(12) STANDARD PATENT (11) Application No. **AU 2006230413 B8**
(19) AUSTRALIAN PATENT OFFICE

(54) Title
Fc variants with optimized properties

(51) International Patent Classification(s)
C07K 16/28 (2006.01) ***C07K 16/30*** (2006.01)
C07K 16/00 (2006.01)

(21) Application No: **2006230413** (22) Date of Filing: **2006.03.31**

(87) WIPO No: **WO06/105338**

(30) Priority Data

(31) Number	(32) Date	(33) Country
60/723,294	**2005.10.03**	**US**
60/705,378	**2005.08.03**	**US**
11/124,620	**2005.05.05**	**US**
60/667,197	**2005.03.31**	**US**
60/723,335	**2005.10.03**	**US**

(43) Publication Date: **2006.10.05**
(44) Accepted Journal Date: **2010.09.23**
(48) Corrigenda Journal Date: **2011.01.20**

(71) Applicant(s)
Xencor, Inc

(72) Inventor(s)
Desjarlais, John R.;Lazar, Gregory Alan;Dang, Wei;Karki, Sher Bahadur

(74) Agent / Attorney
Davies Collison Cave, 1 Nicholson Street, Melbourne, VIC, 3000

(56) Related Art
WO 2004/063351 (Macrogenics, Inc) 29 July 2004
Kabat et al 'Sequences of proteins of immunological interest' (1991) NIH Publication No. 91-3242, pages 679-687

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
5 October 2006 (05.10.2006)

PCT

(10) International Publication Number
WO 2006/105338 A3

(51) International Patent Classification:
C07K 16/28 (2006.01) *C07K 16/30* (2006.01)
C07K 16/00 (2006.01)

(21) International Application Number:
PCT/US2006/011752

(22) International Filing Date: 31 March 2006 (31.03.2006)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

60/667,197	31 March 2005 (31.03.2005)	US
11/124,620	5 May 2005 (05.05.2005)	US
60/705,378	3 August 2005 (03.08.2005)	US
60/723,335	3 October 2005 (03.10.2005)	US
60/723,294	3 October 2005 (03.10.2005)	US

(63) Related by continuation (CON) or continuation-in-part (CIP) to earlier application:
US 11/124,620 (CIP)
Filed on 5 May 2005 (05.05.2005)

(71) Applicant *(for all designated States except US)*: **XENCOR, INC.** [US/US]; 111 West Lemon Avenue, Monrovia, CA 91016 (US).

(72) Inventors; and
(75) Inventors/Applicants *(for US only)*: **LAZAR, Gregory, Alan** [US/US]; 750 Arcadia Avenue #6, Arcadia, CA 91007 (US). **DANG, Wei** [CN/US]; 1111 Blanche Street, Apt. 312, Pasadena, CA 91106 (US). **DESJARLAIS, John, R.** [US/US]; 1030 North Michigan Avenue, Pasadena, CA 91104 (US). **KARKI, Sher, Bahadur** [NP/US]; 2833 Providence Way, Ponoma, CA 91767 (US).

(74) Agents: **SILVA, Robin, M.** et al.; DORSEY & WHITNEY LLP, 555 California Street, Suite 1000, San Francisco, CA 94104 (US).

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

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, LV, MC, NL, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Declarations under Rule 4.17:
— *as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii))*
— *as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii))*
— *of inventorship (Rule 4.17(iv))*

Published:
— *with international search report*

(88) Date of publication of the international search report:
29 March 2007

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: Fc VARIANTS WITH OPTIMIZED PROPERTIES

(57) Abstract: The present invention relates to Fc variants with optimized properties, methods for their generation, Fc polypeptides comprising Fc variants with optimized properties, and methods for using Fc variants with optimized properties.

WO 2006/105338 A3

Fc VARIANTS WITH OPTIMIZED PROPERTIES

[1] This application claims benefit under 35 U.S.C. §119(e) to USSNs 60/667,197, filed March 31, 2005; 60/705,378 filed August 3, 2005; 60/723,294 filed October 3, 2005; and 60/723,335 filed October 3, 2005; and is contination-in-part of USSNs 11/124,620, filed May 5, 2005, each of which is incorporated by reference herein in its entirety. The disclosures of U.S. Patent Application No. 10/822,231, filed March 26, 2004 is also expressly incorporated by reference in their entirety.

FIELD OF THE INVENTION

[2] The present invention relates to Fc variant polypeptides with optimized properties, engineering methods for their generation, and their application, particularly for therapeutic purposes.

BACKGROUND OF THE INVENTION

[3] Antibodies are immunological proteins that bind a specific antigen. In most mammals, including humans and mice, antibodies are constructed from paired heavy and light polypeptide chains. Each chain is made up of individual immunoglobulin (Ig) domains, and thus the generic term immunoglobulin is used for such proteins. Each chain is made up of two distinct regions, referred to as the variable and constant regions. The light and heavy chain variable regions show significant sequence diversity between antibodies, and are responsible for binding the target antigen. The constant regions show less sequence diversity, and are responsible for binding a number of natural proteins to elicit important biochemical events. In humans there are five different classes of antibodies including IgA (which includes subclasses IgA1 and IgA2), IgD, IgE, IgG (which includes subclasses IgG1, IgG2, IgG3, and IgG4), and IgM. The distinguishing features between these antibody classes are their constant regions, although subtler differences may exist in the V region. Figure 1 shows an IgG1 antibody, used here as an example to describe the general structural features of immunoglobulins. IgG antibodies are tetrameric proteins composed of two heavy chains and two light chains. The IgG heavy chain is composed of four immunoglobulin domains linked from N- to C-terminus in the order V_H-CH1-CH2-CH3, referring to the heavy chain variable domain, heavy chain constant domain 1, heavy chain constant domain 2, and heavy chain constant domain 3 respectively (also referred to as V_H-C□1-C□2-C□3, referring to the heavy chain variable domain, constant gamma 1 domain, constant gamma 2 domain, and constant gamma 3 domain respectively). The IgG light chain is composed of two immunoglobulin domains linked from N- to C-terminus in the order V_L-C_L, referring to the light chain variable domain and the light chain constant domain respectively.

[4] The variable region of an antibody contains the antigen binding determinants of the molecule, and thus determines the specificity of an antibody for its target antigen. The variable region is so named because it is the most distinct in sequence from other antibodies within the same class. The majority of sequence variability occurs in the complementarity determining regions (CDRs). There are 6 CDRs total, three each per heavy and light chain, designated V_H CDR1, V_H CDR2, V_H CDR3, V_L CDR1, V_L CDR2, and V_L CDR3. The variable region outside of the CDRs is referred to as the framework (FR) region. Although not as diverse as the CDRs, sequence variability does occur in the FR region between different antibodies. Overall, this characteristic architecture of antibodies provides a stable scaffold (the FR region) upon which substantial antigen binding diversity (the CDRs) can be

explored by the immune system to obtain specificity for a broad array of antigens. A number of high-resolution structures are available for a variety of variable region fragments from different organisms, some unbound and some in complex with antigen. The sequence and structural features of antibody variable regions are well characterized (Morea *et al.*, 1997, *Biophys Chem* 68:9-16; Morea *et al.*, 2000, *Methods* 20:267-279, hereby entirely incorporated by reference), and the conserved features of antibodies have enabled the development of a wealth of antibody engineering techniques (Maynard *et al.*, 2000, *Annu Rev Biomed Eng* 2:339-376, hereby entirely incorporated by reference). For example, it is possible to graft the CDRs from one antibody, for example a murine antibody, onto the framework region of another antibody, for example a human antibody. This process, referred to in the art as "humanization", enables generation of less immunogenic antibody therapeutics from nonhuman antibodies. Fragments comprising the variable region can exist in the absence of other regions of the antibody, including for example the antigen binding fragment (Fab) comprising V_H-Cγ1 and V_H-C_L, the variable fragment (Fv) comprising V_H and V_L, the single chain variable fragment (scFv) comprising V_H and V_L linked together in the same chain, as well as a variety of other variable region fragments (Little *et al.*, 2000, *Immunol Today* 21:364-370, hereby entirely incorporated by reference).

[5] The Fc region of an antibody interacts with a number of Fc receptors and ligands, imparting an array of important functional capabilities referred to as effector functions. For IgG the Fc region, as shown in Figure 1, comprises Ig domains Cγ2 and Cγ3 and the N-terminal hinge leading into Cγ2. An important family of Fc receptors for the IgG class are the Fc gamma receptors (FcγRs). These receptors mediate communication between antibodies and the cellular arm of the immune system (Raghavan *et al.*, 1996, *Annu Rev Cell Dev Biol* 12:181-220; Ravetch *et al.*, 2001, *Annu Rev Immunol* 19:275-290, both hereby entirely incorporated by reference). In humans this protein family includes FcγRI (CD64), including isoforms FcγRIa, FcγRIb, and FcγRIc; FcγRII (CD32), including isoforms FcγRIIa (including allotypes H131 and R131), FcγRIIb (including FcγRIIb-1 and FcγRIIb-2), and FcγRIIc; and FcγRIII (CD16), including isoforms FcγRIIIa (including allotypes V158 and F158) and FcγRIIIb (including allotypes FcγRIIIb-NA1 and FcγRIIIb-NA2) (Jefferis *et al.*, 2002, *Immunol Lett* 82:57-65, hereby entirely incorporated by reference). These receptors typically have an extracellular domain that mediates binding to Fc, a membrane spanning region, and an intracellular domain that may mediate some signaling event within the cell. These receptors are expressed in a variety of immune cells including monocytes, macrophages, neutrophils, dendritic cells, eosinophils, mast cells, platelets, B cells, large granular lymphocytes, Langerhans' cells, natural killer (NK) cells, and $\gamma\gamma$ T cells. Formation of the Fc/FcγR complex recruits these effector cells to sites of bound antigen, typically resulting in signaling events within the cells and important subsequent immune responses such as release of inflammation mediators, B cell activation, endocytosis, phagocytosis, and cytotoxic attack. The ability to mediate cytotoxic and phagocytic effector functions is a potential mechanism by which antibodies destroy targeted cells. The cell-mediated reaction wherein nonspecific cytotoxic cells that express FcγRs recognize bound antibody on a target cell and subsequently cause lysis of the target cell is referred to as antibody dependent cell-mediated cytotoxicity (ADCC) (Raghavan *et al.*, 1996, *Annu Rev Cell Dev Biol* 12:181-220; Ghetie *et al.*, 2000, *Annu Rev Immunol* 18:739-766;

Ravetch *et al.*, 2001, *Annu Rev Immunol* 19:275-290, both hereby entirely incorporated by reference). The cell-mediated reaction wherein nonspecific cytotoxic cells that express FcγRs recognize bound antibody on a target cell and subsequently cause phagocytosis of the target cell is referred to as antibody dependent cell-mediated phagocytosis (ADCP). A number of structures have been solved of the extracellular domains of human FcγRs, including FcγRIIa (pdb accession code 1H9V)(Sondermann *et al.*, 2001, *J Mol Biol* 309:737-749, hereby entirely incorporated by reference) (pdb accession code 1FCG)(Maxwell *et al.*, 1999, *Nat Struct Biol* 6:437-442, hereby entirely incorporated by reference), FcγRIIb (pdb accession code 2FCB)(Sondermann *et al.*, 1999, *Embo J* 18:1095-1103, hereby entirely incorporated by reference); and FcγRIIIb (pdb accession code 1E4J)(Sondermann *et al.*, 2000, *Nature* 406:267-273, hereby entirely incorporated by reference). All FcγRs bind the same region on Fc, at the N-terminal end of the Cγ2 domain and the preceding hinge, shown in Figure 2. This interaction is well characterized structurally (Sondermann *et al.*, 2001, *J Mol Biol* 309:737-749, hereby entirely incorporated by reference), and several structures of the human Fc bound to the extracellular domain of human FcγRIIIb have been solved (pdb accession code 1E4K)(Sondermann *et al.*, 2000, *Nature* 406:267-273, hereby entirely incorporated by reference) (pdb accession codes 1IIS and 1IIX)(Radaev *et al.*, 2001, *J Biol Chem* 276:16469-16477, hereby entirely incorporated by reference), as well as has the structure of the human IgE Fc/Fc□RI□ complex (pdb accession code 1F6A)(Garman *et al.*, 2000, *Nature* 406:259-266, hereby entirely incorporated by reference).

