dying cells become leaky, colorimetric assays may be employed that measure reduction in the metabolic activity of mitochondria based on the knowledge that mitochondria in dead cells cannot metabolize dyes, while mitochondria in live cells can. Bioluminescent cytotoxicity assays (*e.g.* CytoTox-Glo™, Promega) were developed to measure the release of stable protease markers into the cell culture medium. Protease activity is considered a robust enzymatic cell death marker, and may be used as a ratiometric measurement of viable and dead cells (Niles, A.L., et al. *Anal Biochem*, 366(2): 197–206, 15 July 2007).

[00126] One can also measure early indicators for apoptosis such as alterations in membrane asymmetry resulting in occurrence of phosphatidylserine on the outside of the cell surface (Annexin V based assays). Alternatively, later stages of apoptosis, such as activation of caspases can be measured in populations of cells or in individual cells. In addition, measurement of release of cytochrome C and AIF into cytoplasm by mitochondria or fragmentation of chromosomal DNA can be determined. Terminal deoxynucleotidyl transferase dUTP nick end labeling (TUNEL) is a common method for detecting DNA fragmentation that results from apoptotic signaling cascades. The assay relies on the presence of nicks in the DNA which can be identified by terminal deoxynucleotidyl transferase, an enzyme that will catalyze the addition of bromolated dUTPs that are secondarily detected with a specific labelled antibody.

[00127] Cytotoxicity may be complement-directed, or antibody-directed, or directly associated with the binding of a cytotoxic molecule or cell.

[00128] In certain embodiments, antibodies of the invention exhibit cytotoxicity of less than 20% cytolysis (*i.e.* % cytotoxicity), or less than 10%, or 5%, 4%, 3%, 2%, or even 0% or undetectable cytolysis (cytotoxicity), as measured in an *in vitro* or *ex vivo* cell killing assay. In certain embodiments, antibodies of the invention exhibit less than 20%, 10%, or 5%, 4%, 3%, 2%, or even 0% or undetectable cytotoxicity, at an antibody concentration of 10 nM.

[00129] In other embodiments, antibodies exhibit apoptotic activity of less than 20% cytolysis (*i.e.* % cytotoxicity), or less than 10%, or 5%, 4%, 3%, 2%, or even 0% or undetectable cytolysis (cytotoxicity), as measured in an *in vitro* or *ex vivo* cell killing assay. In still other embodiments, In certain embodiments, antibodies of the invention exhibit less than 20%, 10%, or 5%, 4%, 3%, 2%, or even 0% or undetectable apoptotic activity, at an antibody concentration of 10 nM.

[00130] In still other embodiments, antibodies exhibit CDC activity of less than about 50% cytotoxicity, or less than cytotoxicity 40%, 30%, 20%, 10%, or 5%, 4%, 3%, 2%, or even 0% or undetectable cytotoxicity, as measured in an *in vitro* or *ex vivo* cell killing assay. In still other embodiments, In certain embodiments, antibodies of the invention exhibit less than 50%, 40%, 30%, 20%, 10%, or 5%, 4%, 3%, 2%, or even 0% or undetectable CDC activity, at an antibody concentration of 100 nM. In more embodiments, antibodies exhibit ADCC activity of less than about 50% cytotoxicity, or less than cytotoxicity 40%, 30%, 20%, 10%, or 5%, 4%, 3%, 2%, or even 0% or undetectable cytotoxicity, as measured in an *in vitro* or *ex vivo* cell killing assay. In still other embodiments, In certain embodiments, antibodies of the invention exhibit less than 50%, 40%, 30%, 20%, 10%, or 5%, 4%, 3%, 2%, or even 0% or undetectable ADCC activity, at an antibody concentration of 100 nM.

[00131] The present invention provides antibodies, antigen-binding proteins and Fc-fusion proteins that comprise recombinant polypeptides comprising a chimeric hinge, and further provide reduced effector functions. The properties of such recombinant polypeptides of the invention may be compared to the properties of one or more reference proteins. See the examples below for reference, or control antibodies and antigen-binding proteins which have corresponding variable regions and constant regions (*e.g.* having a wild-type IgG1 C_H region (SEQ ID NO:13) or a wild-type IgG4 C_H region (SEQ ID NO:15)) compared to the chimeric antibodies of the invention, and may be used in certain testing methodologies for comparison of functional or pharmacokinetic properties to the antibodies and antigen-binding proteins of the invention. It is understood that a corresponding wild-type IgG C_H region differs from chimeric C_H regions of the invention in that the "wild-type" IgG C_H region is derived from the natural IgG amino acid sequence containing (from N-terminal to C-terminal) a CH1 domain, a hinge, a CH2 domain, and a CH3 domain. Wild-type IgG may include variants having one or more amino acid modifications while retaining essentially the same functional characteristics as natural IgG. A corresponding antibody or polypeptide may be assembled to have the same target binding domain (*e.g.* V_H and/or V_L) as the antibody or polypeptide having the chimeric C_H region, or otherwise has essentially the same functionality for the purpose of comparison in certain assays.

[00132] It has been shown in the Examples that isolated antibodies of the invention bind weakly to FcγR expressing cells, *e.g.* effector cells, but however lack effector functions, such as cytotoxicity and proliferation, compared to the effector functions of a corresponding antibody comprising a wild-type IgG1 or IgG4 C_H region.

Further aspects of the invention

[00133] In one aspect, the invention provides a recombinant polypeptide comprising a chimeric hinge region. In some aspects, the chimeric hinge region comprises a human IgG2 lower hinge amino acid sequence PCPAPPVA (SEQ ID NO: 3) from positions 228 to 236 (EU numbering). In other aspects, the chimeric hinge region comprises: a human IgG1 or a human IgG4 upper hinge amino acid sequence from positions 216 to 227 (EU numbering) and a human IgG2 lower hinge amino acid sequence PCPAPPVA (SEQ ID NO: 3) from positions 228 to 236 (EU numbering), from N-terminus to C-terminus.

[00134] In other aspects, the chimeric hinge region comprises: an upper hinge amino acid sequence from positions 216 to 227 (EU numbering) selected from the group consisting of SEQ ID NO:4 and SEQ ID NO:5, and a lower hinge amino acid sequence PCPAPPVA (SEQ ID NO: 3) from positions 228 to 236 (EU numbering), from N-terminus to C-terminus.

[00135] The invention provides a recombinant polypeptide comprising, from N-terminus to C-terminus, a CH1 domain, a chimeric hinge, a CH2 domain, and a CH3 domain wherein:

the CH1 domain comprises at least the amino acid sequence DKKV or DKRV from positions 212 to 215 (EU numbering), the chimeric hinge comprises a human IgG1 or a human IgG4 upper hinge amino acid sequence from positions 216 to 227 (EU numbering) and a human IgG2 lower hinge amino acid sequence PCPAPPVA (SEQ ID NO: 3) from positions 228 to 236 (EU numbering), the CH2 domain comprises a human IgG4 CH2 domain amino acid sequence from positions 237 to 340 (EU numbering), and the CH3 domain comprises a human IgG1 or a human IgG4 CH3 domain sequence from positions 341 to 447 (EU numbering), or a variant thereof. In one embodiment, the present invention provides a monoclonal antibody comprising a heavy chain constant region comprising or consisting of SEQ NO: 1, SEQ ID NO: 2, SEQ ID NO: 30, or SEQ ID NO: 31. In another embodiment, the present invention provides a monoclonal antibody comprising at least one heavy chain with a constant region comprising or consisting of SEQ ID NO: 38 or 37.

[00136] Table 7. Representative chimeric C_H constructs

C_H construct SEQ ID NO	**CH1**	**Upper Hinge**	**Lower Hinge**	**CH2**	**CH3**
1	DKRV (SEQ ID NO:5)	ESKYGPPCP (SEQ ID NO:7)	PCPAPPVA (SEQ ID NO:3)	SEQ ID NO:10	SEQ ID NO:12
2	DKKV (SEQ ID NO:4)	EPKSCDKTHTCP (SEQ ID NO:6)	PCPAPPVA (SEQ ID NO:3)	SEQ ID NO:10	SEQ ID NO:11
30	SEQ ID NO: 43	EPKSCDKTHTCP (SEQ ID NO:6)	PCPAPPVA (SEQ ID NO:3)	SEQ ID NO:10	SEQ ID NO:11
31	SEQ ID NO: 44	ESKYGPPCP (SEQ ID NO:7)	PCPAPPVA (SEQ ID NO:3)	SEQ ID NO:10	SEQ ID NO:12
37	SEQ ID NO: 43	EPKSCDKTHTCP (SEQ ID NO:6)	PCPAPPVA (SEQ ID NO:3)	SEQ ID NO:10	SEQ ID NO:41
38	SEQ ID NO: 44	ESKYGPPCP (SEQ ID NO:7)	PCPAPPVA (SEQ ID NO:3)	SEQ ID NO:10	SEQ ID NO:42

[00137] In some embodiments, the recombinant polypeptide is selected from the group consisting of an antibody, antigen-binding protein and receptor-Fc fusion protein.

[00138] In some embodiments, the isolated antibody, antigen-binding protein, or receptor-Fc fusion protein comprises a heavy chain construct comprising a CH region, from N-terminus to C-terminus, a CH1 domain, a chimeric hinge, a CH2 domain, and a CH3 domain, wherein the CH1 domain comprises the amino acid sequence DKKV or DKRV, the chimeric hinge comprises a human IgG1 or a human IgG4 upper hinge amino acid sequence from positions 216 to 227 (EU numbering), or a natural variant thereof, and a human IgG2 lower hinge amino acid sequence from positions 228 to 236 (EU numbering), the CH2 domain comprises a human IgG4 CH2 domain sequence from positions 237 to 340 (EU numbering), or a natural variant thereof, and the CH3 domain comprises a human IgG1 or a human IgG4 CH3 domain sequence from positions 341 to 447 (EU numbering), or a natural variant thereof, and the CH region has an amino acid sequence with at least about 95%, or about 96%, or about 97%, or about 98%, or about 99% identity to SEQ ID NO:1 or SEQ ID NO:2.

