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[Continued on next page]

(54) Title: FC VARIANTS

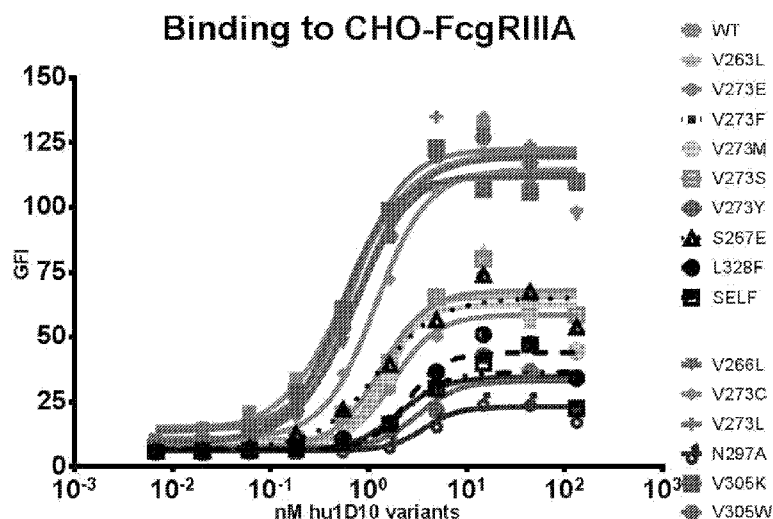


FIGURE 11A

(57) Abstract: The present disclosure relates to polypeptide variants having modified Fc domains with altered affinity to Fc receptors.



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## FC VARIANTS

### 1. CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit under 35 U.S.C. § 119(e) of provisional application no. 61/791,624, which was filed March 15, 2013, and is incorporated by reference in its entirety.

### 2. SEQUENCE LISTING

[0002] The application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on March 13, 2014, is named 381493-884WO (125234)\_SL.txt and is 31,705 bytes in size.

### 3. BACKGROUND

[0003] The fragment crystallizable (“Fc”) region of an antibody is composed of two identical protein fragments, derived from the second and third constant domains of the antibody's two heavy chains. Fc regions bind to receptors on immune cells known as Fc receptors (“FcRs”), leading to both activating and inhibitory signals. For example, the FcγRIIIA (also known as CD16 or CD16a) is found on natural killer cells and macrophages, and has a low affinity for Fc regions. Binding of Fc ligand to an FcγRIIIA receptor can result in induction of antibody-dependent cell-mediated cytotoxicity (ADCC) and induction of cytokine release by macrophages. In contrast, the FcγRIIB receptor (also known as CD32b) is found on macrophages, neutrophils, B cells and eosinophils, and binding of Fc ligand to an FcγRIIB receptor inhibits cell activity.

[0004] The differences in downstream signaling affected by different FcRs are based on structural differences. Within the Fc gamma receptor (“FcγR”) family—including FcγRI (CD64), FcγRIIA (CD32), FcγRIIIA (CD16a), and FcγRIIIB (CD16b)—Fc receptors generate activation signals via a motif known as an Immunoreceptor Tyrosine-based Activation Motif (ITAM). FcγRIIA, FcγRI, and FcγRIIIA all produce activating signals through their ITAMs, or by interaction with an ITAM-containing subunit. Alternatively, an Fc receptor can contain an Immunoreceptor Tyrosine-based Inhibitory Motif (ITIM) that generates inhibitory signals. FcγRIIB1 and FcγRIIB2, alternatively spliced forms of FcγRIIB (collectively referred to as “FcγRIIB”) have ITIM sequences, and thus function as inhibitory Fc receptors (*see* Blank *et al.*, 2009, *Immunol Rev.* 232(1):59-71).

[0005] By altering the Fc regions of antibodies, improvements can be made to increase antibody therapeutic efficacy, increase antibody half-life, and reduce unwanted side effects.

#### 4. SUMMARY

[0006] Because Fc $\gamma$ RIIIA generates signals that activate immune cells, in particular cells that mediate ADCC, it is believed that decreasing Fc binding to Fc $\gamma$ RIIIA will result in decreased immune cell activation and reduced levels of ADCC. Moreover, because Fc $\gamma$ RIIB generates signals that inhibit immune cells, the dual effect of increasing Fc binding to Fc $\gamma$ RIIB coupled with decreasing Fc binding to Fc $\gamma$ RIII will result in greater inhibition of immune cell activation as compared to modulating binding of a single receptor. The present inventors have identified single amino acid substitutions or point mutations in the CH2 domains of Fc molecules that impact binding to both Fc receptors. For example, as will be discussed in more detail below, amino acid substitutions at a single position (*e.g.*, V263) can significantly increase binding to Fc $\gamma$ RIIB and decrease binding to Fc $\gamma$ RIIIA. The incorporation of such amino acid substitutions into antibodies and other Fc-based therapeutic molecules can result in variant polypeptides with a greater inhibition of immune cell activation as compared to substitutions that modulate binding to a single receptor. The variant polypeptides are particularly suited for treatment of indications for which induction of immune activation is not desirable, for example in the treatment of immune disorders.

[0007] Accordingly, in one aspect, the present disclosure provides polypeptides comprising modified (or variant) CH2 domains or entire Fc domains (collectively referred to as “variant polypeptides” or “variant Fc polypeptides”) that include amino acid substitutions that increase binding to Fc $\gamma$ RIIB and/or reduced binding to Fc $\gamma$ RIIIA as compared to the binding of a corresponding wild-type CH2 (SEQ ID NO:2) or Fc region (SEQ ID NO:1). A polypeptide of the disclosure can be a monomer or multimer (*e.g.*, dimer or tetramer), each monomeric unit comprising one or more CH2 or Fc domains. A polypeptide of the disclosure is typically an antibody or an Fc fusion protein comprising a variant CH2 or Fc domain of the disclosure. A variant CH2 or variant Fc domain of the present disclosure typically includes one or more substitutions at position 263, position 266, position 273, and position 305, wherein the numbering of the residues in the Fc domain is that of the EU index as in Kabat. These amino acid positions are indicated by asterisk (\*), dagger (†), double dagger (‡), and the number sign (#), respectively, in Figure 2.

[0008] Thus, in one aspect, the present disclosure provides polypeptides comprising a variant CH2 domain which has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% sequence identity to the CH2 domain of SEQ ID NO:2. Relative to the CH2 domain of SEQ ID NO:2, disclosed polypeptides can comprise one or

more substitutions selected from: (a) a V263 substitution that increases affinity towards Fc $\gamma$ RIIB and decreases affinity towards Fc $\gamma$ RIIA; (b) a V266 substitution that increases affinity towards Fc $\gamma$ RIIB and decreases affinity towards Fc $\gamma$ RIIA; and (c) a V273 substitution that increases affinity towards Fc $\gamma$ RIIB and decreases affinity towards Fc $\gamma$ RIIA.

**[0009]** In some embodiments, the polypeptides comprise one or more substitutions selected from V263L, V266L, V273C, V273E, V273F, V273L, V273M, V273S, V273Y, V305K, and V305W, relative to the CH2 domain of SEQ ID NO:2. In specific embodiments, the one or more substitutions of the CH2 domain are selected from V263L, V273E, V273F, V273M, V273S, and V273Y.

**[0010]** In another aspect, the present disclosure provides polypeptides comprising a variant CH2 domain which has up to 6, up to 5, up to 4, up to 3, up to 2 substitutions, or a single amino acid substitution as compared to an CH2 domain of SEQ ID NO:2, including one or more substitutions selected from: (a) a V263 substitution that increases affinity towards Fc $\gamma$ RIIB and decreases affinity towards Fc $\gamma$ RIIA; (b) a V266 substitution that increases affinity towards Fc $\gamma$ RIIB and decreases affinity towards Fc $\gamma$ RIIA; and (c) a V273 substitution that increases affinity towards Fc $\gamma$ RIIB and decreases affinity towards Fc $\gamma$ RIIA.

**[0011]** Polypeptides of the disclosure can also comprise a variant CH2 domain which has up to 6, up to 5, up to 4, up to 3, up to 2 substitutions, or a single amino acid substitution, as compared to an CH2 domain of SEQ ID NO:2, including one or more substitutions selected from V263L, V266L, V273C, V273E, V273F, V273L, V273M, V273S, V273Y, V305K, and V305W. In specific embodiments, the one or more substitutions of the CH2 domain are selected from V263L, V273E, V273F, V273M, V273S, and V273Y.

**[0012]** As discussed in detail herein, the CH2 domain is a component of the Fc domain of an antibody. Accordingly, in one aspect polypeptides are provided that comprise an Fc domain, said Fc domain comprising a CH2 domain of the disclosure. In some embodiments, the Fc domain has up to 20, up to 15, up to 12, up to 10, up to 9, up to 8, up to 7, up to 6, up to 5 or up to 4 amino acid substitutions as compared to the CH2 domain of the Fc domain of SEQ ID NO:1. Overall, the Fc domain of the polypeptide can have at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% sequence identity to the Fc domain of SEQ ID NO:1.

**[0013]** Skilled artisans will appreciate that disclosed Fc domains can comprise any of the one or more CH2 substitutions described herein. Thus, polypeptides are provided including those in which comprise a V263 substitution (*e.g.*, V263L), a V266 substitution (*e.g.*, V266L), a V273 substitution (*e.g.*, V273E, V273F, V273L, V273M, V273S, or V273Y), or a V305 substitution (*e.g.*, V305K or V305W).

**[0014]** In various embodiments, the polypeptides comprise a variant CH2 domain which has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% sequence identity to the CH2 domain of SEQ ID NO:2, and which has relative to the CH2 domain of SEQ ID NO:2 one or more substitutions selected from: a V263 substitution that increases affinity towards FcγRIIB and decreases affinity towards FcγRIIIA; and a V273 substitution that increases affinity towards FcγRIIB and decreases affinity towards FcγRIIIA.

**[0015]** In various embodiments, the polypeptides comprise a variant CH2 domain which has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% sequence identity to the CH2 domain of SEQ ID NO:2, and which has relative to the CH2 domain of SEQ ID NO:2: the substitution V263L; and/or a V273 substitution selected from V273C, V273E, V273F, V273L, V273M, V273S, V273Y.

**[0016]** In various embodiments, the polypeptides comprise a variant CH2 domain which has up to 6, up to 5, up to 4, up to 3, up to 2 substitutions, or a single amino acid substitution, as compared to an CH2 domain of SEQ ID NO:2, including one or more substitutions selected from: a V263 substitution that increases affinity towards FcγRIIB and decreases affinity towards FcγRIIIA; a V266 substitution that increases affinity towards FcγRIIB and decreases affinity towards FcγRIIIA; and a V273 substitution that increases affinity towards FcγRIIB and decreases affinity towards FcγRIIIA.

**[0017]** In various embodiments, the polypeptides comprise a variant CH2 domain which has up to 6, up to 5, up to 4, up to 3, up to 2 substitutions, or a single amino acid substitution, as compared to an CH2 domain of SEQ ID NO:2, including one or more substitutions selected from: the substitution V263L; and/or a V273 substitution selected from V273C, V273E, V273F, V273L, V273M, V273S, V273Y.

**[0018]** Fc domains are known to mediate Fc effector functions, as described in Section 3.5. Accordingly, the disclosure provides polypeptides that further comprise one or more additional

substitutions or combinations of substitutions that modify Fc effector function. Typically, Fc effector functions that can be modified include (a) reduction or increase in binding to FcRN; (b) reduction or increase in binding to FcγRI; (c) reduction or increase in binding to FcγRIIA or FcγRIIB; (d) reduction or increase in binding to FcγRIIIA; or (e) a combination of two, three, four or all of the foregoing.

**[0019]** An exemplary substitution known to modify Fc effector function is the Fc substitution M428L, which can occur in combination with the Fc substitution T250Q. Additionally, an Fc domain of the disclosure can comprise one or more additional substitutions selected from Table 1, as compared to the Fc domain of SEQ ID NO:1.

**[0020]** In one aspect, the disclosure provides polypeptides that are antibodies, discussed in further detail in Section 3.1. These antibodies can be human or humanized antibodies. In typical embodiments, an antibody specifically binds to CD40, CD25, CD3, an HLA molecule, a costimulatory molecule, a cytokine (*e.g.*, TNF-α or IL-2), a chemokine, an adhesion molecule (*e.g.*, α4 integrin), an activation markers, or an immunomodulatory protein. The costimulatory molecule can be CD28, PD-1, CTLA-4, CD80, CD86, TIM3, OX40, BB-1, GITR, CD27, B7-H4, or DC-SIGN. In some embodiments, the immunomodulatory protein is a cell surface molecule. In other embodiments, the immunomodulatory protein is a soluble molecule.

**[0021]** In typical embodiments, the antibody specifically binds to CD25. In other embodiments, the antibody specifically binds to CD40.

**[0022]** Polypeptides of the disclosure also include Fc fusion proteins in which the CH2 domain is part of an Fc domain operably linked to at least one fusion partner. Fc fusion proteins are discussed in detail in Section 3.3. In such Fc proteins, said at least one fusion partner can be the extracellular domain (“ECD”) of TNF receptor II; the first ECD of lymphocyte function-associated antigen 3 (LFA-3); the ECD of human cytotoxic T lymphocyte associated molecule-4 (CTLA-4); the C-terminus of the IL-1R accessory protein ligand binding region; the N-terminus of the IL-1RI ECD; peptide thrombopoietin (TPO) mimetic; ECD of CTLA-4 with the two amino acid substitutions L104E and A29Y; and the ECDs of VEGF receptor 1 and/or the ECD of VEGF receptor 2.

**[0023]** In another aspect, the disclosure provides conjugate compounds comprising polypeptides the disclosure linked to an effector moiety or a detectable label. Conjugate compounds are discussed

further in section 3.6. In some embodiments, the conjugate compound comprises a polypeptide linked to a detectable label, such as a radioactive compound, a fluorescent compound, an enzyme, a substrate, an epitope tag or a toxin. In some embodiments, the conjugate compound comprises a polypeptide linked to an effector moiety, such as a cytotoxic agent. Skilled artisans will appreciate the various cytotoxic agents that can be linked to polypeptides of the disclosure, including an auristatin, a DNA minor groove binding agent, a DNA minor groove alkylating agent, an enediyne, a duocarmycin, a maytansinoid or a vinca alkaloid. Other exemplary cytotoxic agents are anti-tubulins, AFP, MMAF, or MMAE.

**[0024]** The present disclosure further provides pharmaceutical compositions comprising polypeptides of the disclosure and a pharmaceutically acceptable carrier or a conjugate compound of the disclosure. Pharmaceutical compositions and methods of treatment are discussed in detail in Section 3.7.

**[0025]** Nucleic acids comprising nucleotide sequences encoding the polypeptides of the disclosure are provided herein, as are vectors comprising nucleic acids. Additionally, prokaryotic and eukaryotic host cells transformed with a vector comprising a nucleotide sequence encoding a disclosed polypeptide are provided herein, as well as eukaryotic (such as mammalian) host cells engineered to express the nucleotide sequences. Methods of producing polypeptides, by culturing host cells and recovering the polypeptides are also provided, and discussed further in section 3.4, below.

**[0026]** Skilled artisans will appreciate that the polypeptides of the disclosure are useful in the treatment of various diseases or disorders such as an immune disorder or cancer for which it would be suitable to administer to a patient in need thereof an appropriate polypeptide, pharmaceutical composition, or conjugate compound of the disclosure.

**[0027]** In some embodiments, the polypeptide is an anti-CD40 antibody useful for treatment of a cancer. In particular embodiments, the cancer is a hematological cancer optionally selected from chronic lymphocytic leukemia, Burkitt's lymphoma, multiple myeloma, a T cell lymphoma, Non-Hodgkin's Lymphoma, Hodgkin's Disease, Waldenstrom's macroglobulinemia or Kaposi's sarcoma. In particular embodiments, the cancer is a solid tumor, optionally selected from ovarian cancer, breast cancer, lung cancer, melanoma, pancreatic cancer, and renal cancer. Exemplary VL and VH



sequences of an anti-CD40 antibody are provided as SEQ ID NO:3 and SEQ ID NO:4, respectively. In specific embodiments, the anti-CD40 antibody is a multi-specific antibody.

**[0028]** In other embodiments, the polypeptide is an anti-CD20 antibody useful for treatment of an immune disorder which is rheumatoid arthritis or multiple sclerosis. Exemplary VL and VH sequences of an anti-CD20 antibody are provided as SEQ ID NO:5 and SEQ ID NO:6, respectively.

**[0029]** In yet other embodiments, the polypeptide is an anti-CD25 antibody useful for treatment of an immune disorder which is multiple sclerosis, asthma, psoriasis, uveitis, ocular inflammation or organ transplant rejection or of a cancer which is human T cell leukemia virus-1 associated T-cell leukemia. Exemplary VL sequences of an anti-CD25 antibody include SEQ ID NO:7 and SEQ ID NO:9. Exemplary VL sequences of an anti-CD25 antibody include SEQ ID NO:8 and SEQ ID NO:10.

**[0030]** In still other embodiments, the polypeptide is an anti-TNF $\alpha$  antibody useful for treatment of an immune disorder which is rheumatoid arthritis, juvenile idiopathic arthritis, psoriatic arthritis, ankylosing spondylitis, Crohn's disease, ulcerative colitis or plaque psoriasis. Exemplary VL sequences of an anti-TNF $\alpha$  antibody include SEQ ID NO:11 and SEQ ID NO:13. Exemplary VL sequences of an anti-TNF $\alpha$  antibody include SEQ ID NO:12 and SEQ ID NO:14.

**[0031]** In still further embodiments, the polypeptide is an anti-IL-6 receptor antibody useful for treatment of an immune disorder which is rheumatoid arthritis or Castleman's Disease. Exemplary VL and VH sequences of an anti-IL-6 receptor antibody are provided as SEQ ID NO:15 and SEQ ID NO:16, respectively. The polypeptide can also be an anti- $\alpha$ 4-integrin antibody useful for treatment of an immune disorder which is multiple sclerosis. In some embodiments, the polypeptide is an anti-IL-1 antibody useful for treatment of an immune disorder which is Cryopyrin-Associated Periodic Syndromes ("CAPS"). Exemplary VL and VH sequences of an anti-IL-6 receptor antibody are provided as SEQ ID NO:17 and SEQ ID NO:18, respectively. The polypeptide can also be an anti-BAFF antibody and useful for treatment of an immune disorder which is systemic lupus erythematosus or allergy. Exemplary VL and VH sequences of an anti-BAFF antibody are provided as SEQ ID NO:19 and SEQ ID NO:20, respectively.

**[0032]** It should be understood that the above summary is not intended to describe every embodiment or every implementation of the various inventions disclosed herein. The Detailed

Description and Examples Section further exemplify illustrative embodiments. The various embodiments described herein are intended to be disclosed in combinations, as if each specific combination were explicitly disclosed. The Examples are representative only and should not be interpreted as exclusive, or limiting the scope of the various inventions disclosed herein.

**[0033]** A more complete appreciation of the various inventions disclosed herein, and many of the attendant advantages thereof, is provided by the detailed description that follows.

**[0034]** As used herein throughout the specification and in the appended claims, the following terms and expressions are intended to have the following meanings:

**[0035]** The indefinite articles “a” and “an” and the definite article “the” are intended to include both the singular and the plural, unless the context in which they are used clearly indicates otherwise.

**[0036]** “At least one” and “one or more” are used interchangeably to mean that the article may include one or more than one of the listed elements.

**[0037]** Unless otherwise indicated, it is to be understood that all numbers expressing quantities, ratios, and numerical properties of ingredients, reaction conditions, and so forth, used in the specification and claims are contemplated to be able to be modified in all instances by the term “about.”

## **5. BRIEF DESCRIPTION OF THE FIGURES**

**[0038] FIGURE 1** provides a schematic representation of a native IgG. Disulfide bonds are represented by heavy lines between CH1 and CL domains and the two CH2 domains. V is variable domain; C is constant domain; L stands for light chain and H stands for heavy chain.

**[0039] FIGURES 2A-2B. FIGURE 2A** provides the sequence of a wild type Fc domain, from human IgG1 (SEQ ID NO:1). Within the Fc domain the CH2 domain (whose sequence is APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK; SEQ ID NO:2) is double underlined and the CH3 domain (whose sequence is GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK; SEQ ID NO:21) is bolded. Residues 263, 266, 273, and 305 are indicated by asterisk (\*), dagger (†), double dagger

( $\pm$ ), and the number sign (#), respectively. **FIGURE 2B** shows the amino acid sequences and the numbering of the amino acids in the CH1, hinge, CH2 and CH3 domains. The full-length sequence of the CH1, hinge, CH2 and CH3 domains in **FIGURE 2B** is referred to as SEQ ID NO: 38.

**[0040]** **FIGURE 3** provides a schematic of complexes used to measure binding of polypeptides of the disclosure to Fc receptors.

**[0041]** **FIGURE 4** provides FACS titration curves and EC<sub>50</sub> measurements for binding of wild-type hu1D10 to (A) FcγRIIB1 and (B) FcγRIIIA.

**[0042]** **FIGURE 5** provides a representative FACS sort result.

**[0043]** **FIGURE 6** provides a plot displaying enrichment ratios for individual clones significantly increased for FcγRIIB binding and decreased for binding to FcγRIIIA.

**[0044]** **FIGURE 7** provides positions and substitutions that were identified as having significantly increased FcγRIIB binding and decreased binding to FcγRIIIA. The enrichment ratios for each mutant are tabulated.

**[0045]** **FIGURE 8** provides single-point FACS data for binding of polypeptides of the disclosure to FcγRIIB.

**[0046]** **FIGURE 9** provides single-point FACS data for binding of polypeptides of the disclosure to FcγRIIIA.

**[0047]** **FIGURES 10A-10B** provides confirmatory data showing that polypeptides of the disclosure demonstrated higher maximal binding to FcγRIIB than the wild-type antibody. **FIGURE 10A** shows binding curves of WT and variant Fc regions to FcγRIIB; **FIGURE 10B** shows the EC<sub>50</sub> of binding for each variant and the fold over wild type binding.

**[0048]** **FIGURES 11A-11B** provides confirmatory data showing that polypeptides of the disclosure demonstrated higher maximal binding to FcγRIIIA than the wild-type antibody. **FIGURE 11A** shows binding curves of WT and variant Fc regions to FcγRIIIA; **FIGURE 11B** shows the EC<sub>50</sub> of binding for each variant and the fold over wild type binding.

**[0049]** **FIGURE 12** provides FACS data from testing polypeptides of the disclosure using a non-radioactive ADCC assay.

[0050] **FIGURES 13A-13D.** **FIGURE 13A** provides data showing percent cytotoxicity graphed against IgG concentration to determine the EC<sub>50</sub>. **FIGURE 13B** shows FcγRIIB up-mutants having some ADCC activity, though lower than wild-type. **FIGURE 13C** shows polypeptides with little to no ADCC activity. **FIGURE 13D** compares the non-ADCC hu1D10 polypeptides to previously known substitutions that result in decreased binding to FcγRIIA (S267E, L328F, double mutant “SELF”).

[0051] **FIGURES 14A-14B.** **FIGURE 14A** provides results for induction of ADCC for polypeptides of the disclosure using a chromium release assay. **FIGURE 14B** provides symbol key for **FIGURE 14A**.

[0052] **FIGURES 15A-15C** provides results for dendritic cell activation for polypeptides of the disclosure using monocyte-derived immature dendritic cells. **FIGURE 15A** shows dendritic cell activation by ADCC-inducing variants. **FIGURE 15B** shows dendritic cell activation by non-ADCC-inducing variants. **FIGURE 15C** shows the EC<sub>50</sub> for IL-12 induction.

[0053] **FIGURE 16** shows Fc variants with lowest ADCC activity with retained/improved FcγRIIB binding in bold font.

## **6. DETAILED DESCRIPTION**

### **6.1. Fc Variant Polypeptides**

[0054] Fc domains of immunoglobulin are involved in non-antigen binding function and have several effector functions mediated by binding of effector molecules. As illustrated in Figure 1, Fc domains are composed of two main domains, the CH<sub>2</sub> domain and the CH<sub>3</sub> domain, and have a small hinge region N-terminal to the CH<sub>2</sub> domain. The present disclosure provides polypeptides comprising modified CH<sub>2</sub> domains (and modified Fc domains comprising modified CH<sub>2</sub> domains), collectively referred to herein as variant polypeptides, Fc variants, or simply variants or polypeptides. The variant polypeptides are typically antibodies or antibody fragments (referred to herein collectively as antibody variants) or Fc fusion proteins.

[0055] As used herein, numbering of antibody amino acid residues is done according to Kabat EU nomenclature unless otherwise indicated.

[0056] As used herein, the term “Fc domain” refers to a C-terminal region of an immunoglobulin heavy chain. Although the generally accepted boundaries of the Fc domain of an immunoglobulin heavy chain might vary, the human IgG heavy chain Fc domain is usually defined to stretch from an

amino acid residue at position Cys226, or from Pro230, to the carboxyl-terminus thereof. In some embodiments, variants comprise only portions of the Fc domain and can include or not include the carboxyl-terminus. The Fc domain of an immunoglobulin generally comprises two constant domains, CH2 and CH3. The Fc variant polypeptides of the disclosure typically include at a CH2 domain and oftentimes also include a CH3 domain.

**[0057]** As used herein, the “CH2 domain” (also referred to as “C $\gamma$ 2” domain) generally comprises the stretch of residues that extends from about amino acid 231 to about amino acid 340 in an Fc domain (*e.g.*, in the human IgG Fc domain). The CH2 domain is unique in that it is not closely paired with another domain. Rather, two N-linked branched carbohydrate chains are interposed between the two CH2 domains of an intact native IgG molecule.

**[0058]** As used herein, the “CH3 domain” (also referred to as “C $\gamma$ 3” domain) generally comprises the stretch of residues C-terminal to a CH2 domain in an Fc domain (*e.g.*, from about amino acid residue 341 to about amino acid residue 447 of a human IgG Fc region).

**[0059]** The terms “Fc receptor” and “FcR” are used to describe a receptor that binds to an Fc domain (*e.g.* the Fc domain of an antibody or antibody fragment). Portions of Fc receptors are specifically contemplated in some embodiments of the present invention. In preferred embodiments, the FcR is a native sequence human FcR. In other preferred embodiments, the FcR is one which binds an IgG antibody (a gamma receptor) and includes receptors of the Fc $\gamma$ RI, Fc $\gamma$ RII, and Fc $\gamma$ RIII subclasses, including allelic variants and alternatively spliced forms of these receptors. Fc $\gamma$ RII receptors include Fc $\gamma$ RIIA (an “activating receptor”) and Fc $\gamma$ RIIB (an “inhibiting receptor”), which have similar amino acid sequences that differ primarily in the cytoplasmic domains thereof. Activating receptor Fc $\gamma$ RIIA contains an immunoreceptor tyrosine based activation motif (ITAM) in its cytoplasmic domain. Inhibiting receptor Fc $\gamma$ RIIB contains an immunoreceptor tyrosine-based inhibition motif (ITIM) in its cytoplasmic domain. Other FcRs, including those to be identified in the future, are encompassed by the term “FcR” herein. The term also includes the neonatal receptor, FcRn.

**[0060]** The polypeptides of the disclosure comprise an Fc variant domain having an amino acid sequence substantially homologous to all or part of a human immunoglobulin constant region, preferably an IgG C-domain.

**[0061]** Numerous sequences for human C regions have been published; see, *e.g.*, Clark, 1997, Chem. Immunol. 65:88-110. Other sequences for human immunoglobulin heavy chains can be obtained from the SwissProt and PIR databases using Lasergene software (DNASar Limited, London UK)

under accession numbers A93433, B90563, A90564, B91668, A91723 and A02146 for human Ig $\gamma$ -1 chain C region, A93906, A92809, A90752, A93132, A02148 for human Ig  $\gamma$ -2 chain C region, A90933, A90249, A02150 for human Ig $\gamma$ -4 chain C region, and A23511 for human Ig $\gamma$ -3 chain C region. An exemplary Fc domain has the amino acid sequence of SEQ ID NO:1.

**[0062]** In various embodiments, the amino acid sequence of the Fc variant domain shares at least about 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% sequence identity with the reference any of the foregoing Fc domains. In a preferred embodiment, the reference Fc domain comprises SEQ ID NO:1.