[6] The different IgG subclasses have different affinities for the FcγRs, with IgG1 and IgG3 typically binding substantially better to the receptors than IgG2 and IgG4 (Jefferis *et al.*, 2002, *Immunol Lett* 82:57-65, hereby entirely incorporated by reference). All FcγRs bind the same region on IgG Fc, yet with different affinities: the high affinity binder FcγRI has a Kd for IgG1 of 10^{-8} M^{-1}, whereas the low affinity receptors FcγRII and FcγRIII generally bind at 10^{-6} and 10^{-5} respectively. The extracellular domains of FcγRIIIa and FcγRIIIb are 96% identical, however FcγRIIIb does not have a intracellular signaling domain. Furthermore, whereas FcγRI, FcγRIIa/c, and FcγRIIIa are positive regulators of immune complex-triggered activation, characterized by having an intracellular domain that has an immunoreceptor tyrosine-based activation motif (ITAM), FcγRIIb has an immunoreceptor tyrosine-based inhibition motif (ITIM) and is therefore inhibitory. Thus the former are referred to as activation receptors, and FcγRIIb is referred to as an inhibitory receptor. The receptors also differ in expression pattern and levels on different immune cells. Yet another level of complexity is the existence of a number of FcγR polymorphisms in the human proteome. A particularly relevant polymorphism with clinical significance is V158/F158 FcγRIIIa. Human IgG1 binds with greater affinity to the V158 allotype than to the F158 allotype. This difference in affinity, and presumably its effect on ADCC and/or ADCP, has been shown to be a significant determinant of the efficacy of the anti-CD20 antibody rituximab (Rituxan®, BiogenIdec). Patients with the V158 allotype respond favorably to rituximab treatment; however, patients with the lower affinity F158 allotype respond poorly (Cartron *et al.*, 2002, *Blood* 99:754-758, hereby entirely incorporated by reference). Approximately 10-20% of humans are V158/V158 homozygous, 45% are V158/F158 heterozygous, and 35-45% of humans are

F158/F158 homozygous (Lehrnbecher *et al.*, 1999, *Blood* 94:4220-4232; Cartron *et al.*, 2002, *Blood* 99:754-758, both hereby entirely incorporated by reference). Thus 80-90% of humans are poor responders, *e.g.*, they have at least one allele of the F158 FcγRIIIa.

[7] An overlapping but separate site on Fc, shown in Figure 1, serves as the interface for the complement protein C1q. In the same way that Fc/FcγR binding mediates ADCC, Fc/C1q binding mediates complement dependent cytotoxicity (CDC). C1q forms a complex with the serine proteases C1r and C1s to form the C1 complex. C1q is capable of binding six antibodies, although binding to two IgGs is sufficient to activate the complement cascade. Similar to Fc interaction with FcγRs, different IgG subclasses have different affinity for C1q, with IgG1 and IgG3 typically binding substantially better to the FcγRs than IgG2 and IgG4 (Jefferis *et al.*, 2002, *Immunol Lett* 82:57-65, hereby entirely incorporated by reference). There is currently no structure available for the Fc/C1q complex; however, mutagenesis studies have mapped the binding site on human IgG for C1q to a region involving residues D270, K322, K326, P329, and P331, and E333 (Idusogie *et al.*, 2000, *J Immunol* 164:4178-4184; Idusogie *et al.*, 2001, *J Immunol* 166:2571-2575, both hereby entirely incorporated by reference).

[8] A site on Fc between the Cγ2 and Cγ3 domains, shown in Figure 1, mediates interaction with the neonatal receptor FcRn, the binding of which recycles endocytosed antibody from the endosome back to the bloodstream (Raghavan *et al.*, 1996, *Annu Rev Cell Dev Biol* 12:181-220; Ghetie *et al.*, 2000, *Annu Rev Immunol* 18:739-766, both hereby entirely incorporated by reference). This process, coupled with preclusion of kidney filtration due to the large size of the full length molecule, results in favorable antibody serum half-lives ranging from one to three weeks. Binding of Fc to FcRn also plays a key role in antibody transport. The binding site for FcRn on Fc is also the site at which the bacterial proteins A and G bind. The tight binding by these proteins is typically exploited as a means to purify antibodies by employing protein A or protein G affinity chromatography during protein purification. Thus, the fidelity of this region on Fc is important for both the clinical properties of antibodies and their purification. Available structures of the rat Fc/FcRn complex (Martin *et al.*, 2001, *Mol Cell* 7:867-877, hereby entirely incorporated by reference), and of the complexes of Fc with proteins A and G (Deisenhofer, 1981, *Biochemistry* 20:2361-2370; Sauer-Eriksson *et al.*, 1995, *Structure* 3:265-278; Tashiro *et al.*, 1995, *Curr Opin Struct Biol* 5:471-481, all hereby entirely incorporated by reference) provide insight into the interaction of Fc with these proteins.

[9] A key feature of the Fc region is the conserved N-linked glycosylation that occurs at N297, shown in Figure 1. This carbohydrate, or oligosaccharide as it is sometimes referred, plays a critical structural and functional role for the antibody, and is one of the principle reasons that antibodies must be produced using mammalian expression systems. While not wanting to be limited to one theory, it is believed that the structural purpose of this carbohydrate may be to stabilize or solubilize Fc, determine a specific angle or level of flexibility between the Cγ3 and Cγ2 domains, keep the two Cγ2 domains from aggregating with one another across the central axis, or a combination of these. Efficient Fc binding to FcγR and C1q requires this modification, and alterations in the composition of the N297 carbohydrate or its elimination affect binding to these proteins (Umaña *et al.*, 1999, *Nat*

Biotechnol 17:176-180; Davies *et al.*, 2001, *Biotechnol Bioeng* 74:288-294; Mimura *et al.*, 2001, *J Biol Chem* 276:45539-45547.; Radaev *et al.*, 2001, *J Biol Chem* 276:16478-16483; Shields *et al.*, 2001, *J Biol Chem* 276:6591-6604; Shields *et al.*, 2002, *J Biol Chem* 277:26733-26740; Simmons *et al.*, 2002, *J Immunol Methods* 263:133-147, all hereby entirely incorporated by reference). Yet the carbohydrate makes little if any specific contact with FcγRs (Radaev *et al.*, 2001, *J Biol Chem* 276:16469-16477, hereby entirely incorporated by reference), indicating that the functional role of the N297 carbohydrate in mediating Fc/FcγR binding may be via the structural role it plays in determining the Fc conformation. This is supported by a collection of crystal structures of four different Fc glycoforms, which show that the composition of the oligosaccharide impacts the conformation of Cγ2 and as a result the Fc/FcγR interface (Krapp *et al.*, 2003, *J Mol Biol* 325:979-989, hereby entirely incorporated by reference).

[10] The features of antibodies discussed above - specificity for target, ability to mediate immune effector mechanisms, and long half-life in serum - make antibodies powerful therapeutics. Monoclonal antibodies are used therapeutically for the treatment of a variety of conditions including cancer, inflammation, and cardiovascular disease. There are currently over ten antibody products on the market and hundreds in development. In addition to antibodies, an antibody-like protein that is finding an expanding role in research and therapy is the Fc fusion (Chamow *et al.*, 1996, *Trends Biotechnol* 14:52-60; Ashkenazi *et al.*, 1997, *Curr Opin Immunol* 9:195-200, both hereby entirely incorporated by reference). An Fc fusion is a protein wherein one or more polypeptides is operably linked to Fc. 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 invention extends also to Fc fusions.

[11] Antibodies have found widespread application in oncology, particularly for targeting cellular antigens selectively expressed on tumor cells with the goal of cell destruction. There are a number of possible mechanisms by which antibodies destroy tumor cells, including anti-proliferation via blockage of needed growth pathways, intracellular signaling leading to apoptosis, enhanced down regulation and/or turnover of receptors, CDC, ADCC, ADCP, and promotion of an adaptive immune response (Cragg *et al.*, 1999, *Curr Opin Immunol* 11:541-547; Glennie *et al.*, 2000, *Immunol Today* 21:403-410, both hereby entirely incorporated by reference). Anti-tumor efficacy may be due to a combination of these mechanisms, and their relative importance in clinical therapy appears to be cancer dependent. Despite this arsenal of anti-tumor weapons, the potency of antibodies as anti-cancer agents is unsatisfactory, particularly given their high cost. Patient tumor response data show that monoclonal antibodies provide only a small improvement in therapeutic success over normal single-agent cytotoxic chemotherapeutics. For example, just half of all relapsed low-grade non-Hodgkin's lymphoma patients respond to the anti-CD20 antibody rituximab (McLaughlin *et al.*, 1998, *J Clin Oncol* 16:2825-2833, hereby entirely incorporated by reference). Of 166 clinical patients, 6% showed a complete response and 42% showed a partial response, with median response duration of

approximately 12 months. Trastuzumab (Herceptin®, Genentech), an anti-HER2/neu antibody for treatment of metastatic breast cancer, has less efficacy. The overall response rate using trastuzumab for the 222 patients tested was only 15%, with 8 complete and 26 partial responses and a median response duration and survival of 9 to 13 months (Cobleigh *et al.*, 1999, *J Clin Oncol* 17:2639-2648, hereby entirely incorporated by reference). Currently for anticancer therapy, any small improvement in mortality rate defines success. Thus there is a significant need to enhance the capacity of antibodies to destroy targeted cancer cells.

[12] A promising means for enhancing the anti-tumor potency of antibodies is via enhancement of their ability to mediate cytotoxic effector functions such as ADCC, ADCP, and CDC. The importance of FcγR-mediated effector functions for the anti-cancer activity of antibodies has been demonstrated in mice (Clynes *et al.*, 1998, *Proc Natl Acad Sci U S A* 95:652-656; Clynes *et al.*, 2000, *Nat Med* 6:443-446, both hereby entirely incorporated by reference), and the affinity of interaction between Fc and certain FcγRs correlates with targeted cytotoxicity in cell-based assays (Shields *et al.*, 2001, *J Biol Chem* 276:6591-6604; Presta *et al.*, 2002, *Biochem Soc Trans* 30:487-490; Shields *et al.*, 2002, *J Biol Chem* 277:26733-26740, all hereby entirely incorporated by reference). Additionally, a correlation has been observed between clinical efficacy in humans and their allotype of high (V158) or low (F158) affinity polymorphic forms of FcγRIIIa (Cartron *et al.*, 2002, *Blood* 99:754-758, hereby entirely incorporated by reference). Together these data suggest that an antibody that is optimized for binding to certain FcγRs may better mediate effector functions and thereby destroy cancer cells more effectively in patients. The balance between activating and inhibiting receptors is an important consideration, and optimal effector function may result from an antibody that has enhanced affinity for activation receptors, for example FcγRI, FcγRIIa/c, and FcγRIIIa, yet reduced affinity for the inhibitory receptor FcγRIIb. Furthermore, because FcγRs can mediate antigen uptake and processing by antigen presenting cells, optimized FcγR affinity may also improve the capacity of antibody therapeutics to elicit an adaptive immune response (Dhodapkar & Dhodapkar, 2005, Proc Natl Acad Sci USA, 102, 6243–6244, hereby entirely incorporated by reference). The importance of complement-mediated effector function for anti-cancer therapy of antibodies is not as well characterized. Antibodies optimized for CDC would provide a way to investigate the role of complement in antibody clinical applications, and provide a potential mechanism for improving the tumor killing capacity of antibodies.