[00139] In another embodiment, the present invention provides an isolated antibody, antigen-binding protein, or receptor-Fc fusion protein comprising a heavy chain construct comprising a CH region, from N-terminus to C-terminus, a CH1 domain, a chimeric hinge, a

CH2 domain, and a CH3 domain, wherein the CH1 domain comprises the amino acid sequence DKKV or DKRV, the chimeric hinge comprises a human IgG1 or a human IgG4 upper hinge amino acid sequence from positions 216 to 227 (EU numbering), or a natural variant thereof, and a human IgG2 lower hinge amino acid sequence from positions 228 to 236 (EU numbering), the CH2 domain comprises a human IgG4 CH2 domain sequence from positions 237 to 340 (EU numbering), or a natural variant thereof, and the CH3 domain comprises a human IgG1 or a human IgG4 CH3 domain sequence from positions 341 to 447 (EU numbering), or a natural variant thereof, and the CH region has an amino acid sequence with at least about 95%, or about 96%, or about 97%, or about 98%, or about 99% identity to SEQ ID NO: 30 or SEQ ID NO: 31. In some embodiments, the CH region has an amino acid sequence with at least about 95%, or about 96%, or about 97%, or about 98%, or about 99% identity to SEQ ID NO: 38 or SEQ ID NO: 37.

[00140] Such “variant” or ”natural variant” C_H domains of the invention, *e.g.* Fc domains and Fc domain fragments, comprise one or more additions, deletions, or substitutions of amino acids when compared to the wild-type sequence that such C_H domains of the invention are derived from, but essentially function as desired. In some examples, the C_H domain or Fc domain exhibits weak or no binding to certain FcγR expressing cells, *e.g.* effector cells, resulting in altered effector functions, such as cytotoxicity and proliferation. In one example, such variants include modifications such as additions, deletions, or substitutions of amino acids in the CH3 domain engineered for the isolation of bispecific molecules.

[00141] In one embodiment, the present invention provides a monoclonal antibody comprising a heavy chain variable region and a heavy chain constant region comprising or consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 38, or SEQ ID NO: 37, or a sequence with at least about 95%, or about 96%, or about 97%, or about 98%, or about 99% to such heavy chain constant region. In another embodiment, the present invention provides a monoclonal antibody comprising a light chain variable region, a heavy chain variable region and a heavy chain constant region comprising or consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 38, or SEQ ID NO: 37, or a sequence with at least about 95%, or about 96%, or about 97%, or about 98%, or about 99% to such heavy chain constant region.

[00142] In another embodiment, the invention is an isolated antibody, or antigen-binding fragment thereof, comprising a heavy chain constant region (C_H) having (i) the amino acid sequence of SEQ NO: 1 or having the amino acid sequence encoded by SEQ ID NO: 33, or (ii) the amino acid sequence of SEQ NO: 31 or having the amino acid sequence

encoded by SEQ ID NO: 29, or (iii) a sequence with at least about 95%, or about 96%, or about 97%, or about 98%, or about 99% identity to a sequence described in (i) or (ii). In another embodiment, the invention is an isolated antibody, or antigen-binding fragment thereof, comprising a heavy chain constant region (C_H) having (i) the amino acid sequence of SEQ NO: 2 or having the amino acid sequence encoded by SEQ ID NO: 32, or (ii) the amino acid sequence of SEQ NO: 30 or having the amino acid sequence encoded by SEQ ID NO: 28, or (iii) a sequence with at least about 95%, or about 96%, or about 97%, or about 98%, or about 99% identity to a sequence described in (i) or (ii).

[00143] In still another embodiment, the invention is an isolated antibody, or antigen-binding fragment thereof, comprising a heavy chain constant region (C_H) having (i) the amino acid sequence of SEQ NO: 38 or having the amino acid sequence encoded by SEQ ID NO: 36, or (ii) the amino acid sequence of SEQ NO: 37 or having the amino acid sequence encoded by SEQ ID NO: 35, or (iii) a sequence with at least about 95%, or about 96%, or about 97%, or about 98%, or about 99% identity to a sequence described in (i) or (ii).

[00144] In some embodiments, the isolated antibody is a monoclonal antibody. In other embodiments, the isolated antibody, or antigen binding fragment thereof, is a humanized, chimeric, single-chain antibody or bispecific antibody.

[00145] In another embodiment, the invention is an Fc-containing protein comprising (i) the amino acid sequence of SEQ NO: 1 or the amino acid sequence encoded by SEQ ID NO: 33, or (ii) the amino acid sequence of SEQ NO: 31 or the amino acid sequence encoded by SEQ ID NO: 29, or (iii) a sequence with at least about 95%, or about 96%, or about 97%, or about 98%, or about 99% identity to a sequence described in (i) or (ii). In another embodiment, the invention is an Fc-containing protein comprising (i) the amino acid sequence of SEQ NO: 2 or the amino acid sequence encoded by SEQ ID NO: 32, or (ii) the amino acid sequence of SEQ NO: 30 or the amino acid sequence encoded by SEQ ID NO: 28, or (iii) a sequence with at least about 95%, or about 96%, or about 97%, or about 98%, or about 99% identity to a sequence described in (i) or (ii).

[00146] In another embodiment, the invention is an Fc-containing protein comprising (i) the amino acid sequence of SEQ NO: 38 or the amino acid sequence encoded by SEQ ID NO: 36, or (ii) the amino acid sequence of SEQ NO: 37 or the amino acid sequence encoded by SEQ ID NO: 35, or (iii) a sequence with at least about 95%, or about 96%, or about 97%, or about 98%, or about 99% identity to a sequence described in (i) or (ii).

[00147] In another embodiment, the present invention provides a composition comprising the antibody, antigen-binding protein or Fc fusion protein described.

[00148] The present invention provides an antibody or antigen-binding protein that lacks cytotoxic or cytolytic effector function. In some aspects, the antibody or antigen-binding protein lacks cytotoxic or cytolytic effector function and comprises SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 38, or SEQ ID NO: 37.

[00149] The present invention provides an antibody or antigen-binding protein having cytotoxic activity that is at least 10-fold less, or at least 50-fold less, or at least 100-fold less, or at least 1000-fold less, or at least 10000-fold less than the cytotoxic activity of a corresponding antibody comprising a wild-type IgG1 or wild-type IgG4 CH region.

[00150] The present invention provides an antibody capable of binding to an FcγR, wherein such antibody comprises a recombinant polypeptide comprising SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 38, or SEQ ID NO: 37. In some embodiments, the antibody is capable of binding to an FcγR with lower affinity compared to the binding affinity of a corresponding antibody comprising a wild-type IgG1 or wild-type IgG4 heavy chain constant region. In some embodiments, the antibody is capable of activating an FcγR at a half-maximal concentration (EC_{50}) of greater than about 10 nM, or about 20 nM, or about 30 nM, or about 40 nM, about 50 nM, about 100 nM. In some embodiments, the FcγR is a human or cynomolgus FcγRII. In other embodiments, the FcγR is FcγRIIA or FcγRIIB. In some embodiments, the antibody is capable of binding to FcγRIIA having an affinity (K_D value) of about 10 μM, or about 20 μM, or about 30 μM, or about 40 μM, about 50 μM, about 100 μM. In other embodiments, the antibody or recombinant polypeptide binds to FcγRIIA with an affinity greater than the affinity of the antibody or recombinant polypeptide to FcγRIIB.

[00151] In some embodiments, the antibody is capable of binding to FcγRIIB having an affinity (KD value) of about 10 μM, or about 20 μM, or about 30 μM, or about 40 μM, about 50 μM, about 100 μM. In some embodiments, the antibody or recombinant polypeptide binds to FcγRIIA with an affinity (K_D value) substantially similar to the affinity of the antibody or recombinant polypeptide to FcγRIIB.

[00152] For certain embodiments, it may be desirable for the chimeric antibodies of the invention to engage, and even indirectly enhance FcγRIIA-mediated activity, even though the chimeric antibodies may have wild-type affinities for FcγRIIA. Without being bound to any one theory, certain antibodies, and thus therapeutics, may benefit from a weakened interaction (compared to wild-type antibodies) with the inhibitory receptor FcγRIIB, which may shift the balance between the activating FcγRIIA and the inhibitory FcγRIIB receptors in favor of activation.

[00153] The present invention encompasses the production of monoclonal antibodies comprising a recombinant polypeptide comprising SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 38, or SEQ ID NO: 37 and having specificities for various target antigens. The invention provides a method for producing an antibody comprising: a) introducing the vector comprising a nucleic acid molecule encoding an antibody, or fragment thereof, of the invention into a mammalian host cell, b) culturing the host cell capable of expressing the antibody, and c) isolating the antibody from the cell culture media.

[00154] Monoclonal antibodies of the present invention may *e.g.* be produced by the hybridoma method first described by Kohler et al., *Nature* 256, 495 (1975), or may be produced by recombinant DNA methods. Monoclonal antibodies may also be isolated from phage antibody libraries using the techniques described in, for example, Clackson et al., *Nature* 352, 624-628 (1991) and Marks et al., J. Mol. Biol. 222, 581-597 (1991). Monoclonal antibodies may be obtained from any suitable source. Thus, for example, monoclonal antibodies may be obtained from hybridomas prepared from murine splenic B lymphocyte cells obtained from mice immunized with an antigen of interest, for instance, in the form of cells expressing the antigen on the surface, or a nucleic acid encoding an antigen of interest. Monoclonal antibodies may also be obtained from hybridomas derived from antibody-expressing cells of immunized humans or non-human mammals such as rats, rabbits, dogs, primates, etc.

[00155] In one embodiment, the antibody of the invention is a human antibody. Human monoclonal antibodies may be generated using transgenic or transchromosomal mice carrying parts of the human immune system rather than the mouse system. Such transgenic and transchromosomic mice include mice referred to herein as VELOCIMMUNE mice, HuMAb mice and KM mice, respectively, and are collectively referred to herein as "transgenic mice" and are described hereinabove.

[00156] Splenocytes from these transgenic mice may be used to generate hybridomas that secrete human monoclonal antibodies according to well-known techniques. Human monoclonal or polyclonal antibodies of the present invention, or antibodies of the present invention originating from other species may also be generated transgenically through the generation of another non-human mammal or plant that is transgenic for the immunoglobulin heavy and light chain sequences of interest and production of the antibody in a recoverable form therefrom. In connection with the transgenic production in mammals, antibodies may be produced in, and recovered from, the milk of goats, cows, or other mammals. See for instance US 5,827,690, US 5,756,687, US 5,750,172 and US 5,741,957.