**[0063]** Sequence comparisons are typically performed by comparing sequences over a “comparison window” to identify and compare local regions of sequence similarity. A “comparison window” refers to a conceptual segment of typically 12 contiguous residues that is compared to a reference sequence. The comparison window may comprise additions or deletions (*i.e.*, gaps) of about 20% or less as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the respective sequences. Optimal alignment of sequences for aligning a comparison window may be conducted by computerised implementations of algorithms (Geneworks program by Intelligenetics; GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package Release 7.0, Genetics Computer Group, 575 Science Drive Madison, Wis., USA, incorporated herein by reference) or by inspection and the best alignment (*i.e.*, resulting in the highest percentage homology over the comparison window) generated by any of the various methods selected. Reference also may be made to the BLAST family of programs as for example disclosed by Altschul *et al.*, 1997, *Nucl. Acids Res.* 25(17):3389-402, which is incorporated herein by reference.

**[0064]** The present disclosure provides polypeptides comprising a modified Fc domain wherein the binding of the polypeptide to a first Fc receptor, *e.g.*, Fc $\gamma$ RIIB, is increased compared to that of the wild-type Fc domain, and the binding of the polypeptide to a second Fc receptor, *e.g.*, Fc $\gamma$ RIIA, is decreased compared to that of an antibody having a wild-type Fc domain. The polypeptide can be an antibody or an Fc fusion protein.

**[0065]** The Fc variant polypeptides can comprise a single substitution that results in both increased binding to Fc $\gamma$ RIIB and decreased binding to Fc $\gamma$ RIIA, as compared to that of a polypeptide having a wild-type Fc domain.

**[0066]** The Fc variant polypeptides can comprise a variant constant region heavy chain domain 2 (“CH2”) having at least one substitution selected from V263L, V266L, V273C, V273E, V273F,

V273L, V273M, V273S, V273Y, V305K, and V305W as compared to a CH2 domain of SEQ ID NO:2. The variant CH2 domain preferably has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity to the CH2 domain of SEQ ID NO:2. In various embodiments, the CH2 domain includes at least one substitution selected from V263L, V273E, V273F, V273M, V273S, and V273Y.

**[0067]** In some embodiments, the variant CH2 domain has altogether up to 20, up to 15, up to 12, up to 10, up to 9, up to 8, up to 7, up to 6, up to 5 or up to 4 amino acid substitutions as compared to a CH2 domain of SEQ ID NO:2. In some embodiments, the CH2 domain can have no more than 6, no more than 5, no more than 4, no more than 3, or no more than 2 amino acid substitutions as compared to the CH2 domain of SEQ ID NO:2.

**[0068]** The Fc variant polypeptides can comprise a variant Fc region comprising a CH2 domain having at least one substitution selected from V263L, V266L, V273C, V273E, V273F, V273L, V273M, V273S, V273Y, V305K, and V305W as compared to a CH2 domain of SEQ ID NO:2. The variant Fc region preferably has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity to the Fc region of SEQ ID NO:1. In various embodiments, the CH2 domain includes at least one substitution selected from V263L, V273E, V273F, V273M, V273S, and V273Y.

**[0069]** In some embodiments, the variant Fc region domain has altogether up to 20, up to 15, up to 12, up to 10, up to 9, up to 8, up to 7, up to 6, up to 5 or up to 4 amino acid substitutions as compared to an Fc domain of SEQ ID NO:1. In some embodiments, the variant Fc region can have no more than 6, no more than 5, no more than 4, no more than 3, or no more than 2 amino acid substitutions as compared to the Fc region of SEQ ID NO:1.

**[0070]** The variant polypeptides of the disclosure can be antibodies or Fc fusion proteins. For example but not by way of limitation, an Fc fusion proteins can be an antibody that is recombinantly expressed as a fusion protein, *e.g.*, with a cytokine protein, a toxin protein or other bioactive protein. In other embodiments, an Fc fusion protein contains an Fc domain of an antibody, such as a variant Fc domain as disclosed herein, recombinantly expressed as a fusion protein with a fusion partner. In other embodiments, an Fc fusion protein contains a CH2 or CH3 domain of an Fc region, such as a variant CH2 domain as disclosed herein, recombinantly expressed as a fusion protein with a fusion partner. The variant antibodies of the disclosure can be antibody-drug conjugates. For example but

not by way of limitation the variant antibodies can be conjugated to mole molecule toxins or bioactive small molecule compounds. Exemplary antibodies and fusion proteins are described in Sections

**[0071]** The variant Fc domains of the disclosure can comprise (in addition to the one or more substitutions that give rise to increased affinity to Fc $\gamma$ RIIB and reduced affinity to Fc $\gamma$ RIIA) one or more substitutions that impact effector function.

**[0072]** In one embodiment, the variant Fc domain contains one or more substitutions that result in reduced binding to an Fc $\gamma$ R and comprises an amino acid modification at any one or more of amino acid positions 238, 239, 248, 249, 252, 254, 265, 268, 269, 270, 272, 278, 289, 292, 293, 294, 295, 296, 298, 301, 303, 322, 324, 327, 329, 333, 335, 338, 340, 373, 376, 382, 388, 389, 414, 416, 419, 434, 435, 437, 438 or 439 of the Fc domain, wherein the numbering of the residues in the Fc domain is that of the EU index as in Kabat.

**[0073]** For example, the variant Fc domain can contain one or more substitutions that result in reduced binding to an Fc $\gamma$ RI and comprise an amino acid modification at any one or more of amino acid positions 238, 265, 269, 270, 327 or 329 of the Fc domain, wherein the numbering of the residues in the Fc domain is that of the EU index as in Kabat.

**[0074]** The variant Fc domain can contain one or more substitutions that result in reduced binding to an Fc $\gamma$ RII and comprise an amino acid modification at any one or more of amino acid positions 238, 265, 269, 270, 292, 294, 295, 298, 303, 324, 327, 329, 333, 335, 338, 373, 376, 414, 416, 419, 435, 438 or 439 of the Fc domain, wherein the numbering of the residues in the Fc domain is that of the EU index as in Kabat.

**[0075]** The variant Fc domain of interest can contain one or more substitutions that result in reduced binding to an Fc $\gamma$ RIII and comprise an amino acid modification at one or more of amino acid positions 238, 239, 248, 249, 252, 254, 265, 268, 269, 270, 272, 278, 289, 293, 294, 295, 296, 301, 303, 322, 327, 329, 338, 340, 373, 376, 382, 388, 389, 416, 434, 435 or 437 of the Fc domain, wherein the numbering of the residues in the Fc domain is that of the EU index as in Kabat.

**[0076]** In another embodiment, the variant Fc domain with altered Fc $\gamma$ R binding affinity contains one or more substitutions that result in improved binding to the Fc $\gamma$ R and comprises an amino acid modification at any one or more of amino acid positions 255, 256, 258, 267, 268, 272, 276, 280, 283, 285, 286, 290, 298, 301, 305, 307, 309, 312, 315, 320, 322, 326, 330, 331, 333, 334, 337, 340, 360,



378, 398 or 430 of the Fc domain, wherein the numbering of the residues in the Fc domain is that of the EU index as in Kabat.

**[0077]** For example, the variant Fc domain can contain one or more substitutions that result in increased binding to an Fc $\gamma$ RIII and, optionally, may further contains one or more substitutions that result in decreased binding to an Fc $\gamma$ RII. An exemplary such variant comprises amino acid modification(s) at position(s) 298 and/or 333 of the Fc domain, wherein the numbering of the residues in the Fc domain is that of the EU index as in Kabat.

**[0078]** The variant Fc domain can contain one or more substitutions that result in increased binding to an Fc $\gamma$ RII and comprise an amino acid modification at any one or more of amino acid positions 255, 256, 258, 267, 268, 272, 276, 280, 283, 285, 286, 290, 301, 305, 307, 309, 312, 315, 320, 322, 326, 330, 331, 337, 340, 378, 398 or 430 of the Fc domain, wherein the numbering of the residues in the Fc domain is that of the EU index as in Kabat. Such variant Fc domains with increased binding to an Fc $\gamma$ RII may optionally further contains one or more substitutions that result in decreased binding to an Fc $\gamma$ RIII and may, for example, comprise an amino acid modification at any one or more of amino acid positions 268, 272, 298, 301, 322 or 340 of the Fc domain, wherein the numbering of the residues in the Fc domain is that of the EU index as in Kabat.

**[0079]** In yet another aspect, the Fc variant polypeptides can be modified to increase or reduce their binding affinities to the fetal Fc receptor, FcRn, for example, by mutating the immunoglobulin constant region segment at particular regions involved in FcRn interactions (See, *e.g.*, WO 2005/123780). Accordingly, the disclosure further provides a polypeptide comprising a variant Fc domain with altered neonatal Fc receptor (FcRn) binding affinity, which polypeptide comprises an amino acid modification at any one or more of amino acid positions 238, 252, 253, 254, 255, 256, 265, 272, 286, 288, 303, 305, 307, 309, 311, 312, 317, 340, 356, 360, 362, 376, 378, 380, 382, 386, 388, 400, 413, 415, 424, 433, 434, 435, 436, 439 or 447 of the Fc domain, wherein the numbering of the residues in the Fc domain is that of the EU index as in Kabat. Such variant Fc domains with reduced binding to an FcRn can comprise an amino acid modification at any one or more of amino acid positions 252, 253, 254, 255, 288, 309, 386, 388, 400, 415, 433, 435, 436, 439 or 447 of the Fc domain, wherein the numbering of the residues in the Fc domain is that of the EU index as in Kabat. The above-mentioned variant Fc domains may, alternatively, contains one or more substitutions that result in increased binding to FcRn and comprise an amino acid modification at any one or more of amino acid positions 238, 256, 265, 272, 286, 303, 305, 307, 311, 312, 317, 340, 356, 360, 362, 376,

378, 380, 382, 413, 424 or 434 of the Fc domain, wherein the numbering of the residues in the Fc domain is that of the EU index as in Kabat. In yet further embodiments, the variant Fc domains have at least one or more modification that enhances the affinity to FcRn, *e.g.*, a modification of one or more amino acid residues 251-256, 285-290, 308-314, 385-389, and 428-436 (*e.g.*, M428L), or a modification at positions 250 and 428 (*e.g.*, T250Q/M428L), see, *e.g.*, Hinton *et al.*, 2004, *J Biol Chem* 279(8): 6213-6; PCT Publication No. WO 97/34631; and WO 02/060919, all of which are incorporated herein by reference in their entirety. In particular embodiments, an antibody of the IgG class is mutated such that at least one of amino acid residues 250, 314, and 428 of the heavy chain constant region is substituted alone, or in any combinations thereof, such as at positions 250 and 428, or at positions 250 and 314, or at positions 314 and 428, or at positions 250, 314, and 428, with positions 250 and 428 a specific combination. For position 250, the substituting amino acid residue can be any amino acid residue other than threonine, including, but not limited to, alanine, cysteine, aspartic acid, glutamic acid, phenylalanine, glycine, histidine, isoleucine, lysine, leucine, methionine, asparagine, proline, glutamine, arginine, serine, valine, tryptophan, or tyrosine. For position 314, the substituting amino acid residue can be any amino acid residue other than leucine, including, but not limited to, alanine, cysteine, aspartic acid, glutamic acid, phenylalanine, glycine, histidine, isoleucine, lysine, methionine, asparagine, proline, glutamine, arginine, serine, threonine, valine, tryptophan, or tyrosine. For position 428, the substituting amino acid residues can be any amino acid residue other than methionine, including, but not limited to, alanine, cysteine, aspartic acid, glutamic acid, phenylalanine, glycine, histidine, isoleucine, lysine, leucine, asparagine, proline, glutamine, arginine, serine, threonine, valine, tryptophan, or tyrosine. Such mutations increase the antibody's binding to FcRn, which protects the antibody from degradation and increases its half-life.

**[0080]** Other exemplary substitutions leading to modification in Fc effector function are those disclosed in U.S. Patent No. 7,632,497, hereby incorporated by reference in its entirety. In specific embodiments, the additional substitutions are selected from those in Table 1, below. Table 1 shows the effect on binding (up, down or no change "nc") to the indicated FcγRs for the indicated substitutions (Shields *et al.*, 2001, *J Biol Chem* 276(9):6591-604).

<b>Table 1</b>					
<b>Substitution</b>	<b>FcRn</b>	<b>RI</b>	<b>RIIA</b>	<b>RIIB</b>	<b>RIII</b>
E233P	down	down	down	down	down
L234V	down	down	down	down	down

Table 1					
Substitution	FcRn	RI	RIIA	RIIB	RIII
L235A	down	down	down	down	down
P238A	down	down	down	down	down
S239A	nc	nc	nc	nc	down
I253A	down	nc	nc	nc	nc
S254A	down	nc	nc	nc	nc
R255A	nc	nc	up	up	nc
T256A	nc	nc	up	up	up
E258A	nc	nc	up	up	nc
D265A	down	down	down	down	down
D265N	--	--	down	down	down
D265E	--	--	down	down	down
S267A	nc	nc	up	up	nc
S267G	--	--	nc	nc	down
S267T	--	--	down	down	down
H268A	nc	nc	up	up	down
E269A	nc	nc	nc	nc	down
D270A	nc	nc	down	down	down
D270N	--	--	down	down	down
D270E	--	--	down	down	nc
E272A	nc	nc	up	up	nc
N276A	nc	nc	up	up	nc
D280A	nc	nc	up	up	nc
H285A	nc	nc	up	up	nc
N286A	nc	nc	up	up	nc
K288A	down	nc	nc	nc	nc
K290A	nc	nc	up	up	up
R292A	nc	nc	down	down	nc
E293A	nc	nc	nc	nc	down
E293D	--	--	down	down	down
Q295A	nc	nc	down	down	down
Y296F	nc	nc	nc	nc	down
N297A	down	down	down	down	down

Table 1					
Substitution	FcRn	RI	RIIA	RIIB	RIII
S298A	nc	nc	down	down	up
S298T	--	--	down	down	nc
S298N	--	--	down	down	down
R301A	nc	nc	up	up	down
R301M	--	--	up	up	down
V303A	nc	nc	nc	nc	down
V305A	up	nc	nc	nc	nc
T307A	nc	nc	up	up	nc
L309A	nc	nc	up	up	nc
Q311A	up	nc	nc	nc	nc
D312A	up	nc	nc	nc	nc
N315A	nc	nc	up	up	nc
K317A	up	nc	nc	nc	nc
K322A	nc	nc	up	up	down
K326A	nc	nc	up	up	nc
A327Q	down	down	down	down	down
A327S	nc	nc	down	down	down
A327G	nc	nc	nc	nc	down
P329A	down	down	down	down	down
P331A	nc	nc	up	up	nc
P331S	--	--	nc	down	down
E333A	nc	nc	nc	nc	up
E333Q	--	--	down	down	nc
E333N	--	--	down	down	down
E333D	--	--	--	--	up
K334A	nc	nc	nc	nc	up
K334R	--	--	nc	up	down
K334Q	--	--	nc	nc	up
K334E	--	--	down	nc	up
K334V	--	--	up	nc	up
S337A	nc	nc	up	up	nc
K338A	nc	nc	nc	nc	down

Table 1					
Substitution	FcRn	RI	RIIA	RIIB	RIII
K338M	--	--	nc	nc	down
A339T	nc	nc	nc	nc	up
K360A	up	nc	nc	nc	nc
Q362A	up	nc	nc	nc	nc
D376A	nc	nc	nc	nc	down
A378Q	nc	nc	up	up	nc
E380A	up	nc	nc	nc	nc
E382A	up	nc	nc	nc	nc
K414A	nc	nc	down	down	nc
S415A	down	nc	nc	nc	nc
S424A	up	nc	nc	nc	nc
E430A	nc	nc	up	up	nc
H433A	down	nc	nc	nc	nc
N434A	up	nc	nc	nc	nc
H435A	down	nc	nc	nc	nc
Y436A	down	nc	nc	nc	nc

[0081] In certain embodiments, the variant Fc regions of the disclosure can have one or more substitutions in their hinge regions (the portion of SEQ ID NO:1 N-terminal to the CH2 domain) that impact effector function, for example as described in WO2009/006520, particularly at the amino acid position set forth in claim 7 of WO2009/006520. In specific embodiment, the hinge region can include at least one of the combinations of substitutions designated a through ff as set forth in claim 8 of WO2009/006520. WO2009/006520 is incorporated by reference herein in its entirety.

## 6.2. Variant Antibodies

[0082] The polypeptides of the disclosure can be antibodies comprising the variant Fc sequences described herein, referred to as “variant antibodies”.

[0083] In certain embodiments, the variant antibodies of the disclosure are monoclonal antibodies. The term “monoclonal antibody” as used herein is not limited to antibodies produced through hybridoma technology. The term “monoclonal antibody” refers to an antibody that is derived from a single clone, including any eukaryotic, prokaryotic, or phage clone and not the method by which it is

produced. Monoclonal antibodies useful in connection with the present disclosure can be prepared using a wide variety of techniques known in the art including the use of hybridoma, recombinant, and phage display technologies or a combination thereof. The Fc variants of the disclosure include chimeric, primatized, humanized, or human antibodies.

**[0084]** The variant antibodies of the disclosure can be chimeric antibodies. The term “chimeric” antibody as used herein refers to an antibody having variable sequences derived from a non-human immunoglobulin, such as rat or mouse antibody, and human immunoglobulin constant regions, typically chosen from a human immunoglobulin template. Methods for producing chimeric antibodies are known in the art. See, *e.g.*, Morrison, 1985, *Science* 229(4719):1202-7; Oi *et al.*, 1986, *BioTechniques* 4:214-221; Gillies *et al.*, 1985, *J Immunol Methods* 125:191-202; U.S. Pat. Nos. 5,807,715; 4,816,567; and 4,816,397, which are incorporated herein by reference in their entireties.

**[0085]** The variant antibodies of the disclosure can be humanized. “Humanized” forms of non-human (*e.g.*, murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')<sub>2</sub> or other target-binding subdomains of antibodies) which contain minimal sequences derived from non-human immunoglobulin. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin sequence. The humanized antibody can also comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin consensus sequence. Methods of antibody humanization are known in the art. See, *e.g.*, Riechmann *et al.*, 1988, *Nature* 332:323-7; U.S. Patent Nos: 5,530,101; 5,585,089; 5,693,761; 5,693,762; and 6,180,370 to Queen *et al.*; EP239400; PCT publication WO 91/09967; U.S. Patent No. 5,225,539; EP592106; EP519596; Padlan, 1991, *Mol Immuno*, 28:489-498; Studnicka *et al.*, 1994, *Prot. Eng.* 7:805-814; Roguska *et al.*, 1994, *Proc. Natl. Acad. Sci.* 91:969-973; and U.S. Patent No. 5,565,332, all of which are hereby incorporated by reference in their entireties.

**[0086]** The variant antibodies of the disclosure can be human antibodies. Completely “human” Fc variants can be desirable for therapeutic treatment of human patients. As used herein, “human antibodies” include antibodies having the amino acid sequence of a human immunoglobulin and include antibodies isolated from human immunoglobulin libraries or from animals transgenic for one or more human immunoglobulin and that do not express endogenous immunoglobulins. Human

antibodies can be made by a variety of methods known in the art including phage display methods using antibody libraries derived from human immunoglobulin sequences. See U.S. Patent Nos. 4,444,887 and 4,716,111; and PCT publications WO 98/46645; WO 98/50433; WO 98/24893; WO 98/16654; WO 96/34096; WO 96/33735; and WO 91/10741, each of which is incorporated herein by reference in its entirety. Human antibodies can also be produced using transgenic mice which are incapable of expressing functional endogenous immunoglobulins but which can express human immunoglobulin genes. See, *e.g.*, PCT publications WO 98/24893; WO 92/01047; WO 96/34096; WO 96/33735; U.S. Patent Nos. 5,413,923; 5,625,126; 5,633,425; 5,569,825; 5,661,016; 5,545,806; 5,814,318; 5,885,793; 5,916,771; and 5,939,598, which are incorporated by reference herein in their entireties. In addition, companies such as Medarex (Princeton, NJ), Astellas Pharma (Deerfield, IL), Amgen (Thousand Oaks, CA) and Regeneron (Tarrytown, NY) can be engaged to provide human antibodies directed against a selected antigen using technology similar to that described above. Completely human antibodies that recognize a selected epitope can be generated using a technique referred to as “guided selection.” In this approach a selected non-human monoclonal antibody, *e.g.*, a mouse antibody, is used to guide the selection of a completely human antibody recognizing the same epitope (Jespers *et al.*, 1988, *Biotechnology* 12:899-903).

**[0087]** The variant antibodies of the disclosure can be primatized. The term “primatized antibody” refers to an antibody comprising monkey variable regions and human constant regions. Methods for producing primatized antibodies are known in the art. See *e.g.*, U.S. Patent Nos. 5,658,570; 5,681,722; and 5,693,780, which are incorporated herein by reference in their entireties.

**[0088]** The variant antibodies of the disclosure can be bispecific antibodies. Bispecific antibodies are monoclonal, often human or humanized, antibodies that have binding specificities for at least two different antigens. Non-limiting examples of antigen targets of bispecific antibodies include a cell-surface protein, receptor, receptor subunit, tissue-specific antigen, virally derived protein, virally encoded envelope protein, bacterially derived protein, or bacterial surface protein, *etc.*

**[0089]** The variant antibodies of the disclosure can be dual variable domain (“DVD”) immunoglobulins (“DVD-Ig”) (see, Gu & Ghayur, 2012, *Methods in Enzymology* 502:25-41, incorporated by reference herein in its entirety). A DVD-Ig combines the target-binding variable domains of two monoclonal antibodies via linkers to create a tetravalent, dual-targeting single agent. Suitable linkers for use in the light chains of the DVDs of the present disclosure include those identified on Table 2.1 on page 30 of Gu & Ghayur, 2012, *Methods in Enzymology* 502:25-41,

incorporated by reference herein: the short  $\kappa$  chain linkers ADAAP (SEQ ID NO: 22) (murine) and TVAAP (SEQ ID NO: 23) (human); the long  $\kappa$  chain linkers ADAAPTVSIFP (SEQ ID NO: 24) (murine) and TVAAPSVFIFPP (SEQ ID NO: 25) (human); the short  $\lambda$  chain linker QPKAAP (SEQ ID NO: 26) (human); the long  $\lambda$  chain linker QPKAAPSVTLFPP (SEQ ID NO: 27) (human); the GS-short linker GGS GG (SEQ ID NO: 28), the GS-medium linker GGS GG GG GG (SEQ ID NO: 29), and the GS-long linker GGS GG GG GG GG GG (SEQ ID NO: 30) (all GS linkers are murine and human). Suitable linkers for use in the heavy chains of the DVDs of the present disclosure include those identified on Table 2.1 on page 30 of Gu & Ghayur, 2012, *Methods in Enzymology* 502:25-41, incorporated by reference herein: the short linkers AKTTAP (SEQ ID NO: 31) (murine) and ASTKGP (SEQ ID NO: 32) (human); the long linkers AKTTAPSVYPLAP (SEQ ID NO: 33) (murine) and ASTKGPSVFPLAP (SEQ ID NO: 34) (human); the GS-short linker GGGGSG (SEQ ID NO: 35), the GS-medium linker GGGGSGGGGS (SEQ ID NO: 36), and the GS-long linker GGGGSGGGGSGGGG (SEQ ID NO: 37) (all GS linkers are murine and human). Preferably human linkers are used for human or humanized DVD-Igs.

**[0090]** In the present disclosure, the DVD-Ig is directed towards two different targets. The targets can be selected from EGFR, HER2, ErbB3, or any other target described in Tariq *et al.*, U.S. Patent Application Publication No. 2011/0044980, published February 24, 2011 (incorporated by reference herein in its entirety).

**[0091]** Target binding domains of DVD immunoglobulins are typically arranged in tandem, with one variable domain stacked on top of another to form inner and outer Fv domains.

**[0092]** The variant antibodies of the disclosure include derivatized antibodies. For example, but not by way of limitation, derivatized antibodies are typically modified by glycosylation, acetylation, pegylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to a cellular ligand or other protein (see Section 6.5 for a discussion of antibody conjugates), *etc.* Any of numerous chemical modifications can be carried out by known techniques, including, but not limited to, specific chemical cleavage, acetylation, formylation, metabolic synthesis of tunicamycin, *etc.* Additionally, the derivative can contain one or more non-natural amino acids, *e.g.*, using Ambrx technology (*See, e.g.*, Wolfson, 2006, *Chem. Biol.* 13(10):1011-2).