[13] In contrast antibody therapeutics and indications wherein effector functions contribute to clinical efficacy, for some antibodies and clinical applications it may be favorable to reduce or eliminate binding to one or more FcγRs, or reduce or eliminate one or more FcγR- or complement-mediated effector functions including but not limited to ADCC, ADCP, and/or CDC. This is often the case for therapeutic antibodies whose mechanism of action involves blocking or antagonism but not killing of the cells bearing target antigen. In these cases depletion of target cells is undesirable and can be considered a side effect. For example, the ability of anti-CD4 antibodies to block CD4 receptors on T cells makes them effective anti-inflammatories, yet their ability to recruit FcγR receptors also directs immune attack against the target cells, resulting in T cell depletion (Reddy *et*

al., 2000, *J Immunol* 164:1925-1933, hereby entirely incorporated by reference). Effector function may also be a problem for radiolabeled antibodies, referred to as radioconjugates, and antibodies conjugated to toxins, referred to as immunotoxins. These drugs can be used to destroy cancer cells, but the recruitment of immune cells via Fc interaction with FcγRs brings healthy immune cells in proximity to the deadly payload (radiation or toxin), resulting in depletion of normal lymphoid tissue along with targeted cancer cells (Hutchins *et al.*, 1995, *Proc Natl Acad Sci U S A* 92:11980-11984; White *et al.*, 2001, *Annu Rev Med* 52:125-145, both entirely incorporated by reference). IgG isotypes that poorly recruit complement or effector cells, for example IgG2 and IgG4, can be used to address this problem in part. Fc variants that reduce or ablate Fc ligand binding are also known in the art (Alegre et al., 1994, Transplantation 57:1537-1543; Hutchins et al., 1995, Proc Natl Acad Sci USA 92:11980-11984; Armour et al., 1999, Eur J Immunol 29:2613-2624; Reddy et al., 2000, J Immunol 164:1925-1933; Xu et al., 2000, Cell Immunol 200:16-26; Shields et al., 2001, J Biol Chem 276:6591-6604; Armour et al., 1999, Eur J Immunol 29:2613-2624; US 6,194,551; US 5,885,573; PCT WO 99/58572; USSN 10/267,286, all hereby entirely incorporated by reference). However the complete Fc ligand-binding properties and effector function capacity of these variants, and their properties relative to the WT IgG isotypes, are unclear. What is needed is a general and robust means to completely ablate all FcγR binding and FcγR- and complement-mediated effector functions. A further consideration is that other important antibody properties not be perturbed. Fc variants should be engineered that not only ablate binding to FcγRs and/or C1q, but also maintain antibody stability, solubility, and structural integrity, as well as ability to interact with other important Fc ligands such as FcRn and proteins A and G.

[14] Recent success has been achieved at obtaining Fc variants with modulated binding to FcγRs and C1q, and in some cases these Fc variants have been test in for capacity to mediate FcγR- and complement-mediated effector functions (USSN 10/672,280, USSN 10/822,231, USSN 11/124,620, filed May 5, 2005, and USSN 11/256,060, filed October 21, 2005, all herein entirely incorporated by reference). Fc variants obtained in these studies provide a variety of optimal enhancements in Fc ligand and effector function properties, including but not limited to selectively improved binding to FcγRs, enhanced ADCC, improved binding to complement protein C1q, reduced binding to FcγRs, reduced binding to complement protein C1q, and other optimized properties. The present invention aims to further characterize the properties of select Fc variants from these studies, and to utilize the data to generate novel variants with optimized properties.

SUMMARY OF THE INVENTION

[15] The present invention provides Fc variants with optimized properties. Said optimized properties include altered binding to FcγR's, altered antibody dependent cell-mediated cytotoxicity, and altered complement dependent cytotoxicity relative to a parent Fc polypeptide.

[16] In one embodiment, the Fc variants of the present invention improve binding to one or more FcγR's relative to a parent Fc polypeptide. In an alternate embodiment, the Fc variants of the invention improve antibody dependent cell-mediated cytotoxicity relative to a parent Fc polypeptide. In

a preferred embodiment, said Fc variants comprise an amino acid modification at one or more positions selected from the group consisting of: 227, 234, 235, 236, 239, 246, 255, 258, 260, 264, 267, 268, 272, 281, 282, 283, 284, 293, 295, 304, 324, 327, 328, 330, 332, 335, wherein numbering is according to the EU index.

[17] In an alternate embodiment, the Fc variants of the present invention improve complement dependent cytotoxicity relative to a parent Fc polypeptide. In a preferred embodiment, said Fc variants comprise an amino acid modification at one or more positions selected from the group consisting of: 233, 234, 235, 239, 267, 268, 271, 272, 274, 276, 278, 281, 282, 284, 285, 293, 300, 320, 322, 324, 326, 327, 328, 330, 331, 332, 333, 334, and 335, wherein numbering is according to the EU index.

[18] In an alternate embodiment, the Fc variants of the present invention reduce binding to one or more FcγRs relative to a parent Fc polypeptide. In an alternate embodiment, the Fc variants of the invention reduce antibody dependent cell-mediated cytotoxicity relative to a parent Fc polypeptide. In an alternate embodiment, the Fc variants of the invention reduce complement dependent cytotoxicity relative to a parent Fc polypeptide. In a preferred embodiment, the Fc variants of the invention reduce binding to one or more FcγRs, reduce antibody dependent cell-mediated cytotoxicity, and reduce complement dependent cytotoxicity relative to a parent Fc polypeptide. In a most preferred embodiment, said Fc variants comprise one or more amino acid modifications at a position selected from the group consisting of: 232, 234, 235, 236, 237, 238, 239, 265, 267, 269, 270, 297, 299, 325, 327, 328, 329, 330, and 331, wherein numbering is according to the EU index.

[19] The present invention provides methods for engineering Fc variants with optimized properties. It is a further object of the present invention to provide experimental production and screening methods for obtaining optimized Fc variants.

[20] The present invention provides isolated nucleic acids encoding the Fc variants described herein.The present invention provides vectors comprising said nucleic acids, optionally, operably linked to control sequences. The present invention provides host cells containing the vectors, and methods for producing and optionally recovering the Fc variants.

[21] The present invention provides novel Fc polypeptides, including antibodies, Fc fusions, isolated Fc, and Fc fragments, that comprise the Fc variants disclosed herein. Said novel Fc polypeptides may find use in a therapeutic product. In a most preferred embodiment, the Fc polypeptides of the invention are antibodies.

[22] The present invention provides compositions comprising Fc polypeptides that comprise the Fc variants described herein, and a physiologically or pharmaceutically acceptable carrier or diluent.

[23] The present invention contemplates therapeutic and diagnostic uses for Fc polypeptides that comprise the Fc variants disclosed herein.

BRIEF DESCRIPTION OF THE DRAWINGS

[24] Figure 1. Antibody structure and function. Shown is a model of a full length human IgG1 antibody, modeled using a humanized Fab structure from pdb accession code 1CE1 (James et al.,

1999, J Mol Biol 289:293-301, hereby entirely incorporated by reference) and a human IgG1 Fc structure from pdb accession code 1DN2 (DeLano et al., 2000, Science 287:1279-1283, hereby entirely incorporated by reference). The flexible hinge that links the Fab and Fc regions is not shown. IgG1 is a homodimer of heterodimers, made up of two light chains and two heavy chains. The Ig domains that comprise the antibody are labeled, and include V_L and C_L for the light chain, and V_H, Cgamma1 (Cγ1), Cgamma2 (Cγ2), and Cgamma3 (Cγ3) for the heavy chain. The Fc region is labeled. Binding sites for relevant proteins are labeled, including the antigen binding site in the variable region, and the binding sites for FcγRs, FcRn, C1q, and proteins A and G in the Fc region.

[25] Figure 2. The Fc/FcγRIIIb complex structure 1IIS. Fc is shown as a gray ribbon diagram, and FcγRIIIb is shown as a black ribbon. The N297 carbohydrate is shown as black sticks.

[26] Figures 3a – 3b. Alignment of the amino acid sequences of the human IgG immunoglobulins IgG1, IgG2, IgG3, and IgG4. Figure 3a provides the sequences of the CH1 (Cγ1) and hinge domains, and Figure 3b provides the sequences of the CH2 (Cγ2) and CH3 (Cγ3) domains. Positions are numbered according to the EU index of the IgG1 sequence, and differences between IgG1 and the other immunoglobulins IgG2, IgG3, and IgG4 are shown in grey. Polymorphisms exist at a number of positions (Kim et al., 2001, J. Mol. Evol. 54:1-9, hereby entirely incorporated by reference), and thus slight differences between the presented sequences and sequences in the prior art may exist. The possible beginnings of the Fc region are labeled, defined herein as either EU position 226 or 230.

[27] Figure 4. Allotypes and isoallotypes of the gamma1 chain of human IgG1 showing the positions and the relevant amino acid substitutions (Gorman & Clark, 1990, Semin Immunol 2(6):457-66, hereby entirely incorporated by reference). For comparison the amino acids found in the equivalent positions in human IgG2, IgG3 and IgG4 gamma chains are also shown.

[28] Figure 5. Fc variants and FcγR binding data. All Fc variants were constructed in the context of the antibody PRO70769 IgG1. Fold indicates the fold IC50 relative to WT PRO70769 IgG1 for binding to human V158 and F158 FcγRIIIa as measured by the competition AlphaScreen assay.

[29] Figure 6. Binding to human V158 FcγRIIIa (Figure 6a) and F158 FcγRIIIa (Figure 6b) by select PRO70769 Fc variants as determined by the competition AlphaScreen assay. In the presence of competitor antibody (Fc variant or WT) a characteristic inhibition curve is observed as a decrease in luminescence signal. The binding data were normalized to the maximum and minimum luminescence signal for each particular curve, provided by the baselines at low and high antibody concentrations respectively. The curves represent the fits of the data to a one site competition model using nonlinear regression.

[30] Figure 7. Binding to human V158 FcγRIIIa and F158 FcγRIIIa by PRO70769 Fc variants as measured by competition AlphaScreen assay. Figure 7a provides data for select variants, Figure 7b provides the IC50's and folds relative to WT PRO70769 IgG1.

[31] Figure 8. Fc variants and FcγR binding data. All Fc variants were constructed in the context of the variable region PRO70769 and either human IgG1 or IgG(1/2) ELLGG. Figure 8a provides the

IC50's and fold IC50's relative to WT PRO70769 IgG1 for binding to human activating receptors V158 and F158 FcγRIIIa, and the inhibitory receptor FcγRIIb, as measured by competition AlphaScreen assay. Figure 8b shows the AlphaScreen data for select variants.

[32] Figure 9. Competition Surface Plasmon Resonance (SPR) experiment measuring binding affinities of I332E and S239D/I332E variants in the context of trastuzumab to human V158 FcγRIIIa. Figure 9a provides the sensorgram raw data, Figure 9b provides a plot of the log of receptor concentration against the initial rate obtained at each concentration, and Figure 9c provides the affinities obtained from the fits to these data as described in Example 1.

[33] Figure 10. Cell-based ADCC assays of select Fc variants in the context of the anti-CD20 antibody PRO70769. ADCC was measured by the release of lactose dehydrogenase using a LDH Cytotoxicity Detection Kit (Roche Diagnostic). CD20+ lymphoma WIL2-S cells were used as target cells and human PBMCs were used as effector cells. Shown is the dose-dependence of ADCC on antibody concentration for the indicated antibodies, normalized to the minimum and maximum fluorescence signal for each particular curve, provided by the baselines at low and high antibody concentrations respectively. The curves represent the fits of the data to a sigmoidal dose-response model using nonlinear regression.

[34] Figure 11. Cell-based ADCC assay of select Fc variants in the context of PRO70769 IgG1 in the absence and presence of serum levels of human IgG. ADCC was measured by the release of lactose dehydrogenase using a LDH Cytotoxicity Detection Kit (Roche Diagnostic). CD20+ lymphoma WIL2-S cells were used as target cells and human PBMCs were used as effector cells.

[35] Figure 12. Residues mutated in Fc variants designed to enhance CDC. The structure of the human IgG1 Fc region is shown (pdb accession code 1E4K, Sondermann *et al.*, 2000, *Nature* 406:267-273, hereby entirely incorporated by reference). Black ball and sticks indicate residues D270, K322, P329, and P331, which have been shown to be important in mediating binding to complement protein C1q, and grey sticks indicate residues that were mutated in the present invention to explore variants that affect CDC.