Expression vectors comprising a mouse UP-II promoter operatively linked to the DNA encoding the Ig heavy and light chain sequences of interest may be engineered for expression and secretion of the proteins of interest in urine of a transgenic animal (See, *e.g.*, US 5,824,543).

[00157] Further, human antibodies of the present invention or antibodies of the present invention from other species may be generated through display-type technologies, including, without limitation, phage display, retroviral display, ribosomal display, and other techniques, using techniques well known in the art and the resulting molecules may be subjected to additional maturation, such as affinity maturation, as such techniques are well known in the art (see for instance Hoogenboom et al., *J. Mol. Biol.* 227, 381 (1991) (phage display), Vaughan et al., *Nature Biotech* 14, 309 (1996) (phage display), Hanes and Plucthau, *PNAS USA* 94, 4937-4942 (1997) (ribosomal display), Parmley and Smith, *Gene* 73, 305-318 (1988) (phage display), Scott *TIBS* 17, 241-245 (1992), Cwirla et al., *PNAS USA* 87, 6378-6382 (1990), Russel et al., *Nucl. Acids Research* 21, 1081-1085 (1993), Hogenboom et al., *Immunol. Reviews* 130, 43-68 (1992), Chiswell and McCafferty *TIBTECH* 10, 80-84 (1992), and US 5,733,743). If display technologies are utilized to produce antibodies that are not human, such antibodies may be humanized.

[00158] The engineered heavy chain constant (C_H) regions of the invention will provide reduced effector functions. Either of the human light chain constant (C_L) regions, kappa or lambda, may be used. If desired, the class of an antibody of the present invention may be switched by known methods.

[00159] The present invention provides the antibodies of the invention produced by a host cell. In one embodiment, the invention provides a method for producing a monoclonal antibody comprising a) immunizing VELOCIMMUNE® mice with an antigen sufficient to cause an antibody immune response, b) obtaining serum from such mice and testing for antibody titer against said antigen, c) harvesting B cells from the spleens of such immunized mice shown to have elevated antibody titers and fusing said B cells with mouse myeloma cells to form such hybridoma, d) isolating chimeric antibody from such hybridoma by protein A chromatography, such chimeric antibody having a human variable region and a mouse constant region, e) selecting a chimeric antibody having desirable characteristics, and f) replacing the mouse constant regions of such antibodies with a human constant region of the invention, for example, such human constant region comprising SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 38, or SEQ ID NO: 37.

[00160] In one embodiment, the antibody of the invention is a full-length IgG antibody. In another embodiment, the antibody of the invention is an antibody fragment or a single-

chain antibody. In still another embodiment, the antibody of the invention is a fully human IgG antibody.

[00161] In some aspects of the invention, the antibody is a bispecific antibody wherein each antigen-binding domain of such molecule or antibody comprises a V_H region paired with a V_L region. In certain embodiments, the bispecific antibody comprises a first antigen-binding domain and a second antigen binding domain each comprise different, distinct V_H regions ith a common V_L region. In some embodiments, the bispecific antibodies are constructed comprising a first antigen-binding domain that specifically binds a first antigen, wherein the first antigen-binding domain comprises an V_H region / V_L region pair derived from a first antibody directed against the first antigen; and a second antigen-binding domain that specifically binds a second antigen, wherein the second antigen-binding domain comprises an V_H region derived from a second antibody directed against a second antigen paired with an V_L region derived from the first antibody (*e.g.*, the same V_L region that is included in the antigen-binding domain of the first antibody). In some embodiments, the heavy chain of at least one of the antibodies, i.e. the first antibody or the second antibody or both antibodies, in a bispecific antibody is modified to comprise a chimeric heavy chain constant region (C_H region). In other embodiments, the bispecific antibody comprises SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 38, or SEQ ID NO: 37.

[00162] In some aspects of the invention, two antibodies of different specificity use the same light chain. In certain embodiments, the heavy chain of at least one of the Ig heavy chains in a bispecific antibody is modified to comprise a chimeric heavy chain constant region comprising a recombinant polypeptide of the invention. In some embodiments, at least one of the heavy chains is modified in the CH3 domain resulting in a differential affinity for the bispecific antibody for an affinity reagent, such as Protein A, for ease of isolation. In another embodiment, at least one of the heavy chains in such bispecific antibody comprises an amino acid modification at i) 95R or ii) 95R and 96F in the IMGT numbering system (95R and 96F correspond to 435R and 436F in the EU numbering system).

[00163] In other aspects, the antibody is a bispecific antibody wherein the bispecific antibody comprises:

(a) a first heavy chain comprising an antigen-binding domain capable of recognizing and binding to a first target antigen,

(b) a second heavy chain comprising an antigen-binding domain capable of recognizing and binding to a second target antigen,

(c) a common light chain antigen-binding domain capable of recognizing and binding to the first or second target antigen,

wherein the heavy chain of (a) or (b) or both (a) and (b) further comprises the heavy chain constant region comprising SEQ ID NO:1 or SEQ ID NO: 31.

[00164] In still other aspects, the antibody is a bispecific antibody wherein the bispecific antibody comprises:

(a) a first heavy chain comprising an antigen-binding domain capable of recognizing and binding to a first target antigen,

(b) a second heavy chain comprising an antigen-binding domain capable of recognizing and binding to a second target antigen,

(c) a common light chain antigen-binding domain capable of recognizing and binding to the first or second target antigen,

wherein the heavy chain of (a) or (b) or both (a) and (b) further comprises the heavy chain constant region comprising SEQ ID NO:2 or SEQ ID NO: 30.

[00165] In another aspect, at least one of the heavy chains of (a) or (b) in such bispecific antibody hereinabove comprises an amino acid modification at (i) 435R or (ii) 435R and 436F (EU numbering) ((i)95R or (ii) 95R and 96F in the IMGT numbering system).

[00166] In other aspects, the antibody is a bispecific antibody wherein the bispecific antibody comprises (a) a first heavy chain comprising an antigen-binding domain capable of recognizing and binding to a first target antigen, and a first heavy chain constant region comprising SEQ ID NO: 1, SEQ ID NO:2, SEQ ID NO: 30, or SEQ ID NO: 31; (b) a second heavy chain comprising an antigen-binding domain capable of recognizing and binding to a second target antigen, and a second heavy chain constant region comprising SEQ ID NO: 38 or SEQ ID NO: 37; and (c) common light chain antigen-binding domain capable of recognizing and binding to the first or second target antigen.

[00167] In one embodiment, the antibody is a monovalent antibody. Accordingly, in one embodiment, the antibody is a monovalent antibody, wherein said antibody is constructed by a method comprising : i) providing a nucleic acid molecule encoding the light chain of said monovalent antibody, said construct comprising a nucleotide sequence encoding the V_L region of a selected antigen specific antibody and a nucleotide sequence encoding the constant C_L region of an Ig, wherein said nucleotide sequence encoding the V_L region of a selected antigen specific antibody and said nucleotide sequence encoding the C_L region of an Ig are operably linked together, and wherein the nucleotide sequence encoding the C_L region has been modified such that the C_L region does not contain any amino acids capable of forming disulfide bonds or covalent bonds with other peptides comprising an

identical amino acid sequence of the C_L region in the presence of polyclonal human IgG or when administered to an animal or human being; ii) providing a nucleic acid construct encoding the heavy chain of said monovalent antibody, said construct comprising a nucleotide sequence encoding the V_H region of a selected antigen specific antibody and a nucleotide sequence encoding a constant C_H region of a human Ig, wherein the nucleotide sequence encoding the C_H region comprises nucleic acids encoding SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 38, or SEQ ID NO: 37, wherein such nucleotide sequence has been modified and does not comprise any amino acid residues which participate in the formation of disulphide bonds or covalent or stable non- covalent inter-heavy chain bonds with other peptides comprising an identical amino acid sequence of the C_H region of the human Ig in the presence of polyclonal human IgG or when administered to an animal, such as a human, wherein said nucleotide sequence encoding the V_H region of a selected antigen specific antibody and said nucleotide sequence encoding the C_H region of said Ig are operably linked together; iii) providing a cell expression system for producing said monovalent antibody; iv) producing said monovalent antibody by co-expressing the nucleic acid constructs of (i) and (ii) in cells of the cell expression system of (iii).

[00168] Similarly, in one embodiment, the antibody is a monovalent antibody, which comprises: i) a variable region or an antigen-binding domain of said region, and ii) a C_H region of an immunoglobulin or a fragment thereof comprising SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 38, or SEQ ID NO: 37, wherein the C_H region or fragment thereof has been modified such that the region does not comprise any amino acid residues which are capable of forming disulfide bonds with an identical C_H region or other covalent or stable non-covalent inter-heavy chain bonds with an identical C_H region in the presence of polyclonal human IgG.

[00169] In another further embodiment, the sequence of said monovalent antibody has been modified so that it does not comprise any acceptor sites for N-linked glycosylation.

[00170] In general, antibodies described herein may be modified by inclusion of any suitable number of such modified amino acids and/or associations with conjugated substituents. Suitability in this context is generally determined by the ability to at least substantially retain the antibody or antigen binding fragment's selectivity and/or specificity associated. The modified amino acid may, for instance, be selected from a glycosylated amino acid, a PEGylated amino acid, a farnesylated amino acid, an acetylated amino acid, a biotinylated amino acid, an amino acid conjugated to a lipid moiety, or an amino acid conjugated to an organic derivatizing agent. The inclusion of one or more modified amino

acids may be advantageous in, for example, further increasing polypeptide serum half-life, reducing polypeptide antigenicity, or increasing polypeptide storage stability. Amino acid(s) are modified, for example, co-translationally or post-translationally during recombinant production (*e.g.*, N-linked glycosylation at N-X-S/T motifs during expression in mammalian cells) or modified by synthetic means. Non-limiting examples of a modified amino acid include a glycosylated amino acid, a sulfated amino acid, a prenylated (e. g., farnesylated, geranylgeranylated) amino acid, an acetylated amino acid, an acylated amino acid, a PEGylated amino acid, a biotinylated amino acid, a carboxylated amino acid, a phosphorylated amino acid, and the like. References adequate to guide one of skill in the modification of amino acids are replete throughout the literature. Example protocols are found in Walker (1998) Protein Protocols On CD-Rom, Humana Press, Totowa, NJ.