### 6.2.1. Targets of Fc Variant Antibodies

[0093] Virtually any antigen may be targeted by antibodies of the disclosure, including but not limited to proteins, subunits, domains, motifs, and/or epitopes belonging to the following list of target antigens, which includes both soluble factors such as cytokines and membrane-bound factors, including transmembrane receptors: 17-IA, 4-1BB, 4Dc, 6-keto-PGF1a, 8-iso-PGF2a, 8-oxo-dG, A1 Adenosine Receptor, A33, ACE, ACE-2, Activin, Activin A, Activin AB, Activin B, Activin C, Activin RIA, Activin RIA ALK-2, Activin RIB ALK-4, Activin RIIA, Activin RIIB, ADAM, ADAM10, ADAM12, ADAM15, ADAM17/TACE, ADAM8, ADAM9, ADAMTS, ADAMTS4, ADAMTS5, Addressins, aFGF, ALCAM, ALK, ALK-1, ALK-7, alpha-1-antitrypsin, alpha-V/beta-1 antagonist, ANG, Ang, APAF-1, APE, APJ, APP, APRIL, AR, ARC, ART, Artemin, anti-Id, ASPARTIC, Atrial natriuretic factor, av/b3 integrin, Axl, b2M, B7-1, B7-2, B7-H, B-lymphocyte Stimulator (BlyS), BACE, BACE-1, Bad, BAFF, BAFF-R, Bag-1, BAK, Bax, BCA-1, BCAM, Bcl, BCMA, BDNF, b-ECGF, bFGF, BID, Bik, BIM, BLC, BL-CAM, BLK, BMP, BMP-2 BMP-2a, BMP-3 Osteogenin, BMP-4 BMP-2b, BMP-5, BMP-6 Vgr-1, BMP-7 (OP-1), BMP-8 (BMP-8a, OP-2), BMPR, BMPR-IA (ALK-3), BMPR-IB (ALK-6), BRK-2, RPK-1, BMPR-II (BRK-3), BMPs, b-NGF, BOK, Bombesin, Bone-derived neurotrophic factor, BPDE, BPDE-DNA, BTC, complement factor 3 (C3), C3a, C4, C5, C5a, C10, CA125, CAD-8, Calcitonin, cAMP, carcinoembryonic antigen (CEA), carcinoma-associated antigen, Cathepsin A, Cathepsin B, Cathepsin C/DPPI, Cathepsin D, Cathepsin E, Cathepsin H, Cathepsin L, Cathepsin O, Cathepsin S, Cathepsin V, Cathepsin X/Z/P, CBL, CCI, CCK2, CCL, CCL1, CCL11, CCL12, CCL13, CCL14, CCL15, CCL16, CCL17, CCL18, CCL19, CCL2, CCL20, CCL21, CCL22, CCL23, CCL24, CCL25, CCL26, CCL27, CCL28, CCL3, CCL4, CCL5, CCL6, CCL7, CCL8, CCL9/10, CCR, CCR1, CCR10, CCR10, CCR2, CCR3, CCR4, CCR5, CCR6, CCR7, CCR8, CCR9, CD1, CD2, CD3, CD3E, CD4, CD5, CD6, CD7, CD8, CD10, CD11a, CD11b, CD11c, CD13, CD14, CD15, CD16, CD18, CD19, CD20, CD21, CD22, CD23, CD25, CD27L, CD28, CD29, CD30, CD30L, CD32, CD33 (p67 proteins), CD34, CD38, CD40, CD40L, CD44, CD45, CD46, CD49a, CD52, CD54, CD55, CD56, CD61, CD64, CD66e, CD74, CD80 (B7-1), CD89, CD95, CD123, CD137, CD138, CD140a, CD146, CD147, CD148, CD152, CD164, CEACAM5, CFTR, cGMP, CINC, *Clostridium botulinum* toxin, *Clostridium perfringens* toxin, CKb8-1, CLC, CMV, CMV UL, CNTF, CNTN-1, COX, C-Ret, CRG-2, CT-1, CTACK, CTGF, CTLA-4, CX3CL1, CX3CR1, CXCL, CXCL1, CXCL2, CXCL3, CXCL4, CXCL5, CXCL6, CXCL7, CXCL8, CXCL9, CXCL10, CXCL11, CXCL12, CXCL13, CXCL14, CXCL15, CXCL16, CXCR, CXCR1, CXCR2, CXCR3, CXCR4, CXCR5, CXCR6, cytokeratin tumor-

associated antigen, DAN, DCC, DcR3, DC-SIGN, Decay accelerating factor, des(1-3)-IGF-I (brain IGF-1), Dhh, digoxin, DNAM-1, Dnase, Dpp, DPPIV/CD26, Dtk, ECAD, EDA, EDA-A1, EDA-A2, EDAR, EGF, EGFR (ErbB-1), EMA, EMMPRIN, ENA, endothelin receptor, Enkephalinase, eNOS, Eot, eotaxin1, EpCAM, Ephrin B2/EphB4, EPO, ERCC, E-selectin, ET-1, Factor 10a, Factor VII, Factor VIIIc, Factor IX, fibroblast activation protein (FAP), Fas, FcR1, FEN-1, Ferritin, FGF, FGF-19, FGF-2, FGF3, FGF-8, FGFR, FGFR-3, Fibrin, FL, FLIP, Flt-3, Flt-4, Follicle stimulating hormone, Fractalkine, FZD1, FZD2, FZD3, FZD4, FZD5, FZD6, FZD7, FZD8, FZD9, FZD10, G250, Gas 6, GCP-2, GCSF, GD2, GD3, GDF, GDF-1, GDF-3 (Vgr-2), GDF-5 (BMP-14, CDMP-1), GDF-6 (BMP-13, CDMP-2), GDF-7 (BMP-12, CDMP-3), GDF-8 (Myostatin), GDF-9, GDF-15 (MIC-1), GDNF, GDNF, GFAP, GFRa-1, GFR-alpha1, GFR-alpha2, GFR-alpha3, GTR, Glucagon, Glut 4, glycoprotein 10b/IIIa (GP 10b/IIIa), GM-CSF, gp130, gp72, GRO, Growth hormone releasing factor, Hapten (NP-cap or NIP-cap), HB-EGF, HCC, HCMV gB envelope glycoprotein, HCMV gH envelope glycoprotein, HCMV UL, Hemopoietic growth factor (HGF), Hep B gp120, heparanase, Her2, Her2/neu (ErbB-2), Her3 (ErbB-3), Her4 (ErbB-4), herpes simplex virus (HSV) gB glycoprotein, HSV gD glycoprotein, HGFA, High molecular weight melanoma-associated antigen (HMW-MAA), HIV gp120, HIV IIIB gp120 V3 loop, HLA, HLA-DR, HM1.24, HMFG PEM, HRG, Hrk, human cardiac myosin, human cytomegalovirus (HCMV), human growth hormone (HGH), HVEM, I-309, IAP, ICAM, ICAM-1, ICAM-3, ICE, ICOS, IFNg, Ig, IgA receptor, IgE, IGF, IGF binding proteins, IGF-1R, IGFBP, IGF-I, IGF-II, IL, IL-1, IL-1R, IL-2, IL-2R, IL-4, IL-4R, IL-5, IL-5R, IL-6, IL-6R, IL-8, IL-9, IL-10, IL-12, IL-13, IL-15, IL-18, IL-18R, IL-23, interferon (INF)-alpha, INF-beta, INF-gamma, Inhibin, iNOS, Insulin A-chain, Insulin B-chain, Insulin-like growth factor 1, integrin alpha2, integrin alpha3, integrin alpha4, integrin alpha4/beta1, integrin alpha4/beta7, integrin alpha5 (alphaV), integrin alpha5/beta1, integrin alpha5/beta3, integrin alpha6, integrin beta1, integrin beta2, interferon gamma, IP-10, I-TAC, JE, Kallikrein 2, Kallikrein 5, Kallikrein 6, Kallikrein 11, Kallikrein 12, Kallikrein 14, Kallikrein 15, Kallikrein L1, Kallikrein L2, Kallikrein L3, Kallikrein L4, KC, KDR, Keratinocyte Growth Factor (KGF), laminin 5, LAMP, LAP, LAP (TGF-1), Latent TGF-1, Latent TGF-1 bp1, LBP, LDGF, LECT2, Lefty, Lewis-Y antigen, Lewis-Y related antigen, LFA-1, LFA-3, Lfo, LIF, LIGHT, lipoproteins, LIX, LKN, Lptn, L-Selectin, LT-a, LT-b, LTB4, LTBP-1, Lung surfactant, Luteinizing hormone, Lymphotoxin Beta Receptor, Mac-1, MAdCAM, MAG, MAP2, MARC, MCAM, MCAM, MCK-2, MCP, M-CSF, MDC, Mer, METALLOPROTEASES, MGDF receptor, MGMT, MHC (HLA-DR), MIF, MIG, MIP, MIP-1-alpha, MK, MMAC1, MMP, MMP-1, MMP-10, MMP-11, MMP-12, MMP-13, MMP-14, MMP-15, MMP-2, MMP-24, MMP-3,

MMP-7, MMP-8, MMP-9, MPIF, Mpo, MSK, MSP, mucin (Muc1), MUC18, Muellerian-inhibitin substance, Mug, MuSK, NAIP, NAP, NCAD, N-Cadherin, NCA 90, NCAM, NCAM, Neprilysin, Neurotrophin-3, -4, or -6, Neurturin, Neuronal growth factor (NGF), NGFR, NGF-beta, nNOS, NO, NOS, Npn, NRG-3, NT, NTN, OB, OGG1, OPG, OPN, OSM, OX40L, OX40R, p150, p95, PADPr, Parathyroid hormone, PARC, PARP, PBR, PBSF, PCAD, P-Cadherin, PCNA, PDGF, PDGF, PDK-1, PECAM, PEM, PF4, PGE, PGF, PGI2, PGJ2, PIN, PLA2, placental alkaline phosphatase (PLAP), PIGF, PLP, PP14, Proinsulin, Prorelaxin, Protein C, PS, PSA, PSCA, prostate specific membrane antigen (PSMA), PTEN, PTHrp, Ptk, PTN, R51, RANK, RANKL, RANTES, RANTES, Relaxin A-chain, Relaxin B-chain, renin, respiratory syncytial virus (RSV) F, RSV Fgp, Ret, Rheumatoid factors, RLIP76, RPA2, RSK, S100, SCF/KL, SDF-1, SERINE, Serum albumin, sFRP-3, Shh, SIGIRR, SK-1, SLAM, SLPI, SMAC, SMDF, SMOH, SOD, SPARC, Stat, STEAP, STEAP-II, TACE, TACI, TAG-72 (tumor-associated glycoprotein-72), TARC, TCA-3, T-cell receptors (*e.g.*, T-cell receptor alpha/beta), TdT, TECK, TEM1, TEM5, TEM7, TEM8, TERT, testicular PLAP-like alkaline phosphatase, Tfr, TGF, TGF-alpha, TGF-beta, TGF-beta Pan Specific, TGF-beta RI (ALK-5), TGF-beta RII, TGF-beta RIIB, TGF-beta RIII, TGF-beta1, TGF-beta2, TGF-beta3, TGF-beta4, TGF-beta5, Thrombin, Thymus Ck-1, Thyroid stimulating hormone, Tie, TIMP, TIQ, Tissue Factor, TMEFF2, Tmpo, TMPRSS2, TNF, TNF-alpha, TNF-alpha beta, TNF-beta2, TNF-c, TNF-RI, TNF-RII, TNFRSF10A (TRAIL R1 Apo-2, DR4), TNFRSF10B (TRAIL R2 DR5, KILLER, TRICK-2A, TRICK-B), TNFRSF10C (TRAIL R3 DcR1, LIT, TRID), TNFRSF10D (TRAIL R4 DcR2, TRUNDD), TNFRSF11A (RANK ODF R, TRANCE R), TNFRSF11B (OPG OCIF, TR1), TNFRSF12 (TWEAK R FN14), TNFRSF13B (TACI), TNFRSF13C (BAFF R), TNFRSF14 (HVEM ATAR, HveA, LIGHT R, TR2), TNFRSF16 (NGFR p75NTR), TNFRSF17 (BCMA), TNFRSF18 (GITR AITR), TNFRSF19 (TROY TAJ, TRADE), TNFRSF19L (RELT), TNFRSF1A (TNF RI CD120a, p55-60), TNFRSF1B (TNF RII CD120b, p75-80), TNFRSF26 (TNFRH3), TNFRSF3 (LTbR TNF RIII, TNFC R), TNFRSF4 (OX40 ACT35, TXGP1 R), TNFRSF5 (CD40 p50), TNFRSF6 (Fas Apo-1, APT1, CD95), TNFRSF6B (DcR3M68, TR6), TNFRSF7 (CD27), TNFRSF8 (CD30), TNFRSF9 (4-1BB CD137, ILA), TNFRSF21 (DR6), TNFRSF22 (DcTRAIL R2TNFRH2), TNFRST23 (DcTRAIL R1TNFRH1), TNFRSF25 (DR3 Apo-3, LARD, TR-3, TRAMP, WSL-1), TNFSF10 (TRAIL Apo-2 Ligand, TL2), TNFSF11 (TRANCE/RANK Ligand ODF, OPG Ligand), TNFSF12 (TWEAK Apo-3 Ligand, DR3 Ligand), TNFSF13 (APRIL TALL2), TNFSF13B (BAFF BLYS, TALL1, THANK, TNFSF20), TNFSF14 (LIGHT HVEM Ligand, LTg), TNFSF15 (TL1A/VEGI), TNFSF18 (GITR Ligand AITR Ligand, TL6), TNFSF1A (TNF-a Conectin, DIF,

TNFSF2), TNFSF1B (TNF- $\beta$  LTa, TNFSF1), TNFSF3 (LT $\beta$  TNFC, p33), TNFSF4 (OX40 Ligand gp34, TXGP1), TNFSF5 (CD40 Ligand CD154, gp39, HIGM1, IMD3, TRAP), TNFSF6 (Fas Ligand Apo-1 Ligand, APT1 Ligand), TNFSF7 (CD27 Ligand CD70), TNFSF8 (CD30 Ligand CD153), TNFSF9 (4-1BB Ligand CD137 Ligand), TP-1, t-PA, Tpo, TRAIL, TRAIL R, TRAIL-R1, TRAIL-R2, TRANCE, transferring receptor, TRF, Trk, TROP-2, TSG, TSLP, tumor-associated antigen CA 125, tumor-associated antigen expressing Lewis Y related carbohydrate, TWEAK, TXB2, Ung, uPAR, uPAR-1, Urokinase, VCAM, VCAM-1, VECAD, VE-Cadherin, VE-cadherin-2, VEGFR-1 (flt-1), VEGF, VEGFR, VEGFR-3 (flt-4), VEGI, VIM, Viral antigens, VLA, VLA-1, VLA-4, VNR integrin, von Willebrands factor, WIF-1, WNT1, WNT2, WNT2B/13, WNT3, WNT3A, WNT4, WNT5A, WNT5B, WNT6, WNT7A, WNT7B, WNT8A, WNT8B, WNT9A, WNT9A, WNT9B, WNT10A, WNT10B, WNT11, WNT16, XCL1, XCL2, XCR1, XCR1, XEDAR, XIAP, XPD, and receptors for hormones and growth factors.

**[0094]** An antibody of the disclosure, comprising the variant Fc domains described herein, can include the CDR sequences or the variable domain sequences of a known “parent” antibody. In some embodiments, the parent antibody and the antibody of the disclosure can share similar or identical sequences except for modifications to the Fc domain as disclosed herein.

**[0095]** For example, a parent antibody can be substantially similar to rituximab (Rituxan®, IDEC/Genentech/Roche) (see for example U.S. Pat. No. 5,736,137), a chimeric anti-CD20 antibody approved to treat Non-Hodgkin's lymphoma; HuMax-CD20, an anti-CD20 currently being developed by Genmab, an anti-CD20 antibody described in U.S. Pat. No. 5,500,362, AME-133 (Applied Molecular Evolution), hA20 (Immunomedics, Inc.), HumaLYM (Intracel), and PRO70769 (PCT/US2003/040426, entitled “Immunoglobulin Variants and Uses Thereof”). A number of antibodies that target members of the family of epidermal growth factor receptors, including EGFR (ErbB-1), Her2/neu (ErbB-2), Her3 (ErbB-3), Her4 (ErbB-4), may benefit from the Fc polypeptides of the present invention. For example the Fc polypeptides of the present invention may find use in an antibody that is substantially similar to trastuzumab (Herceptin®, Genentech) (see for example U.S. Pat. No. 5,677,171), a humanized anti-Her2/neu antibody approved to treat breast cancer; pertuzumab (rhuMab-2C4, Omnitarg™), currently being developed by Genentech; an anti-Her2 antibody described in U.S. Pat. No. 4,753,894; cetuximab (Erbix®, Imclone) (U.S. Pat. No. 4,943,533; PCT WO 96/40210), a chimeric anti-EGFR antibody in clinical trials for a variety of cancers; ABX-EGF (U.S. Pat. No. 6,235,883), currently being developed by Abgenix-Immunex-Amgen; HuMax-EGFr

(U.S. Ser. No. 10/172,317), currently being developed by Genmab; 425, EMD55900, EMD62000, and EMD72000 (Merck KGaA) (U.S. Pat. No. 5,558,864; Murthy *et al.* 1987, *Arch Biochem Biophys.* 252(2):549-60; Rodeck *et al.*, 1987, *J Cell Biochem.* 35(4):315-20; Kettleborough *et al.*, 1991, *Protein Eng.* 4(7):773-83); ICR62 (Institute of Cancer Research) (PCT WO 95/20045; Modjtahedi *et al.*, 1993, *J Cell Biophys.* 1993, 22(1-3):129-46; Modjtahedi *et al.*, 1993, *Br J Cancer.* 1993, 67(2):247-53; Modjtahedi *et al.*, 1996, *Br J Cancer.* 73(2):228-35; Modjtahedi *et al.*, 2003, *Int J Cancer.* 105(2):273-80); TheraCIM hR3 (YM Biosciences, Canada and Centro de Immunologia Molecular, Cuba (U.S. Pat. No. 5,891,996; U.S. Pat. No. 6,506,883; Mateo *et al.*, 1997, *Immunotechnology*, 3(1):71-81); mAb-806 (Ludwig Institute for Cancer Research, Memorial Sloan-Kettering) (Jungbluth *et al.* 2003, *Proc Natl Acad Sci USA.* 100(2):639-44); KSB-102 (KS Biomedix); MR1-1 (IVAX, National Cancer Institute) (PCT WO 0162931A2); and SC100 (Scancell) (PCT WO 01/88138). In another preferred embodiment, the Fc polypeptides of the present invention may find use in alemtuzumab (Campath®, Millenium), a humanized monoclonal antibody currently approved for treatment of B-cell chronic lymphocytic leukemia. The Fc polypeptides of the present invention may find use in a variety of antibodies or Fc fusions that are substantially similar to other clinical products and candidates, including but not limited to muromonab-CD3 (Orthoclone OKT3®), an anti-CD3 antibody developed by Ortho Biotech/Johnson & Johnson, ibritumomab tiuxetan (Zevalin®), an anti-CD20 antibody developed by IDEC/Schering AG, gemtuzumab ozogamicin (Mylotarg®), an anti-CD33 (p67 protein) antibody developed by Celltech/Wyeth, abciximab (ReoPro®), developed by Centocor/Lilly, basiliximab (Simulect®), developed by Novartis, palivizumab (Synagis®), developed by MedImmune, infliximab (Remicade®), an anti-TNFalpha antibody developed by Centocor, adalimumab (Humira®), an anti-TNFalpha antibody developed by Abbott, Humicade™ an anti-TNFalpha antibody developed by Celltech, ABX-CBL, an anti-CD147 antibody being developed by Abgenix, ABX-IL8, an anti-IL8 antibody being developed by Abgenix, ABX-MA1, an anti-MUC18 antibody being developed by Abgenix, Pemtumomab (R1549, 90Y-muHMFG1), an anti-MUC1 In development by Antisoma, Therex (R1550), an anti-MUC1 antibody being developed by Antisoma, AngioMab (AS1405), being developed by Antisoma, HuBC-1, being developed by Antisoma, Thioplatin (AS1407) being developed by Antisoma, Antegren® (natalizumab), an anti-alpha-4-beta-1 (VLA-4) and alpha-4-beta-7 antibody being developed by Biogen, VLA-1 mAb, an anti-VLA-1 integrin antibody being developed by Biogen, LTBR mAb, an anti-lymphotoxin beta receptor (LTBR) antibody being developed by Biogen, CAT-152, an anti-TGF-β2 antibody being developed by Cambridge Antibody Technology, J695, an anti-IL-12 antibody

being developed by Cambridge Antibody Technology and Abbott, CAT-192, an anti-TGF $\beta$ 1 antibody being developed by Cambridge Antibody Technology and Genzyme, CAT-213, an anti-Eotaxin1 antibody being developed by Cambridge Antibody Technology, LymphoStat-B™ an anti-Blys antibody being developed by Cambridge Antibody Technology and Human Genome Sciences Inc., TRAIL-R1 mAb, an anti-TRAIL-R1 antibody being developed by Cambridge Antibody Technology and Human Genome Sciences, Inc., Avastin™ (bevacizumab, rhuMAb-VEGF), an anti-VEGF antibody being developed by Genentech, an anti-HER receptor family antibody being developed by Genentech, Anti-Tissue Factor (ATF), an anti-Tissue Factor antibody being developed by Genentech, Xolair™ (Omalizumab), an anti-IgE antibody being developed by Genentech, Raptiva™ (Efalizumab), an anti-CD11a antibody being developed by Genentech and Xoma, MLN-02 Antibody (formerly LDP-02), being developed by Genentech and Millenium Pharmaceuticals, HuMax CD4, an anti-CD4 antibody being developed by Genmab, HuMax-IL15, an anti-IL15 antibody being developed by Genmab and Amgen, HuMax-Inflam, being developed by Genmab and Medarex, HuMax-Cancer, an anti-Heparanase I antibody being developed by Genmab and Medarex and Oxford GcoSciences, HuMax-Lymphoma, being developed by Genmab and Amgen, HuMax-TAC, being developed by Genmab, IDEC-131, and anti-CD40L antibody being developed by IDEC Pharmaceuticals, IDEC-151 (Clenoliximab), an anti-CD4 antibody being developed by IDEC Pharmaceuticals, IDEC-114, an anti-CD80 antibody being developed by IDEC Pharmaceuticals, IDEC-152, an anti-CD23 being developed by IDEC Pharmaceuticals, anti-macrophage migration factor (MIF) antibodies being developed by IDEC Pharmaceuticals, BEC2, an anti-idiotypic antibody being developed by Imclone, IMC-1C11, an anti-KDR antibody being developed by Imclone, DC101, an anti-flk-1 antibody being developed by Imclone, anti-VE cadherin antibodies being developed by Imclone, CEA-Cide™ (labetuzumab), an anti-carcinoembryonic antigen (CEA) antibody being developed by Immunomedics, LymphoCide™ (Epratuzumab), an anti-CD22 antibody being developed by Immunomedics, AFP-Cide, being developed by Immunomedics, MyelomaCide, being developed by Immunomedics, LkoCide, being developed by Immunomedics, ProstaCide, being developed by Immunomedics, MDX-010, an anti-CTLA4 antibody being developed by Medarex, MDX-060, an anti-CD30 antibody being developed by Medarex, MDX-070 being developed by Medarex, MDX-018 being developed by Medarex, Osidem™ (IDM-1), and anti-Her2 antibody being developed by Medarex and Immuno-Designed Molecules, HuMax™-CD4, an anti-CD4 antibody being developed by Medarex and Genmab, HuMax-IL15, an anti-IL15 antibody being developed by Medarex and Genmab, CNTO 148, an anti-TNF $\alpha$  antibody being developed by Medarex and

Centocor/J&J, CNTO 1275, an anti-cytokine antibody being developed by Centocor/J&J, MOR101 and MOR102, anti-intercellular adhesion molecule-1 (ICAM-1) (CD54) antibodies being developed by MorphoSys, MOR201, an anti-fibroblast growth factor receptor 3 (FGFR-3) antibody being developed by MorphoSys, Nuvion® (visilizumab), an anti-CD3 antibody being developed by Protein Design Labs, HuZAF™, an anti-gamma interferon antibody being developed by Protein Design Labs, Anti- $\alpha 5\beta 1$  Integrin, being developed by Protein Design Labs, anti-IL-12, being developed by Protein Design Labs, ING-1, an anti-Ep-CAM antibody being developed by Xoma, and MLN01, an anti-Beta2 integrin antibody being developed by Xoma, all of the above-cited references in this paragraph are expressly incorporated herein by reference.

**[0096]** In one embodiment, the variants of the present invention are used for the treatment of autoimmune, inflammatory, or transplant indications. Target antigens and clinical products and candidates that are relevant for such diseases include but are not limited to anti- $\alpha 4\beta 7$  integrin antibodies such as LDP-02, anti-beta2 integrin antibodies such as LDP-01, anti-complement (C5) antibodies such as 5G1.1, anti-CD2 antibodies such as BTI-322, MEDI-507, anti-CD3 antibodies such as OKT3, SMART anti-CD3, anti-CD4 antibodies such as IDEC-151, MDX-CD4, OKT4A, anti-CD11a antibodies, anti-CD14 antibodies such as IC14, anti-CD18 antibodies, anti-CD23 antibodies such as IDEC 152, anti-CD25 antibodies such as Zenapax, anti-CD40L antibodies such as 5c8, Antova, IDEC-131, anti-CD64 antibodies such as MDX-33, anti-CD80 antibodies such as IDEC-114, anti-CD147 antibodies such as ABX-CBL, anti-E-selectin antibodies such as CDP850, anti-gpIIb/IIIa antibodies such as ReoPro/Abcixima, anti-ICAM-3 antibodies such as ICM3, anti-ICE antibodies such as VX-740, anti-FcR1 antibodies such as MDX-33, anti-IgE antibodies such as rhuMab-E25, anti-IL-4 antibodies such as SB-240683, anti-IL-5 antibodies such as SB-240563, SCH55700, anti-IL-8 antibodies such as ABX-IL8, anti-interferon gamma antibodies, anti-TNF (TNF, TNFa, TNFa, TNF-alpha) antibodies such as CDP571, CDP870, D2E7, Infliximab, MAK-195F, and anti-VLA-4 antibodies such as Antegren.

**[0097]** Exemplary antibodies which can be engineered to incorporated the variant Fc regions of the disclosure are set forth in Table 2 below:

Table 2			
Antibody target & name	Chain	Sequence Identifier	Sequence
Anti-CD40 (S2C6)	VL	SEQ ID NO:3	DVVVTQTPLSLPVSLGQAQASISCRSSQSLVHSN GNTFLHWYLQKPGQSPKLLIYTVSNRFGVDP RFGSGSGTDFTLKISRVEAEDLGVYFCSQTTH

Table 2			
Antibody target & name	Chain	Sequence Identifier	Sequence
			VPWTFGGGTKLEIQ
	VH	SEQ ID NO:4	EVQLQQSGPDLVKPGASVKISCKASGYSFTGY YIHMVKQSKGHSLEWIGRVIPNNGGTSYNQKF KGKAILTVDKSSSTAYMELRSLTSEDSAVYYC AREGIYWWGHGTTTLTVSS
Anti-CD20 (rituximab)	VL	SEQ ID NO:5	QIVLSQSPAILSASPGEKVTMTCRASSSVSYIH WFQQKPGSSPKPWIYATSNLASGVPVRFSGSG SGTSYSLTISRVEAEDAATYYCQQWTSNPPTFG GGTKLEIK
	VH	SEQ ID NO:6	QVQLQQPGAELVKPGASVKMSCKASGYTFTS YNMHVWKQTPGRGLEWIGAIYPNGDTSYNQ KFKGKATLTADKSSSTAYMQLSSLTSEDSAVY YCARSTYYGGDWYFNVWGAGTTVTVSA
Anti-CD25 (daclizumab)	VL	SEQ ID NO:7	DIQMTQSPSTLSASVGDRTITCSASSSISYMH WYQQKPGKAPKLLIYTTSNLASGVPARFSGSG SGTEFTLTISLQPDDEFATYYCHQRSTYPLTFG QGKTKVEIK
	VH	SEQ ID NO:8	QVQLVQSGAEVKKPGSSVKVSKASGYTFTSY RMHWVRQAPGQGLEWIGYINPSTGYTEYNQK FKDKATITADESTNTAYMELSSLRSEDTAVYY CARGGGVFDYWGQGTLLTVSS
Anti-CD25 (basiliximab)	VL	SEQ ID NO:9	QIVLTQSPAISASPGEKVTMTCSASSSISYMQ WYQQKPGTSPKRWIYDTSKLASGVPARFSGSG SGTSYSLTISSMEAEDAATYYCHQRSSYTFGGG TKLEIK
	VH	SEQ ID NO:10	EVQLQQSGTVLARPGASVKMSCKASGYSFTRY WMHWIKQRPQGQGLEWIGAIYPGNSDTSYNQK FEGKAKLTAVTSASTAYMELSSLTHEDSAVYY CSRDYGYFDYFWGQGTLLTVSS
Anti-TNF $\alpha$ (adalimumab)	VL	SEQ ID NO:11	DIQMTQSPSSLSASVGDRTITCRASQGIRNYL AWYQQKPGKAPKLLIYAASLTQSGVPSRFGSG GSGTDFTLTISLQPEDVATYYCQRYNRAPYTF GQGKTKVEIK
	VH	SEQ ID NO:12	EVQLVESGGGLVQPGRSLRLSCAASGFTFDDY AMHWVRQAPGKGLEWVSAITWNSGHIDYADS VEGRFTISRDNKNSLYLQMNSLRAEDTAVYY CAKVSYLSTASSLDYWGQGTLLTVSS
Anti-TNF $\alpha$ (infliximab)	VL	SEQ ID NO:13	SIVMTQTPKFLVLSAGDRTITCTASQSVSNDV VWYQQKPGQSPKMLMYSAFNRYTGVPDRFTG RGYGTDFTFITISSVQAEDLAVYFCQQDYNspr TFGGGTKLEIKR
	VH	SEQ ID NO:14	QIQLVQSGPELKKPGETVKISCKASGYTFTHYG MNWVKQAPGKGLKWMGWINTYTGEPTYADD FKEHFAFSLETASTVFLQINNLIKNEATATYFC ARERGDAMDYWGQGTSTVTVSS
Anti-IL-6R (tocilizumab)	VL	SEQ ID NO:15	DIQMTQSPSSLSASVGDRTITCRASQDISSYLN WYQQKPGKAPKLLIYYTSRLHSGVPSRFGSGG SGTDFTFTISLQPEDATYYCQQGNTLPYTFGQ



Table 2			
Antibody target & name	Chain	Sequence Identifier	Sequence
			GTKVEIK
	VH	SEQ ID NO:16	QVQLQESGPGLV RPSQTL SLTCTVSGYSITSDH AWSWVRQPPGRGLEWIGYISYSGITTYNPSLKS RVTMLRDTSKNQFSLRLSSVTAADTAVYCARS LARTTAMDYWGQGSLVTVSS
Anti-IL-1 (canakinumab)	VL	SEQ ID NO:17	EIVLTQSPDFQSVTPKEKVTITCRASQSIGSSLH WYQQKPDQSPKLLIKYASQSFSGVPSRFSGSGS GTDFTLTINSLEAEDAAAYYCHQSSSLPFTFGP GTK
	VH	SEQ ID NO:18	QVQLVESGGGVVQPGRSLRLSCAASGFTFSVY GMNWVRQAPGKGLEWVAIIWYDGDNQYYAD SVKGRFTISRDNKNTLYLQMNGLRAEDTAVY YCARDLRTGPFDYWGQGLTVT
Anti-BAFF (belimumab)	VL	SEQ ID NO:19	SSELTQDPAVSVALGQTVRVTCQGDLSRSYYA SWYQQKPGQAPVLVIYGKNNRPSGIPDRFSGSS GNRPSGIPNRFSGSSSGNASLTITGAQAEDAD YYCSSRDSSGNHWVFVGGGTELTVLG
	VH	SEQ ID NO:20	QVQLQQSGAEVKKPGSSVRVSKASGGTFNN NAINWVRQAPGQGLEWMGGIIPMFGTAKYSE NFQGRVAITADESTGTASMESSLRSEDVAVY YCARSRDLLFPFHALSPWGRGTMVTVSS

[0098] Several of the antibodies described in this section have been subject to mutational analysis to improve their biological properties. Such mutant antibodies having desirable properties can be modified to incorporate the variant CH2 domains and Fc regions of the disclosure. US 2010/0266613 A1, for example, discloses variant V<sub>L</sub> and V<sub>H</sub> sequences of the anti-TNF $\alpha$  antibody adalimumab. The variant CH2 domains and Fc regions of the disclosure can be incorporated into any of the variant anti-TNF $\alpha$  antibodies disclosed in US 2010/0266613 A1, which is incorporated by reference herein in its entirety. In some embodiments, the variant anti-TNF $\alpha$  antibody comprises one or more of the substitutions in Table 5 of US 2010/0266613, *i.e.*, A25W, Q27R, Q27T, I29V, R30Q, and L33E in the V<sub>L</sub> chain. In other embodiments, the variant anti-TNF $\alpha$  antibody comprises a combination of substitutions from Table 10 of US 2010/0266613, *i.e.*, 129T/A34G, N31T/A34G, R30Q/A34S, R30Q, Q27G/A34G, Q27H/A34S, Q27R/A34S, G28S/A34S, N31T/A34S, or N31S/A34S in the V<sub>L</sub> chain, most preferably G28S/A34S. The stretch of amino acids spanning A25 through A34 is in bold, underlined font in Table 2 above.