[36] Figure 13. Fc variants screened for complement-mediated cytotoxicity (CDC) and CDC data. The variable region is that of the anti-CD20 antibody PRO70769, and the heavy chain constant region is IgG1 unless noted IgG(1/2) ELLGG. Fold CDC provides the relative CDC activity compared to WT PRO70769 IgG1.

[37] Figure 14. CDC assays of Fc variant anti-CD20 antibodies. The dose-dependence on antibody concentration of complement-mediated lysis is shown for the indicated PRO70769 antibodies against CD20+ WIL2-S lymphoma target cells. Lysis was measured using release of Alamar Blue, and data were normalized to the minimum and maximum fluorescence signal for each particular curve, provided by the baselines at low and high antibody concentrations respectively. The curves represent the fits of the data to a sigmoidal dose-response model with variable slope using nonlinear regression.

[38] Figure 15. Amino acid modifications that provide enhanced and reduced CDC, and positions that may be modified that may provide enhanced/modulated CDC. Positions are numbered according to the EU index.

[39] Figure 16. Fc variants screened for reduced FcγR affinity, FcγR-mediated effector function, and complement-mediated effector function. The variable region is that of the anti-CD20 antibody PRO70769, and the heavy chain constant region is IgG1. The figure provides the Fold IC50 for binding to human V158 FcγRIIIa and the Fold EC50 of CDC activity relative to WT PRO70769 IgG1.

[40] Figure 17. Binding to human V158 FcγRIIIa by select PRO70769 Fc variants as determined by the competition AlphaScreen assay.

[41] Figure 18. CDC assays of select Fc variant anti-CD20 antibodies against CD20+ WIL2-S lymphoma target cells. Lysis was measured by Alamar Blue release.

[42] Figure 19. Cell-based ADCC activity of select anti-CD20 Fc variants against CD20+ lymphoma WIL2-S cells. Human PBMCs were used as effector cells, and lysis was measured by LDH release.

[43] Figure 20. Fc variants screened for reduced FcγR affinity, FcγR-mediated effector function, and complement-mediated effector function. The variable region is that of the anti-CD20 antibody PRO70769, and the heavy chain constant region is IgG1. The figure provides the Fold IC50 relative to WT for binding to human V158 FcγRIIIa by two separate experiments, the Fold IC50 relative to WT for binding to human FcγRI, and the Fold EC50 relative to WT for CDC activity.

[44] Figure 21. Binding to the low affinity human activating receptor V158 FcγRIIIa and the high affinity human activating receptor FcγRI by select PRO70769 Fc variants as determined by the competition AlphaScreen assay.

[45] Figure 22. CDC activity of select PRO70769 Fc variants against CD20+ WIL2-S lymphoma target cells. Lysis was measured by release of Alamar Blue.

[46] Figure 23. Cell-based ADCC activity of anti-Her2 Fc variant and WT IgG antibodies against Her2/neu+ SkBr-3 breast carcinoma target cells. Human PBMCs were used as effector cells, and lysis was measured by LDH release.

[47] Figure 24. Amino acid sequences of variable light (VL) and heavy (VH) chains used in the present invention, including PRO70769 (Figures 24a and 24b), trastuzumab (Figures 24c and 24d), and ipilimumab (Figures 24e and 24f).

[48] Figure 25. Amino acid sequences of human constant light kappa (Figure 25a) and heavy (Figures 25b – 25f) chains used in the present invention.

[49] Figure 26. Sequences showing possible constant heavy chain sequences with reduced Fc ligand binding and effector function properties (Figure 26a), and sequences of improved anti-CTLA-4 antibodies (Figures 26b – 26d). Figure 26a shows potential Fc variant constant heavy chain sequences, with variable positions designated in bold as X1, X2, X3, X4, X5, X6, X7, and X8. The

table below the sequence provides the WT amino acid and possible substitutions for these positions. Improved antibody sequences may comprise one or more non-WT amino acid selected from this group of possible modifications. Figure 26b provides the light chain sequence of an anti-CTLA-4 antibody, and Figures 26c and 26d provide heavy chain sequences of anti-CTLA-4 antibodies with reduced Fc ligand binding and Fc-mediated effector function. These include an L235G/G236R IgG1 heavy chain (Figure 26c) and an IgG2 heavy chain (Figure 26d). The positions are numbered according to the EU index as in Kabat, and thus do not correspond to the sequential order in the sequence.

DETAILED DESCRIPTION OF THE INVENTION

[50] In order that the invention may be more completely understood, several definitions are set forth below. Such definitions are meant to encompass grammatical equivalents.

[51] By "ADCC" or "antibody dependent cell-mediated cytotoxicity" as used herein is meant the cell-mediated reaction wherein nonspecific cytotoxic cells that express Fc□Rs recognize bound antibody on a target cell and subsequently cause lysis of the target cell.

[52] By "ADCP" or antibody dependent cell-mediated phagocytosis as used herein is meant the cell-mediated reaction wherein nonspecific cytotoxic cells that express Fc□Rs recognize bound antibody on a target cell and subsequently cause phagocytosis of the target cell.

[53] By "amino acid modification" herein is meant an amino acid substitution, insertion, and/or deletion in a polypeptide sequence. By "amino acid substitution" or "substitution" herein is meant the replacement of an amino acid at a particular position in a parent polypeptide sequence with another amino acid. For example, the substitution L328R refers to a variant polypeptide, in this case an Fc variant, in which the leucine at position 328 is replaced with arginine. By "amino acid insertion" or "insertion" as used herein is meant the addition of an amino acid at a particular position in a parent polypeptide sequence. For example, insert G > 235-236 designates an insertion of glycine between positions 235 and 236. By "amino acid deletion" or "deletion" as used herein is meant the removal of an amino acid at a particular position in a parent polypeptide sequence. For example, G236- designates the deletion of glycine at position 236. Amino acids of the invention may be further classified as either isotypic or novel.

[54] By "CDC" or "complement dependent cytotoxicity" as used herein is meant the reaction wherein one or more complement protein components recognize bound antibody on a target cell and subsequently cause lysis of the target cell.

[55] By "isotypic modification" as used herein is meant an amino acid modification that converts one amino acid of one isotype to the corresponding amino amino acid in a different, aligned isotype. For example, because IgG1 has a tyrosine and IgG2 a phenylalanine at EU position 296, a F296Y substitution in IgG2 is considered an isotypic modification.

[56] By "novel modification" as used herein is meant an amino acid modification that is not isotypic. For example, because none of the IgGs has a glutamic acid at position 332, the substitution I332E in IgG1, IgG2, IgG3, or IgG4 is considered a novel modification.

[57] By "amino acid" and "amino acid identity" as used herein is meant one of the 20 naturally occurring amino acids or any non-natural analogues that may be present at a specific, defined position.

[58] By "effector function" as used herein is meant a biochemical event that results from the interaction of an antibody Fc region with an Fc receptor or ligand. Effector functions include FcγR-mediated effector functions such as ADCC and ADCP, and complement-mediated effector functions such as CDC.

[59] By "effector cell" as used herein is meant a cell of the immune system that expresses one or more Fc receptors and mediates one or more effector functions. Effector cells include but are not limited to monocytes, macrophages, neutrophils, dendritic cells, eosinophils, mast cells, platelets, B cells, large granular lymphocytes, Langerhans' cells, natural killer (NK) cells, and □□ T cells, and may be from any organism including but not limited to humans, mice, rats, rabbits, and monkeys.

[60] By "Fab" or "Fab region" as used herein is meant the polypeptides that comprise the V_H, CH1, V_H, and C_L immunoglobulin domains. Fab may refer to this region in isolation, or this region in the context of a full length antibody or antibody fragment.

[61] By "Fc" or "Fc region", as used herein is meant the polypeptide comprising the constant region of an antibody excluding the first constant region immunoglobulin domain. Thus Fc refers to the last two constant region immunoglobulin domains of IgA, IgD, and IgG, and the last three constant region immunoglobulin domains of IgE and IgM, and the flexible hinge N-terminal to these domains. For IgA and IgM, Fc may include the J chain. For IgG, as illustrated in Figure 1, Fc comprises immunoglobulin domains Cgamma2 and Cgamma3 (Cγ2 and Cγ3) and the hinge between Cgamma1 (Cγ1) and Cgamma2 (Cγ2). Although the boundaries of the Fc region may vary, the human IgG heavy chain Fc region is usually defined to comprise residues C226 or P230 to its carboxyl-terminus, wherein the numbering is according to the EU index as in Kabat. Fc may refer to this region in isolation, or this region in the context of an Fc polypeptide, as described below. By "Fc polypeptide" as used herein is meant a polypeptide that comprises all or part of an Fc region. Fc polypeptides include antibodies, Fc fusions, isolated Fcs, and Fc fragments.

[62] By "Fc fusion" as used herein is meant a protein wherein one or more polypeptides is operably linked to Fc. Fc fusion is herein meant to be synonymous with the terms "immunoadhesin", "Ig fusion", "Ig chimera", and "receptor globulin" (sometimes with dashes) as used in the prior art (Chamow *et al.*, 1996, *Trends Biotechnol* 14:52-60; Ashkenazi *et al.*, 1997, *Curr Opin Immunol* 9:195-200, both hereby entirely incorporated by reference). An Fc fusion combines the Fc region of an immunoglobulin with a fusion partner, which in general may be any protein, polypeptide or small molecule. The role of the non-Fc part of an Fc fusion, *i.e.,* the fusion partner, is to mediate target binding, and thus it is functionally analogous to the variable regions of an antibody. Virtually any protein or small molecule may be linked to Fc to generate an Fc fusion. Protein fusion partners may include, but are not limited to, the target-binding region of a receptor, an adhesion molecule, a ligand, an enzyme, a cytokine, a chemokine, or some other protein or protein domain. Small molecule fusion

partners may include any therapeutic agent that directs the Fc fusion to a therapeutic target. Such targets may be any molecule, preferrably an extracellular receptor that is implicated in disease.

[63] By "Fc gamma receptor" or "Fc□R" as used herein is meant any member of the family of proteins that bind the IgG antibody Fc region and are substantially encoded by the Fc□R genes. In humans this family includes but is not limited to FcγRI (CD64), including isoforms FcγRIa, FcγRIb, and FcγRIc; FcγRII (CD32), including isoforms FcγRIIa (including allotypes H131 and R131), FcγRIIb (including FcγRIIb-1 and FcγRIIb-2), and FcγRIIc; and FcγRIII (CD16), including isoforms FcγRIIIa (including allotypes V158 and F158) and FcγRIIIb (including allotypes FcγRIIIb-NA1 and FcγRIIIb-NA2) (Jefferis *et al.*, 2002, *Immunol Lett* 82:57-65, hereby entirely incorporated by reference), as well as any undiscovered human Fc□Rs or FcγR isoforms or allotypes. An FcγR may be from any organism, including but not limited to humans, mice, rats, rabbits, and monkeys. Mouse Fc□Rs include but are not limited to Fc□RI (CD64), Fc□RII (CD32), Fc□RIII (CD16), and Fc□RIII-2 (CD16-2), as well as any undiscovered mouse Fc□Rs or FcγR isoforms or allotypes.

[64] By "Fc ligand" as used herein is meant a molecule, preferably a polypeptide, from any organism that binds to the Fc region of an antibody to form an Fc / Fc ligand complex. Fc ligands include but are not limited to FcγRs, FcγRs, FcγRs, FcRn, C1q, C3, mannan binding lectin, mannose receptor, *staphylococcal* protein A, *streptococcal* protein G, and viral FcγR. Fc ligands also include Fc receptor homologs (FcRH), which are a family of Fc receptors that are homologous to the Fc□Rs (Davis *et al.*, 2002, *Immunological Reviews* 190:123-136, hereby entirely incorporated by reference). Fc ligands may include undiscovered molecules that bind Fc.