[00171] Antibodies of the invention may also be chemically modified by covalent conjugation to a polymer to, for instance, further increase their circulating half-life. Exemplary polymers, and methods to attach them to peptides, are illustrated in for instance US 4,766,106, US 4,179,337, US 4,495,285 and US 4,609,546. Additional illustrative polymers include polyoxyethylated polyols and polyethylene glycol (PEG) (*e.g.*, a PEG with a molecular weight of between about 1,000 and about 40,000, such as between about 2,000 and about 20,000, *e.g.*, about 3,000-12,000 g/mol).

[00172] In one embodiment, antibodies comprising one or more radiolabeled amino acids are provided. A radiolabeled antibody may be used for both diagnostic and therapeutic purposes. In another embodiment, antibodies of the present invention may be conjugated to a molecule which is a therapeutic agent or a detectable marker. In one embodiment, the therapeutic agent is a cytotoxic agent, such as a radioisotope. Examples of radioisotopes for polypeptides include, but are not limited to, ^{3}H, ^{14}C, ^{15}N, ^{35}S, ^{90}Y, ^{99}Tc, and ^{125}I, ^{131}I, ^{186}Re, and ^{225}Ac. Methods for preparing radiolabeled amino acids and related peptide derivatives are known in the art (see for instance Junghans et al., in Cancer Chemotherapy and Biotherapy 655-686 (2nd edition, Chafner and Longo, eds., Lippincott Raven (1996)) and US 4,681,581, US 4,735,210, US 5,101,827, US 5,102,990 (US RE35,500), US 5,648,471 and US 5,697,902. For example, a radioisotope may be conjugated by a chloramine T method. In further embodiments, a detectable marker may be a radiolabel, an enzyme, a chromophore, or a fluorescent label.

[00173] In a further aspect, the invention relates to an expression vector encoding a polypeptide, *e.g.* an antibody, antigen-binding protein or receptor-Fc fusion protein of the invention. Such expression vectors may be used for recombinant production of polypeptides of the invention.

[00174] An expression vector in the context of the present invention may be any suitable vector, including chromosomal, non-chromosomal, and synthetic nucleic acid vectors (a nucleic acid sequence comprising a suitable set of expression control elements). Examples of such vectors include derivatives of SV40, bacterial plasmids, phage DNA, baculovirus, yeast plasmids, vectors derived from combinations of plasmids and phage DNA, and viral nucleic acid (RNA or DNA) vectors. In one embodiment, an antibody-encoding nucleic acid molecule is comprised in a naked DNA or RNA vector, including, for example, a linear expression element (as described in, for instance, Sykes and Johnston, *Nat Biotech* 12, 355-59 (1997)), a compacted nucleic acid vector (as described in for instance US 6,077,835 and/or WO 00/70087), or a plasmid vector such as pBR322, pUC 19/18, or pUC 118/119. Such nucleic acid vectors and the usage thereof are well known in the art (see, for instance, US 5,589,466 and US 5,973,972).

[00175] In another embodiment, the vector comprises the nucleic acid molecule encoding an antibody or polypeptide of the invention, including an expression vector comprising the nucleic acid molecules described wherein the nucleic acid molecule is operatively linked to an expression control sequence.

[00176] In one embodiment, the vector is suitable for expression of a polypeptide or antibody of the invention in a bacterial cell. Examples of such vectors include expression vectors such as BlueScript (Stratagene), pIN vectors (Van Heeke & Schuster, *J Biol Chem* 264, 5503-5509 (1989), pET vectors (Novagen, Madison, WI) and the like).

[00177] An expression vector may also or alternatively be a vector suitable for expression in a yeast system. Any vector suitable for expression in a yeast system may be employed. Suitable vectors include, for example, vectors comprising constitutive or inducible promoters such as yeast alpha factor, alcohol oxidase and PGH (reviewed in: F. Ausubel et al., ed. Current Protocols in Molecular Biology, Greene Publishing and Wiley InterScience New York (1987), and Grant et al., *Methods in Enzymol* 153, 516-544 (1987)).

[00178] A vector comprising a nucleic acid molecule of the invention is provided, wherein the nucleic acid molecule is operatively linked to an expression control sequence suitable for expression in a mammalian host cell.

[00179] Expression control sequences are engineered to control and drive the transcription of genes of interest, and subsequent expression of proteins in various cell systems. Plasmids combine an expressible gene of interest with expression control sequences (*i.e.* expression cassettes) that comprise desirable elements such as, for example, promoters, enhancers, selectable markers, operators, *etc.* In an expression vector of the invention, antibody-encoding nucleic acid molecules may comprise or be associated

with any suitable promoter, enhancer, selectable marker, operator, repressor protein, polyA termination sequences and other expression-facilitating elements.

[00180] "Promoter" as used herein indicates a DNA sequence sufficient to direct transcription of a DNA sequence to which it is operably linked, i.e., linked in such a way as to permit transcription of the antibody-encoding nucleotide sequence when the appropriate signals are present. The expression of a antibody-encoding nucleotide sequence may be placed under control of any promoter or enhancer element known in the art. Examples of such elements include strong expression promoters (e. g., human CMV IE promoter/enhancer or CMV major IE (CMV-MIE) promoter, as well as RSV, SV40 late promoter, SL3-3, MMTV, ubiquitin (Ubi), ubiquitin C (UbC), and HIV LTR promoters).

[00181] In some embodiments, the vector comprises a promoter selected from the group consisting of SV40, CMV, CMV-IE, CMV-MIE, RSV, SL3-3, MMTV, Ubi, UbC and HIV LTR.

[00182] Nucleic acid molecules of the invention may also be operatively linked to an effective poly (A) termination sequence, an origin of replication for plasmid product in E. coli, an antibiotic resistance gene as selectable marker, and/or a convenient cloning site (*e.g.*, a polylinker). Nucleic acids may also comprise a regulatable inducible promoter (inducible, repressable, developmentally regulated) as opposed to a constitutive promoter such as CMV IE (the skilled artisan will recognize that such terms are actually descriptors of a degree of gene expression under certain conditions).

[00183] Selectable markers are elements well-known in the art. Under the selective conditions, only cells that express the appropriate selectable marker can survive. Commonly, selectable marker genes express proteins, usually enzymes, that confer resistance to various antibiotics in cell culture. In other selective conditions, cells that express a flourescent protein marker are made visible, and are thus selectable. Embodiments include beta-lactamase (bla) (beta- lactam antibiotic resistance or ampicillin resistance gene or ampR), bls (blasticidin resistance acetyl transferase gene), bsd (blasticidin-S deaminase resistance gene), bsr (blasticidin-S resistance gene), Sh ble (Zeocin® resistance gene), hygromycin phosphotransferase (hpt) (hygromycin resistance gene), tetM (tetracycline resistance gene or tetR), neomycin phosphotransferase II (npt) (neomycin resistance gene or neoR), kanR (kanamycin resistance gene), and pac (puromycin resistance gene).

[00184] In certain embodiments, the vector comprises one or more selectable marker genes selected from the group consisting of bla, bls, BSD, bsr, Sh ble, hpt, tetR, tetM, npt, kanR and pac. In other embodiments, the vector comprises one or more selectable marker genes encoding green fluorescent protein (GFP), enhanced green fluorescent protein

(eGFP), cyano fluorescent protein (CFP), enhanced cyano fluorescent protein (eCFP), or yellow fluorescent protein (YFP).

[00185] For the purposes of this invention, gene expression in eukaryotic cells may be tightly regulated using a strong promoter that is controlled by an operator that is in turn regulated by a regulatory fusion protein (RFP). The RFP consists essentially of a transcription blocking domain, and a ligand-binding domain that regulates its activity. Examples of such expression systems are described in US20090162901A1, which is herein incorporated by reference in its entirety.

[00186] As used herein "operator" indicates a DNA sequence that is introduced in or near a gene in such a way that the gene may be regulated by the binding of the RFP to the operator and, as a result, prevents or allow transcription of the gene of interest, *i.e.* a nucleotide encoding a polypeptide of the invention. A number of operators in prokaryotic cells and bacteriophage have been well characterized (Neidhardt, ed. Escherichia coli and Salmonella; Cellular and Molecular Biology 2d. Vol 2 ASM Press, Washington D.C. 1996). These include, but are not limited to, the operator region of the *LexA* gene of *E. coli*, which binds the LexA peptide, and the lactose and tryptophan operators, which bind the repressor proteins encoded by the *LacI* and *trpR* genes of *E. coli*. These also include the bacteriophage operators from the lambda P_R and the phage P22 *ant/mnt* genes which bind the repressor proteins encoded by lambda cI and P22 arc. In some embodiments, when the transcription blocking domain of the RFP is a restriction enzyme, such as NotI, the operator is the recognition sequence for that enzyme. One skilled in the art will recognize that the operator must be located adjacent to, or 3' to the promoter such that it is capable of controlling transcription by the promoter. For example, U.S. Pat. No. 5,972,650, which is incorporated by reference herein, specifies that *tetO* sequences be within a specific distance from the TATA box. In specific embodiments, the operator is preferably placed immediately downstream of the promoter. In other embodiments, the operator is placed within 10 base pairs of the promoter.

[00187] In certain embodiments, the operator is selected from the group consisting of tet operator (tetO), NotI recognition sequence, LexA operator, lactose operator, tryptophan operator and Arc operator (AO). In some embodiments, the repressor protein is selected from the group consisting of TetR, LexA, LacI, TrpR, Arc, LambdaC1 and GAL4. In other embodiments, the transcription blocking domain is derived from a eukaryotic repressor protein, *e.g.* a repressor domain derived from GAL4.

[00188] In an exemplary cell expression system, cells are engineered to express the tetracycline repressor protein (TetR) and a protein of interest is placed under transcriptional

control of a promoter whose activity is regulated by TetR. Two tandem TetR operators (tetO) are placed immediately downstream of a CMV-MIE promoter/enhancer in the vector. Transcription of the gene encoding the protein of interest directed by the CMV-MIE promoter in such vector may be blocked by TetR in the absence of tetracycline or some other suitable inducer (*e.g.* doxycycline). In the presence of an inducer, TetR protein is incapable of binding tetO, hence transcription then translation (expression) of the protein of interest occurs. (See, *e.g.*, US Patent No. 7,435,553, which is herein incorporated by reference in its entirety.)