[0099] In some embodiments, antibodies against infectious diseases are used. Antibodies against eukaryotic cells include antibodies targeting yeast cells, including but not limited to *Saccharomyces cerevisiae*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia*

*guillerimondii* and *P. pastoris*, *Schizosaccharomyces pombe*, *plasmodium falciparum*, and *Yarrowia lipolytica*.

**[0100]** Antibodies against additional fungal cells are also useful, including target antigens associated with *Candida* strains including *Candida glabrata*, *Candida albicans*, *C. krusei*, *C. lusitanae* and *C. maltosa*, as well as species of *Aspergillus*, *Cryptococcus*, *Histoplasma*, *Coccidioides*, *Blastomyces*, and *Penicillium*, among others.

**[0101]** Antibodies directed against target antigens associated with protozoa include, but are not limited to, antibodies associated with *Trypanosoma*, *Leishmania* species including *Leishmania donovani*; *Plasmodium* spp., *Pneumocystis carinii*, *Cryptosporidium parvum*, *Giardia lamblia*, *Entamoeba histolytica*, and *Cyclospora cayetanensis*.

**[0102]** Antibodies against prokaryotic antigens are also useful, including antibodies against suitable bacteria such as pathogenic and non-pathogenic prokaryotes including but not limited to *Bacillus*, including *Bacillus anthracis*; *Vibrio*, e.g. *V. cholerae*; *Escherichia*, e.g. Enterotoxigenic *E. coli*, *Shigella*, e.g. *S. dysenteriae*; *Salmonella*, e.g. *S. typhi*; *Mycobacterium* e.g. *M. tuberculosis*, *M. leprae*; *Clostridium*, e.g. *C. botulinum*, *C. tetani*, *C. difficile*, *C. perfringens*; *Corynebacterium*, e.g. *C. diphtheriae*; *Streptococcus*, *S. pyogenes*, *S. pneumoniae*; *Staphylococcus*, e.g. *S. aureus*; *Haemophilus*, e.g. *H. influenzae*; *Neisseria*, e.g. *N. meningitidis*, *N. gonorrhoeae*; *Yersinia*, e.g. *Y. lamblia*, *Y. pestis*, *Pseudomonas*, e.g. *P. aeruginosa*, *P. putida*; *Chlamydia*, e.g. *C. trachomatis*; *Bordetella*, e.g. *B. pertussis*; *Treponema*, e.g. *T. palladium*; *B. anthracis*, *Y. pestis*, *Brucella* spp., *F. tularensis*, *B. mallei*, *B. pseudomallei*, *B. mallei*, *B. pseudomallei*, *C. botulinum*, *Salmonella* spp., SEB *V. cholerae* toxin B, *E. coli* O157:H7, *Listeria* spp., *Trichosporon beigeli*, *Rhodotorula* species, *Hansenula anomala*, *Enterobacter* sp., *Klebsiella* sp., *Listeria* sp., *Mycoplasma* sp. and the like.

**[0103]** In some aspects, the antibodies are directed against viral infections; these viruses include, but are not limited to, including orthomyxoviruses, (e.g. influenza virus), paramyxoviruses (e.g. respiratory syncytial virus, mumps virus, measles virus), adenoviruses, rhinoviruses, coronaviruses, reoviruses, togaviruses (e.g. rubella virus), parvoviruses, poxviruses (e.g. variola virus, vaccinia virus), enteroviruses (e.g. poliovirus, coxsackievirus), hepatitis viruses (including A, B and C), herpesviruses (e.g. Herpes simplex virus, varicella-zoster virus, cytomegalovirus, Epstein-Barr virus), rotaviruses, Norwalk viruses, hantavirus, arenavirus, rhabdovirus (e.g. rabies virus), retroviruses

(including HIV, HTLV-I and -II), papovaviruses (e.g. papillomavirus), polyomaviruses, and picornaviruses, and the like.

### 6.3. Fc Fusion Proteins

[0104] In one embodiment, the polypeptides of the invention are Fc fusion proteins. Fc-based fusion proteins are typically composed of an immunoglobulin Fc domain that is directly linked to another peptide. As explained by Czajkowsky et al., 2012, *EMBO Mol Med* 4:1015–1028, the fusion partner can be any other proteinaceous molecule of interest, such as a ligand that activates upon interaction with a cell-surface receptor, a peptidic antigen (Ag) against a challenging pathogen or a ‘bait’ protein to identify binding partners assembled in a protein microarray. Most frequently, an Fc domain is fused to a polypeptide with therapeutic potential to endow the fusion with a number of additional beneficial biological and pharmacological properties. The presence of an Fc domain can markedly increase a protein’s plasma half life, which prolongs its therapeutic activity owing to its interaction with the salvage neonatal Fc-receptor (FcRn; Roopenian & Akilesh, 2007, *Nat Rev Immunol* 7: 715-725), as well as to the slower renal clearance for larger sized molecules (Kontermann, 2011, *Curr Opin Biotechnol* 22: 868-876). The attached Fc domain also enables these molecules to interact with Fc-receptors (FcRs) found on immune cells (Nimmerjahn & Ravetch, 2008, *Nat Rev Immunol* 8: 34-47).

[0105] Accordingly, an Fc fusion combines the Fc region of an antibody, and thus its favorable effector functions and pharmacokinetics, with the target-binding region of a receptor, ligand, or some other protein or protein domain. The role of the latter is to mediate target recognition, and thus it is functionally analogous to the antibody variable region. Because of the structural and functional overlap of Fc fusions with antibodies, the discussion on antibodies in the present disclosure extends to Fc fusions unless indicated otherwise.

[0106] In exemplary embodiments, the Fc fusion partner is the extracellular domain (“ECD”) of TNF receptor II; the first ECD of lymphocyte function-associated antigen 3 (LFA-3); the ECD of human cytotoxic T lymphocyte associated molecule-4 (CTLA-4); the C-terminus of the IL-1R accessory protein ligand binding region fused to the N-terminus of the IL-1RI ECD; peptide thrombopoietin (TPO) mimetic; ECD of CTLA-4 with the two amino acid substitutions L104E and A29Y; or ECDs of VEGF receptors 1 and 2.

[0107] An Fc fusion protein of the disclosure, comprising the variant Fc domains described herein, can be based on a known “parent” Fc fusion, such as the approved biologics described in Table 3.

<b>Table 3</b>			
<b>International non-proprietary (trade) name</b>	<b>Description</b>	<b>Mode of action</b>	<b>Year &amp; Indication of first US approval</b>
Etanercept (Enbrel®)	75 kDa soluble extracellular domain (ECD) of tumor necrosis factor (TNF) receptor II fused to human IgG1 Fc	Binds membrane-bound and soluble forms of TNF, thereby reducing concentrations of inflammatory cytokines	1998 Rheumatoid arthritis
Alefacept (Amevive®)	First ECD of lymphocyte function-associated antigen 3 (LFA-3) fused to human IgG1 Fc	Binds CD2; blocks the interactions between LFA on APCs with CD2 on T cells, thereby inhibiting T-cell activation	2003 Plaque psoriasis
Abatacept (Orencia®)	ECD of human cytotoxic T lymphocyte associated molecule-4 (CTLA-4) fused to human IgG1 Fc	Blocks the interactions between CD80 or CD86 on APCs and CD28 on T cells, thereby inhibiting T-cell activation	2005 Rheumatoid arthritis
Rilonacept (Arcalyst®)	Two chains, each comprising the C-terminus of the IL-1R accessory protein ligand binding region fused to the N-terminus of the IL-1RI ECD, fused to human IgG1 Fc	Binds IL-1, thereby preventing interaction with endogenous cell-surface receptors	2008 Plaque psoriasis
Romiplostim (Nplate®)	Peptide thrombopoietin (TPO) mimetic fused to the C-terminus of aglycosylated human IgG1 Fc; produced in <i>E. Coli</i>	Binds and agonizes the TPO receptor; Fc functionality minimized due to lack of glycosylation	2008 Thrombocytopenia
Belatacept (Nulojix®)	ECD of CTLA-4 fused to human IgG1 Fc; differs from abatacept by two amino acid substitutions (L104E, A29Y) in the CTLA-4 region	Blocks the interactions between CD80 or CD86 on APCs and CD28 on T cells, thereby inhibiting T-cell activation	2011 Prophylaxis of organ rejection in adult kidney transplant recipients
Aflibercept (Eylea™)	ECDs of VEGF receptors 1 and 2 fused to human IgG1 Fc	Binds all forms of VEGF-A, as well as placental growth factor, thereby inhibiting angiogenesis	2011 Wet age-related macular degeneration

**[0108]** In some embodiments, the parent Fc fusion and the Fc fusion of the disclosure can share similar or identical sequences except for modifications to the Fc domain as disclosed herein.

**[0109]** Fc fusion proteins can also contain just a variant CH2 domain instead of a whole Fc region. Fusion proteins containing a variant CH2 domain can be used, for example, as a dimerization domain

and/or to direct the fusion polypeptide to FC $\gamma$ IIB. In one embodiment, the fusion partner is another Fc domain, such as an IgE Fc domain, creating a “tandem” Fc polypeptide. An IgG-IgE fusion polypeptide was shown to binds Fc $\epsilon$ R and Fc $\gamma$ RIIB and shut down mast cell degranulation. See Cermerski *et al.*, 2012, *Immunol. Lett.* 143:34-43

#### **6.4. Nucleic Acids and Expression Systems**

[0110] The present disclosure encompasses nucleic acid molecules and host cells encoding the Fc variant polypeptides of the disclosure.

[0111] A variant antibody of the disclosure that is an antibody can be prepared by recombinant expression of immunoglobulin light and heavy chain genes in a host cell. For example, to express an antibody recombinantly, a host cell is transfected with one or more recombinant expression vectors carrying DNA fragments encoding the immunoglobulin light and heavy chains of the antibody such that the light and heavy chains are expressed in the host cell and, optionally, secreted into the medium in which the host cells are cultured, from which medium the antibodies can be recovered. Standard recombinant DNA methodologies are used to obtain antibody heavy and light chain genes, incorporate these genes into recombinant expression vectors and introduce the vectors into host cells, such as those described in *Molecular Cloning; A Laboratory Manual*, Second Edition (Sambrook, Fritsch and Maniatis (eds), Cold Spring Harbor, N. Y., 1989), *Current Protocols in Molecular Biology* (Ausubel, F.M. *et al.*, eds., Greene Publishing Associates, 1989) and in U.S. Patent No. 4,816,397.

[0112] In one embodiment, the Fc variant polypeptides are similar to their wild-type equivalents but for changes in their Fc domains. To generate nucleic acids encoding such Fc variant polypeptides, a DNA fragment encoding the Fc domain or a portion of the Fc domain of the wild-type antibody (referred to as the “wild-type Fc domain”) can be synthesized and used as a template for mutagenesis to generate a polypeptide as described herein using routine mutagenesis techniques; alternatively, a DNA fragment encoding the polypeptide can be directly synthesized.

[0113] Once DNA fragments encoding wild-type Fc domains are obtained, these DNA fragments can be further manipulated by standard recombinant DNA techniques, for example, to convert the constant region genes to full-length antibody chain genes. In these manipulations, a CH-encoding DNA fragment is operatively linked to another DNA fragment encoding another protein, such as an antibody variable region or a flexible linker. The term “operatively linked,” as used in this context, is

intended to mean that the two DNA fragments are joined such that the amino acid sequences encoded by the two DNA fragments remain in-frame.

[0114] To express the Fc variant polypeptides of the disclosure, DNAs encoding partial or full-length light and heavy chains, obtained as described above, are inserted into expression vectors such that the genes are operatively linked to transcriptional and translational control sequences. In this context, the term “operatively linked” is intended to mean that a polypeptide gene is ligated into a vector such that transcriptional and translational control sequences within the vector serve their intended function of regulating the transcription and translation of the polypeptide gene. The expression vector and expression control sequences are chosen to be compatible with the expression host cell used. A variant antibody light chain gene and the antibody heavy chain gene can be inserted into separate vectors or, more typically, both genes are inserted into the same expression vector.

[0115] The polypeptide genes are inserted into the expression vector by standard methods (*e.g.*, ligation of complementary restriction sites on the polypeptide gene fragment and vector, or blunt end ligation if no restriction sites are present). Prior to insertion of the variant Fc domain sequences, the expression vector can already carry antibody variable region sequences. Additionally or alternatively, the recombinant expression vector can encode a signal peptide that facilitates secretion of the antibody chain from a host cell. The antibody chain gene can be cloned into the vector such that the signal peptide is linked in-frame to the amino terminus of the antibody chain gene. The signal peptide can be an immunoglobulin signal peptide or a heterologous signal peptide (*i.e.*, a signal peptide from a non-immunoglobulin protein).

[0116] In addition to the antibody chain genes, the recombinant expression vectors of the disclosure carry regulatory sequences that control the expression of the antibody chain genes in a host cell. The term “regulatory sequence” is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals) that control the transcription or translation of the antibody chain genes. Such regulatory sequences are described, for example, in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185 (Academic Press, San Diego, CA, 1990). It will be appreciated by those skilled in the art that the design of the expression vector, including the selection of regulatory sequences may depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, *etc.* Suitable regulatory sequences for mammalian host cell expression include viral elements that direct high levels of protein expression in mammalian cells, such as promoters and/or enhancers derived from cytomegalovirus (CMV) (such as the CMV

promoter/enhancer), Simian Virus 40 (SV40) (such as the SV40 promoter/enhancer), adenovirus, (*e.g.*, the adenovirus major late promoter (AdMLP)) and polyoma. For further description of viral regulatory elements, and sequences thereof, see, *e.g.*, U.S. Patent No. 5,168,062 by Stinski, U.S. Patent No. 4,510,245 by Bell *et al.*, and U.S. Patent No. 4,968,615 by Schaffner *et al.*

**[0117]** In addition to the antibody chain genes and regulatory sequences, the recombinant expression vectors of the disclosure can carry additional sequences, such as sequences that regulate replication of the vector in host cells (*e.g.*, origins of replication) and selectable marker genes. The selectable marker gene facilitates selection of host cells into which the vector has been introduced (*See, e.g.*, U.S. Patents Nos. 4,399,216, 4,634,665 and 5,179,017, all by Axel *et al.*). For example, typically the selectable marker gene confers resistance to drugs, such as G418, puromycin, blasticidin, hygromycin or methotrexate, on a host cell into which the vector has been introduced. Suitable selectable marker genes include the dihydrofolate reductase (DHFR) gene (for use in DHFR<sup>-</sup> host cells with methotrexate selection/amplification) and the neo gene (for G418 selection). For expression of the light and heavy chains, the expression vector(s) encoding the heavy and light chains is transfected into a host cell by standard techniques. The various forms of the term “transfection” are intended to encompass a wide variety of techniques commonly used for the introduction of exogenous DNA into a prokaryotic or eukaryotic host cell, *e.g.*, electroporation, lipofection, calcium-phosphate precipitation, DEAE- dextran transfection and the like.

**[0118]** It is possible to express the polypeptides of the disclosure in either prokaryotic or eukaryotic host cells. In certain embodiments, expression of polypeptides is performed in eukaryotic cells, *e.g.*, mammalian host cells, for optimal secretion of a properly folded and immunologically active polypeptide. Exemplary mammalian host cells for expressing the recombinant polypeptides of the disclosure include Chinese Hamster Ovary (CHO cells) (including DHFR<sup>-</sup> CHO cells, described in Urlaub and Chasin, 1980, *Proc. Natl. Acad. Sci. USA* 77:4216-4220, used with a DHFR selectable marker, *e.g.*, as described in Kaufman and Sharp, 1982, *Mol. Biol.* 159:601-621), NS0 myeloma cells, COS cells, 293 cells and SP2/0 cells. When recombinant expression vectors encoding polypeptide genes are introduced into mammalian host cells, the polypeptides are produced by culturing the host cells for a period of time sufficient to allow for expression of the polypeptide in the host cells or secretion of the polypeptide into the culture medium in which the host cells are grown. Polypeptides can be recovered from the culture medium using standard protein purification methods. Host cells

can also be used to produce portions of intact polypeptides, such as Fab fragments or scFv molecules. It is understood that variations on the above procedure are within the scope of the present disclosure.

[0119] Recombinant DNA technology can also be used to remove some or all of the DNA encoding either or both of the light and heavy chains that is not necessary for binding to antigen. The molecules expressed from such truncated DNA molecules are also encompassed by the polypeptides of the disclosure.

[0120] In some embodiments, polypeptides of the disclosure can be bifunctional antibodies. Such antibodies, in which one heavy and one light chain are specific for one antigen and the other heavy and light chain are specific for a second antigen, can be produced by crosslinking an antibody of the disclosure to a second antibody by standard chemical crosslinking methods. Bifunctional antibodies can also be made by expressing a nucleic acid engineered to encode a bifunctional antibody.

[0121] In certain embodiments, dual specific antibodies, *i.e.* antibodies that bind one antigen and a second, unrelated antigen using the same binding site, can be produced by mutating amino acid residues in the light chain and/or heavy chain CDRs. Exemplary second antigens include a proinflammatory cytokine (such as, for example, lymphotoxin, interferon- $\gamma$ , or interleukin-1). Dual specific polypeptides can be produced, *e.g.*, by mutating amino acid residues in the periphery of the antigen binding site (*See, e.g., Bostrom et al., 2009, Science 323:1610-1614*). Dual functional polypeptides can be made by expressing a nucleic acid engineered to encode a dual specific polypeptide.

[0122] Polypeptides of the disclosure can also be produced by chemical synthesis (*e.g.*, by the methods described in *Solid Phase Peptide Synthesis*, 2<sup>nd</sup> ed., 1984 The Pierce Chemical Co., Rockford, Ill.). Polypeptides can also be generated using a cell-free platform (*see, e.g., Chu et al., Biochemia No. 2, 2001 (Roche Molecular Biologicals)*).

[0123] Methods for recombinant expression of Fc fusion proteins are described in Flanagan *et al., Methods in Molecular Biology*, vol. 378: Monoclonal Antibodies: Methods and Protocols.

[0124] Once a polypeptide of the disclosure has been produced by recombinant expression, it can be purified by any method known in the art for purification of an immunoglobulin molecule, for example, by chromatography (*e.g.*, ion exchange, affinity, particularly by affinity for antigen after Protein A or Protein G selection, and sizing column chromatography), centrifugation, differential solubility, or by any other standard technique for the purification of proteins. Further, the



polypeptides of the present disclosure or fragments thereof can be fused to heterologous polypeptide sequences described herein or otherwise known in the art to facilitate purification.

[0125] Once isolated, a polypeptide can, if desired, be further purified, *e.g.*, by high performance liquid chromatography (See, *e.g.*, Fisher, *Laboratory Techniques In Biochemistry And Molecular Biology* (Work and Burdon, eds., Elsevier, 1980)), or by gel filtration chromatography on a Superdex™ 75 column (Pharmacia Biotech AB, Uppsala, Sweden).

#### **6.5. Biological Activity of Fc Variant Polypeptides**

[0126] Due to the incorporation of amino acid substitutions in the Fc region that impact binding to FcγRIIIA and/or FcγRIIB, the polypeptides of the disclosure display modified biological activity, *e.g.*, modified effector function and/or binding to FcγRIIIA and/or FcγRIIB.

[0127] In one embodiment, the effector function is ADCC. Accordingly, the disclosure provides variant Fc polypeptide that are characterized by exhibiting ADCC that is reduced by at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70% or even more as compared to a non-variant Fc polypeptide, *i.e.*, a polypeptide that is identical but for the substitution(s) that increase binding to FcγRIIB and/or decrease binding to FcγRIIIA, for example one or more of the substitutions V263L, V266L, V273C, V273E, V273F, V273L, V273M, V273S, V273Y, V305K, and V305W.

[0128] In certain embodiments, the reduction in ADCC is measured in an *in vitro* assay at a polypeptide concentration of 1 μg/mL or 2 μg/mL or more (*e.g.*, 3 μg/mL, 4 μg/mL or 5 μg/mL) using an effector to target cell ratio of, for example, 25:1, 40:1, 50:1 or 60:1, for example when using PBMC effector cells from 3 or more, 6 or more, 10 or more, or 50 or more healthy donors. ADCC activity can be measured by flow cytometry, as described in Example 9, or by measuring <sup>51</sup>Chromium release, as described in Example 10. The target cell utilized in an ADCC assay will depend on the binding specificity of the variant polypeptide, and can be readily determined by one of skill in the art. For example, as described in Example 9, Raji cells are suitable target cells for assaying ADCC activity of antibody Hu1D10 (and Fc variants thereof) and, as described in Example 10, Lymphoma RL cells are suitable target cells for assaying ADCC activity of an anti-CD40 antibody (and Fc variants thereof).

[0129] In another embodiment, the effector function is immune activation of a target cell by a cross-linking Fc polypeptide. For example in one assay, the target cell is a dendritic cell and the cross-linking Fc polypeptide is an anti-CD40 antibody. Typically, binding of an Fc region to FcγRIIB

provides a negative signal to Fc $\gamma$ RIIB positive cells via the receptor's ITAM motif. However, binding of an Fc region of an anti-CD40 antibody to Fc $\gamma$ RIIB on the surface of dendritic cells improves crosslinking of CD40, resulting in increased IL-12 production by the dendritic cells. Increasing affinity to Fc $\gamma$ RIIB therefore results in higher IL-12 secretion. Accordingly, the disclosure provides variant Fc polypeptide whose Fc region increases IL-12 secretion in dendritic cells when grafted onto a CD40 antibody. In various embodiments, the Fc region can activate dendritic cells by at least about 10%, at least about 15%, at least about 20%, at least about 25%, at least 30% , at least about 35%, at least about 40%, or even more as compared to a non-variant anti-CD40 antibody, *i.e.*, an anti-CD40 antibody that is identical but for the substitution(s) that increase binding to Fc $\gamma$ RIIB and optionally also decrease binding to Fc $\gamma$ RIIIA, for example one or more of the substitutions V263L, V266L, V273C, V273E, V273F, V273L, V273M, V273S, V273Y, V305K, and V305W.

**[0130]** In certain embodiments, the immune activation of dendritic cells is measured in an IL-12p70 secretion assay. Briefly, monocyte-derived immature dendritic cells ("moDC") can be stimulated with a polypeptide of the disclosure and primed with IFN $\gamma$ , and the resulting amount of IL-12p70 produced assayed, for example by ELISA. In an exemplary embodiment, the IL-12p70 secretion assay is performed as described in Example 11 below.

**[0131]** In yet other embodiment, a variant polypeptide of the disclosure displays increased binding to Fc $\gamma$ RIIB and/or reduced binding to Fc $\gamma$ RIIIA. Exemplary binding assays are described in Examples 7 and 8. In certain embodiments, the binding of a variant polypeptide to Fc $\gamma$ RIIB is at least about 10%, at least about 20%, by at least about 30%, at least about 40%, or at least about 50% greater than the binding to Fc $\gamma$ RIIB of a non-variant Fc polypeptide, *e.g.*, a polypeptide that is identical but for the one or more of the substitutions of V263L, V266L, V273C, V273E, V273F, V273L, V273M, V273S, V273Y, V305K, and V305W. In further embodiments, the binding of a variant polypeptide to Fc $\gamma$ RIIIA is at least about 10%, at least about 20%, by at least about 30%, at least about 40%, or at least about 50% less than the binding to Fc $\gamma$ RIIIA of a non-variant Fc polypeptide, *e.g.*, a polypeptide that is identical but for the one or more of the substitutions of V263L, V266L, V273C, V273E, V273F, V273L, V273M, V273S, V273Y, V305K, and V305W.

#### **6.6. Polypeptide Conjugates**

**[0132]** The polypeptides of the disclosure include polypeptide conjugates that are modified, *e.g.*, by the covalent attachment of any type of molecule to the polypeptide, such that covalent attachment does not interfere with binding to antigen.

[0133] In certain aspects, a polypeptide of the disclosure can be conjugated to an effector moiety or a label. The term “effector moiety” as used herein includes, for example, antineoplastic agents, drugs, toxins, biologically active proteins, for example enzymes, antibody or antibody fragments, synthetic or naturally occurring polymers, nucleic acids (*e.g.*, DNA and RNA), radionuclides, particularly radioiodide, radioisotopes, chelated metals, nanoparticles and reporter groups such as fluorescent compounds or compounds which can be detected by NMR or ESR spectroscopy.

[0134] In one example, polypeptides can be conjugated to an effector moiety, such as a cytotoxic agent, a radionuclide or drug moiety to modify a given biological response. The effector moiety can be a protein or polypeptide, such as, for example and without limitation, a toxin (such as abrin, ricin A, *Pseudomonas* exotoxin, or *Diphtheria* toxin), a signaling molecule (such as  $\alpha$ -interferon,  $\beta$ -interferon, nerve growth factor, platelet derived growth factor or tissue plasminogen activator), a thrombotic agent or an anti-angiogenic agent (*e.g.*, angiostatin or endostatin) or a biological response modifier such as a cytokine or growth factor (*e.g.*, interleukin-1 (IL-1), interleukin-2 (IL-2), interleukin-6 (IL-6), granulocyte macrophage colony stimulating factor (GM-CSF), granulocyte colony stimulating factor (G-CSF), or nerve growth factor (NGF)).

[0135] In another example the effector moieties can be cytotoxins or cytotoxic agents. Examples of cytotoxins and cytotoxic agents include taxol, cytochalasin B, gramicidin D, ethidium bromide, emetine, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicin, doxorubicin, daunorubicin, dihydroxy anthracin dione, mitoxantrone, mithramycin, actinomycin D, 1-dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and puromycin and analogs or homologs thereof.

[0136] Effector moieties also include, but are not limited to, antimetabolites (*e.g.* methotrexate, 6-mercaptopurine, 6-thioguanine, cytarabine, 5-fluorouracil decarbazine), alkylating agents (*e.g.*, mechlorethamine, thioepa chlorambucil, melphalan, carmustine (BSNU) and lomustine (CCNU), cyclophosphamide, busulfan, dibromomannitol, streptozotocin, mitomycin C5 and cis-dichlorodiamine platinum (II) (DDP) cisplatin), anthracyclines (*e.g.*, daunorubicin (formerly daunomycin) and doxorubicin), antibiotics (*e.g.*, dactinomycin (formerly actinomycin), bleomycin, mithramycin, anthramycin (AMC), calicheamicins or duocarmycins), and anti-mitotic agents (*e.g.*, vincristine and vinblastine).