[65] By "full length antibody"as used herein is meant the structure that constitutes the natural biological form of an antibody, including variable and constant regions. For example, in most mammals, including humans and mice, the full length antibody of the IgG isotype is a tetramer and consists of two identical pairs of two immunoglobulin chains, each pair having one light and one heavy chain, each light chain comprising immunoglobulin domains V_L and C_L, and each heavy chain comprising immunoglobulin domains V_H, C□1, C□2, and C□3. In some mammals, for example in camels and llamas, IgG antibodies may consist of only two heavy chains, each heavy chain comprising a variable domain attached to the Fc region.

[66] By "IgG" as used herein is meant a polypeptide belonging to the class of antibodies that are substantially encoded by a recognized immunoglobulin gamma gene. In humans this IgG comprises the subclasses or isotypes IgG1, IgG2, IgG3, and IgG4. In mice IgG comprises IgG1, IgG2a, IgG2b, IgG3.

[67] By "immunoglobulin (Ig)" herein is meant a protein consisting of one or more polypeptides substantially encoded by immunoglobulin genes. Immunoglobulins include but are not limited to antibodies. Immunoglobulins may have a number of structural forms, including but not limited to full length antibodies, antibody fragments, and individual immunoglobulin domains.

[68] By "immunoglobulin (Ig) domain"as used herein is meant a region of an immunoglobulin that exists as a distinct structural entity as ascertained by one skilled in the art of protein structure. Ig

domains typically have a characteristic □-sandwich folding topology. The known Ig domains in the IgG isotype of antibodies are V_H, C□1, C□2, C□3, V_L, and C_L.

[69] By "IgG" or "IgG immunoglobulin" as used herein is meant a polypeptide belonging to the class of antibodies that are substantially encoded by a recognized immunoglobulin gamma gene. In humans this class comprises the subclasses or isotypes IgG1, IgG2, IgG3, and IgG4. By "isotype" as used herein is meant any of the subclasses of immunoglobulins defined by the chemical and antigenic characteristics of their constant regions. The known human immunoglobulin isotypes are IgG1, IgG2, IgG3, IgG4, IgA1, IgA2, IgM, IgD, and IgE.

[70] By "parent polypeptide", "parent protein", "precursor polypeptide", or "precursor protein" as used herein is meant an unmodified polypeptide that is subsequently modified to generate a variant. Said parent polypeptide may be a naturally occurring polypeptide, or a variant or engineered version of a naturally occurring polypeptide. Parent polypeptide may refer to the polypeptide itself, compositions that comprise the parent polypeptide, or the amino acid sequence that encodes it. Accordingly, by "parent Fc polypeptide" as used herein is meant an Fc polypeptide that is modified to generate a variant, and by "parent antibody" as used herein is meant an antibody that is modified to generate a variant antibody.

[71] By "position" as used herein is meant a location in the sequence of a protein. Positions may be numbered sequentially, or according to an established format, for example the EU index as in Kabat. For example, position 297 is a position in the human antibody IgG1.

[72] By "polypeptide" or "protein" as used herein is meant at least two covalently attached amino acids, which includes proteins, polypeptides, oligopeptides and peptides.

[73] By "residue" as used herein is meant a position in a protein and its associated amino acid identity. For example, Asparagine 297 (also referred to as Asn297, also referred to as N297) is a residue in the human antibody IgG1.

[74] By "target antigen" as used herein is meant the molecule that is bound specifically by the variable region of a given antibody. A target antigen may be a protein, carbohydrate, lipid, or other chemical compound.

[75] By "target cell" as used herein is meant a cell that expresses a target antigen.

[76] By "variable region" as used herein is meant the region of an immunoglobulin that comprises one or more Ig domains substantially encoded by any of the V□, V□, and/or V_H genes that make up the kappa, lambda, and heavy chain immunoglobulin genetic loci respectively.

[77] By "variant polypeptide", "polypeptide variant", or "variant" as used herein is meant a polypeptide sequence that differs from that of a parent polypeptide sequence by virtue of at least one amino acid modification. The parent polypeptide may be a naturally occurring or wild-type (WT) polypeptide, or may be a modified version of a WT polypeptide. Variant polypeptide may refer to the polypeptide itself, a composition comprising the polypeptide, or the amino sequence that encodes it. Preferably, the variant polypeptide has at least one amino acid modification compared to the parent

polypeptide, e.g. from about one to about ten amino acid modifications, and preferably from about one to about five amino acid modifications compared to the parent. The variant polypeptide sequence herein will preferably possess at least about 80% homology with a parent polypeptide sequence, and most preferably at least about 90% homology, more preferably at least about 95% homology. Accordingly, by "Fc variant" or "variant Fc" as used herein is meant an Fc sequence that differs from that of a parent Fc sequence by virtue of at least one amino acid modification. An Fc variant may only encompass an Fc region, or may exist in the context of an antibody, Fc fusion, isolated Fc, Fc fragment, or other polypeptide that is substantially encoded by Fc. Fc variant may refer to the Fc polypeptide itself, compositions comprising the Fc variant polypeptide, or the amino acid sequence that encodes it. By "Fc polypeptide variant" or "variant Fc polypeptide" as used herein is meant an Fc polypeptide that differs from a parent Fc polyeptide by virtue of at least one amino acid modification. By "protein variant" or "variant protein" as used herein is meant a protein that differs from a parent protein by virtue of at least one amino acid modification. By "antibody variant" or "variant antibody" as used herein is meant an antibody that differs from a parent antibody by virtue of at least one amino acid modification. By "IgG variant" or "variant IgG" as used herein is meant an antibody that differs from a parent IgG by virtue of at least one amino acid modification. By "immunoglobulin variant" or "variant immunoglobluin" as used herein is meant an immunoglobulin sequence that differs from that of a parent immunoglobulin sequence by virtue of at least one amino acid modification.

[78] By "wild type or WT" herein is meant an amino acid sequence or a nucleotide sequence that is found in nature, including allelic variations. A WT protein, polypeptide, antibody, immunoglobulin, IgG, etc. has an amino acid sequence or a nucleotide sequence that has not been intentionally modified.

Antibodies

[79]Accordingly, the present invention provides variant antibodies.

[80]Traditional antibody structural units typically comprise a tetramer. Each tetramer is typically composed of two identical pairs of polypeptide chains, each pair having one "light" (typically having a molecular weight of about 25 kDa) and one "heavy" chain (typically having a molecular weight of about 50-70 kDa). Human light chains are classified as kappa and lambda light chains. Heavy chains are classified as mu, delta, gamma, alpha, or epsilon, and define the antibody's isotype as IgM, IgD, IgG, IgA, and IgE, respectively. IgG has several subclasses, including, but not limited to IgG1, IgG2, IgG3, and IgG4. IgM has subclasses, including, but not limited to, IgM1 and IgM2. Thus, "isotype" as used herein is meant any of the subclasses of immunoglobulins defined by the chemical and antigenic characteristics of their constant regions. The known human immunoglobulin isotypes are IgG1, IgG2, IgG3, IgG4, IgA1, IgA2, IgM1, IgM2, IgD, and IgE.

[81]The amino-terminal portion of each chain includes a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. In the variable region, three loops are gathered for each of the V domains of the heavy chain and light chain to form an antigen-binding site. Each of the loops is referred to as a complementarity-determining region (hereinafter referred to as a "CDR"), in which the variation in the amino acid sequence is most significant.

[82]The carboxy-terminal portion of each chain defines a constant region primarily responsible for effector function. Kabat et al. collected numerous primary sequences of the variable regions of heavy chains and light chains. Based on the degree of conservation of the sequences, they classified individual primary sequences into the CDR and the framework and made a list thereof (see SEQUENCES OF IMMUNOLOGICAL INTEREST, 5th edition, NIH publication, No. 91-3242, E.A. Kabat et al.).

[83]In the IgG subclass of immunoglobulins, there are several immunoglobulin domains in the heavy chain. By "immunoglobulin (Ig) domain" herein is meant a region of an immunoglobulin having a distinct tertiary structure. Of interest in the present invention are the heavy chain domains, including, the constant heavy (CH) domains and the hinge domains. In the context of IgG antibodies, the IgG isotypes each have three CH regions. Accordingly, "CH" domains in the context of IgG are as follows: "CH1" refers to positions 118-220 according to the EU index as in Kabat. "CH2" refers to positions 237-340 according to the EU index as in Kabat, and "CH3" refers to positions 341-447 according to the EU index as in Kabat.

[84]Another type of Ig domain of the heavy chain is the hinge region. By "hinge" or "hinge region" or "antibody hinge region" or "immunoglobulin hinge region" herein is meant the flexible polypeptide comprising the amino acids between the first and second constant domains of an antibody. Structurally, the IgG CH1 domain ends at EU position 220, and the IgG CH2 domain begins at residue EU position 237. Thus for IgG the antibody hinge is herein defined to include positions 221 (D221 in IgG1) to 236 (G236 in IgG1), wherein the numbering is according to the EU index as in Kabat. In some embodiments, for example in the context of an Fc region, the lower hinge is included, with the "lower hinge" generally referring to positions 226 or 230.

[85]Of particular interest in the present invention are the Fc regions. By "Fc" or "Fc region", as used herein is meant the polypeptide comprising the constant region of an antibody excluding the first constant region immunoglobulin domain and in some cases, part of the hinge. Thus Fc refers to the last two constant region immunoglobulin domains of IgA, IgD, and IgG, and the last three constant region immunoglobulin domains of IgE and IgM, and the flexible hinge N-terminal to these domains. For IgA and IgM, Fc may include the J chain. For IgG, as illustrated in Figure 1, Fc comprises immunoglobulin domains Cgamma2 and Cgamma3 (Cg2 and Cg3) and the lower hinge region between Cgamma1 (Cg1) and Cgamma2 (Cg2). Although the boundaries of the Fc region may vary, the human IgG heavy chain Fc region is usually defined to include residues C226 or P230 to its carboxyl-terminus, wherein the numbering is according to the EU index as in Kabat. Fc may refer to this region in isolation, or this region in the context of an Fc polypeptide, as described below. By "Fc polypeptide" as used herein is meant a polypeptide that comprises all or part of an Fc region. Fc polypeptides include antibodies, Fc fusions, isolated Fcs, and Fc fragments.

[86]In some embodiments, the antibodies are full length. By "full length antibody" herein is meant the structure that constitutes the natural biological form of an antibody, including variable and constant regions, including one or more modifications as outlined herein.

[87]Alternatively, the antibodies can be a variety of structures, including, but not limited to, antibody fragments, monoclonal antibodies, bispecific antibodies, minibodies, domain antibodies, synthetic antibodies (sometimes referred to herein as "antibody mimetics"), chimeric antibodies, humanized antibodies, antibody fusions (sometimes referred to as "antibody conjugates"), and fragments of each, respectively.

Antibody Fragments

[88]In one embodiment, the antibody is an antibody fragment. Of particular interest are antibodies that comprise Fc regions, Fc fusions, and the constant region of the heavy chain (CH1-hinge-CH2-CH3), again also including constant heavy region fusions.

[89]Specific antibody fragments include, but are not limited to, (i) the Fab fragment consisting of VL, VH, CL and CH1 domains, (ii) the Fd fragment consisting of the VH and CH1 domains, (iii) the Fv fragment consisting of the VL and VH domains of a single antibody; (iv) the dAb fragment (Ward et al., 1989, Nature 341:544-546) which consists of a single variable, (v) isolated CDR regions, (vi) F(ab')2 fragments, a bivalent fragment comprising two linked Fab fragments (vii) single chain Fv molecules (scFv), wherein a VH domain and a VL domain are linked by a peptide linker which allows the two domains to associate to form an antigen binding site (Bird et al., 1988, Science 242:423-426, Huston et al., 1988, Proc. Natl. Acad. Sci. U.S.A. 85:5879-5883), (viii) bispecific single chain Fv dimers (PCT/US92/09965) and (ix) "diabodies" or "triabodies", multivalent or multispecific fragments constructed by gene fusion (Tomlinson et. al., 2000, Methods Enzymol. 326:461-479; WO94/13804; Holliger et al., 1993, Proc. Natl. Acad. Sci. U.S.A. 90:6444-6448). The antibody fragments may be modified. For example, the molecules may be stabilized by the incorporation of disulphide bridges linking the VH and VL domains (Reiter et al., 1996, Nature Biotech. 14:1239-1245).