[00189] Another exemplary cell expression system includes regulatory fusion proteins such as TetR-ER_{LBD}T2 fusion protein, in which the transcription blocking domain of the fusion protein is TetR and the ligand-binding domain is the estrogen receptor ligand-binding domain (ER_{LBD}) with T2 mutations (ER_{LBD}T2; Feil et al. (1997) Biochem. Biophys. Res. Commun. 237:752-757). When *tetO* sequences were placed downstream and proximal to the strong CMV-MIE promoter, transcription of the nucleotide sequence of interest from the CMV-MIE/*tetO* promoter was blocked in the presence of tamoxifen and unblocked by removal of tamoxifen. In another example, use of the fusion protein Arc2-ER_{LBD}T2, a fusion protein consisting of a single chain dimer consisting of two Arc proteins connected by a 15 amino acid linker and the ER_{LBD}T2 (*supra*), involves an Arc operator (AO), more specifically two tandem arc operators immediately downstream of the CMV-MIE promoter/enhancer. Cell lines may be regulated by Arc2-ER_{LBD}T2, wherein cells expressing the protein of interest are driven by a CMV-MIE/ArcO2 promoter and are inducible with the removal of tamoxifen. (See, *e.g.*, US 20090162901A1, which is herein incorporated by reference.)

[00190] In some embodiments, a vector of the invention comprises a CMV-MIE/TetO or CMV-MIE/AO2 hybrid promoter.

[00191] The vectors of the invention may also employ Cre-*lox* tools for recombination technology in order to facilitate the replication of a gene of interest. A Cre-*lox* strategy requires at least two components: 1) Cre recombinase, an enzyme that catalyzes recombination between two loxP sites; and 2) *lox*P sites (*e.g.* a specific 34-base pair bp sequence consisting of an 8-bp core sequence, where recombination takes place, and two flanking 13-bp inverted repeats) or mutant *lox* sites. (See, e.g. Araki et al. *PNAS* 92:160-4 (1995); Nagy, A. et al. *Genesis* 26:99-109 (2000); Araki et al. *Nuc Acids Res* 30(19):e103 (2002); and US20100291626A1, all of which are herein incorporated by reference). In another recombination strategy, yeast-derived FLP recombinase may be utilized with the consensus sequence FRT (see also, *e.g.* Dymecki, S. *PNAS* 93(12): 6191-6196).

[00192] In another aspect, a gene (*i.e.* a nucleotide sequence encoding a

recombinant polypeptide of the invention) is inserted within an expression-enhancing sequence of the expression cassette, and is optionally operably linked to a promoter, wherein the promoter-linked gene is flanked 5' by a first recombinase recognition site and 3' by a second recombinase recognition site. Such recombinase recognition sites allow Cre-mediated recombination in the host cell of the expression system. In some instances, a second promoter-linked gene is downstream (3') of the first gene and is flanked 3' by the second recombinase recognition site. In still other instances, a second promoter-linked gene is flanked 5' by the second recombinase site, and flanked 3' by a third recombinase recognition site. In some embodiments, the recombinase recognition sites are selected from a *lox*P site, a *lox*511 site, a *lox*2272 site, and a FRT site. In other embodiments, the recombinase recognition sites are different. In a further embodiment, the host cell comprises a gene capable of expressing a Cre recombinase.

[00193] In one embodiment, the vector comprises a first gene encoding a light chain of an antibody or a heavy chain of an antibody of the invention, and a second gene encoding a light chain of an antibody or a heavy chain of an antibody of the invention.

[00194] In some embodiments, the vector further comprises an X-box-binding-protein 1 (mXBP1) gene capable of enhancing protein production/protein secretion through control of the expression of genes involved in protein folding in the endoplasmic reticulum (ER). (See, *e.g.* Ron D, and Walter P. *Nat Rev Mol Cell Biol*.8:519–529 (2007)).

[00195] The term "cell" includes any cell that is suitable for expressing a recombinant nucleic acid sequence. Cells include those of prokaryotes and eukaryotes (single-cell or multiple-cell), bacterial cells (*e.g.*, strains of *E. coli, Bacillus* spp*., Streptomyces* spp*.,* etc.), mycobacteria cells, fungal cells, yeast cells (*e.g. S. cerevisiae*, *S. pombe*, *P. partoris*, *P. methanolica*, etc.), plant cells, insect cells (e.g. SF-9, SF-21, baculovirus-infected insect cells, *Trichoplusia ni*, etc.), non-human animal cells, human cells, or cell fusions such as, for example, hybridomas or quadromas. In certain embodiments, the cell is a human, monkey, ape, hamster, rat or mouse cell. In other embodiments, the cell is eukaryotic and is selected form the following cells: CHO (e.g. CHO K1, DXB-11 CHO, Veggie-CHO), COS (e.g. COS-7), retinal cells, Vero, CV1, kidney (e.g. HEK293, 293 EBNA, MSR 293, MDCK, HaK, BHK21), HeLa, HepG2, WI38, MRC 5, Colo25, HB 8065, HL-60, Jurkat, Daudi, A431 (epidermal), CV-1, U937, 3T3, L cell, C127 cell, SP2/0, NS-0, MMT cell, tumor cell, and a cell line derived from an aforementioned cell. In some embodiments, the cell comprises one or more viral genes, *e.g.* a retinal cell that expresses a viral gene (e.g. a PER.C6® cell).

[00196] In an even further aspect, the invention relates to a recombinant eukaryotic or prokaryotic host cell, such as a transfectoma, which produces an antibody of the invention

as defined herein or a bispecific molecule of the invention as defined herein. Examples of host cells include yeast, bacterial, and mammalian cells, such as CHO or HEK cells. For example, in one embodiment, the present invention provides a cell comprising a nucleic acid stably integrated into the cellular genome that comprises a sequence coding for expression of an antibody comprising a recombinant polypeptide of the present invention. In another embodiment, the present invention provides a cell comprising a non-integrated (i.e., episomal) nucleic acid, such as a plasmid, cosmid, phagemid, or linear expression element, which comprises a sequence coding for expression of an antibody comprising the recombinant polypeptide of the invention. In other embodiments, the present invention provides a cell line produced by stably transfecting a host cell with a plasmid comprising an expression vector of the invention.

[00197] In a further aspect, the invention relates to a method for producing an antibody, or antigen-binding protein, or receptor-Fc fusion protein of the invention, said method comprising the steps of a) culturing a hybridoma or a host cell of the invention as described herein above, and b) purifying the antibody, or antigen-binding protein, or receptor-Fc fusion *(supra)* from the culture media.

[00198] In an even further aspect, the invention relates to a composition comprising: an antibody or antigen-binding fragment thereof, antigen-binding protein or receptor-Fc fusion protein as defined herein, or a bispecific molecule as defined herein.

[00199] The compositions may be formulated with pharmaceutically acceptable carriers or diluents as well as any other known adjuvants and excipients in accordance with conventional techniques such as those disclosed in Remington: The Science and Practice of Pharmacy, 19th Edition, Gennaro, Ed., Mack Publishing Co., Easton, PA, 1995.

[00200] The pharmaceutically acceptable carriers or diluents as well as any other known adjuvants and excipients should be suitable for the chosen antibody of the present invention and the chosen mode of administration. The actual dosage levels of the active ingredients in the pharmaceutical compositions of the present invention may be varied so as to obtain an amount of the active ingredient which is effective to achieve the appropriate stability of drug substance, desired therapeutic response for a particular patient, composition, and mode of administration. The selected dosage level will depend upon a variety of pharmacokinetic factors.

[00201] The pharmaceutical composition may be administered by any suitable route and mode. Suitable routes of administering an antibody of the present invention *in vivo* are well known in the art and may be selected by those of ordinary skill in the art. (Daugherty, AL, and Msrny, RJ, *Adv Drug Delivery Rev*, 58(5-6): 686-706 (2006)).

[00202] Labeled antibodies of the invention can be used for diagnostic purposes to detect, diagnose, or monitor diseases or disorders. The invention provides for the detection or diagnosis of a disease or disorder, comprising: (a) assaying the existence of antigen in cells or tissue samples of a subject using one or more antibodies that immunospecifically bind to the target antigen; and (b) comparing the level of the antigen with a control level, *e.g.* levels in normal tissue samples, whereby an increase in the assayed level of antigen compared to the control level of antigen is indicative of the disease or disorder, or indicative of the severity of the disease or disorder.

[00203] Antibodies of the invention can be used to assay antigen levels in a biological sample using immunohistochemical methods well-known in the art. Other antibody-based methods useful for detecting protein include immunoassays such as the enzyme linked immunoassay (ELISA) and the radioimmunoassay (RIA). Suitable antibody labels may be used in such kits and methods, and labels known in the art include enzyme labels, such as alkaline phophatase and glucose oxidase; radioisotope labels, such as iodine (^{125}I, ^{131}I), carbon (^{14}C), sulfur (^{35}S), tritium (^{3}H), indium (^{121}In), and technetium (^{99m}Tc); and luminescent labels, such as luminol and luciferase; and flourescent labels, such as flourescein and rhodamine.

[00204] Presence of labeled antibodies may be detected *in vivo* for diagnosis purposes. In one embodiment, diagnosis comprises: a) administering to a subject an effective amount of a labeled antibody; b) waiting for a time interval following administration for permitting labeled antibody to concentrate at sites where antigen may be detected and to allow for unbound labeled antibody to be cleared to background level; c) determining a background level; and d) detecting the labeled antibody in the subject, such that detection of labeled antibody above the background level is indicative that the subject has the disease or disorder, or is indicative of the severity of the disease or disorder. In accordance with such embodiment, the antibody is labeled with an imaging moiety suitable for detection using a particular imaging system known to those skilled in the art. Background levels may be determined by various methods known in the art, including comparing the amount of labeled antibody detected to a standard value previously determined for a particular imaging system. Methods and systems that may be used in the diagnostic methods of the invention include, but are not limited to, computed tomography (CT), whole body scan such as positron emission tomography (PET), magnetic resonance imaging (MRI), and sonography.

EXAMPLES

[00205] The following examples are provided to describe to those of ordinary skill in the art how to make and use methods and compositions of the invention, and are not intended to limit the scope of what the inventors regard as their invention. Efforts have been made to ensure the accuracy with respect to numbers used (*e.g.* amounts, concentrations, temperature, etc.) but some experimental errors and deviations should be accounted for.