[0137] Other effector moieties can include radionuclides such as, but not limited to,  $^{111}\text{In}$  and  $^{90}\text{Y}$ ,  $\text{Lu}^{177}$ , Bismuth $^{213}$ , Californium $^{252}$ , Iridium $^{192}$  and Tungsten $^{188}$ /Rhenium $^{188}$  and drugs such as, but not limited to, alkylphosphocholines, topoisomerase I inhibitors, taxoids and suramin.

[0138] Techniques for conjugating such effector moieties to polypeptides are well known in the art (See, *e.g.*, Hellstrom *et al.*, *Controlled Drug Delivery*, 2nd Ed., at pp. 623-53 (Robinson *et al.*, eds., 1987)); Thorpe *et al.*, 1982, *Immunol. Rev.* 62:119-58 and Dubowchik *et al.*, 1999, *Pharmacology and Therapeutics* 83:67-123).

[0139] In one example, the polypeptide is fused via a covalent bond (*e.g.*, a peptide bond), through the polypeptide's N-terminus or the C-terminus or internally, to an amino acid sequence of another protein (or portion thereof; for example, at least a 10, 20 or 50 amino acid portion of the protein). The polypeptide can be linked to the other protein at the N-terminus of the Fc domain of the polypeptide. Recombinant DNA procedures can be used to create such fusions, for example as described in WO 86/01533 and EP0392745. In another example the effector molecule can increase half life *in vivo*, and/or enhance the delivery of a polypeptide across an epithelial barrier to the immune system. Examples of suitable effector molecules of this type include polymers, albumin, albumin binding proteins or albumin binding compounds such as those described in WO 2005/117984.

[0140] In certain aspects, a polypeptide is conjugated to a small molecule toxin. In certain exemplary embodiments, a polypeptide of the disclosure is conjugated to a dolastatin or a dolostatin peptidic analogs or derivatives, *e.g.*, an auristatin (U.S. Pat. Nos. 5,635,483 and 5,780,588). The dolastatin or auristatin drug moiety may be attached to the polypeptide through its N (amino) terminus, C (carboxyl) terminus or internally (WO 02/088172). Exemplary auristatin embodiments include the N-terminus linked monomethylauristatin drug moieties DE and DF, as disclosed in U.S. Patent No. 7,498,298, which is hereby incorporated by reference in its entirety (disclosing, *e.g.*, linkers and methods of preparing monomethylvaline compounds such as MMAE and MMAF conjugated to linkers).

[0141] In other exemplary embodiments, small molecule toxins include but are not limited to calicheamicin, maytansine (U.S. Pat. No. 5,208,020), trichothene, and CC1065. In one embodiment of the disclosure, the polypeptide is conjugated to one or more maytansine molecules (*e.g.*, about 1 to about 10 maytansine molecules per polypeptide molecule). Maytansine may, for example, be converted to May-SS-Me which may be reduced to May-SH3 and reacted with a polypeptide (Chari *et al.*, 1992, *Cancer Research* 52: 127-131) to generate a maytansinoid- polypeptide or maytansinoid-

Fc fusion conjugate. Structural analogues of calicheamicin that can also be used include but are not limited to  $\gamma_1^1$ ,  $\gamma_3^1$ ,  $\gamma_3^1$  N-acetyl-  $\gamma_1^1$ , PSAG, and  $\theta_1^1$ , (Hinman *et al.*, 1993, *Cancer Research* 53:3336-3342; Lode *et al.*, 1998, *Cancer Research* 58:2925-2928; U.S. Patent No. 5,714,586; U.S. Patent No. 5,712,374; U.S. Patent No. 5,264,586; U.S. Patent No. 5,773,001).

[0142] Polypeptides of the disclosure can also be conjugated to liposomes for targeted delivery (See, *e.g.*, Park *et al.*, 1997, *Adv. Pharmacol.* 40:399–435; Marty & Schwendener, 2004, *Methods in Molecular Medicine* 109:389-401).

[0143] In one example polypeptides of the present disclosure can be attached to poly(ethyleneglycol) (PEG) moieties. In one particular example the polypeptide is an antibody fragment and the PEG moieties can be attached through any available amino acid side-chain or terminal amino acid functional group located in the antibody fragment, for example any free amino, imino, thiol, hydroxyl or carboxyl group. Such amino acids can occur naturally in the antibody fragment or can be engineered into the fragment using recombinant DNA methods. See, for example, U.S. Patent No. 5,219,996. Multiple sites can be used to attach two or more PEG molecules. PEG moieties can be covalently linked through a thiol group of at least one cysteine residue located in the antibody fragment. Where a thiol group is used as the point of attachment, appropriately activated effector moieties (for example, thiol selective derivatives such as maleimides and cysteine derivatives) can be used.

[0144] The word “label” when used herein refers to a detectable compound or composition which can be conjugated directly or indirectly to a polypeptide of the disclosure. The label can itself be detectable (*e.g.*, radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, can catalyze chemical alteration of a substrate compound or composition which is detectable. Useful fluorescent moieties include, but are not limited to, fluorescein, fluorescein isothiocyanate, rhodamine, 5- dimethylamine-1-naphthalenesulfonyl chloride, phycoerythrin and the like. Useful enzymatic labels include, but are not limited to, alkaline phosphatase, horseradish peroxidase, glucose oxidase and the like.

#### **6.7. Pharmaceutical Compositions and Therapeutic Methods**

[0145] Due to their low ADCC activity, polypeptides of the disclosure are particularly useful in the context of immune diseases and disorders, including autoimmune diseases, where cell killing may not be desirable. Examples of such diseases and disorders include Addison’s disease, autoimmune diseases of the ear, autoimmune diseases of the eye such as uveitis, autoimmune hepatitis, Crohn’s

disease, diabetes (Type I), epididymitis, glomerulonephritis, Graves' disease, Guillain-Barre syndrome, Hashimoto's disease, hemolytic anemia, systemic lupus erythematosus (SLE), multiple sclerosis, myasthenia gravis, pemphigus vulgaris, psoriasis, rheumatoid arthritis, sarcoidosis, scleroderma, psoriasis, Sjogren's syndrome, spondyloarthropathies, thyroiditis, ulcerative colitis and/or vasculitis. However, the polypeptides of the disclosure can also be used to treat indications where cell killing is desirable, *e.g.*, oncology indications, particularly when the polypeptide is capable of signaling through the target molecule and/or when conjugated to an effector moiety. The specific indication or indications that are suitable for treatment using an Fc variant polypeptide will depend on the sequence and/or properties of the non-Fc or portion of the Fc variant polypeptide, and can be readily determined by a person of ordinary skill in the art. Exemplary embodiments are set forth below.

**[0146]** In one embodiment, a variant polypeptide of the disclosure is an anti-CD40 antibody and is used to treat a CD40-expressing cancer, such as chronic lymphocytic leukemia, Burkitt's lymphoma, multiple myeloma, a T cell lymphoma, Non-Hodgkin's Lymphoma, Hodgkin's Disease, Waldenstrom's macroglobulinemia, Kaposi's sarcoma, ovarian cancer, breast cancer, lung cancer, melanoma, pancreatic cancer, or renal cancer. The anti-CD40 antibody can be a multi-specific antibody.

**[0147]** In another embodiment, a variant polypeptide of the disclosure is an anti-CD20 antibody and is used to treat rheumatoid arthritis or multiple sclerosis.

**[0148]** In another embodiment, a variant polypeptide of the disclosure is an anti-CD25 antibody and is used to treat multiple sclerosis, psoriasis, asthma, uveitis, ocular inflammation or human T cell leukemia virus-1 associated T-cell leukemia or to prevent organ transplant rejection.

**[0149]** In another embodiment, a variant polypeptide of the disclosure is an anti-TNF $\alpha$  antibody and is used to treat rheumatoid arthritis, juvenile idiopathic arthritis, psoriatic arthritis, ankylosing spondylitis, Crohn's disease, ulcerative colitis or plaque psoriasis.

**[0150]** In another embodiment, a variant polypeptide of the disclosure is an anti-IL-6 receptor antibody and is used to treat rheumatoid arthritis or Castleman's Disease.

**[0151]** In another embodiment, a variant polypeptide of the disclosure is an anti- $\alpha$ 4-integrin antibody and is used to treat multiple sclerosis.

[0152] In another embodiment, a variant polypeptide of the disclosure is an anti-IL-1 antibody and is used to treat Cryopyrin-Associated Periodic Syndromes (“CAPS”).

[0153] In another embodiment, a variant polypeptide of the disclosure is an anti-BAFF antibody and is used to treat systemic lupus erythmatosis or allergy.

[0154] The disclosure provides methods of treating any of the foregoing diseases in a patient in need thereof, comprising: administering to the patient an appropriate polypeptide of the disclosure in a therapeutically effective dose.

[0155] As used herein, a “therapeutically effective” amount of a polypeptide can be administered as a single dose or over the course of a therapeutic regimen, *e.g.*, over the course of a week, two weeks, three weeks, one month, three months, six months, one year, or longer.

[0156] The dosage of a polypeptides of the disclosure to be administered of will vary according to the particular antigen specificity, the type of autoimmune or inflammatory disease, the subject, and the nature and severity of the disease, the physical condition of the subject, the therapeutic regimen (*e.g.*, whether a combination therapeutic agent is used), and the selected route of administration; the appropriate dosage can be readily determined by a person skilled in the art.

[0157] For the treatment and/or prophylaxis of autoimmune or inflammatory disease in humans and animals, pharmaceutical compositions comprising polypeptides can be administered to patients (*e.g.*, human subjects) at therapeutically or prophylactically effective dosages (*e.g.*, dosages which result in inhibition of an autoimmune or inflammatory disease and/or relief of autoimmune or inflammatory disease symptoms) using any suitable route of administration, such as injection and other routes of administration known in the art for antibody-based clinical products.

[0158] It will be recognized by one of skill in the art that the optimal quantity and spacing of individual dosages of a polypeptide of the disclosure will be determined by the nature and extent of the condition being treated, the form, route and site of administration, and the age and condition of the particular subject being treated, and that a physician will ultimately determine appropriate dosages to be used. This dosage can be repeated as often as appropriate. If side effects develop the amount and/or frequency of the dosage can be altered or reduced, in accordance with normal clinical practice.

[0159] According to the present disclosure, treatment of a disease encompasses the treatment of patients already diagnosed as having any form of the disease at any clinical stage or manifestation;

the delay of the onset or evolution or aggravation or deterioration of the symptoms or signs of the disease; and/or preventing and/or reducing the severity of the disease.

[0160] A “subject” or “patient” to whom the polypeptide of the disclosure is administered is preferably a mammal such as a non-primate (*e.g.*, cow, pig, horse, cat, dog, rat, *etc.*) or a primate (*e.g.*, monkey or human). In certain embodiments, the subject or patient is a human. In certain aspects, the human is a pediatric patient. In other aspects, the human is an adult patient.

[0161] Compositions comprising a polypeptide of the disclosure are provided herein. The compositions will typically be supplied as part of a sterile, pharmaceutical composition that will normally include a pharmaceutically acceptable carrier. This composition can be in any suitable form (depending upon the desired method of administering it to a patient).

[0162] Pharmaceutical compositions can be conveniently presented in unit dose forms containing a predetermined amount of a polypeptide of the disclosure per dose. Such a unit can contain for example but without limitation 5 mg to 5 g, for example 10 mg to 1 g, or 20 to 50 mg, 40 mg to 100 mg, or 50 mg to 300 mg. Pharmaceutically acceptable carriers for use in the disclosure can take a wide variety of forms depending, *e.g.*, on the condition to be treated or route of administration.

[0163] Therapeutic formulations of the polypeptides of the disclosure can be prepared for storage as lyophilized formulations or aqueous solutions by mixing the polypeptide having the desired degree of purity with optional pharmaceutically-acceptable carriers, excipients or stabilizers typically employed in the art (all of which are referred to herein as “carriers”), *i.e.*, buffering agents, stabilizing agents, preservatives, isotonicifiers, non-ionic detergents, antioxidants, and other miscellaneous additives. See, *Remington's Pharmaceutical Sciences*, 16th edition (Osol, ed. 1980). Such additives must be nontoxic to the recipients at the dosages and concentrations employed.

[0164] Buffering agents help to maintain the pH in the range which approximates physiological conditions. They can be present at concentration ranging from about 2 mM to about 50 mM. Suitable buffering agents for use with the present disclosure include both organic and inorganic acids and salts thereof such as citrate buffers (*e.g.*, monosodium citrate-disodium citrate mixture, citric acid-trisodium citrate mixture, citric acid-monosodium citrate mixture, *etc.*), succinate buffers (*e.g.*, succinic acid-monosodium succinate mixture, succinic acid-sodium hydroxide mixture, succinic acid-disodium succinate mixture, *etc.*), tartrate buffers (*e.g.*, tartaric acid-sodium tartrate mixture, tartaric acid-potassium tartrate mixture, tartaric acid-sodium hydroxide mixture, *etc.*), fumarate buffers (*e.g.*, fumaric acid-monosodium fumarate mixture, fumaric acid-disodium fumarate mixture, monosodium



fumarate-disodium fumarate mixture, *etc.*), gluconate buffers (*e.g.*, gluconic acid-sodium gluconate mixture, gluconic acid-sodium hydroxide mixture, gluconic acid-potassium gluconate mixture, *etc.*), oxalate buffer (*e.g.*, oxalic acid-sodium oxalate mixture, oxalic acid-sodium hydroxide mixture, oxalic acid-potassium oxalate mixture, *etc.*), lactate buffers (*e.g.*, lactic acid-sodium lactate mixture, lactic acid-sodium hydroxide mixture, lactic acid-potassium lactate mixture, *etc.*) and acetate buffers (*e.g.*, acetic acid-sodium acetate mixture, acetic acid-sodium hydroxide mixture, *etc.*). Additionally, phosphate buffers, histidine buffers and trimethylamine salts such as Tris can be used.

**[0165]** Preservatives can be added to retard microbial growth, and can be added in amounts ranging from 0.2%-1% (w/v). Suitable preservatives for use with the present disclosure include phenol, benzyl alcohol, meta-cresol, methyl paraben, propyl paraben, octadecyldimethylbenzyl ammonium chloride, benzalconium halides (*e.g.*, chloride, bromide, and iodide), hexamethonium chloride, and alkyl parabens such as methyl or propyl paraben, catechol, resorcinol, cyclohexanol, and 3-pentanol. Isotonicifiers sometimes known as “stabilizers” can be added to ensure isotonicity of liquid compositions of the present disclosure and include polyhydric sugar alcohols, for example trihydric or higher sugar alcohols, such as glycerin, erythritol, arabitol, xylitol, sorbitol and mannitol. Stabilizers refer to a broad category of excipients which can range in function from a bulking agent to an additive which solubilizes the therapeutic agent or helps to prevent denaturation or adherence to the container wall. Typical stabilizers can be polyhydric sugar alcohols (enumerated above); amino acids such as arginine, lysine, glycine, glutamine, asparagine, histidine, alanine, ornithine, L-leucine, 2-phenylalanine, glutamic acid, threonine, *etc.*, organic sugars or sugar alcohols, such as lactose, trehalose, stachyose, mannitol, sorbitol, xylitol, ribitol, myoinositol, galactitol, glycerol and the like, including cyclitols such as inositol; polyethylene glycol; amino acid polymers; sulfur containing reducing agents, such as urea, glutathione, thiocetic acid, sodium thioglycolate, thioglycerol,  $\alpha$ -monothioglycerol and sodium thio sulfate; low molecular weight polypeptides (*e.g.*, peptides of 10 residues or fewer); proteins such as human serum albumin, bovine serum albumin, gelatin or immunoglobulins; hydrophylic polymers, such as polyvinylpyrrolidone monosaccharides, such as xylose, mannose, fructose, glucose; disaccharides such as lactose, maltose, sucrose and trisaccharides such as raffinose; and polysaccharides such as dextran. Stabilizers can be present in the range from 0.1 to 10,000 weights per part of weight active protein.

**[0166]** Non-ionic surfactants or detergents (also known as “wetting agents”) can be added to help solubilize the therapeutic agent as well as to protect the therapeutic protein against agitation-induced

aggregation, which also permits the formulation to be exposed to shear surface stressed without causing denaturation of the protein. Suitable non-ionic surfactants include polysorbates (20, 80, *etc.*), polyoxamers (184, 188 *etc.*), Pluronic polyols, polyoxyethylene sorbitan monoethers (TWEEN®-20, TWEEN®-80, *etc.*). Nonionic surfactants can be present in a range of about 0.05 mg/mL to about 1.0 mg/mL, for example about 0.07 mg/mL to about 0.2 mg/mL.

[0167] Additional miscellaneous excipients include bulking agents (*e.g.*, starch), chelating agents (*e.g.*, EDTA), antioxidants (*e.g.*, ascorbic acid, methionine, vitamin E), and cosolvents. Further formulations suitable for the polypeptides of the disclosure are disclosed in U.S. Pat. App. No. 2004/0033228 A1, the contents of which are incorporated by reference herein in their entirety.

## 7. EXAMPLES

### **Example 1: Construction of a CH2 Point-by-point (PxP) library**

[0168] Hu1D10, a monoclonal antibody specific for the beta-chain of HLA-DR (Shi *et al.*, 2002, *Leuk Lymphoma*. 43(6):1303-12) was used as a model system. Synthetic VL and VH domains for Hu1D10 were constructed by a commercial gene synthesis supplier (DNA 2.0 Inc., Menlo Park, CA) and cloned into vector pYA206 to create the pYA206-Hu1D10 plasmid. The vector pYA206 is an Epstein-Barr virus derived episomal vector designed for expression and display of antibodies on the surface of mammalian cells.

[0169] 84 amino acid positions in the constant region heavy chain domain 2 (CH2) were targeted for mutagenesis using an NNK randomization approach. The NNK coding scheme was used (in which N = A, C, G, or T and K = G or T) because 1) only 32 codons are required to encode all 20 naturally occurring amino acids, 2) only a single stop codon (TAG) is included in the 32, and 3) the maximum degeneracy (number of different codons encoding a single amino acid) is 3, rather than the maximum 6-fold degeneracy that occurs in the complete 64 codon genetic code.

[0170] 84 different DNA fragments encoding the human Fc $\gamma$  isotype (Fc $\gamma$ ), each with NNK degeneracy at a different CH2 position, were synthesized by a commercial supplier of synthetic genes (DNA 2.0, Menlo Park, CA). The synthetic Fc $\gamma$  genes were digested with Sall and NotI restriction enzymes and subcloned into plasmid pYA206-hu1D10. Ligations were transformed into *E. coli* Top10 cells (Invitrogen, CA) such that at least 10 times more *E. coli* transformants were obtained than the total number of possible codons in that sub-library. The resulting CH2 library was composed of 1680 total different codons at 84 different positions.

**Example 2: Fc $\gamma$ RIIB binding determination**

[0171] A Fluorescence Activated Cell Sorter (FACS) titration was performed to assess binding of Fc $\gamma$ RIIB to unmodified control Fc $\gamma$ . Because of the low-affinity interaction between Fc $\gamma$ RIIB and Fc $\gamma$ , an 8:4:1 complex was used for flow cytometry (FIGURE 3): Five micrograms of Fc $\gamma$ RIIB (R&D Systems, 1875-CD) was pre-incubated with 12.5  $\mu$ g of biotinylated anti-poly histidine (R&D Systems, BAM050), then added to 3.5  $\mu$ g of Streptavidin-APC (Southern Biotech, cat # 7100-11L). This complex was then serially diluted 4-fold and combined with goat anti-human kappa-PE (Southern Biotech, 2060-09). To determine the EC<sub>50</sub> of Fc $\gamma$ R-complex binding, 100  $\mu$ l of complex was added to  $2 \times 10^5$  cells at each concentration and incubated for 1hr. After three washes in a FACS buffer, cells were analyzed by flow cytometry in a FACSCalibur (BD Biosciences). The percent of cells in the double positive quadrant was determined and plotted against Fc $\gamma$ RIIB concentration. The EC<sub>50</sub> was determined to be 3.6  $\mu$ g/mL (FIGURE 4A).

**Example 3: Fc $\gamma$ RIIIA binding determination**

[0172] A FACS titration was performed to assess binding of Fc $\gamma$ RIIIA to Fc $\gamma$ . Because of the low-affinity interaction between Fc $\gamma$ RIIIA and Fc $\gamma$ , a 2:1:1 complex was used for flow cytometry (FIGURE 3). 9  $\mu$ g of Fc $\gamma$ RIIIA (R&D Systems, cat # 4325-FC) was pre-incubated with 15  $\mu$ g of biotinylated anti-poly histidine (R&D Systems, BAM050), then added to 15  $\mu$ g of Streptavidin-APC (Southern Biotech, cat # 7100-11L). This complex was then serially diluted 4-fold and combined with goat anti-human kappa-PE (Southern Biotech, 2060-09). To determine the EC<sub>50</sub> of Fc $\gamma$ R-complex binding, 100  $\mu$ l of complex was added to  $2 \times 10^5$  cells at each concentration and incubated for 1hr. After three washes in a FACS buffer, cells were analyzed by flow cytometry in a FACSCalibur (BD Bioscience). The percent of cells in the double positive quadrant was determined and plotted against Fc $\gamma$ RIIIA concentration. The EC<sub>50</sub> was determined to be 0.17  $\mu$ g/mL (Fig 2B).

**Example 4: Fluorescence activated cell sorting (FACS) of the CH2 library**

[0173] The CH2 library was transfected into 293c18 cells with 0.5  $\mu$ g library plasmid, 100  $\mu$ g pACYC184 carrier plasmid and 250  $\mu$ l lipofectamine; selected using 0.8  $\mu$ g/ml puromycin after 2 days, and cultured for an additional 18 days prior to FACS sorting.

[0174] Cells were co-stained with 1:200 PE-labeled anti-human Kappa-PE antibody (Southern Biotech) and either Fc $\gamma$ RIIIA- or Fc $\gamma$ RIIB-complex (FIGURE 3) at or below 50% maximal binding as determined by titration. A minimum of  $1 \times 10^5$  cells were sorted from three populations – high (H),

medium (M), and low (L) – based on differential binding to the Fc $\gamma$ R. A representative FACS sort result is shown in FIGURE 5. Variants with desired properties were enriched in the H-gate in the Fc $\gamma$ RIIB binding and enriched in L-gate in the Fc $\gamma$ RIIIA binding.

**Example 5: Massively parallel sequencing of the “expressed” and “sorted” populations**

[0175] Plasmids were recovered from the sorted H, M, and L cell populations as described in Example 4, and PCR amplification was performed to prepare short amplicons suitable for massively parallel sequencing. Amplicons were then sequenced using the Genome Sequencer FLX as directed by manufacturer (454 Life Sciences, Branford, CT). Approximately 800,000 individual sequences were determined for each population of the FACS-sorted cells.

[0176] The sequences were examined and the number of times each point mutation was found in the “expressed” and “sorted” population was tabulated. Each amino acid codon was initially identified and tabulated. For amino acids with more than one codon, the occurrence of the different codons for each amino acid were added together to make an overall summary of the behavior of that amino acid variant in each subpopulation. For the 3-way sort of the CH2 library to assess binding to Fc $\gamma$ RIIIA or Fc $\gamma$ RIIB, an Enrichment Ratio (ER) score was assigned for each codon variant. The ER denotes how much more or less frequent the variant is found in the H population compared to its overall frequency. Similarly, Enrichment Ratios can be calculated for each variant in each of the M, and L populations. Higher affinity variants are expected to be enriched in the H population (ER>1) and depleted (ER<1) in the L population. Conversely, lower affinity mutants are expected to be depleted in the H population (ER<1) and enriched in the L population (ER>1). It is possible to identify higher, lower, and neutral affinity variants simply by observing the Enrichment Ratios for the H population.

**Example 6: Identification of Point Mutants With Desired Properties**

[0177] Comprehensive mutagenesis of 84 positions in CH2 identified variants with a significantly increased Fc $\gamma$ RIIB binding and decreased binding to Fc $\gamma$ RIIIA (lower than WT), lower right quadrant in FIGURE 6. In this example, 2 standard deviations above the wild-type average was taken to be significantly increased, and lower than the wild-type average was taken to be decreased.

[0178] Positions and substitutions that were identified as having significantly increased Fc $\gamma$ RIIB binding and decreased binding to Fc $\gamma$ RIIIA are shown in FIGURE 7. Variant human IgG were

expressed with the Hu1D10 binding domain either as soluble IgG1 or surface-expressed on 293c18 cells.

**Example 7: Confirmation of improved binding using single-point (one-point) FACS**

**[0179]** To confirm improved binding to FcγRIIB, one-point FACS analysis was performed comparing variants to parent IgG expressed on 293c18 cells. IgG variant-expressing 293c18 and controls were stained with FcγRIIB complex at the EC50 concentration. 293c18 expressing an Fc variant containing the N297A modification was used as a negative control. S267E, L328F, and the double mutant “SELF” were included as positive controls. Samples were analyzed by flow cytometry in a FACSCalibur device and the result for each variant was plotted against the wild-type, with FcγR binding on the y-axis and IgG expression on the x-axis (FIGURE 8).

**[0180]** To confirm decreased binding to FcγRIIA, one-point FACS analysis was performed comparing variants to parent IgG expressed on 293c18 cells. IgG variant-expressing 293c18 and controls were stained with FcγRIIA complex at the EC50 concentration. 293c18 expressing N297A, S267E, L328F, and the double mutant “SELF” were used as controls. Samples were analyzed by flow cytometry using a FACSCalibur device and the result for each variant was plotted against the WT, with FcγR binding on the y-axis and IgG expression on the x-axis (FIGURE 9). The variants with the most significant downward shift were found to be V263L, V273E, V273F, V273M, V273S, and V273Y.

**Example 8: Binding of variants to FcγR-expressing cells**

**[0181]** Hu1D10 IgG variant antibodies were expressed in soluble form, purified, and then used to assess binding to CHO cells expressing FcγRIIB. IgG variants were serially-diluted 3-fold starting at 20 μg/mL, or 133 nM, then added to  $2 \times 10^5$  cells/test. Anti-human kappa antibody was used to detect variant IgG binding. Samples were analyzed in a FACSCalibur and fluorescence was plotted against IgG concentration. FIGURE 10 confirms that all the variants have a higher maximal binding to FcγRIIB than the wild-type antibody.

**[0182]** Hu1D10 IgG variants were purified and used to assess binding to FcγRIIA CHO transfectants. IgG variants were serially-diluted 3-fold starting at 20ug/mL, or 133nM and then added to  $2 \times 10^5$  cells/test. A secondary stain of anti-human kappa antibody was used to detect variant IgG binding. Samples were analyzed in a FACSCalibur and fluorescence was plotted against IgG

concentration in FIGURE 11. All variants bound equivalently or less well than wild-type Fc-containing antibody to Fc $\gamma$ RIIIA.

**Example 9: FACS-based antibody-dependent cell-mediated cytotoxicity**

[0183] A non-radioactive antibody dependent cell cytotoxicity (ADCC) assay was optimized and used to test Hu1D10 IgG variants. Raji cells, and PBMC purified from freshly-drawn whole blood were used as target and effector cells, respectively, at a 1:40 ratio.

[0184] The Raji cells were washed and resuspended at  $10^6$  cells/mL in PBS, then incubated with a 1:2000 dilution of CFSE (Cell Technology, Inc., part 4002) for 30 minutes. CFSE-loaded Raji cells were then washed and resuspended to  $4 \times 10^5$ /mL in growth medium consisting of RPMI + 10% heat-inactivated FBS. 50  $\mu$ L of cell suspension was added to each well of a V-bottom plate. 50  $\mu$ L of three-fold serially diluted IgG variants was added to each well, starting at 18  $\mu$ g/mL.