Chimeric and Humanized Antibodies

[90]In some embodiments, the scaffold components can be a mixture from different species. As such, if the antibody is an antibody, such antibody may be a chimeric antibody and/or a humanized antibody. In general, both "chimeric antibodies" and "humanized antibodies" refer to antibodies that combine regions from more than one species. For example, "chimeric antibodies" traditionally comprise variable region(s) from a mouse (or rat, in some cases) and the constant region(s) from a human. "Humanized antibodies" generally refer to non-human antibodies that have had the variable-domain framework regions swapped for sequences found in human antibodies. Generally, in a humanized antibody, the entire antibody, except the CDRs, is encoded by a polynucleotide of human origin or is identical to such an antibody except within its CDRs. The CDRs, some or all of which are encoded by nucleic acids originating in a non-human organism, are grafted into the beta-sheet framework of a human antibody variable region to create an antibody, the specificity of which is determined by the engrafted CDRs. The creation of such antibodies is described in, e.g., WO 92/11018, Jones, 1986, Nature 321:522-525, Verhoeyen et al., 1988, Science 239:1534-1536. "Backmutation" of selected acceptor framework residues to the corresponding donor residues is often required to regain affinity that is lost in the initial grafted construct (US 5530101; US 5585089; US 5693761; US 5693762; US 6180370; US 5859205; US 5821337; US 6054297; US 6407213). The

humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region, typically that of a human immunoglobulin, and thus will typically comprise a human Fc region. Humanized antibodies can also be generated using mice with a genetically engineered immune system. Roque et al., 2004, Biotechnol. Prog. 20:639-654. A variety of techniques and methods for humanizing and reshaping non-human antibodies are well known in the art (See Tsurushita & Vasquez, 2004, Humanization of Monoclonal Antibodies, Molecular Biology of B Cells, 533-545, Elsevier Science (USA), and references cited therein). Humanization methods include but are not limited to methods described in Jones *et al.*, 1986, *Nature* 321:522-525; Riechmann *et al.*,1988; *Nature* 332:323-329; Verhoeyen *et al.*, 1988, *Science*, 239:1534-1536; *Queen et al.*, 1989, *Proc Natl Acad Sci*, USA 86:10029-33; He et al., 1998, J. Immunol. 160: 1029-1035; Carter *et al.*, 1992, *Proc Natl Acad Sci USA 89:4285-9*, Presta et al., 1997, Cancer Res.57(20):4593-9; Gorman et al., 1991, Proc. Natl. Acad. Sci. USA 88:4181-4185; O'Connor *et al.*, 1998, *Protein Eng* 11:321-8. Humanization or other methods of reducing the immunogenicity of nonhuman antibody variable regions may include resurfacing methods, as described for example in Roguska et al., 1994, Proc. Natl. Acad. Sci. USA 91:969-973. In one embodiment, the parent antibody has been affinity matured, as is known in the art. Structure-based methods may be employed for humanization and affinity maturation, for example as described in USSN 11/004,590. Selection based methods may be employed to humanize and/or affinity mature antibody variable regions, including but not limited to methods described in Wu et al., 1999, J. Mol. Biol. 294:151-162; Baca et al., 1997, J. Biol. Chem. 272(16):10678-10684; Rosok et al., 1996, J. Biol. Chem. 271(37): 22611-22618; Rader et al., 1998, Proc. Natl. Acad. Sci. USA 95: 8910-8915; Krauss et al., 2003, Protein Engineering 16(10):753-759. Other humanization methods may involve the grafting of only parts of the CDRs, including but not limited to methods described in USSN 09/810,502; Tan et al., 2002, J. Immunol. 169:1119-1125; De Pascalis et al., 2002, J. Immunol. 169:3076-3084.

Bispecific Antibodies

[91]In one embodiment, the antibodies of the invention multispecific antibody, and notably a bispecific antibody, also sometimes referred to as "diabodies". These are antibodies that bind to two (or more) different antigens. Diabodies can be manufactured in a variety of ways known in the art (Holliger and Winter, 1993, Current Opinion Biotechnol. 4:446-449), e.g., prepared chemically or from hybrid hybridomas.

Minibodies

[92]In one embodiment, the antibody is a minibody. Minibodies are minimized antibody-like proteins comprising a scFv joined to a CH3 domain. Hu et al., 1996, Cancer Res. 56:3055-3061. In some cases, the scFv can be joined to the Fc region, and may include some or all of the hinge region.

Human Antibodies

[93]In one embodiment, the antibody is a fully human antibody with at least one modification as outlined herein. "Fully human antibody " or "complete human antibody" refers to a human antibody

having the gene sequence of an antibody derived from a human chromosome with the modifications outlined herein.

Antibody Fusions

[94]In one embodiment, the antibodies of the invention are antibody fusion proteins (sometimes referred to herein as an "antibody conjugate"). One type of antibody fusions are Fc fusions, which join the Fc region with a conjugate partner. By "Fc fusion" as used herein is meant a protein wherein one or more polypeptides is operably linked to an Fc region. Fc fusion is herein meant to be synonymous with the terms "immunoadhesin", "Ig fusion", "Ig chimera", and "receptor globulin" (sometimes with dashes) as used in the prior art (Chamow et al., 1996, Trends Biotechnol 14:52-60; Ashkenazi et al., 1997, Curr Opin Immunol 9:195-200). An Fc fusion combines the Fc region of an immunoglobulin with a fusion partner, which in general can be any protein or small molecule. Virtually any protein or small molecule may be linked to Fc to generate an Fc fusion. Protein fusion partners may include, but are not limited to, the variable region of any antibody, the target-binding region of a receptor, an adhesion molecule, a ligand, an enzyme, a cytokine, a chemokine, or some other protein or protein domain. Small molecule fusion partners may include any therapeutic agent that directs the Fc fusion to a therapeutic target. Such targets may be any molecule, preferably an extracellular receptor, that is implicated in disease.

[95]In addition to Fc fusions, antibody fusions include the fusion of the constant region of the heavy chain with one or more fusion partners (again including the variable region of any antibody), while other antibody fusions are substantially or completely full length antibodies with fusion partners. In one embodiment, a role of the fusion partner is to mediate target binding, and thus it is functionally analogous to the variable regions of an antibody (and in fact can be). Virtually any protein or small molecule may be linked to Fc to generate an Fc fusion (or antibody fusion). Protein fusion partners may include, but are not limited to, the target-binding region of a receptor, an adhesion molecule, a ligand, an enzyme, a cytokine, a chemokine, or some other protein or protein domain. Small molecule fusion partners may include any therapeutic agent that directs the Fc fusion to a therapeutic target. Such targets may be any molecule, preferably an extracellular receptor, that is implicated in disease.

[96]The conjugate partner can be proteinaceous or non-proteinaceous; the latter generally being generated using functional groups on the antibody and on the conjugate partner. For example linkers are known in the art; for example, homo-or hetero-bifunctional linkers as are well known (see, 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200, incorporated herein by reference).

[97]Suitable conjugates include, but are not limited to, labels as described below, drugs and cytotoxic agents including, but not limited to, cytotoxic drugs (e.g., chemotherapeutic agents) or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diptheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Additional embodiments utilize calicheamicin, auristatins, geldanamycin, maytansine, and

duocarmycins and analogs; for the latter, see U.S. 2003/0050331, hereby incorporated by reference in its entirety.

Covalent modifications of Antibodies

[98]Covalent modifications of antibodies are included within the scope of this invention, and are generally, but not always, done post-translationally. For example, several types of covalent modifications of the antibody are introduced into the molecule by reacting specific amino acid residues of the antibody with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C-terminal residues.

[99]Cysteinyl residues most commonly are reacted with α-haloacetates (and corresponding amines), such as chloroacetic acid or chloroacetamide, to give carboxymethyl or carboxyamidomethyl derivatives. Cysteinyl residues also are derivatized by reaction with bromotrifluoroacetone, α-bromo-β-(5-imidozoyl)propionic acid, chloroacetyl phosphate, N-alkylmaleimides, 3-nitro-2-pyridyl disulfide, methyl 2-pyridyl disulfide, p-chloromercuribenzoate, 2-chloromercuri-4-nitrophenol, or chloro-7-nitrobenzo-2-oxa-1,3-diazole.

[100] Histidyl residues are derivatized by reaction with diethylpyrocarbonate at pH 5.5-7.0 because this agent is relatively specific for the histidyl side chain. Para-bromophenacyl bromide also is useful; the reaction is preferably performed in 0.1M sodium cacodylate at pH 6.0.

[101] Lysinyl and amino terminal residues are reacted with succinic or other carboxylic acid anhydrides. Derivatization with these agents has the effect of reversing the charge of the lysinyl residues. Other suitable reagents for derivatizing alpha-amino-containing residues include imidoesters such as methyl picolinimidate; pyridoxal phosphate; pyridoxal; chloroborohydride; trinitrobenzenesulfonic acid; O-methylisourea; 2,4-pentanedione; and transaminase-catalyzed reaction with glyoxylate.

[102] Arginyl residues are modified by reaction with one or several conventional reagents, among them phenylglyoxal, 2,3-butanedione, 1,2-cyclohexanedione, and ninhydrin. Derivatization of arginine residues requires that the reaction be performed in alkaline conditions because of the high pKa of the guanidine functional group. Furthermore, these reagents may react with the groups of lysine as well as the arginine epsilon-amino group.

[103] The specific modification of tyrosyl residues may be made, with particular interest in introducing spectral labels into tyrosyl residues by reaction with aromatic diazonium compounds or tetranitromethane. Most commonly, N-acetylimidizole and tetranitromethane are used to form O-acetyl tyrosyl species and 3-nitro derivatives, respectively. Tyrosyl residues are iodinated using 125I or 131I to prepare labeled proteins for use in radioimmunoassay, the chloramine T method described above being suitable.

[104] Carboxyl side groups (aspartyl or glutamyl) are selectively modified by reaction with carbodiimides (R'—N=C=N--R'), where R and R' are optionally different alkyl groups, such as 1-cyclohexyl-3-(2-morpholinyl-4-ethyl) carbodiimide or 1-ethyl-3-(4-azonia-4,4-dimethylpentyl)

carbodiimide. Furthermore, aspartyl and glutamyl residues are converted to asparaginyl and glutaminyl residues by reaction with ammonium ions.

[105] Derivatization with bifunctional agents is useful for crosslinking antibodies to a water-insoluble support matrix or surface for use in a variety of methods, in addition to methods described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis (succinimidylpropionate), and bifunctional maleimides such as bis-N-maleimido-1,8-octane. Derivatizing agents such as methyl-3-[(p-azidophenyl)dithio]propioimidate yield photoactivatable intermediates that are capable of forming crosslinks in the presence of light. Alternatively, reactive water-insoluble matrices such as cyanogen bromide-activated carbohydrates and the reactive substrates described in U.S. Pat. Nos. 3,969,287; 3,691,016; 4,195,128; 4,247,642; 4,229,537; and 4,330,440 are employed for protein immobilization.

[106] Glutaminyl and asparaginyl residues are frequently deamidated to the corresponding glutamyl and aspartyl residues, respectively. Alternatively, these residues are deamidated under mildly acidic conditions. Either form of these residues falls within the scope of this invention.