[00206] **Example 1: Preparation of the recombinant polypeptides**

Generating the recombinant polypeptides, for example a chimeric C_H IgG4 (SEQ ID NO: 31) and a chimeric C_H IgG1 (SEQ ID NO: 30), was done using standard cloning techniques. First, the chimeric IgG4 C_H was generated through a two-step PCR amplification process. Two PCR fragments, Fragment 1 and 2, were amplified using starting construct pR85501 (containing a wild-type hIgG4 C_H DNA) and using primers oSP030-oSP031 and oSP032-oSP033 (see Table 8), respectively. The primers introduced the desired IgG2 lower hinge sequence (which encodes SEQ ID NO:3) and the flanking restriction sites into the fragments. These two fragments were then joined using PCR primers oSP031 and oSP033. The resulting sequence was inserted into pR85501via Xho1-Not1 restriction sites generating a vector construct pR85502 that contains a chimeric IgG4 C_H having an IgG2 lower hinge sequence. The sequence was confirmed using primers KO_oLRC120 and oKO021.

[00207] In addition, a chimeric IgG1 C_H was generated through multiple step PCR amplification. Fragment 1a was generated using primers oSP031 and oSP035 (see Table 8 below) from template pR85503 (which contains a wild-type human IgG1 C_H DNA). Fragment 2a was amplified with primers oSP036 and oSP038 using pR85502 (containing the chimeric IgG4 C_H DNA) as a template. Fragment 3 was made using primers oSP037 and oSP039 from template pR85503 (wild-type hIgG1 C_H DNA). Fragments 1a and 2a were joined using primers oSP031 and oSP038, which generated Fragment 4. Joining Fragments 2a and 3 using primers oSP036 and oSP039 created Fragment 5. Fragment 4 and 5 were then fused using primers oSP031 and oSP039. The resulting sequence was inserted into pR85501 via Xho1-Not1 restriction sites generating a construct pR85504 that has an IgG1 constant region with the IgG2 lower hinge and IgG4 CH2 domain. The sequence was confirmed using primers KO_oLRC120 and oKO021.

Table 8: Primers for PCR generation of chimeric C_H nucleic acid constructs

Primer name	Primer Sequence (SEQ ID NO)
oSP030	5'-TTCGCGCAGCTTAGGTTTATGCCAGGGGGGACGGGTGGCACGGGTCGTGGTGGACACCGT

	-3' (antisense) (SEQ ID NO: 16)
oSP031	5'-AAGCTTATACTCGAGCTCTAGATTGGGAACCCGGGTCTCT-3' (SEQ ID NO: 17)
oSP032	5'-CCCACCGTGCCCAGCACCACCTGTGGCAGGACCATCAGTCTTCCTGTTCCCCCCAAAA-3' (SEQ ID NO: 18)
oSP033	5'-TGTGTCTTCAGGGAGAGGGACAGAGACCCATTTACTCGCC GGCG-3' (antisense) (SEQ ID NO: 19)
oSP035	5'-CTCGGGTTTAGAACACTGTTTTGAGTGTGTACGGGTGGCACGGGTCGTGGTGGACACCGT-3' (antisense) (SEQ ID NO:20)
oSP036	5'-AAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCACCTGTG-3' (SEQ ID NO: 21)
oSP037	5'-GAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC-3' (SEQ ID NO: 22)
oSP038	5'- CTCTTTTGGTAGAGGTTTCGGTTTCCCGTCGGGGCTCTTG GTGTCCACATGTGG-3' (antisense) (SEQ ID NO: 23)
oSP039	5'-CTTCAGGGAGAGGGACAGAGGCCCATTTACTCGCCGGCG-3' (antisense) (SEQ ID NO: 24)
KO_oLRC120	5'-GCTGACAGACTAACAGACTG-3' (SEQ ID NO: 25)
KO_Fc-4-3	5'-GACCTCAGGGGTCCGGGAGATCAT-3' (SEQ ID NO: 26)
oKO021	5'-ATACATTATACGAAGTTATACCGGTA-3' (SEQ ID NO: 27)
oKO014	5'- GTGAGCGCTCTTCGGCAGACGTCCAACTGGTGCAGTCAGGG-3' (SEQ ID NO: 39)
oKO015	5'-CAGCTAGCTCTTCCGGCTGAGGAGACGGTGACCGTGGTGCCTTGGCC-3' (SEQ ID NO: 40)

[00208] Example 2: Generation of Chimeric Heavy Chain Antibodies

Exemplary antibodies were obtained using standard methodologies. An anti-hCD3 antibody (anti-hCD3 antibody "L2K") was used to construct the chimeric antibodies of this example. L2K was obtained by well-known methods based on WO2004/106380. Anti-hCD3_L2K, designated herein as Control Antibody 1, contains a wild-type human IgG1 heavy chain constant region (SEQ ID NO:13).

[00209] The bispecific antibodies created in accordance with the present Example comprise two separate antigen-binding domains (*i.e.*, binding arms). An anti-hCD3 x anti-hCD20 (Bispecific antibody), designated herein as Control Antibody 2, was obtained as described in US Patent Application Publication No. US20100331527A1. The bispecific

antibody was constructed using standard methodologies wherein a heavy chain and a light chain from an “L2K” anti-CD3 antibody of WO2004/106380 were combined with a heavy chain from an anti-CD20 antibody (see *e.g.* PCT International Application No. PCT/US13/60511, filed on September 19, 2013, which is herein incorporated by reference in its entirety). Control Antibody 2 contains wild-type human IgG4 heavy chain constant regions (SEQ ID NO:15), yet the anti-CD3 arm has a modified CH3 domain (SEQ ID NO:42) for ease of purification.

[00210] Control Antibody 3 was obtained using the same methodologies as described herein to combine the variable regions of Control Ab 2 (Anti-hCD3 x anti-hCD20 Bispecific Ab) with a wild-type human IgG1 heavy chain constant regions (SEQ ID NO:13), having a modified CH3 domain (SEQ ID NO:41) in the anti-CD3 heavy chain arm.

[00211] Control Antibody 4 contains an antigen-binding domain capable of binding CA9 antigen and a wild-type human IgG1 heavy chain constant region (SEQ ID NO:13).

[00212] Control Antibody 5 is an anti-hCD3 x anti-hCD20 bispecific antibody obtained according to the methods of PCT International Application No. PCT/US13/60511, filed on September 19, 2013, which is herein incorporated by reference in its entirety. Briefly, a first antigen-binding domain comprising a heavy chain variable region derived from an anti-CD20 antibody ("CD20-VH") is paired with a light chain variable region derived from an anti-CD3 antibody ("CD3-VL"). The CD20-VH/CD3-VL pairing creates an antigen-binding domain that specifically recognizes CD20. A second antigen-binding domain comprising a heavy chain variable region derived from an anti-CD3 antibody ("CD3-VH") is paired with a light chain variable region derived from an anti-CD3 antibody ("CD3-VL"). The CD3-VH/CD3-VL pairing creates an antigen-binding domain that specifically recognizes CD3. Control Antibody 5 is engineered with wild-type human IgG1 heavy chain constant regions (SEQ ID NO:13), yet the anti-CD3 arm has a modified CH3 domain (SEQ ID NO:41) in the heavy chain constant region for ease of purification.

[00213] Isotype controls were made that do not bind to the same target antigen as the tested antibodies, *e.g.* do not bind CD3 or CD20 antigen. Wild-type IgG1 Isotype Control contains the wt heavy chain constant region amino acid sequence of SEQ ID NO:13. Wild-type IgG4 “CPPC” Isotype Control has the wt CH amino acid sequence of SEQ ID NO:15, except having the “CPPC” hinge mutation S228P (according to EU numbering).

[00214] The constant region of Control Antibody 1 was replaced with a chimeric human constant region of the invention, *e.g* SEQ ID NO: 31 or SEQ ID NO: 30. Replacement of the constant region was done by obtaining a L2K variable region nucleic acid sequence (plasmid pR85505) that was amplified using primers oKO014 and oKO015 (see Table 8).

The L2K variable region (SEQ ID NO: 34) was then introduced into plasmid pR85502 using Sap1 restriction site for cloning. The sequence of the resulting plasmid pR85506 was confirmed using primers KO_oLRC120 and oKO_Fc_4-3. This construct was used to generate Antibody 1 of the invention, sIgG4-anti-CD3_L2K (also known herein as sIgG4) (which comprises SEQ ID NO:31), using standard methodologies for isolating antibodies.

[00215] In a second example, the L2K variable region was amplified using primers oKO014 and oKO015 (see Table 8) using plasmid pR85505 as template. The variable region was then introduced into plasmid pR85504 using Sap1 restriction site for cloning. The sequence of the resulting plasmid pR85507 was confirmed using primers KO_oLRC120 and oKO_Fc_4-3. This construct was used to generate Antibody 2 of the invention, sIgG1-anti-CD3_L2K (also known herein as sIgG1) (which comprises SEQ ID NO:30), using standard methodologies.

[00216] Antibody 3 was constructed from the anti-CD3 x anti-CD20 bispecific antibody of Control Antibody (Ab) 5. Control Ab 5 had its heavy chain constant regions replaced with chimeric constant heavy chain regions, the anti-CD20 arm having an heavy chain constant region amino acid sequence comprising SEQ ID NO: 30, and the anti-CD3 arm having a mutation in the CH3 domain of the CH (SEQ ID NO:37) to create Antibody 3 (also known herein as sIgG1*).

[00217] Similarly, Antibody 4 was created from bispecific antibody Control Ab 5 whereas heavy chain constant regions were replaced with chimeric CH, the anti-CD20 arm having an heavy chain constant region amino acid sequence comprising SEQ ID NO: 31, and the anti-CD3 arm having a mutation in the CH3 domain of the CH (SEQ ID NO:38) to create Antibody 4 (also known herein as sIgG4*).

[00218] The chimeric antibodies comprising constant regions of SEQ ID NO:30 or SEQ ID NO:31 (or bispecific antibodies comprising SEQ ID NO:30/37 or SEQ ID NO:31/38), and the control antibodies, were used in certain experiments set out in the Examples that follow.