[0185] PBMCs were purified from freshly-drawn heparinized blood centrifuged over Ficoll-Paque (GE, 17-1440-02) at 665 RCF for 30 minutes. The PBMC layer was collected and washed three times in PBS + 10% FBS, first wash at 1350 RCF for 15 minutes, second wash at 225 RCF for 10 minutes, and the third wash at 225 RCF for 10 minutes. After the final wash, cells were resuspended in growth media and counted using a Vi-Cell Rx. Cells were centrifuged and resuspended to  $8 \times 10^6$  cells/mL in growth media. 100  $\mu$ L of cell suspension was added to each well of the target/IgG suspension and incubated at 37C for four hours. Cell suspensions were stained with 1:5 dilution of 7AAD (BD Biosciences, catalog number 559925) and incubated for 30 minutes. To determine spontaneous death of target cells, CFSE-loaded Raji cells were incubated with media only (0 mg/mL IgG, no PBMC), then stained with 7AAD. Samples were analyzed in a FACSCalibur.

[0186] FACS data were graphed for each sample with CFSE (FL1) on the x-axis and 7AAD (FL3) in the y-axis. A quadrant was drawn, discriminating target cells (CFSE+) from PBMC (CFSE-), as well as 7AAD-positive from 7AAD-negative cells (FIGURE 12). The number of cells in the upper right quadrant was defined as “dead” and those in lower right quadrant as “live.” Percent cytotoxicity was calculated, subtracting spontaneous death. The percent cytotoxicity was graphed against IgG concentration to determine the EC<sub>50</sub> (FIGURE 13A).

[0187] Hu1D10 variants were grouped based on ADCC activity. FIGURE 13B shows Fc $\gamma$ RIIB up-mutants having some ADCC activity, though lower than wild-type; FIGURE13C shows variants with little to no ADCC activity. FIGURE13D compares the non-ADCC hu1D10 variants to substitutions

that result in decreased binding to FcγRIIIA (S267E, L328F, double mutant “SELF”) according to literature. FIGURE14D shows that V263L, V273E, V273F, V273M, V273S, and V273Y elicited comparable responses to L328F and lower ADCC responses than S267E and SELF.

**Example 10: Antibody Dependent Cell-Mediated Cytotoxicity of Fc Binding Variants of an Anti-CD40 mAb**

[0188] An antibody-dependent cell-mediated cytotoxicity (ADCC) assay was designed according to a standard protocol (Law *et al.*, 2005, *Cancer Res.* 65:8331-8) using an anti-CD40 monoclonal antibody with modifications in Fcγ. Lymphoma RL cells were labeled with <sup>51</sup>Chromium for 1 hour as target cells. PBMC were used as effector cells and were mixed with target at a 50:1 ratio. Anti-CD40 was diluted in series and applied to target/effector cell mixtures. After 4 hours incubation at 37C, 5% CO<sub>2</sub>, 100 μl of culture supernatant was harvested and radioactivity released was monitored by gamma counter. Cultures without antibody were recorded as media treated negative controls, and the maximum <sup>51</sup>Chromium release was achieved by Triton X100 treatment of labeled target cells. The final percent of cytotoxicity was calculated using the formula: ((sample - (target + media))/((target + Triton)- (target + media)))\*100. The Fcγ variants V263L, V273E, V273F, V273M, V273S, and V273Y did not induce ADCC activity (FIGURE 14).

**Example 11: Functional Activity of Anti-CD40 mAb with Fcγ Substitutions**

[0189] To test whether the differential binding to FcγRIIB affects immune activation of dendritic cells, anti-CD40 monoclonal antibodies were constructed with the substitutions in Fcγ and tested in an IL-12p70 secretion assay.

[0190] Whole blood from healthy human donors, diluted with an equal volume of PBS, was added to a Leucosep (Greiner Bio One) tube, containing Ficoll-Paque Plus below the frit (15 mL). The blood was then centrifuged at 1,000g for 15 minutes without brake. PBMC were collected and washed once with PBS, centrifuged at 1,300 rpm for 5 minutes at room temperature, and washed once with RPMI 1640. Cells were re-suspended in SN12C culture medium (RPMI1640+10% heat-inactivated FBS).

[0191] Generation of monocyte-derived immature dendritic cell (moDC): Monocytes were isolated from PBMC with an enrichment kit from StemCell and were cultured in StemSep serum free medium supplemented with 10 ng/ml GM-CSF and 20 ng/ml IL-4 at 37 C, 5% CO<sub>2</sub> for 6 days. Fresh GM-CSF and IL-4 were added to the culture at day 3 to help maintaining DC differentiation. After 6 days

culture, monocyte-derived immature DC were subject to FACS analysis to verify immature DC phenotype: Lin<sup>-</sup>, CD80/CD86<sup>+</sup>, HLA-DR<sup>+</sup>, CD11C<sup>+</sup>.

**[0192]** Monitoring agonistic activity of anti-CD40 in stimulating IL-12p70 from moDC: Immature moDC were stimulated with anti-CD40 and primed with IFN $\gamma$  for 48 hours in StemSep serum free medium supplemented with GM-CSF and IL-4. The culture supernatant was harvest and assayed for IL-12p70 production by a commercially available ELISA kit. FIGURE 15 shows IL-12p70 production of ADCC-inducing (FIGURE 15A) and non-ADCC-inducing (FIGURE 15B) variants. Of the non-ADCC variants, V273F and V273Y showed the most enhanced dendritic cells activation as measured by IL-12p70 secretion (FIGURE 15C).

**[0193]** All publications, patents, patent applications and other documents cited in this application are hereby incorporated by reference in their entirety for all purposes to the same extent as if each individual publication, patent, patent application or other document were individually indicated to be incorporated by reference for all purposes.

**[0194]** While various specific embodiments have been illustrated and described, it will be appreciated that various changes can be made without departing from the spirit and scope of the invention(s).



## WHAT IS CLAIMED IS:

1. A polypeptide comprising a variant CH2 domain which has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% sequence identity to the CH2 domain of SEQ ID NO:2, and which has relative to the CH2 domain of SEQ ID NO:2 one or more substitutions selected from:

- (a) a V263 substitution that increases affinity towards FcγRIIB and decreases affinity towards FcγRIIIA;
- (b) a V266 substitution that increases affinity towards FcγRIIB and decreases affinity towards FcγRIIIA; and
- (c) a V273 substitution that increases affinity towards FcγRIIB and decreases affinity towards FcγRIIIA.

2. A polypeptide comprising a variant CH2 domain which has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% sequence identity to the CH2 domain of SEQ ID NO:2, and which has relative to the CH2 domain of SEQ ID NO:2 one or more substitutions selected from:

- (a) a V263 substitution that increases affinity towards FcγRIIB and decreases affinity towards FcγRIIIA; and
- (b) a V273 substitution that increases affinity towards FcγRIIB and decreases affinity towards FcγRIIIA.

3. A polypeptide comprising a variant CH2 domain which has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% sequence identity to the CH2 domain of SEQ ID NO:2, and which has relative to the CH2 domain of SEQ ID NO:2:

- (a) the substitution V263L; and/or
- (b) a V273 substitution selected from V273C, V273E, V273F, V273L, V273M, V273S, V273Y.

4. A polypeptide comprising a variant CH2 domain which has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% sequence identity to the CH2 domain of SEQ ID NO:2, and which has relative to the CH2 domain of SEQ ID NO:2 one or more substitutions selected from V263L, V266L, V273C, V273E, V273F, V273L, V273M, V273S, V273Y, V305K, and V305W.

5. The polypeptide of claim 4, wherein the CH2 domain includes one or more substitutions selected from V263L, V273E, V273F, V273M, V273S, and V273Y.

6. A polypeptide comprising a variant CH2 domain which has up to 6, up to 5, up to 4, up to 3, up to 2 substitutions, or a single amino acid substitution, as compared to an CH2 domain of SEQ ID NO:2, including one or more substitutions selected from:

- (a) a V263 substitution that increases affinity towards FcγRIIB and decreases affinity towards FcγRIIIA;
- (b) a V266 substitution that increases affinity towards FcγRIIB and decreases affinity towards FcγRIIIA; and
- (c) a V273 substitution that increases affinity towards FcγRIIB and decreases affinity towards FcγRIIIA.

7. A polypeptide comprising a variant CH2 domain which has up to 6, up to 5, up to 4, up to 3, up to 2 substitutions, or a single amino acid substitution, as compared to an CH2 domain of SEQ ID NO:2, including one or more substitutions selected from:

- (a) a V263 substitution that increases affinity towards FcγRIIB and decreases affinity towards FcγRIIIA;
- (b) a V266 substitution that increases affinity towards FcγRIIB and decreases affinity towards FcγRIIIA; and
- (c) a V273 substitution that increases affinity towards FcγRIIB and decreases affinity towards FcγRIIIA.

8. A polypeptide comprising a variant CH2 domain which has up to 6, up to 5, up to 4, up to 3, up to 2 substitutions, or a single amino acid substitution, as compared to an CH2 domain of SEQ ID NO:2, including one or more substitutions selected from:
- (a) the substitution V263L; and/or
  - (b) a V273 substitution selected from V273C, V273E, V273F, V273L, V273M, V273S, V273Y.
9. A polypeptide comprising a variant CH2 domain which has up to 6, up to 5, up to 4, up to 3, up to 2 substitutions, or a single amino acid substitution, as compared to an CH2 domain of SEQ ID NO:2, including one or more substitutions selected from V263L, V266L, V273C, V273E, V273F, V273L, V273M, V273S, V273Y, V305K, and V305W.
10. The polypeptide of claim 9, wherein the CH2 domain includes one or more substitutions selected from V263L, V273E, V273F, V273M, V273S, and V273Y.
11. A polypeptide comprising an Fc domain, said Fc domain comprising a CH2 domain of any one of claims 1 to 10.
12. The polypeptide of claim 11, wherein the Fc domain has up to 20, up to 15, up to 12, up to 10, up to 9, up to 8, up to 7, up to 6, up to 5 or up to 4 amino acid substitutions as compared to the CH2 domain of the Fc domain of SEQ ID NO:1.
13. The polypeptide of claim 12, wherein the Fc domain has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% sequence identity to the Fc domain of SEQ ID NO:1 .
14. The polypeptide of any one of claims 1 to 13, wherein the CH2 domain comprises the V263 substitution V263L.
15. The polypeptide of any one of claims 1 to 13, wherein the CH2 domain comprises the V266 substitution V266L.
16. The polypeptide of any one of claims 1 to 13, wherein the CH2 domain comprises the V273 substitution V273C.

17. The polypeptide of any one of claims 1 to 13, wherein the CH2 domain comprises the V273 substitution V273E.
18. The polypeptide of any one of claims 1 to 13, wherein the CH2 domain comprises the V273 substitution V273F.
19. The polypeptide of any one of claims 1 to 13, wherein the CH2 domain comprises the V273 substitution V273L.
20. The polypeptide of any one of claims 1 to 13, wherein the CH2 domain comprises the V273 substitution V273M.
21. The polypeptide of any one of claims 1 to 13, wherein the CH2 domain comprises the V273 substitution V273S.
22. The polypeptide of any one of claims 1 to 13, wherein the CH2 domain comprises the V273 substitution V273Y.
23. The polypeptide of any one of claims 1 to 13, wherein the CH2 domain comprises the V273 substitution V305K.
24. The polypeptide of any one of claims 1 to 13, wherein the CH2 domain comprises the V273 substitution V305W.
25. The polypeptide of any one of claims 1 to 24, wherein the CH2 domain has at least a 10% increase in affinity towards FcγRIIB and a 10% decrease in affinity towards FcγRIIIA.
26. The polypeptide of any one of claims 1 to 25, which further comprises one or more additional substitutions or combinations of substitutions that modify Fc effector function.
27. The polypeptide of claim 25, wherein said one or more additional substitutions or combinations of substitutions that modify Fc effector function:
  - (a) reduce or increase binding to FcRN;
  - (b) reduce or increase binding to FcγRI;

- (c) reduce or increase binding to FcγRIIA or FcγRIIB; or
  - (d) reduce or increase binding to FcγRIIIA;
- or a combination thereof.
28. The polypeptide of claim 27, wherein the variant CH2 domain is part of an Fc domain comprising the substitution M428L.
29. The polypeptide of claim 27, wherein the variant CH2 domain is part of an Fc domain comprising the T250Q and M428L.
30. The polypeptide of any one of claims 1 to 29, wherein the variant CH2 domain is part of an Fc domain comprising one or more additional substitutions selected from Table 1 to as compared to Fc domain of SEQ ID NO:1.
31. The polypeptide of any one of claims 1 to 30 which is an antibody.
32. The polypeptide of claim 31 which is a human or humanized antibody.
33. The polypeptide of claim 31 or claim 32, wherein the antibody specifically binds to CD40, CD25, CD3, an HLA molecule, a costimulatory molecule, a cytokine, a chemokine, an adhesion molecule, an activation markers, or an immunomodulatory protein.
34. The polypeptide of claim 33, wherein the costimulatory molecule is CD28, PD-1, CTLA-4, CD80, CD86, TIM3, OX40, BB-1, GITR, CD27, B7-H4, or DC-SIGN.
35. The polypeptide of claim 33, wherein the cytokine is TNF-α or IL-2.
36. The polypeptide of claim 33, wherein the cell adhesion molecule is α4 integrin.
37. The polypeptide of claim 33, wherein the immunomodulatory protein is a cell surface molecule.
38. The polypeptide of claim 33, wherein the immunomodulatory protein is a soluble molecule.
39. The polypeptide of claim 33, wherein the antibody specifically binds to CD25.

40. The polypeptide of claim 33, wherein the antibody specifically binds to CD40.
41. The polypeptide of any one of claims 1 to 30 which is an Fc fusion protein in which the CH2 domain is part of an Fc domain operably linked to at least one fusion partner.
42. The polypeptide of claim 41 in which said at least one fusion partner is the extracellular domain ("ECD") of TNF receptor II; the first ECD of lymphocyte function-associated antigen 3 (LFA-3); the ECD of human cytotoxic T lymphocyte associated molecule-4 (CTLA-4); the C-terminus of the IL-1R accessory protein ligand binding region; the N-terminus of the IL-1RI ECD; peptide thrombopoietin (TPO) mimetic; ECD of CTLA-4 with the two amino acid substitutions L104E and A29Y; the ECDs of VEGF receptor 1; or the ECD of VEGF receptor 2.
43. A conjugate compound comprising the polypeptide of any one of claims 1 to 42 linked to an effector moiety or a detectable label.
44. The conjugate compound of claim 43 wherein the polypeptide is linked to a detectable label.
45. The conjugate compound of claim 44 in which the detectable label is a radioactive compound, a fluorescent compound, an enzyme, a substrate, an epitope tag or a toxin.
46. The conjugate compound of claim 43 in which the polypeptide is linked to an effector moiety.
47. The conjugate compound of claim 46 in which the effector moiety is a cytotoxic agent.
48. The conjugate compound of claim 47 in which the cytotoxic agent is an auristatin, a DNA minor groove binding agent, a DNA minor groove alkylating agent, an enediyne, a duocarmycin, a maytansinoid or a vinca alkaloid.
49. The conjugate compound of claim 47 in which the cytotoxic agent is an anti-tubulin agent.
50. The conjugate compound of claim 49, wherein the cytotoxic agent is AFP, MMAF, or MMAE.
51. A pharmaceutical composition comprising the polypeptide of any one of claims 1 to 42 and a pharmaceutically acceptable carrier or the conjugate compound of any one of claims 43 to 50.

52. A nucleic acid comprising a nucleotide sequence encoding the polypeptide of any one of claims 1 to 42.
53. A vector comprising the nucleic acid of claim 52.
54. A prokaryotic host cell transformed with the vector of claim 53.
55. A eukaryotic host cell transformed with the vector of claim 53.
56. A eukaryotic host cell engineered to express the nucleic acid of claim 52.
57. The eukaryotic host cell of claim 56 which is a mammalian host cell.
58. A method of producing a polypeptide, comprising: (a) culturing the eukaryotic host cell of claim 56 or claim 57 and (b) recovering the polypeptide.
59. A method of treatment, optionally of an immune disorder or a cancer, comprising administering to a patient in need thereof a suitable polypeptide according to any one of claims 1 to 42, a pharmaceutical composition according to claim 51, or a conjugate compound according to any one of claims 43 to 50.
60. The method of claim 59, wherein the polypeptide is an anti-CD40 antibody and wherein the cancer is a hematological cancer, optionally selected from chronic lymphocytic leukemia, Burkitt's lymphoma, multiple myeloma, a T cell lymphoma, Non-Hodgkin's Lymphoma, Hodgkin's Disease, Waldenstrom's macroglobulinemia, Kaposi's sarcoma, or a solid tumor cancer, optionally selected from ovarian cancer, breast cancer, lung cancer, melanoma, pancreatic cancer, and renal cancer.
61. The method of claim 60, wherein the anti-CD40 antibody comprises a VL of SEQ ID NO:3 and a VH of SEQ ID NO:4.
62. The method of claim 60 or claim 61 wherein the anti-CD40 antibody is a multi-specific antibody.
63. The method of claim 59, wherein the polypeptide is an anti-CD20 antibody and wherein the immune disorder is rheumatoid arthritis or multiple sclerosis.

64. The method of claim 63, wherein the anti-CD20 antibody comprises a VL of SEQ ID NO:5 and a VH of SEQ ID NO:6.
65. The method of claim 59, wherein the polypeptide is an anti-CD25 antibody and wherein the immune disorder is multiple sclerosis, psoriasis, asthma, psoriasis, uveitis, ocular inflammation or organ transplant rejection or wherein the cancer is a human T cell leukemia virus-1 associated T-cell leukemia.
66. The method of claim 65, wherein the anti-CD25 antibody comprises a VL of SEQ ID NO:7 and a VH of SEQ ID NO:8.
67. The method of claim 65, wherein the anti-CD25 antibody comprises a VL of SEQ ID NO:9 and a VH of SEQ ID NO:10.
68. The method of claim 59, wherein the polypeptide is an anti-TNF $\alpha$  antibody and wherein the immune disorder is anti-TNF $\alpha$  antibody and wherein the immune disorder is rheumatoid arthritis, juvenile idiopathic arthritis, psoriatic arthritis, ankylosing spondylitis, Crohn's disease, ulcerative colitis or plaque psoriasis.
69. The method of claim 68, wherein the anti-TNF $\alpha$  antibody comprises a VL of SEQ ID NO:11 and a VH of SEQ ID NO:12.
70. The method of claim 68, wherein the anti-TNF $\alpha$  antibody comprises a VL of SEQ ID NO:13 and a VH of SEQ ID NO:14.
71. The method of claim 59, wherein the polypeptide is an anti-IL-6 receptor antibody and wherein the immune disorder is rheumatoid arthritis or Castleman's Disease.
72. The method of claim 71, wherein the anti-IL-6 receptor antibody comprises a VL of SEQ ID NO:15 and a VH of SEQ ID NO:16.
73. The method of claim 59, wherein the polypeptide is an anti- $\alpha$ 4-integrin antibody and wherein the immune disorder is multiple sclerosis.
74. The method of claim 59, wherein the polypeptide is an anti-IL-1 antibody and wherein the immune disorder is Cryopyrin-Associated Periodic Syndromes ("CAPS").



75. The method of claim 74, wherein the anti-IL-1 antibody comprises a VL of SEQ ID NO:17 and a VH of SEQ ID NO:18.

76. The method of claim 59, wherein the polypeptide is an anti-BAFF antibody and wherein the immune disorder is systemic lupus erythmatosis or allergy.

77. The method of claim 76, wherein the anti-BAFF antibody comprises a VL of SEQ ID NO:19 and a VH of SEQ ID NO:20.

1/22

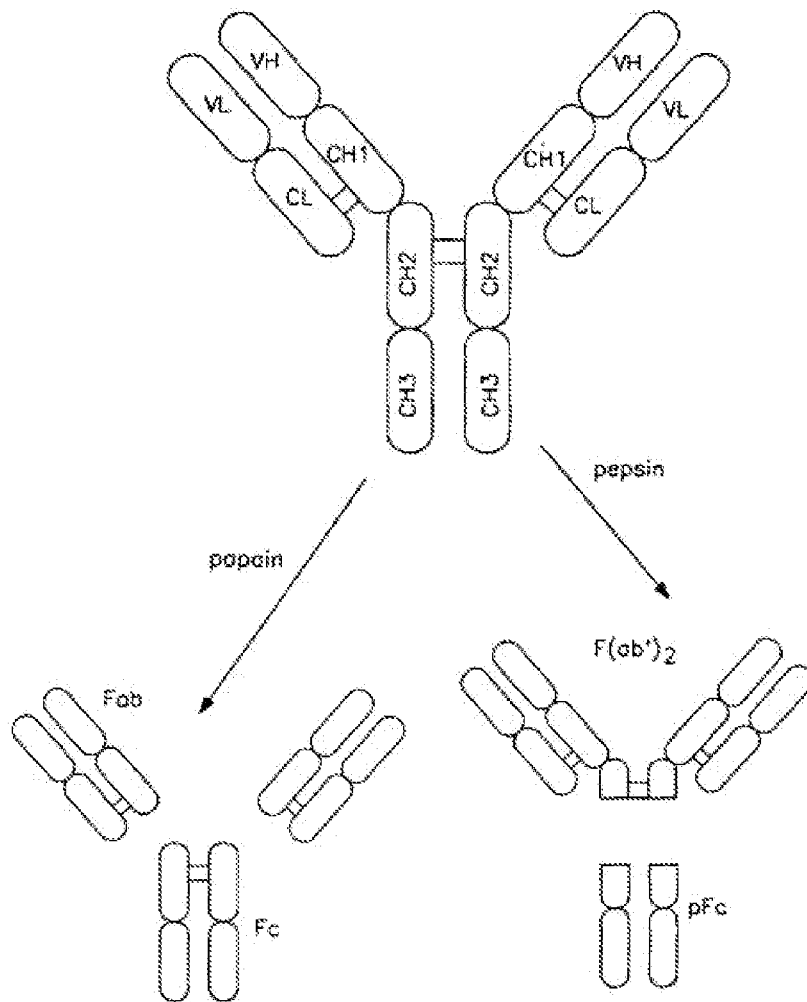


FIGURE 1

2/22

\*

DKTHTCPPCPPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV**VVD**

†

‡

#

**V**SHEDPE**V**KFNWYVDGVEVHNAKTKPREEQYNSTYRVVS**V**LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK**GQPREPQVYTLPPSR****DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD****DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP****GK****FIGURE 2A**

3/22

CH1

118 A S T K G P S V F P L A P S S K S T S G  
138 G T A A L G C L V K D Y F P E P V T V S  
158 W N S G A L T S G V H T F P A V L Q S S  
178 G L Y S L S S V V T V P S S S L G T Q T  
198 Y I C N V N H K P S N T K V D K K V

Hinge

216 E P K S C D K T H T C P P C P

CH2

231 A P E L L G G P S V F L F P P K P K D T  
251 L M I S R T P E V T C V V V D V S H E D  
271 P E V K F N W Y V D G V E V H N A K T K  
291 P R E E Q Y N S T Y R V V S V L T V L H  
311 Q D W L N G K E Y K C K V S N K A L P A  
331 P I E K T I S K A K

CH3

341 G Q P R E P Q V Y T L P P S R E E M T K  
361 N Q V S L T C L V K G F Y P S D I A V E  
381 W E S N G Q P E N N Y K T T P P V L D S  
401 D G S F F L Y S K L T V D K S R W Q Q G  
421 N V F S C S V M H E A L H N H Y T Q K S  
441 L S L S P G K

FIGURE 2B

4/22

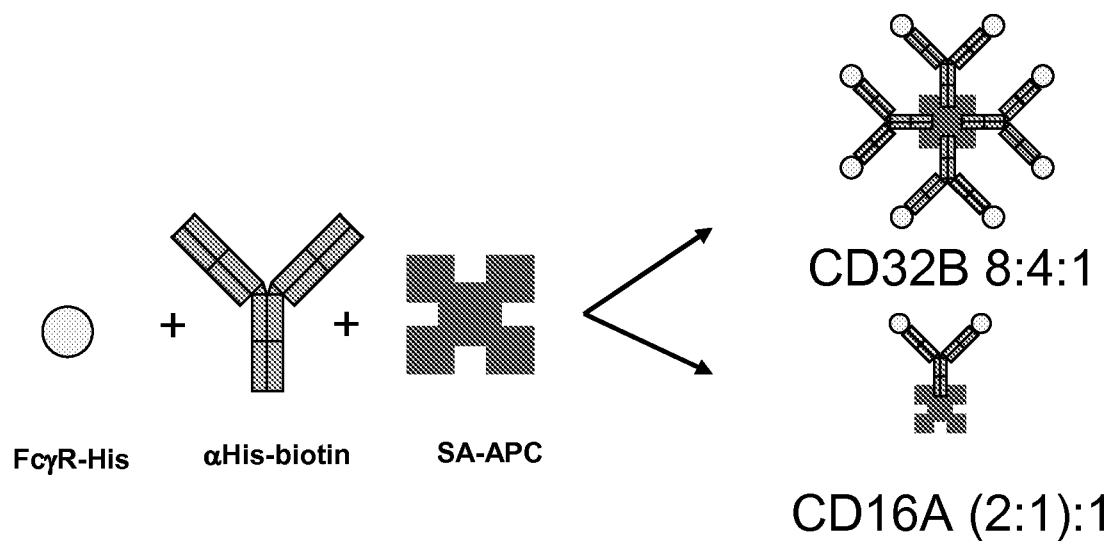
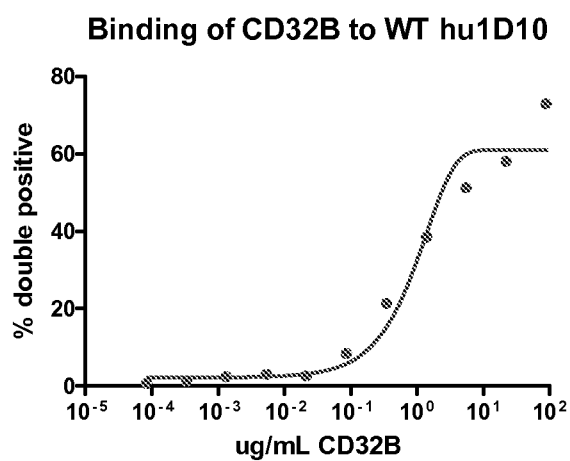