[107] Other modifications include hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α-amino groups of lysine, arginine, and histidine side chains (T. E. Creighton, Proteins: Structure and Molecular Properties, W. H. Freeman & Co., San Francisco, pp. 79-86 [1983]), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Glycosylation

[108] Another type of covalent modification is glycosylation. In another embodiment, the IgG variants disclosed herein can be modified to include one or more engineered glycoforms. By "engineered glycoform" as used herein is meant a carbohydrate composition that is covalently attached to an IgG, wherein said carbohydrate composition differs chemically from that of a parent IgG. Engineered glycoforms may be useful for a variety of purposes, including but not limited to enhancing or reducing effector function. Engineered glycoforms may be generated by a variety of methods known in the art (Umaña et al., 1999, Nat Biotechnol 17:176-180; Davies et al., 2001, Biotechnol Bioeng 74:288-294; Shields et al., 2002, J Biol Chem 277:26733-26740; Shinkawa et al., 2003, J Biol Chem 278:3466-3473); (US 6,602,684; USSN 10/277,370; USSN 10/113,929; PCT WO 00/61739A1; PCT WO 01/29246A1; PCT WO 02/31140A1; PCT WO 02/30954A1); (Potelligent™ technology [Biowa, Inc., Princeton, NJ]; GlycoMAb™ glycosylation engineering technology [GLYCART biotechnology AG, Zürich, Switzerland]). Many of these techniques are based on controlling the level of fucosylated and/or bisecting oligosaccharides that are covalently attached to the Fc region, for example by expressing an IgG in various organisms or cell lines, engineered or otherwise (for example Lec-13 CHO cells or rat hybridoma YB2/0 cells), by regulating enzymes involved in the glycosylation pathway (for example FUT8 [α1,6-fucosyltranserase] and/or β1-4- N-acetylglucosaminyltransferase III [GnTIII]), or by modifying carbohydrate(s) after the IgG has been

expressed. Engineered glycoform typically refers to the different carbohydrate or oligosaccharide; thus an IgG variant, for example an antibody or Fc fusion, can include an engineered glycoform. Alternatively, engineered glycoform may refer to the IgG variant that comprises the different carbohydrate or oligosaccharide. As is known in the art, glycosylation patterns can depend on both the sequence of the protein (e.g., the presence or absence of particular glycosylation amino acid residues, discussed below), or the host cell or organism in which the protein is produced. Particular expression systems are discussed below.

[109] Glycosylation of polypeptides is typically either N-linked or O-linked. N-linked refers to the attachment of the carbohydrate moiety to the side chain of an asparagine residue. The tri-peptide sequences asparagine-X-serine and asparagine-X-threonine, where X is any amino acid except proline, are the recognition sequences for enzymatic attachment of the carbohydrate moiety to the asparagine side chain. Thus, the presence of either of these tri-peptide sequences in a polypeptide creates a potential glycosylation site. O-linked glycosylation refers to the attachment of one of the sugars N-acetylgalactosamine, galactose, or xylose, to a hydroxyamino acid, most commonly serine or threonine, although 5-hydroxyproline or 5-hydroxylysine may also be used.

[110] Addition of glycosylation sites to the antibody is conveniently accomplished by altering the amino acid sequence such that it contains one or more of the above-described tri-peptide sequences (for N-linked glycosylation sites). The alteration may also be made by the addition of, or substitution by, one or more serine or threonine residues to the starting sequence (for O-linked glycosylation sites). For ease, the antibody amino acid sequence is preferably altered through changes at the DNA level, particularly by mutating the DNA encoding the target polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

[111] Another means of increasing the number of carbohydrate moieties on the antibody is by chemical or enzymatic coupling of glycosides to the protein. These procedures are advantageous in that they do not require production of the protein in a host cell that has glycosylation capabilities for N- and O-linked glycosylation. Depending on the coupling mode used, the sugar(s) may be attached to (a) arginine and histidine, (b) free carboxyl groups, (c) free sulfhydryl groups such as those of cysteine, (d) free hydroxyl groups such as those of serine, threonine, or hydroxyproline, (e) aromatic residues such as those of phenylalanine, tyrosine, or tryptophan, or (f) the amide group of glutamine. These methods are described in WO 87/05330 published Sep. 11, 1987, and in Aplin and Wriston, 1981, CRC Crit. Rev. Biochem., pp. 259-306.

[112] Removal of carbohydrate moieties present on the starting antibody may be accomplished chemically or enzymatically. Chemical deglycosylation requires exposure of the protein to the compound trifluoromethanesulfonic acid, or an equivalent compound. This treatment results in the cleavage of most or all sugars except the linking sugar (N-acetylglucosamine or N-acetylgalactosamine), while leaving the polypeptide intact. Chemical deglycosylation is described by Hakimuddin et al., 1987, Arch. Biochem. Biophys. 259:52 and by Edge et al., 1981, Anal. Biochem. 118:131. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., 1987, Meth. Enzymol.

138:350. Glycosylation at potential glycosylation sites may be prevented by the use of the compound tunicamycin as described by Duskin et al., 1982, J. Biol. Chem. 257:3105. Tunicamycin blocks the formation of protein-N-glycoside linkages.

[113] Another type of covalent modification of the antibody comprises linking the antibody to various nonproteinaceous polymers, including, but not limited to, various polyols such as polyethylene glycol, polypropylene glycol or polyoxyalkylenes, in the manner set forth in U.S. Pat. Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337. In addition, as is known in the art, amino acid substitutions may be made in various positions within the antibody to facilitate the addition of polymers such as PEG. See for example, U.S. Publication No. 2005/0114037, incorporated herein by reference in its entirety.

Labeled Antibodies

[114] In some embodiments, the covalent modification of the antibodies of the invention comprises the addition of one or more labels. In some cases, these are considered antibody fusions.

[115] The term "labelling group" means any detectable label. In some embodiments, the labelling group is coupled to the antibody via spacer arms of various lengths to reduce potential steric hindrance. Various methods for labelling proteins are known in the art and may be used in performing the present invention.

[116] In general, labels fall into a variety of classes, depending on the assay in which they are to be detected: a) isotopic labels, which may be radioactive or heavy isotopes; b) magnetic labels (e.g., magnetic particles); c) redox active moieties; d) optical dyes; enzymatic groups (e.g. horseradish peroxidase, β-galactosidase, luciferase, alkaline phosphatase); e) biotinylated groups; and f) predetermined polypeptide epitopes recognized by a secondary reporter (e.g., leucine zipper pair sequences, binding sites for secondary antibodies, metal binding domains, epitope tags, etc.). In some embodiments, the labelling group is coupled to the antibody via spacer arms of various lengths to reduce potential steric hindrance. Various methods for labelling proteins are known in the art and may be used in performing the present invention.

[117] Specific labels include optical dyes, including, but not limited to, chromophores, phosphors and fluorophores, with the latter being specific in many instances. Fluorophores can be either "small molecule" fluores, or proteinaceous fluores.

[118] By "fluorescent label" is meant any molecule that may be detected via its inherent fluorescent properties. Suitable fluorescent labels include, but are not limited to, fluorescein, rhodamine, tetramethylrhodamine, eosin, erythrosin, coumarin, methyl-coumarins, pyrene, Malacite green, stilbene, Lucifer Yellow, Cascade BlueJ, Texas Red, IAEDANS, EDANS, BODIPY FL, LC Red 640, Cy 5, Cy 5.5, LC Red 705, Oregon green, the Alexa-Fluor dyes (Alexa Fluor 350, Alexa Fluor 430, Alexa Fluor 488, Alexa Fluor 546, Alexa Fluor 568, Alexa Fluor 594, Alexa Fluor 633, Alexa Fluor 660, Alexa Fluor 680), Cascade Blue, Cascade Yellow and R-phycoerythrin (PE) (Molecular Probes, Eugene, OR), FITC, Rhodamine, and Texas Red (Pierce, Rockford, IL), Cy5, Cy5.5, Cy7 (Amersham

Life Science, Pittsburgh, PA). Suitable optical dyes, including fluorophores, are described in Molecular Probes Handbook by Richard P. Haugland, hereby expressly incorporated by reference.

[119] Suitable proteinaceous fluorescent labels also include, but are not limited to, green fluorescent protein, including a Renilla, Ptilosarcus, or Aequorea species of GFP (Chalfie et al., 1994, Science 263:802-805), EGFP (Clontech Laboratories, Inc., Genbank Accession Number U55762), blue fluorescent protein (BFP, Quantum Biotechnologies, Inc. 1801 de Maisonneuve Blvd. West, 8th Floor, Montreal, Quebec, Canada H3H 1J9; Stauber, 1998, Biotechniques 24:462-471; Heim et al., 1996, Curr. Biol. 6:178-182), enhanced yellow fluorescent protein (EYFP, Clontech Laboratories, Inc.), luciferase (Ichiki et al., 1993, J. Immunol. 150:5408-5417), β galactosidase (Nolan et al., 1988, Proc. Natl. Acad. Sci. U.S.A. 85:2603-2607) and Renilla (WO92/15673, WO95/07463, WO98/14605, WO98/26277, WO99/49019, U.S. Patent Nos. 5292658, 5418155, 5683888, 5741668, 5777079, 5804387, 5874304, 5876995, 5925558). All of the above-cited references are expressly incorporated herein by reference.

[120] In certain variations, antibody can meant a protein consisting of one or more polypeptides substantially encoded by all or part of the recognized immunoglobulin genes. The recognized immunoglobulin genes, for example in humans, include the kappa (□), lambda (□), and heavy chain genetic loci, which together comprise the myriad variable region genes, and the constant region genes mu (□), delta (□), gamma (□), sigma (□), and alpha (□) which encode the IgM, IgD, IgG (IgG1, IgG2, IgG3, and IgG4), IgE, and IgA (IgA1 and IgA2) isotypes respectively. Antibody herein is meant to include full length antibodies and antibody fragments, and may refer to a natural antibody from any organism, an engineered antibody, or an antibody generated recombinantly for experimental, therapeutic, or other purposes.

[121] An Fc variant comprises one or more amino acid modifications relative to a parent Fc polypeptide, wherein said amino acid modification(s) provide one or more optimized properties. An Fc variant of the present invention differs in amino acid sequence from its parent IgG by virtue of at least one amino acid modification. Thus Fc variants of the present invention have at least one amino acid modification compared to the parent. Alternatively, the Fc variants of the present invention may have more than one amino acid modification as compared to the parent, for example from about one to fifty amino acid modifications, preferrably from about one to ten amino acid modifications, and most preferably from about one to about five amino acid modifications compared to the parent. Thus the sequences of the Fc variants and those of the parent Fc polypeptide are substantially homologous. For example, the variant Fc variant sequences herein will possess about 80% homology with the parent Fc variant sequence, preferably at least about 90% homology, and most preferably at least about 95% homology. Modifications may be made genetically using molecular biology, or may be made enzymatically or chemically.

[122] The Fc variants of the present invention are defined according to the amino acid modifications that compose them. Thus, for example, I332E is an Fc variant with the substitution I332E relative to the parent Fc polypeptide. Likewise, S239D/A330L/I332E defines an Fc variant with the substitutions S239D, A330L, and I332E relative to the parent Fc polypeptide. It is noted that the order in which

substitutions are provided is arbitrary, that is to say that, for example, S239D/A330L/I332E is the same Fc variant as S239D/I332E/A330L, and so on. For all positions discussed in the present invention, numbering is according to the EU index or EU numbering scheme (Kabat *et al.*, 1991, *Sequences of Proteins of Immunological Interest,* 5th Ed., United States Public Health Service, National Institutes of Health, Bethesda, hereby entirely incorporated by reference). The EU index or EU index as in Kabat or EU numbering scheme refers to the numbering of the EU antibody (Edelman et al., 1969, Proc Natl Acad Sci USA 63:78-85, hereby entirely incorporated by reference).

[123] Fc variants of the present invention may be substantially encoded by genes from any organism, preferably mammals, including but not limited to humans, rodents including but not limited to mice and rats, lagomorpha including but not limited to rabbits and hares, camelidae including but not limited to camels, llamas, and dromedaries, and non-human primates, including but not limited to Prosimians, Platyrrhini (New World monkeys), Cercopithecoidea (Old World monkeys), and Hominoidea including the Gibbons and Lesser and Great Apes. In a most preferred embodiment, the Fc variants of the present invention are substantially human.