[00219] Example 3: Chimeric Antibodies Specifically Bind to Jurkat cells

After chimeric antibodies were converted to fully human IgGs, specific antigen binding properties were determined. The example antibody constructs and control antibodies, as set forth in Example 2, were tested using fluorescence-activated cell sorting (FACS) for their ability to bind to Jurkat cells (human T-cell line expressing target antigens CD3+, CD20). FACS data was acquired using the following protocol: Cells at $2x10^5$ per well were incubated with serially diluted antibodies and 100 µl supplements for 1 hour at 4^oC. Post

incubation, cells were washed twice and appropriate secondary antibodies (*e.g.* fluorescent-tagged FITC anti-human IgG) were added and incubated for an additional 30 minutes at 4°C, then washed twice. Cells were re-suspended in cold PBS containing 1% BSA and analyzed by flow cytometry on a FACSCanto II™ flow cytometer (BD Biosciences). Jurkat cells were gated by side and forward scatter sorting. Each EC_{50} for cell binding titration was determined using Prism (GraphPad Software, San Diego, CA) with values calculated using a 4-parameter non-linear regression analysis.

[00220] It was determined that chimeric antibodies bind to Jurkat cells at equal concentrations compared to control antibodies having a wild-type C_H region, therefore chimeric antibodies with altered C_H regions have not lost their ability to bind antigen. See Figure 6.

[00221] Example 4: Characterization of Antibodies- Binding to U937 cells

U937 cells, a monocyte cell line expressing FcγRI and FcγRIIA, were plated and allowed to incubate with serial dilutions of Ab (the highest concentration of Ab used is 50nM). Cells were incubated with Abs for 1hr at 4°C then washed twice. U937 cells were then incubated with secondary Ab (FITC goat anti-human Fab) for 30 min at 4°C then washed twice. Cells were analyzed by flow cytometry using standard methods and median fluorescent intensity (MFI) was recorded. Results are summarized in Table 9 and Figure 7 where it is demonstrated that chimeric Abs, Antibody 1 (sIgG4) and Antibody 2 (sIgG1), bind to U937 cells at high concentrations.

Table 9: Binding of Chimeric Abs vs. Wild-type Abs to U937 cells

Antibody (Ab)	EC_{50} (nM)
Control Ab 1	1.3
sIgG1 (Ab2)	45.4
Control Ab 2	0.91
sIgG4 (Ab 1)	33.5

[00222] Example 5: Characterization of Antibodies- U937 cytotoxic assay

U937 cells were used as a positive killer effector control in the following cytoassay. As such, the ability of antibodies with chimeric C_H regions to kill U937 cells via Fc/FcγR interactions was tested. Calcein killing assays were carried out using the following protocol: Human and cynomolgus Peripheral Blood Mononuclear Cells (PBMCs) were isolated over Ficoll-Paque (GE Healthcare Life Sciences) or via Lympholyte-Mammal density cell separation media

(Cedarlane Laboratories), respectively. The isolated PBMCs were activated over a course of several days with media containing recombinant human IL-2 (30U/ml) and T-cell activation beads (anti-CD3/CD28 for human PBMC, anti-CD2/CD3/CD28 for cynomolgus PBMC). Activated T-cells were isolated from the PBMCs by centrifugation, then resuspended in 1ml media. The magnetized beads were removed from the T-cells. Target cells (U937) were labeled with calcein, then washed and followed by incubation with the isolated activated T-cells (10:1 effector: target ratio) and antibody, using 3-fold serial dilutions of antibody over a course of 3 hours at 37°C. Following incubation, the plates were centrifuged and supernatants were transferred to a translucent black clear bottom plate for fluorescence analysis. Each EC_{50}, defined as the molar concentration of antibody that induces 50% cytotoxicity, was determined using Prism (GraphPad Software, San Diego, CA). Values were calculated using a 4-parameter non-linear regression analysis. Results are summarized in Figure 8.

[00223] The cytotoxic activity of Antibody 1 (sIgG4) and Antibody 2 (sIgG1) is significantly diminished as compared to corresponding antibodies containing wild-type IgG4 and IgG1 hinge regions. See Figure 8. Interestingly, although the chimeric Abs weakly bind at higher concentrations as shown in Example 4, they do not kill U937 cells in the cytoassay.

[00224] **Example 6- Characterization of Antibodies- Proliferation of hPBMCs**

The ability of chimeric antibodies and control constructs to stimulate Peripheral Blood Mononuclear Cells (PBMCs) and induce proliferation was assessed using ATP catalyzed quantification (CellTiter Glo®). The activation of PBMCs results in the release of cytokines, which drive cellular proliferation. Proliferation data was acquired using the following protocol: Human or cynomolgus monkey derived PBMC ($5x10^5$ / well) were incubated with a 3-fold serial dilution of anti-CD20xCD3 or Control antibody (including Control Ab 4 specific to CA9 antigen) in 96 well plates for 72 h at 37°C. Following incubation, CellTiter Glo® was added and luminescence was measured using a VICTOR X5 multi-label plate reader (PerkinElmer). The EC_{50} of cell viability (ATP catalyzed quantification) was determined using Prism (GraphPad Software, San Diego, CA). Values were calculated using a 4-parameter non-linear regression analysis and are shown in Figure 9.

[00225] Antibody 1 (sIgG4) and Antibody 2 (sIgG1) do not activate cellular proliferation in comparison to corresponding antibodies containing wild-type IgG4 and IgG1 hinge regions. See Figure 9.

[00226] Example 7- Surface Plasmon Resonance Derived Binding Affinities and Kinetic Constants of Chimeric Antibodies

The anti-CD3 x anti-CD20 bispecific antibodies having chimeric constant heavy chain regions sIgG1* (Antibody 3) and sIgG4* (Antibody 4) were analyzed using Surface Plasmon Resonance (SPR) (Biacore) technology to determine their kinetic binding parameters to human and cynomolgus Fcγ receptors. Isotype controls, namely wt-IgG1 Isotype Control and wt-IgG4 CPPC Isotype Control, were tested in a similar manner.

[00227] Briefly, SPR experiments were performed at 25°C on a Biacore T200 instrument employing a carboxymethyl dextran-coated (CM-5) chip. A mouse monoclonal anti-penta-histidine antibody (GE Healthcare) was immobilized on the surface of the CM-5 sensor chip using standard amine-coupling chemistry. 140RU-376RU of His-tagged human or monkey FcγR proteins were captured on the anti-penta-histidine amine-coupled CM-5 chip and stock solutions of antibodies were injected at 20 µl/min for 2.5 min over the captured proteins. mAb binding response was monitored and, for low affinity receptors, steady-state binding equilibrium was calculated. Kinetic association (k_a) and dissociation (k_d) rate constants were determined by processing and fitting the data to a 1:1 binding model using Scrubber 2.0 curve fitting software. Binding dissociation equilibrium constants (K_D) and dissociative half-lives ($t_{1/2}$) were calculated from the kinetic rate constants as: K_D (M) = k_d / k_a; and $t_{1/2}$ (min) = (ln2/(60*k_d).

Table 10: Kinetic binding parameters for wild-type (wt) and chimeric heavy chain antibodies

Binding to His-captured human FcγRI at 25°C				
Antibody	**k_a ($M^{-1}sec^{-1}$)**	**k_d ($^1sec^{-1}$)**	**K_D ($10^{-9}M$)**	**$T^{1/2}$ (min)**
wt-IgG1 Isotype Control	1.74E+05	7.48E-04	4.3	15
wt-IgG4 CPPC Isotype Control	1.71E+05	2.36E-03	13.9	5
sIgG1* (Ab 3)	NB	NB	NB	NB
sIgG4* (Ab 4)	NB	NB	NB	NB

NB: No binding

[00228] As the results in Table 10 demonstrate, sIgG1* and sIgG4* bispecific antibodies display no binding to human FcγRI, compared to antibodies having the wild-type (wt) hIgG1 or hIgG4-CPPC CH region. Chimeric heavy chain antibodies of this invention also display weak to no binding for several of the low-affinity FcRγ receptors (*e.g.* FcRγIIa, FcRγIIb) compared to antibodies with wt hIgG1 or hIgG4-CPPC Fc sequence (Table 11).

Table 11: Steady-state equilibrium binding for wild-type (wt) and chimeric heavy chain antibodies

Binding to His-captured low-affinity human and cynomolgus FcγR receptors at 25 °C									
Antibody Tested	K_D (10^{-6} M) Values for Low Affinity FcγR Binding to Chimeric Heavy Chain Antibodies								
	human hFcγRIIA (H131)	*human FcγRIIA (R131)*	*cynomolgus FcγRIIA*	*human FcγRIIB*	*cynomolgus FcγRIIB*	*human FcγRIIIA (V176)*	*human FcγRIIIA (F176)*	*cynomolgus FcγRIIIA*	*human FcγRIIIB*
wtIgG1 Isotype Control	1.1	2	4.2	2	4.2	1.5	1.3	0.6	2.3
wtIgG4 (CPPC) Isotype Control	12	10	19.3	9.8	9.6	10	26	5.8	NB
sIgG1* (Ab 3)	11.7	20.5	23.5	233	14.6	NB	NB	42.4	NB
sIgG4* (Ab 4)	12	19.3	23.1	123	13.9	NB	NB	66.3	NB

NB: No binding

[00229] **Example 8- IgG1 and IgG4 antibodies having chimeric CH regions show decreased effector function in CDC assay**

Antibodies with chimeric CH regions (sIgG1* and sIgG4*), as described above, were generated to produce mAbs with altered or reduced effector function. Compared to antibodies comprising a wild-type (wt) heavy chain constant region of the IgG1 isotype, amino acid substitutions in the CH region may hinder the ability of an Ig Fc to bind to its receptor. Hence, signaling and immune responses, such as B cell activation or phagocytosis, may be altered. The effect of amino acid modifications in the CH region on complement dependent cytoxicity (CDC) (in this example) and antibody-dependent cytoxicity (ADCC) effector function (see Example 9) was examined.

[00230] To examine the effect of Antibody 3 (sIgG1*) and Antibody 4 (sIgG4*) on CDC effector function, CD20-expressing Raji (target) cells (5000/well) or Daudi cells were plated in the presence of 5% human serum complement. Serial dilutions of sIgG1*, sIgG4*

and control antibodies, starting at 100nM, were added to cells for 4 h at 37°C. Target cell lysis was determined using the CytoTox Glo™ kit (Promega) and percent cytoxicity was calculated.