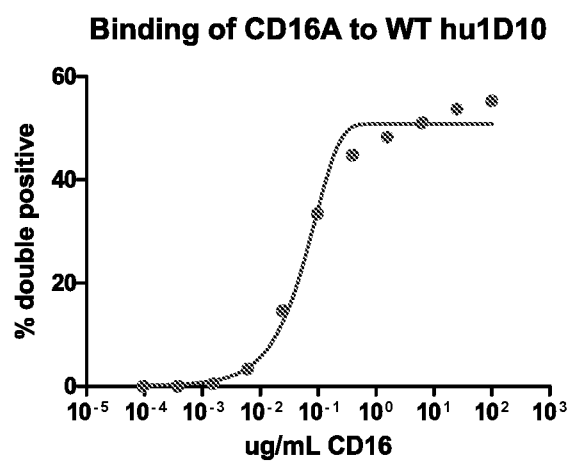
FIGURE 3

A



EC50 3.6 ug/mL

B



EC50 0.17 ug/mL

FIGURE 4

5/22

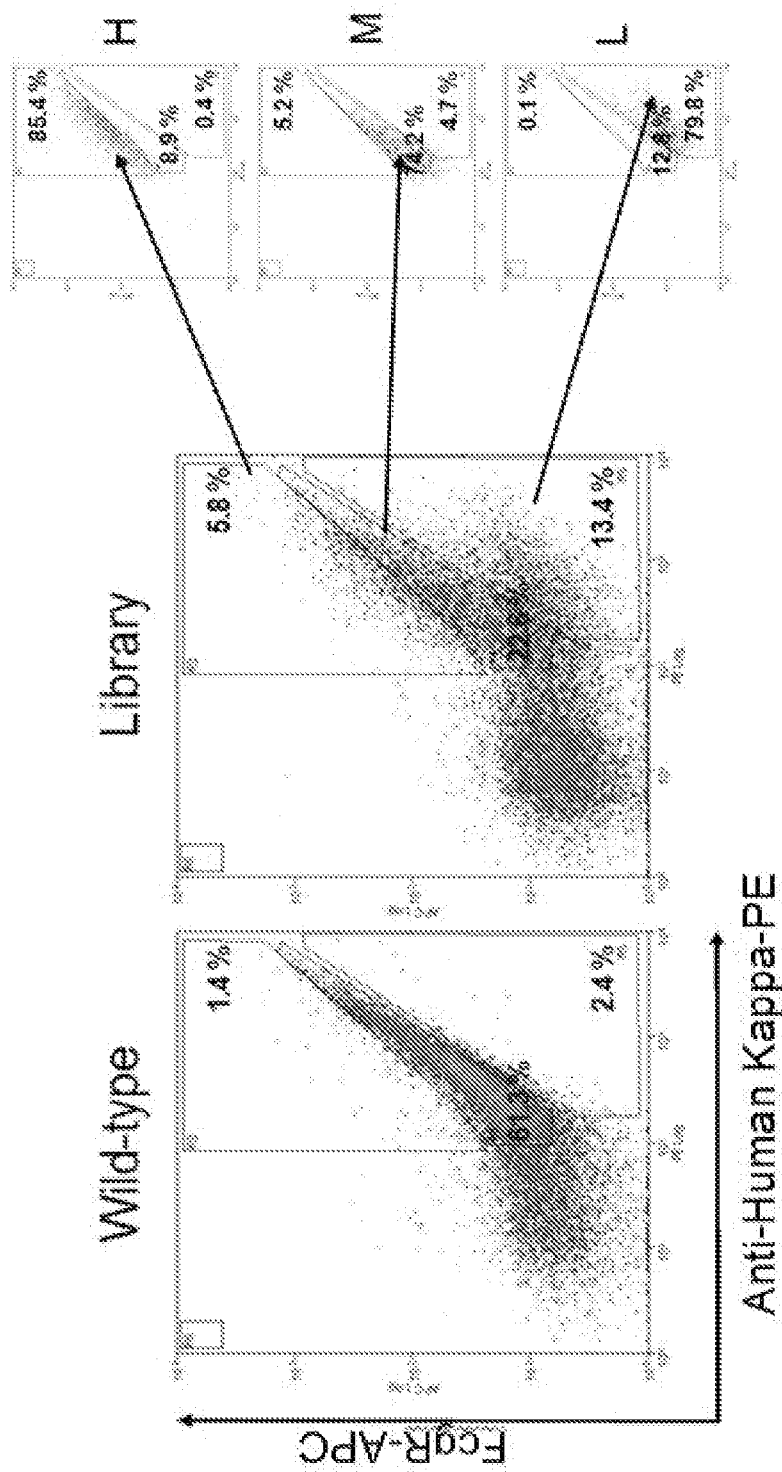


FIGURE 5

6/22

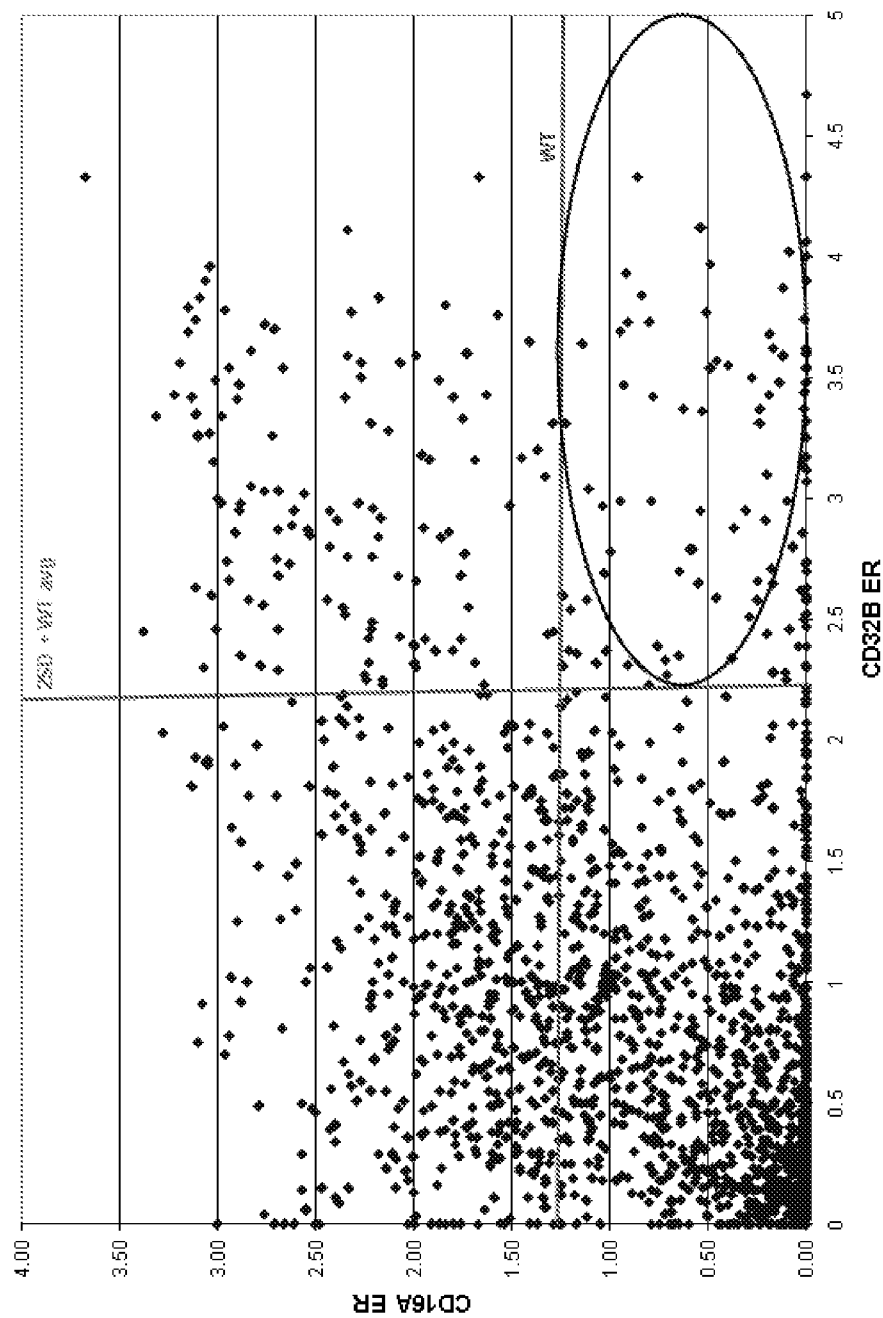


FIGURE 6

7/22

	WT-AA	EU	AA	CD32b_ER	CD16_ER
	V	263	L	2.25	0.10
	V	266	L	3.93	0.92
	V	273	C	2.70	0.65
	V	273	E	3.54	0.49
	V	273	F	4.00	0.00
	V	273	L	3.57	0.28
	V	273	M	3.74	0.01
	V	273	S	3.42	0.75
	V	273	Y	3.97	0.49
	V	305	K	2.14	1.25
	V	305	W	2.03	1.32
		WT			
control	N	297	A		
control	S	267	E		
control	L	328	F		
control		SELF			

FIGURE 7



8/22

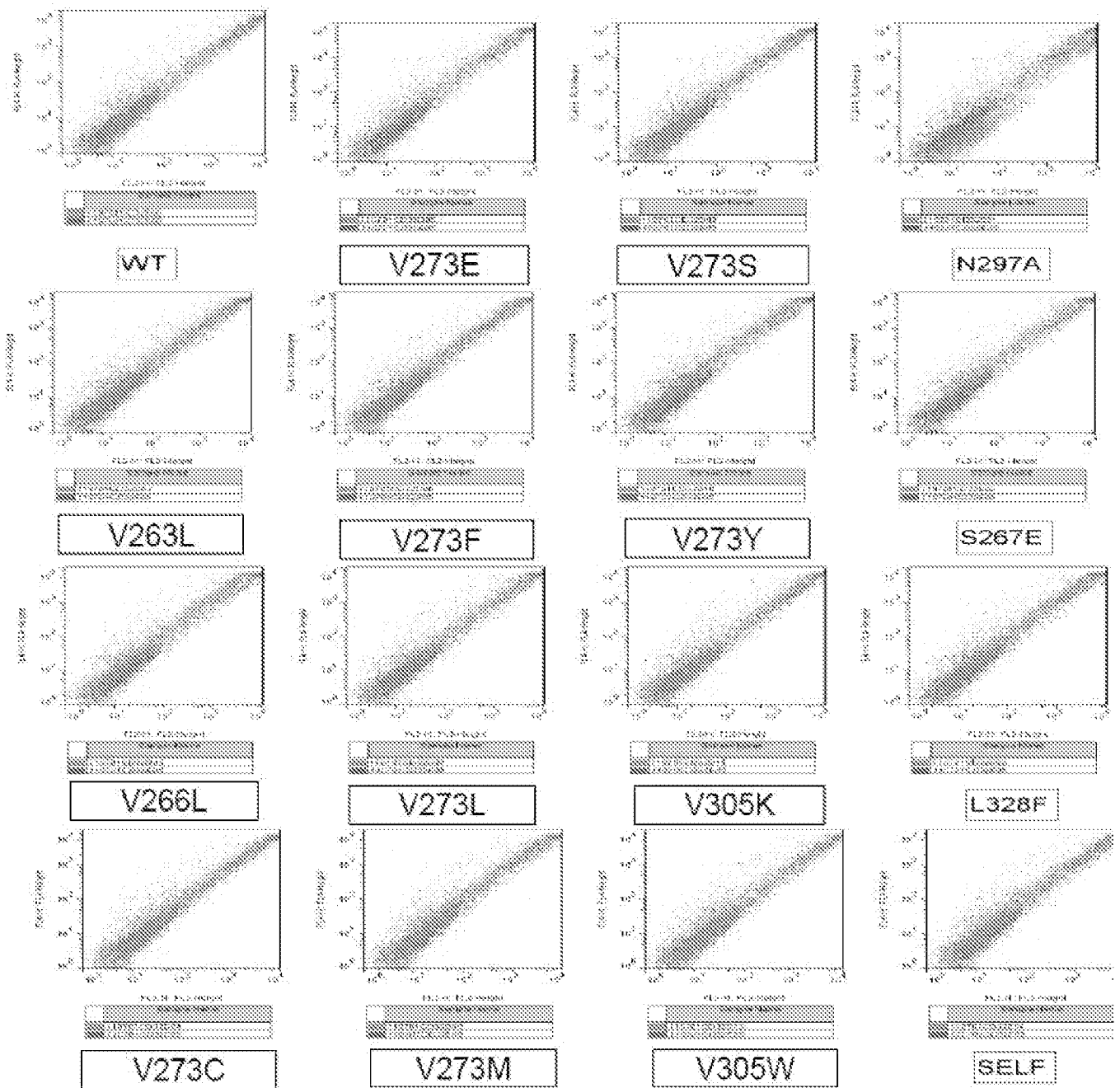


FIGURE 8

9/22

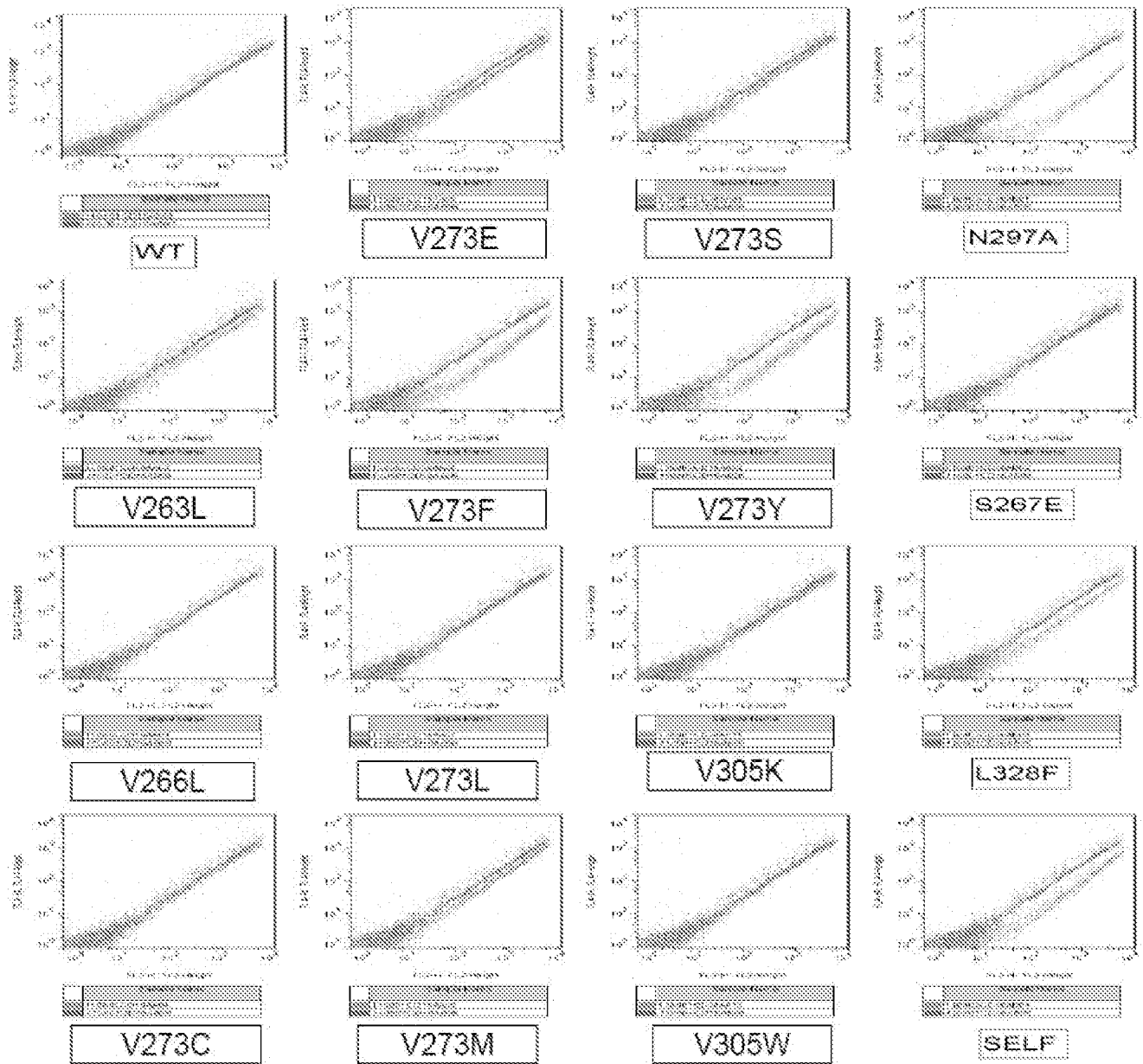


FIGURE 9

10/22

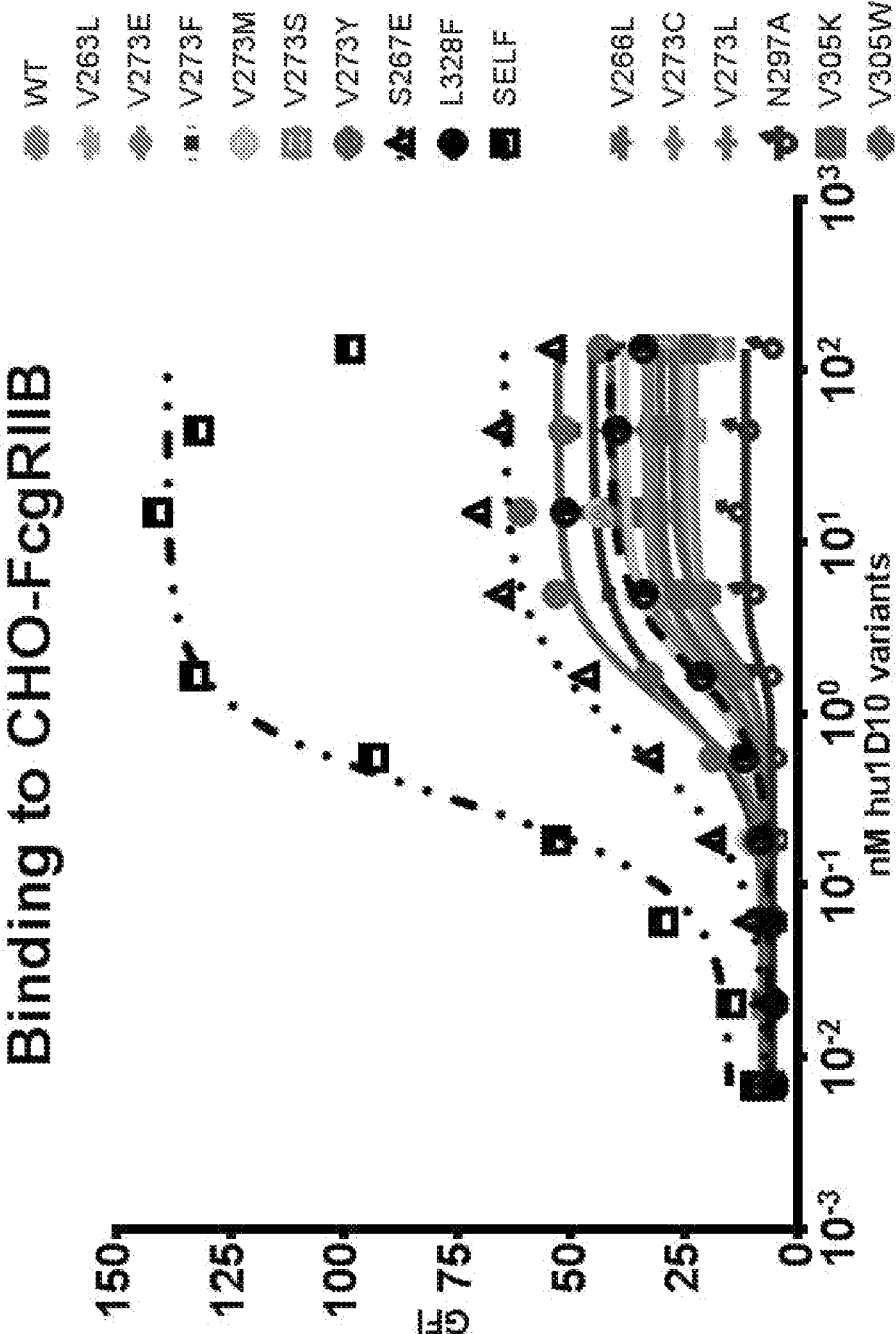


FIGURE 10A

11/22

	Variant	EC50 (nM)	fold over WT
	WT	1.83	1.00
	V263L	1.80	1.02
	V266L	2.22	0.82
	V273C	2.03	0.90
	V273E	1.66	1.10
	V273F	1.08	1.70
	V273L	1.66	1.11
	V273M	1.63	1.12
	V273S	1.72	1.06
	V273Y	1.18	1.55
	V305K	1.93	0.95
	V305W	2.86	0.64
control	N297A	2.00	0.91
control	S267E	0.64	2.85
control	L328F	1.85	0.99
control	SELF	0.32	5.70

FIGURE 10B

12/22

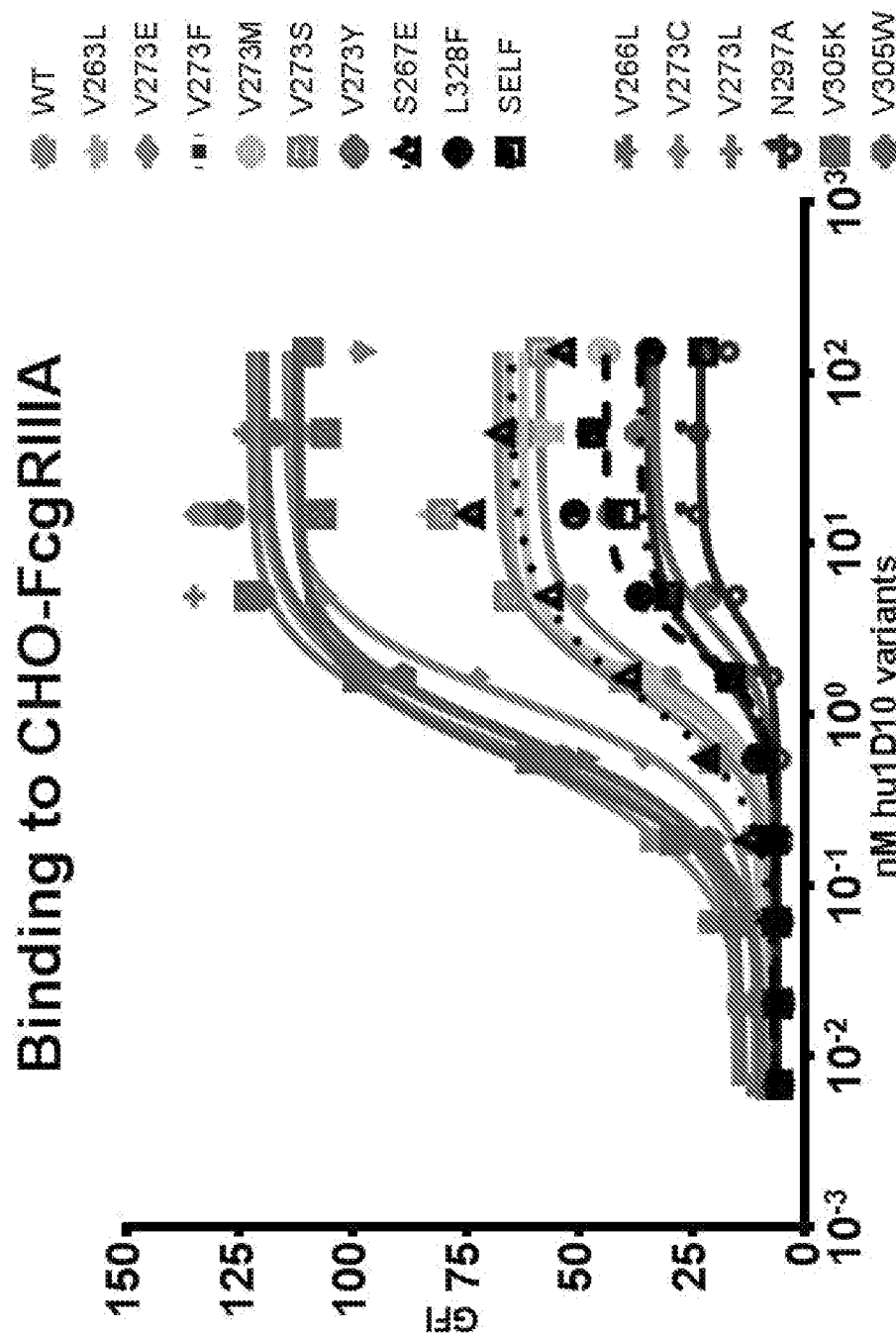


FIGURE 11A

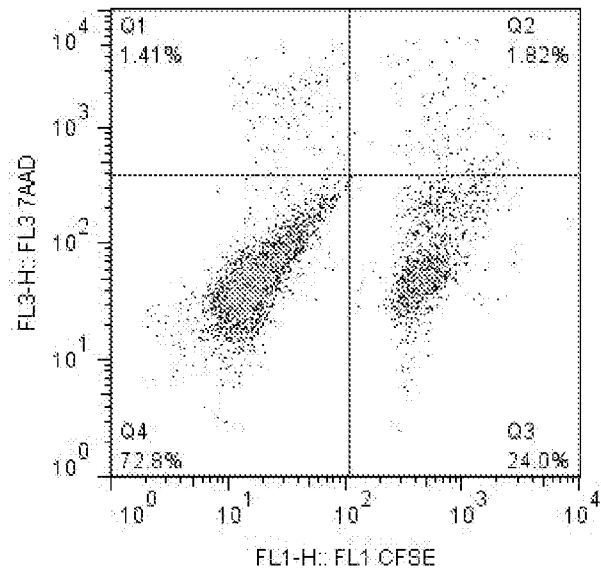
13/22

	Variant	EC50 (nM)	Fold over WT
	WT	0.61	1.00
	V263L	1.52	0.40
	V266L	0.76	0.80
	V273C	1.19	0.51
	V273E	1.78	0.34
	V273F	2.01	0.30
	V273L	0.69	0.88
	V273M	1.59	0.38
	V273S	1.33	0.45
	V273Y	3.19	0.19
	V305K	0.51	1.18
	V305W	0.74	0.82
control	N297A	3.67	0.17
control	S267E	1.24	0.49
control	L328F	2.51	0.24
control	SELF	2.31	0.26