[00231] Percent cytotoxicity was calculated using the equation:

% cytotoxicity = $((L_S - L_{SR})/(L_{MR}-L_{SR}))*100\%$ where L_{SR} is baseline target cell luminescence and L_{MR} is maximal calcein release from cells lysed by digitonin. The EC_{50} for cytoxicity was determined using Prism software (GraphPad). Values were calculated using 4-parameter non-linear regression analysis and are shown in Table 12, and Figures 10A and 10B.

[00232] The CDC activity of Antibody 3 (sIgG1*) and Antibody 4 (sIgG4*) against Daudi and Raji cells is significantly diminished as compared to corresponding antibody having a wt heavy chain constant domain. See Table 12, and Figures 10A/B. Some CDC activity was observed with sIgG4* against Raji cells, however, overall results show that the chimeric antibodies mount weaker effector responses than wt IgG1 Fc control antibodies.

Table 12: sIgG1* and sIgG4* antibodies display reduced activity in CDC assays measuring effector function

CDC				
Target Cell:	Daudi		Raji	
	EC50 [M]	Maximum Cytotoxicity (%)	EC50 [M]	Maximum Cytotoxicity (%)
Control Ab 5	6.12E-08	~95	1.98E-08	~85
Ab 3 (sIgG1*)	NA	NA	3.49E-08	~10
Ab 4 (sIgG4*)	NA	NA	2.86E-08	~45

NA: No activity

[00233] Example 9- IgG1 and IgG4 antibodies having chimeric CH regions show decreased effector function in ADCC assay

To examine the effect of Antibody 3 (sIgG1*) and Antibody 4 (sIgG4*) vs. antibodies with wild-type CH regions on ADCC effector function, freshly isolated unstimulated CD56-positive NK cells or NK92 cells engineered to express the higher affinity V allele of FcγRIIIa were plated with Calcein-labeled CD20-positive Raji or Daudi cells in the presence of chimeric CH-antibodies and wt-CH control antibodies. Calcein release from target cells was monitored and percent cytoxicity was determined. Percent cytotoxicity and EC_{50} were calculated as described for CDC assay, above. Results are shown in Table 13 and Figures 11A and 11B.

[00234] The chimeric CH antibodies, sIgG1* and sIgG4*, do not mediate ADCC activity (Table 13) against Raji or Daudi cells.

Table 13: sIgG1* and sIgG4* antibodies display reduced activity in ADCC assays measuring effector function

ADCC				
Target Cell:	Daudi		Raji	
	EC50 [M]	Maximum Cytotoxicity (%)	EC50 [M]	Maximum Cytotoxicity (%)
Control Ab 5	1.87E-10	~70#	1.48E-09	~65#
Ab 3 (sIgG1*)	NA	NA	NA	NA
Ab 4 (sIgG4*)	NA	NA	NA	NA

NA: No activity; #: background cytotoxicity ~20%

[00235] **Example 10- Pharmacokinetic Profile of Chimeric Antibodies**

The toxicokinetic profile of Antibody 3 (also known herein as sIgG1*) and Antibody 4 (also known herein as sIgG4*) was evaluated by obtaining blood samples from male cynomolgus monkeys (3 animals/treatment group) receiving a single 30-minute IV infusion, followed by a 12-week observation period. Blood samples for toxicokinetic analysis of total drug concentrations in serum were collected pre-dose and post-dose at 5 minutes, and 5, 24, 48, 72 and 168 hours, and Day 14, 21, 35, 49, 66 and 84. The resultant serum samples were analyzed by a direct enzyme linked immunosorbent assay (ELISA) to determine the total drug concentration of the sIgG1* or sIgG4* antibody. The toxicokinetics of the test articles were assessed using non-compartmental analysis (Phoenix WinNonLin) to determine pharmacokinetic parameters. Results are shown in Table 14 (AUC = area under the concentration vs. time curve; C_{max} = observed maximum concentration in serum).

Table 14: Pharmacokinetic Profile of Chimeric Antibodies in Serum of Cynomolgus monkeys Following a Single Intravenous Infusion to Cynomolgus Monkeys

Parameter	Units	1 mg/kg sIgG1*		1 mg/kg sIgG4*	
		Mean	SD	Mean	SD
C_{max}	µg/mL	33.4	3.79	26.0	4.72
C_{max}/Dose	kg*µg/mL/mg	33.4	3.79	26.0	4.72

t_{max}	day	0.0243	0	0.0243	0
$AUC_{0\text{-}168\ h}$	day.µg/mL	100	20.1	61.1	8.04
$AUC_{0\text{-}168\ h}$/ Dose	day*kg*ug/mL/mg	100	20.1	61.1	8.04
T1/2	Day	8.14	1.15	14.0	2.64

[00236] Following a single intravenous dose of 1.0 mg/kg of sIgG1* and sIgG4* in cynomolgus monkeys, mean peak concentrations (C_{max}) of 33.4 and 26.0 µg/mL, respectively, and mean $AUC_{0\text{-}168h}$ values of 100 and 61.1 day*ug/mL, respectively, were observed. The apparent terminal half-life was estimated to be between 8.14-14.0 days of these two molecules. The data indicate that continuous exposure to sIgG1* and sIgG4* was maintained in all animals for the majority of the 12-week observation period and exposure was comparable across treatment groups. No apparent immunogenicity with the test articles was observed. The overall pharmacokinetic profiles of sIgG1* and sIgG4* are typical of monoclonal antibodies dosed in cynomolgus monkey.

What is claimed:

1. An antibody comprising a heavy chain constant (CH) region comprising, from N-terminus to C-terminus, a CH1 domain, a hinge, a CH2 domain, and a CH3 domain wherein:

(a) the CH1 domain comprises a human IgG1 CH1 domain or a human IgG4 CH1 domain having at least the amino acid sequence DKKV or DKRV from positions 212 to 215 (EU numbering),

(b) the hinge comprises a human IgG1 or a human IgG4 upper hinge amino acid sequence from positions 216 to 227 (EU numbering) and a human IgG2 lower hinge amino acid sequence PCPAPPVA (SEQ ID NO: 3) from positions 228 to 236 (EU numbering),

(c) the CH2 domain comprises a human IgG4 CH2 domain amino acid sequence from positions 237 to 340 (EU numbering), and

(d) the CH3 domain comprises a human IgG1 or a human IgG4 CH3 domain sequence from positions 341 to 447 (EU numbering), and

wherein the antibody is capable of binding to an FcγR with lower affinity than a corresponding antibody comprising a wild-type IgG1 or wild-type IgG4 heavy chain constant region, the antibody is capable of binding FcγRIIA and optionally FcγRIIB, and the antibody is capable of binding FcγRIIA with higher affinity compared to its binding affinity to FcγRIIB.

2. The antibody of claim 1, wherein: (a) the CH1 domain comprises the amino acid sequence DKKV (SEQ ID NO: 4), and the hinge comprises the amino acid sequence EPKSCDKTHTCPPCPAPPVA (SEQ ID NO: 8), or (b) the CH1 domain comprises the amino acid sequence DKRV (SEQ ID NO: 5), and the hinge comprises the amino acid sequence ESKYGPPCPPCPAPPVA (SEQ ID NO: 9).

3. The antibody of claim 1 or 2, wherein the CH2 domain comprises the amino acid sequence SEQ ID NO: 10.

4. The antibody of any one of claims 1 to 3, wherein the CH3 domain comprises the amino acid sequence selected from the group consisting of SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 41, and SEQ ID NO: 42.

5. The antibody of claim 1, wherein the CH region has an amino acid sequence identical to SEQ ID NO: 1 or SEQ ID NO: 2.

6. The antibody of claim 1, wherein the CH region has an amino acid sequence identical to SEQ ID NO: 30.

7. The antibody of claim 1, wherein the CH region has an amino acid sequence identical to SEQ ID NO: 31.

8. The antibody of claim 1, wherein the CH region has an amino acid sequence identical to SEQ ID NO: 37.

9. The antibody of claim 1, wherein the CH region has an amino acid sequence identical to SEQ ID NO: 38.

10. The antibody of any one of claims 1 to 9, wherein the antibody exhibits less than 20% CDC cytotoxicity and/or ADCC cytotoxicity, or less than 10%, or 5%, 4%, 3%, 2%, or even 0% or undetectable CDC and/or ADCC cytotoxicity, at an antibody concentration of at least 10 nM.

11. The antibody of claim 10, wherein the CDC and/or ADCC cytotoxic activity is at least 5-fold less, or at least 10-fold less than the CDC and/or ADCC cytotoxic activity of a corresponding antibody comprising a wild-type IgG1 or wild-type IgG4 CH region.

12. The antibody of any one of claims 1 to 11 that is a monospecific antibody.

13. The antibody of any one of claims 1 to 11 that is a bispecific antibody.

14. Nucleic acid molecules encoding an antibody of any one of claims 1 to 13.

15. A vector comprising the nucleic acid molecules of claim 14.

16. The vector of claim 15, wherein:

(a) the nucleic acid molecules are operatively linked to an expression control sequence suitable for expression in a host cell, optionally wherein the expression control sequence comprises (i) a promoter selected from the group consisting of SV40, CMV, CMV-IE, CMV-MIE, UbC, RSV, SL3-3, MMTV, Ubi and HIV LTR, (ii) an expression cassette selected from the group consisting of TetR-ER_{LBD}T2 fusion gene driven by the CMV-MIE promoter, blasticidin resistance gene driven by the SV40 promoter, and Arc-ER_{LBD}T2 fusion gene driven by the CMV-MIE promoter; or (iii) a CMV-MIE/TetO or CMV-MIE/Arc hybrid promoter; and/or

(b) the vector of comprises one or more selectable marker genes selected from the group consisting of bla, bls, BSD, bsr, Sh ble, hpt, tetR, tetM, npt, kanR and pac.

17. A cell comprising the nucleic acid molecules of claim 14.

18. The cell of claim 17, wherein:

(a) the cell comprises a vector of claim 15 or 16; and/or

(b) the nucleic acid molecules are integrated into the genome of the cell; and/or

(c) the cell comprises a nucleic acid encoding a protein expression enhancer and/or

(d) the cell comprises a nucleic acid encoding an XBP polypeptide; and/or

(e) the cell is a eukaryotic cell, an animal cell, a mammalian cell, a CHO cell or a CHO-K1 cell.