FIGURE 11B

14/22

A: 0.0 ug/mL WT hu1D10 = 7% cytotoxicity



B: 1.0 ug/mL WT hu1D10 = 46% cytotoxicity

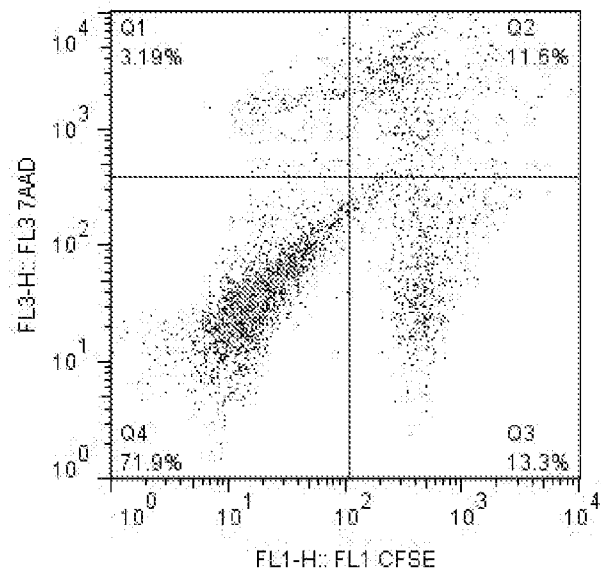


FIGURE 12

15/22

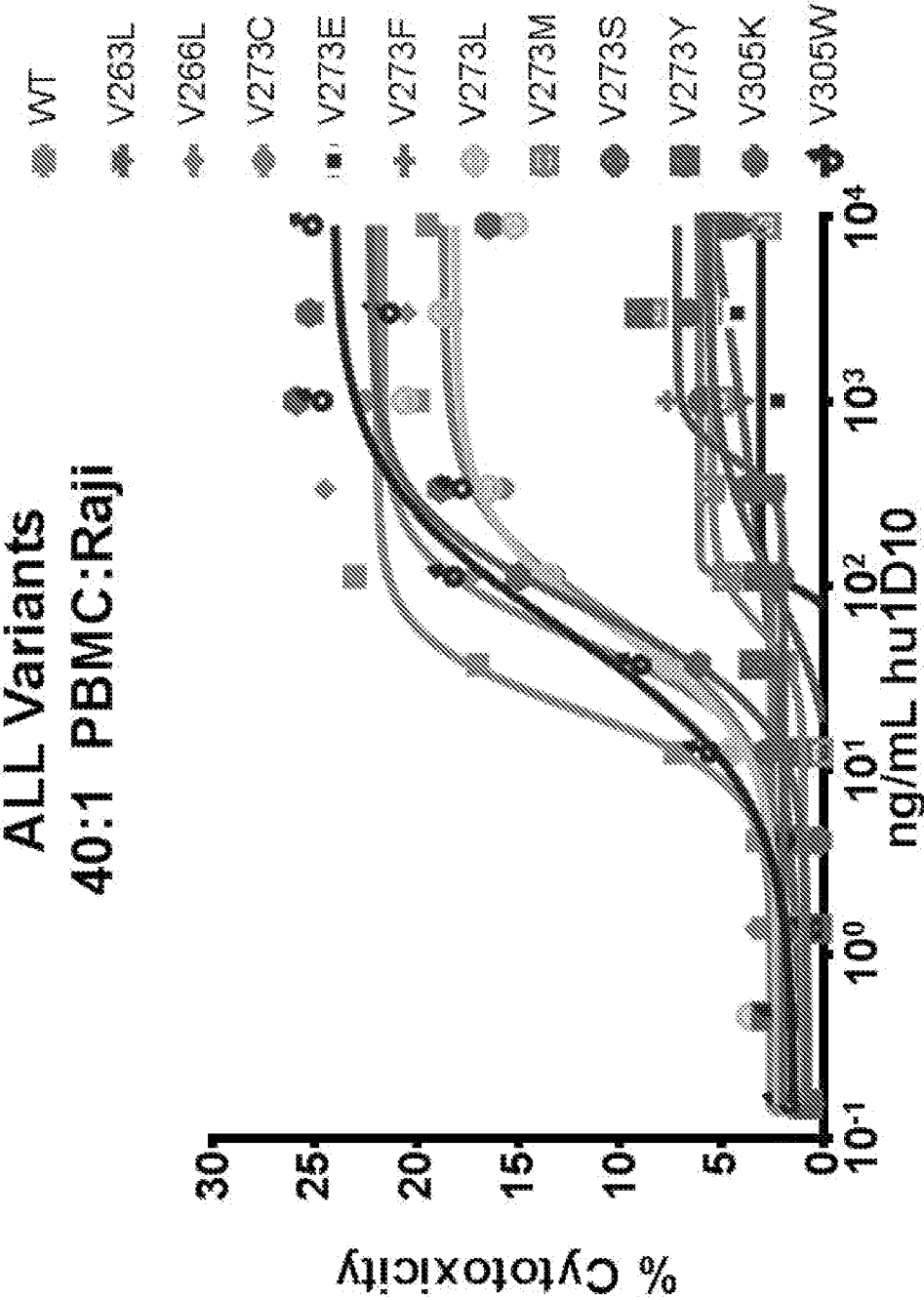


FIGURE 13A



16/22  
ADCC  
40:1 PBMC:Raji

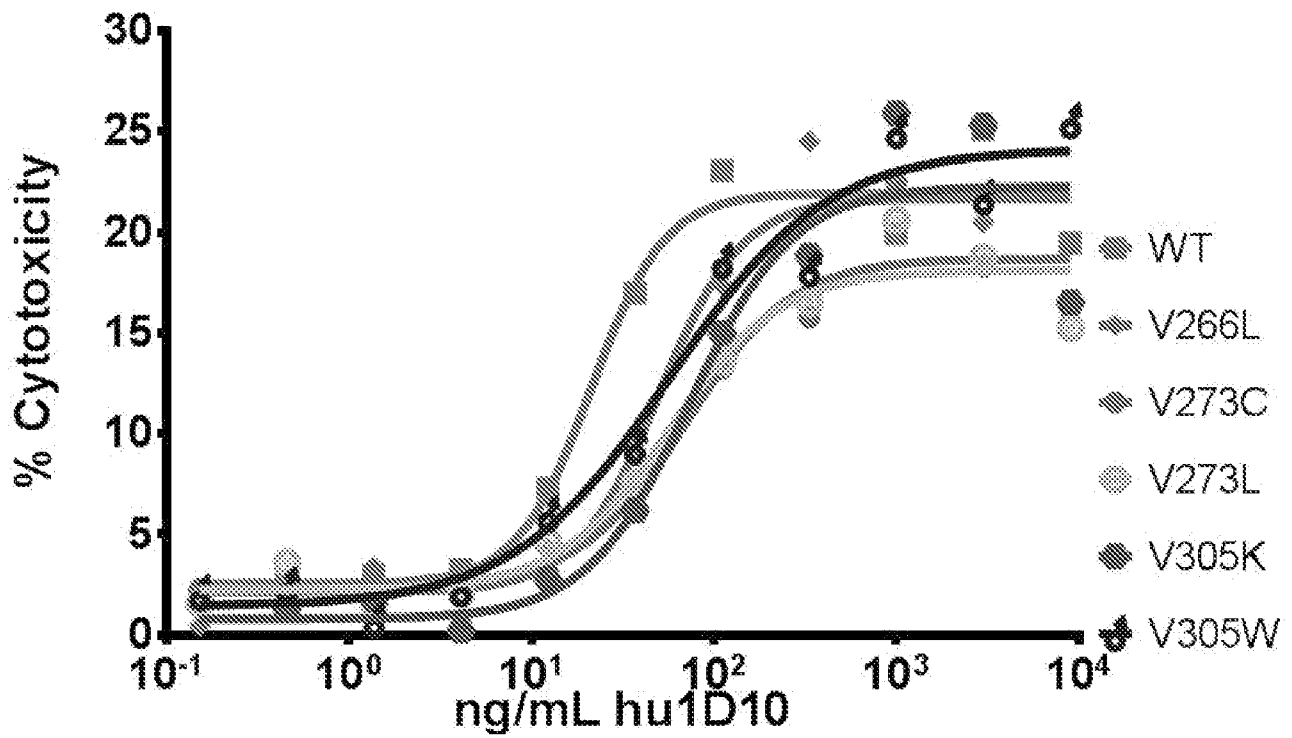


FIGURE 13B

17/22

NO ADCC  
40:1 PBMC:Raji

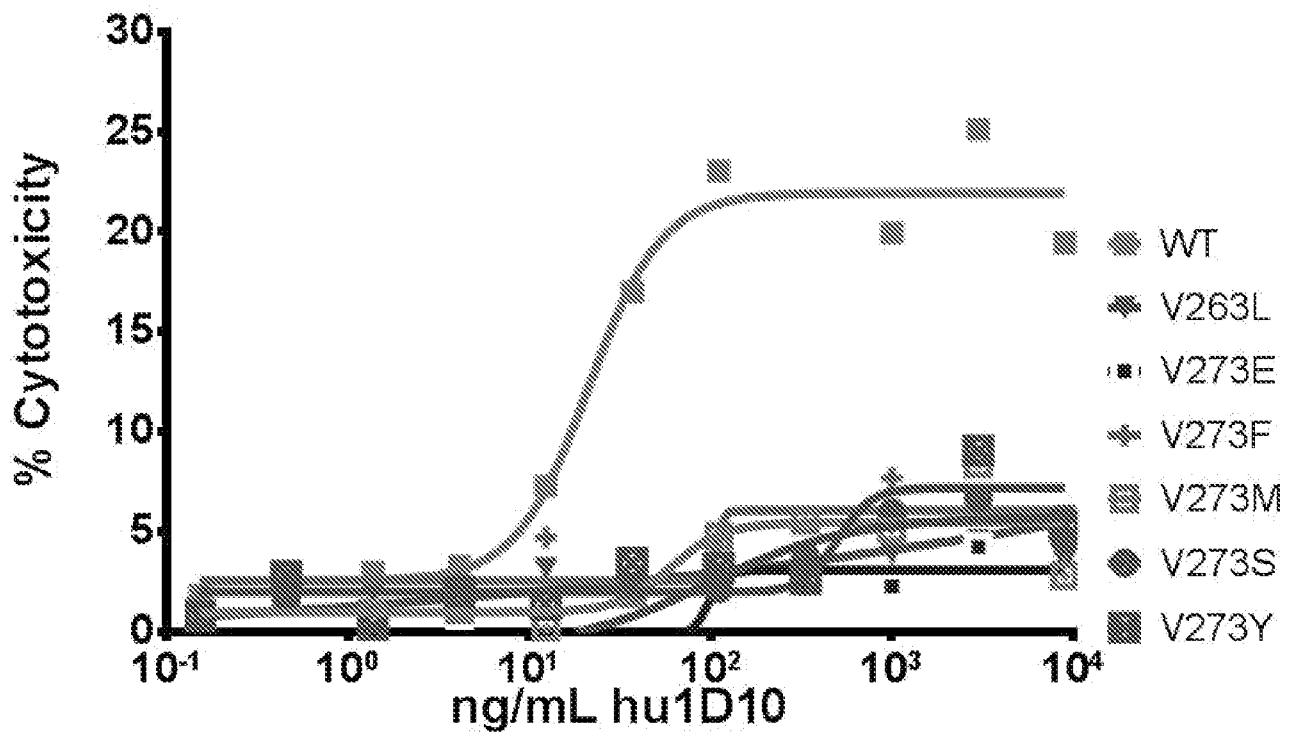


FIGURE 13C

18/22

ADCC  
40:1 PBMC:Raji

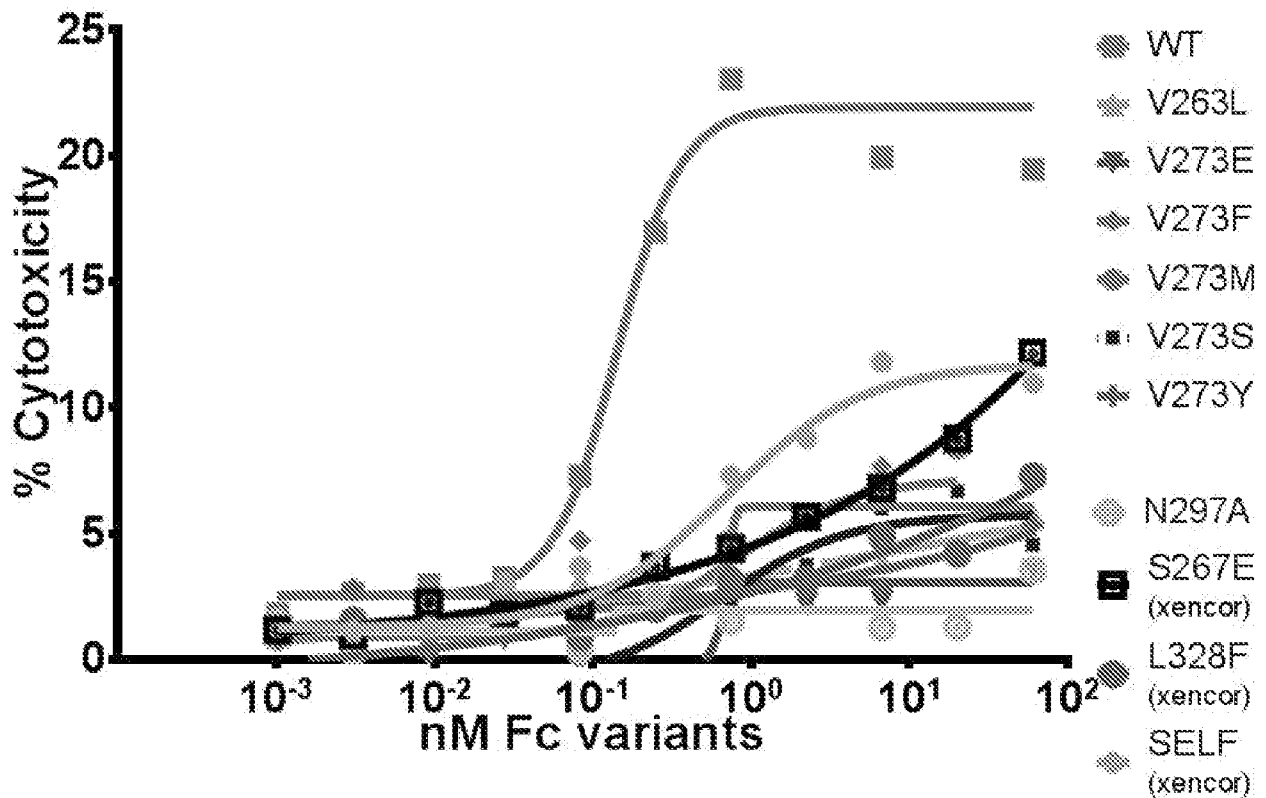


FIGURE 13D

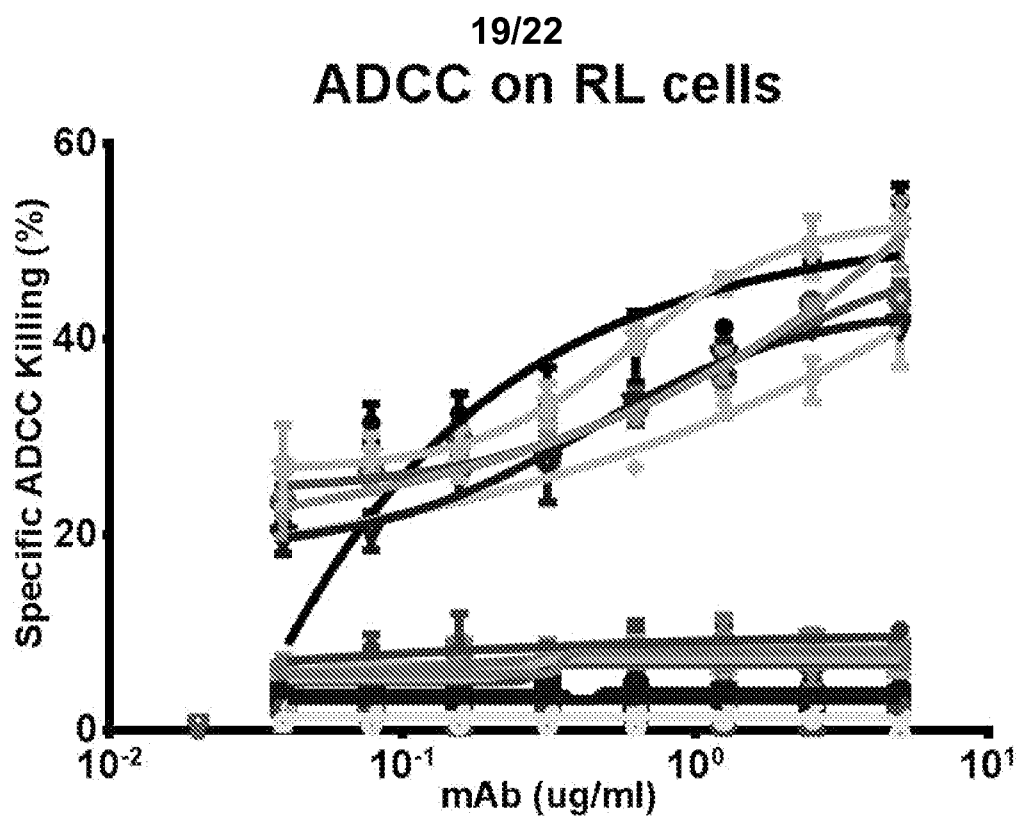


FIGURE 14A

mutations  
w/o ADCC

- ▨ V263L
- ▩ V273E
- ▤ V273F
- ◆ V273M
- ✦ V273S
- ✧ V273Y

mutations  
w/ ADCC

- ▨ V266L
- V273C
- ▼ V273L
- ▨ V305K
- ▨ V305W
- ◆ WT CD40 G1

control mAbs  
w/o ADCC

- ▨ WT CD40 G2
- N297A
- ▨ S267E
- L328F
- SELF
- MSL109
- ▨ hlgG2
- AICC

20/22  
FIGURE 14B

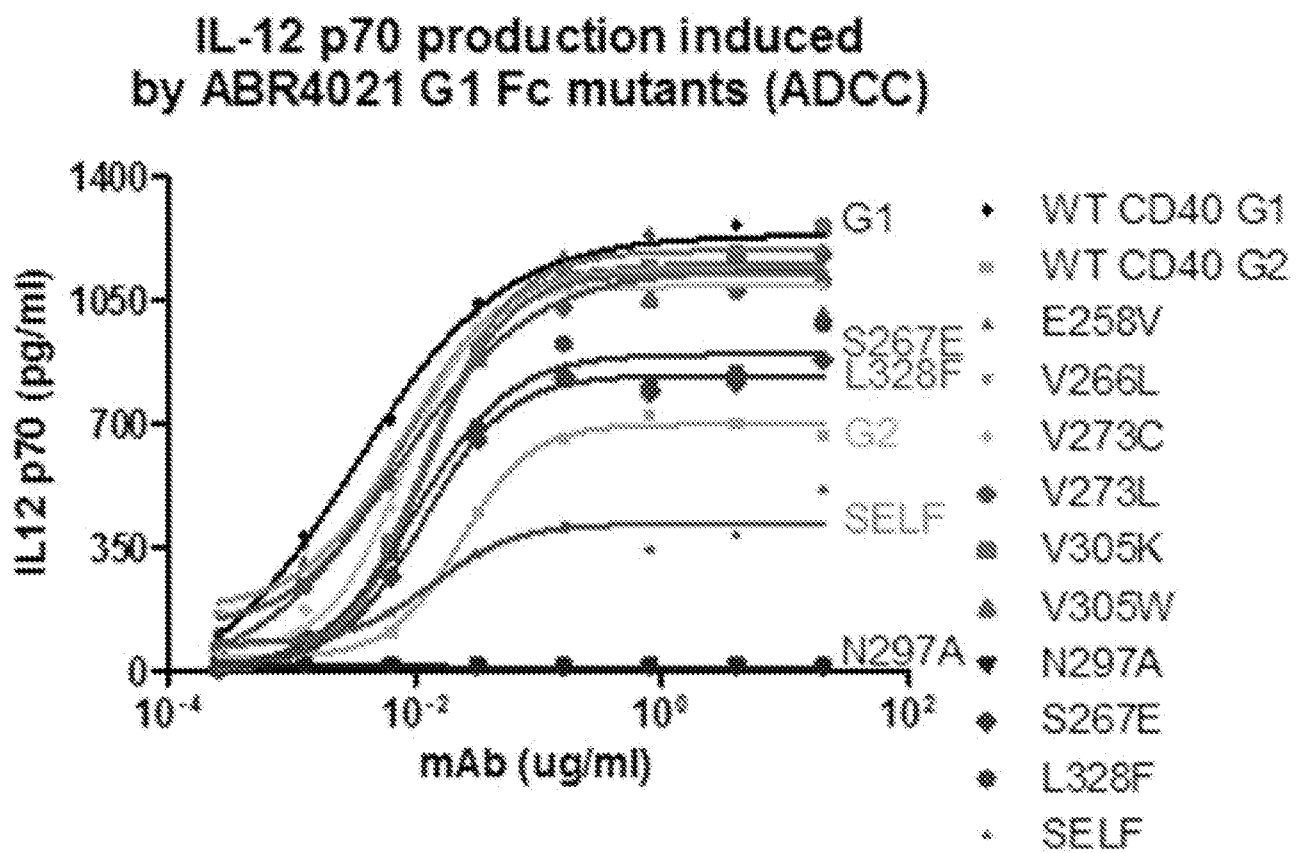
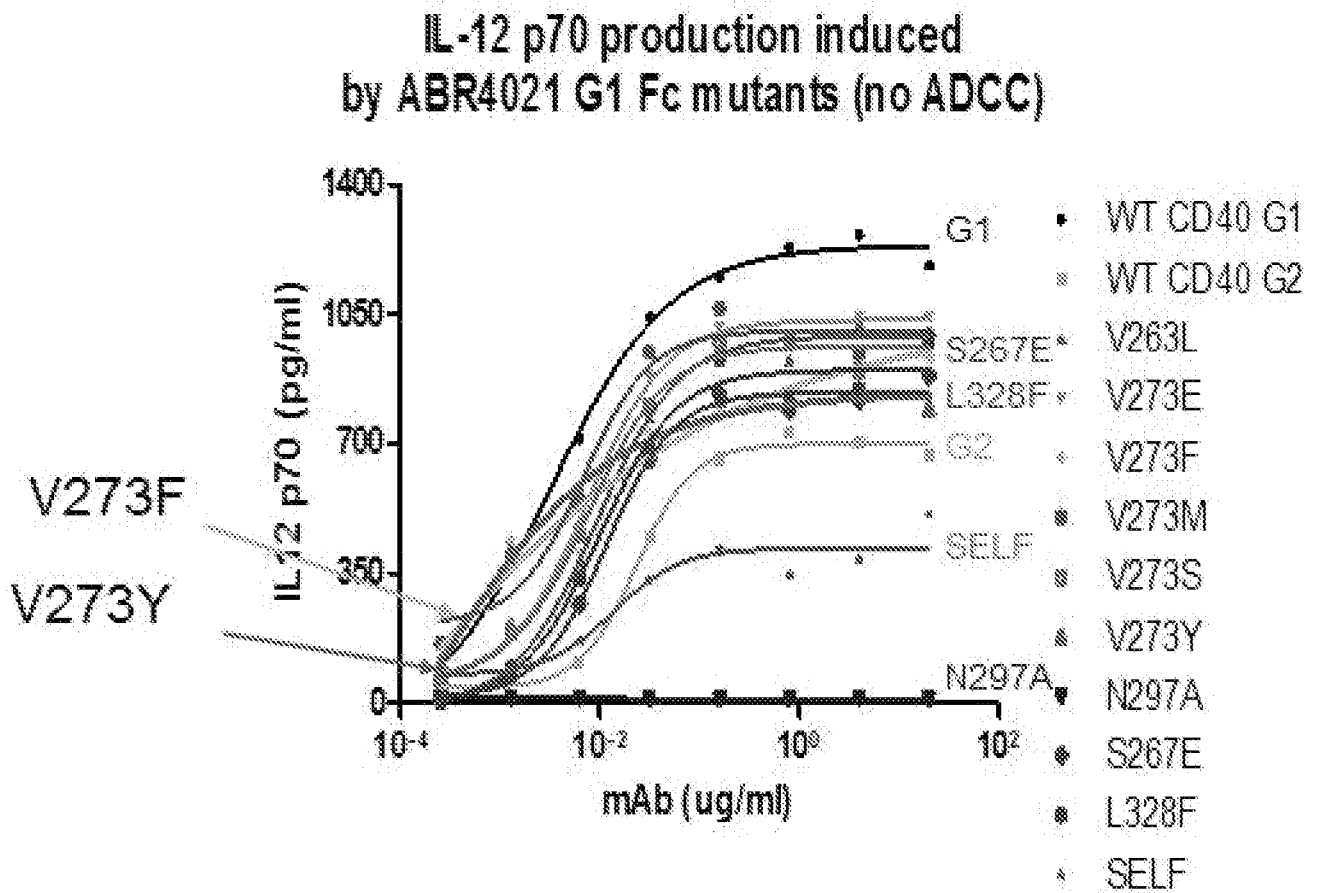


FIGURE 15A

21/22

**FIGURE 15B**

22/22

	EC50, ng/mL
WT CD40 G1	3.25
V263L	9.54
V273E	7.85
V273F	
V273M	8.95
V273S	7.74
V273Y	0.19
N297A	
S267E	11.80
L328F	10.05
SELF	13.97

FIGURE 15C

	WT-AA	EU	AA
	V	263	L
	V	266	L
	V	273	C
	V	273	E
	V	273	F
	V	273	L
	V	273	M
	V	273	S
	V	273	Y
	V	305	K
	V	305	W
		WT	
control	N	297	A
control	S	267	E
control	L	328	F
control		SELF	

FIGURE 16



## (51) International Patent Classification:

C07K 16/00 (2006.01) C07K 16/28 (2006.01)

A61K 39/00 (2006.01)

## (21) International Application Number:

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14 March 2014 (14.03.2014)

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(74) Agents: DECHERT LLP et al.; Suite 700, 2440 W. El Camino Real, Mountain View, California 94040-1499 (US).

(81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JP, KE, KG, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK,

[Continued on next page]

## (54) Title: FC VARIANTS

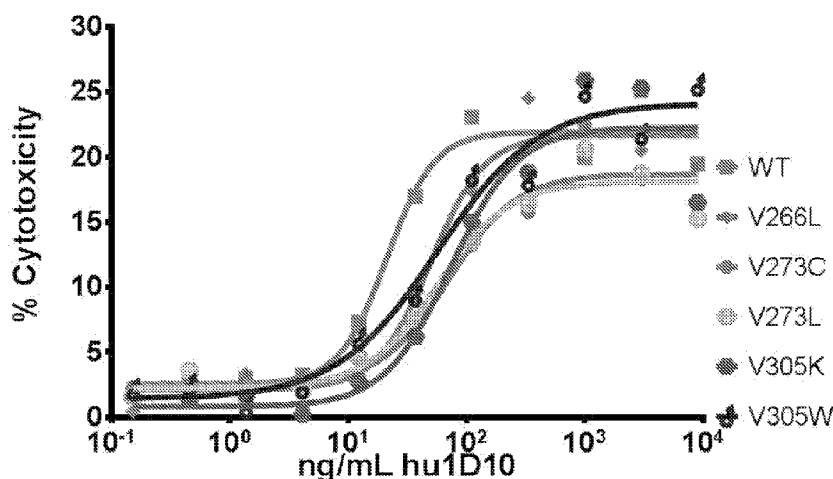
ADCC  
40:1 PBMC:Raji

FIGURE 13B

(57) Abstract: The present disclosure relates to polypeptide variants having modified Fc domains with altered affinity to Fc receptors.





EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU,  
LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK,  
SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ,  
GW, KM, ML, MR, NE, SN, TD, TG).

**Published:**

— with international search report (Art. 21(3))

— before the expiration of the time limit for amending the  
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— with sequence listing part of description (Rule 5.2(a))

**(88) Date of publication of the international search report:**

15 January 2015

## INTERNATIONAL SEARCH REPORT

International application No

PCT/US2014/029585

## A. CLASSIFICATION OF SUBJECT MATTER

INV. C07K16/00 A61K39/00 C07K16/28  
ADD.

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

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

C07K A61K

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

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

EPO-Internal, WPI Data

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2004/099249 A2 (XENCOR INC [US]; LAZAR GREGORY ALAN [US]; CHIRINO ARTHUR J [US]; DANG) 18 November 2004 (2004-11-18)	1,2,6,7, 11-13, 25-77
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	----- -/--	



Further documents are listed in the continuation of Box C.



See patent family annex.

\* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

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"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&amp;" document member of the same patent family

Date of the actual completion of the international search

17 November 2014

Date of mailing of the international search report

01/12/2014

Name and mailing address of the ISA/

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## INTERNATIONAL SEARCH REPORT

International application No

PCT/US2014/029585

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 2007/024249 A2 (MACROGENICS INC [US]; STAVENHAGEN JEFFREY [US]; KOENIG SCOTT [US]) 1 March 2007 (2007-03-01) abstract paragraph [0176]; table 8 -----	3-5, 8-10,14, 16-22
X	WO 2006/034488 A2 (GENENTECH INC [US]; EIGENBROT CHARLES W [US]; JUNUTULA JAGATH REDDY [U]) 30 March 2006 (2006-03-30) abstract page 58, line 18 - line 32; figure 16 -----	1-4,6-9, 11-13, 16,25-77
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## INTERNATIONAL SEARCH REPORT

International application No

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Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	US 2007/231329 A1 (LAZAR GREGORY A [US] ET AL LAZAR GREGORY ALAN [US] ET AL) 4 October 2007 (2007-10-04) abstract figure 41; tables 1,10 -----	1-77
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X,P	WO 2013/109279 A2 (THERAPEUTIC PROTEINS INC [US]; WILTON ROSEMARIE [US]) 25 July 2013 (2013-07-25)  abstract; examples 1-4 -----	1-14, 25-33, 37,41, 43-59, 63,64

# INTERNATIONAL SEARCH REPORT

International application No.

PCT/US2014/029585

## Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application and necessary to the claimed invention, the international search was carried out on the basis of:
- a. (means)
- ☐ on paper
- ☒ in electronic form
- b. (time)
- ☒ in the international application as filed
- ☐ together with the international application in electronic form
- ☐ subsequently to this Authority for the purpose of search
2. ☐ In addition, in the case that more than one version or copy of a sequence listing and/or table relating thereto has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that in the application as filed or does not go beyond the application as filed, as appropriate, were furnished.
3. Additional comments:

## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US2014/029585

### Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

### Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☒ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fees, this Authority did not invite payment of additional fees.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

#### Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- ☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- ☒ No protest accompanied the payment of additional search fees.

**FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210**

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 14(completely); 1-13, 25-77(partially)

A polypeptide comprising a variant CH2 domain which has relative to the CH2 domain of SEQ ID NO:2 at least a V263 substitution and the subject-matter relating thereto.

---

2. claims: 15(completely); 1, 4, 6, 7, 9, 11-13, 25-77(partially)

A polypeptide comprising a variant CH2 domain which has relative to the CH2 domain of SEQ ID NO:2 at least a V266 substitution and the subject-matter relating thereto.

---

3. claims: 16-22(completely); 1-13, 25-77(partially)

A polypeptide comprising a variant CH2 domain which has relative to the CH2 domain of SEQ ID NO:2 at least a V273 substitution and the subject-matter relating thereto.

---

4. claims: 23, 24(completely); 4, 9, 11-13, 25-77(partially)

A polypeptide comprising a variant CH2 domain which has relative to the CH2 domain of SEQ ID NO:2 at least a V305K or V305W substitution and the subject-matter relating thereto.

---

# INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No

PCT/US2014/029585

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-----			

## 摘要

本公开涉及具有经修饰的 Fc 域的多肽变体，其具有改变的对 Fc 受体的亲和力。