[124] The parent Fc polypeptide may be an antibody. Parent antibodies may be fully human, obtained for example using transgenic mice (Bruggemann *et al.*, 1997, *Curr Opin Biotechnol* 8:455-458, hereby entirely incorporated by reference) or human antibody libraries coupled with selection methods (Griffiths *et al.*, 1998, *Curr Opin Biotechnol* 9:102-108, hereby entirely incorporated by reference). The parent antibody need not be naturally occurring. For example, the parent antibody may be an engineered antibody, including but not limited to chimeric antibodies and humanized antibodies (Clark, 2000, *Immunol Today* 21:397-402, hereby entirely incorporated by reference). The parent antibody may be an engineered variant of an antibody that is substantially encoded by one or more natural antibody genes. In one embodiment, the parent antibody has been affinity matured, as is known in the art. Alternatively, the antibody has been modified in some other way, for example as described in USSN 10/339788, filed on March 3, 2003, hereby entirely incorporated by reference.

[125] The Fc variants of the present invention may be substantially encoded by immunoglobulin genes belonging to any of the antibody classes. In a preferred embodiment, the Fc variants of the present invention find use in antibodies or Fc fusions that comprise sequences belonging to the IgG class of antibodies, including IgG1, IgG2, IgG3, or IgG4. Figure 3 provides an alignment of these human IgG sequences. In an alternate embodiment the Fc variants of the present invention find use in antibodies or Fc fusions that comprise sequences belonging to the IgA (including subclasses IgA1 and IgA2), IgD, IgE, IgG, or IgM classes of antibodies. The Fc variants of the present invention may comprise more than one protein chain. That is, the present invention may find use in an antibody or Fc fusion that is a monomer or an oligomer, including a homo- or hetero-oligomer.

[126] As is well known in the art, immunoglobulin polymorphisms exist in the human population. Gm polymorphism is determined by the IGHG1, IGHG2 and IGHG3 genes which have alleles encoding allotypic antigenic determinants referred to as G1m, G2m, and G3m allotypes for markers of the human IgG1, IgG2 and IgG3 molecules (no Gm allotypes have been found on the gamma 4 chain). Markers may be classified into 'allotypes' and 'isoallotypes'. These are distinguished on different

serological bases dependent upon the strong sequence homologies between isotypes. Allotypes are antigenic determinants specified by allelic forms of the Ig genes. Allotypes represent slight differences in the amino acid sequences of heavy or light chains of different individuals. Even a single amino acid difference can give rise to an allotypic determinant, although in many cases there are several amino acid substitutions that have occurred. Allotypes are sequence differences between alleles of a subclass whereby the antisera recognize only the allelic differences. An isoallotype is an allele in one isotype which produces an epitope which is shared with a non-polymorphic homologous region of one or more other isotypes and because of this the antisera will react with both the relevant allotypes and the relevant homologous isotypes (Clark, 1997, IgG effector mechanisms, Chem Immunol. 65:88-110; Gorman & Clark, 1990, Semin Immunol 2(6):457-66, both hereby entirely incorporated by reference).

[127] Allelic forms of human immunoglobulins have been well-characterized (WHO Review of the notation for the allotypic and related markers of human immunoglobulins. J Immunogen 1976, 3: 357-362; WHO Review of the notation for the allotypic and related markers of human immunoglobulins. 1976, Eur. J. Immunol. 6, 599-601; Loghem E van, 1986, Allotypic markers, Monogr Allergy 19: 40-51, all hereby entirely incorporated by reference). Additionally, other polymorphisms have been characterized (Kim et al., 2001, J. Mol. Evol. 54:1-9, hereby entirely incorporated by reference). At present, 18 Gm allotypes are known: G1m (1, 2, 3, 17) or G1m (a, x, f, z), G2m (23) or G2m (n), G3m (5, 6, 10, 11, 13, 14, 15, 16, 21, 24, 26, 27, 28) or G3m (b1, c3, b5, b0, b3, b4, s, t, g1, c5, u, v, g5) (Lefranc, et al., The human IgG subclasses: molecular analysis of structure, function and regulation. Pergamon, Oxford, pp. 43-78 (1990); Lefranc, G. et al., 1979, Hum. Genet.: 50, 199-211, both hereby entirely incorporated by reference). Allotypes that are inherited in fixed combinations are called Gm haplotypes.

[128] Figure 4 shows the allotypes and isoallotypes of the gamma1 chain of human IgG1 showing the positions and the relevant amino acid substitutions (Gorman & Clark, 1990, Semin Immunol 2(6):457-66, hereby entirely incorporated by reference). For comparison the amino acids found in the equivalent positions in human IgG2, IgG3 and IgG4 gamma chains are also shown.

[129] The Fc variants of the present invention may be substantially encoded by any allotype or isoallotype of any immunoglobulin gene. In a preferred embodiment, the Fc variants of the present invention find use in antibodies or Fc fusions that comprise IgG1 sequences that are classified as G1m(1), G1m(2), G1m(3), G1m(17), nG1m(1), nG1m(2), and/or nG1m(17). Thus in the context of an IgG1 isotype, the Fc variants of the present invention may comprise a Lys (G1m(17)) or Arg (G1m(3)) at position 214, an Asp356/Leu358 (G1m(1)) or Glu356/Met358 (nG1m(1)), and/or a Gly (G1m(2)) or Ala (nG1m(2)) at position 431.

[130] In the most preferred embodiment, the Fc variants of the invention are based on human IgG sequences, and thus human IgG sequences are used as the "base" sequences against which other sequences are compared, including but not limited to sequences from other organisms, for example rodent and primate sequences. Fc variants may also comprise sequences from other immunoglobulin classes such as IgA, IgE, IgGD, IgGM, and the like. It is contemplated that, although the Fc variants of the present invention are engineered in the context of one parent IgG, the variants may be engineered

in or "transferred" to the context of another, second parent IgG. This is done by determining the "equivalent" or "corresponding" residues and substitutions between the first and second IgG, typically based on sequence or structural homology between the sequences of the first and second IgGs. In order to establish homology, the amino acid sequence of a first IgG outlined herein is directly compared to the sequence of a second IgG. After aligning the sequences, using one or more of the homology alignment programs known in the art (for example using conserved residues as between species), allowing for necessary insertions and deletions in order to maintain alignment (i.e., avoiding the elimination of conserved residues through arbitrary deletion and insertion), the residues equivalent to particular amino acids in the primary sequence of the first Fc variant are defined. Alignment of conserved residues preferably should conserve 100% of such residues. However, alignment of greater than 75% or as little as 50% of conserved residues is also adequate to define equivalent residues. Equivalent residues may also be defined by determining structural homology between a first and second IgG that is at the level of tertiary structure for IgGs whose structures have been determined. In this case, equivalent residues are defined as those for which the atomic coordinates of two or more of the main chain atoms of a particular amino acid residue of the parent or precursor (N on N, CA on CA, C on C and O on O) are within about 0.13 nm and preferably about 0.1 nm after alignment. Alignment is achieved after the best model has been oriented and positioned to give the maximum overlap of atomic coordinates of non-hydrogen protein atoms of the proteins. Regardless of how equivalent or corresponding residues are determined, and regardless of the identity of the parent IgG in which the IgGs are made, what is meant to be conveyed is that the Fc variants discovered by the present invention may be engineered into any second parent IgG that has significant sequence or structural homology with the Fc variant. Thus for example, if a variant antibody is generated wherein the parent antibody is human IgG1, by using the methods described above or other methods for determining equivalent residues, the variant antibody may be engineered in another IgG1 parent antibody that binds a different antigen, a human IgG2 parent antibody, a human IgA parent antibody, a mouse IgG2a or IgG2b parent antibody, and the like. Again, as described above, the context of the parent Fc variant does not affect the ability to transfer the Fc variants of the present invention to other parent IgGs.

[131] Virtually any antigen may be targeted by the Fc variants of the present invention, including but not limited to proteins, subunits, domains, motifs, and/or epitopes belonging to the following list of targets: 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 IIa, 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, GITR, Glucagon, Glut 4, glycoprotein IIb/IIIa (GP IIb/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 gp 120 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), PlGF, 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, TNFc, 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 (DcR3 M68, TR6), TNFRSF7 (CD27), TNFRSF8 (CD30), TNFRSF9 (4-1BB CD137, ILA), TNFRSF21 (DR6), TNFRSF22 (DcTRAIL R2 TNFRH2), TNFRST23 (DcTRAIL R1 TNFRH1), 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-b LTa, TNFSF1), TNFSF3 (LTb 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, VEFGR-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, etc.

[132] The present invention provides Fc variants that are optimized for a variety of therapeutically relevant properties. An Fc variant that is engineered or predicted to display one or more optimized properties is herein referred to as an "optimized Fc variant". Properties that may be optimized include but are not limited to enhanced or reduced affinity for an FcγR. In a preferred embodiment, the Fc variants of the present invention are optimized to possess enhanced affinity for a human activating FcγR, preferably FcγRI, FcγRIIa, FcγRIIc, FcγRIIIa, and FcγRIIIb, most preferably FcγRIIIa. In an alternately preferred embodiment, the Fc variants are optimized to possess reduced affinity for the human inhibitory receptor FcγRIIb. These preferred embodiments are anticipated to provide IgG polypeptides with enhanced therapeutic properties in humans, for example enhanced effector function and greater anti-cancer potency. In an alternate embodiment, the Fc variants of the present invention are optimized to have reduced or ablated affinity for a human FcγR, including but not limited to FcγRI, FcγRIIa, FcγRIIb, FcγRIIc, FcγRIIIa, and FcγRIIIb. These embodiments are anticipated to provide IgG polypeptides with enhanced therapeutic properties in humans, for example reduced effector function and reduced toxicity. In other embodiments, Fc variants of the present invention provide enhanced affinity for one or more FcγRs, yet reduced affinity for one or more other FcγRs. For example, an Fc variant of the present invention may have enhanced binding to FcγRIIIa, yet reduced binding to FcγRIIb. Alternately, an Fc variant of the present invention may have enhanced binding to FcγRIIa and FcγRI, yet reduced binding to FcγRIIb. In yet another embodiment, an Fc variant of the present invention may have enhanced affinity for FcγRIIb, yet reduced affinity to one or more activating FcγRs.

[133] Preferred embodiments comprise optimization of binding to a human FcγR, however in alternate embodiments the Fc variants of the present invention possess enhanced or reduced affinity for FcγRs from nonhuman organisms, including but not limited to rodents and non-human primates. Fc variants that are optimized for binding to a nonhuman FcγR may find use in experimentation. For example, mouse models are available for a variety of diseases that enable testing of properties such as efficacy, toxicity, and pharmacokinetics for a given drug candidate. As is known in the art, cancer cells can be grafted or injected into mice to mimic a human cancer, a process referred to as xenografting. Testing of Fc variants that comprise Fc variants that are optimized for one or more mouse FcγRs, may provide valuable information with regard to the efficacy of the protein, its mechanism of action, and the like. The Fc variants of the present invention may also be optimized for enhanced functionality and/or solution properties in aglycosylated form. In a preferred embodiment,

the aglycosylated Fc variants of the present invention bind an Fc ligand with greater affinity than the aglycosylated form of the parent Fc variant. Said Fc ligands include but are not limited to FcγRs, C1q, FcRn, and proteins A and G, and may be from any source including but not limited to human, mouse, rat, rabbit, or monkey, preferably human. In an alternately preferred embodiment, the Fc variants are optimized to be more stable and/or more soluble than the aglycosylated form of the parent Fc variant.

[134] Fc variants of the invention may comprise modifications that modulate interaction with Fc ligands other than FcγRs, including but not limited to complement proteins, FcRn, and Fc receptor homologs (FcRHs). FcRHs include but are not limited to FcRH1, FcRH2, FcRH3, FcRH4, FcRH5, and FcRH6 (Davis et al., 2002, Immunol. Reviews 190:123-136, hereby entirely incorporated by reference).

[135] Preferably, the Fc ligand specificity of the Fc variant of the present invention will determine its therapeutic utility. The utility of a given Fc variant for therapeutic purposes will depend on the epitope or form of the Target antigen and the disease or indication being treated. For some targets and indications, enhanced FcγR-mediated effector functions may be preferable. This may be particularly favorable for anti-cancer Fc variants. Thus Fc variants may be used that comprise Fc variants that provide enhanced affinity for activating FcγRs and/or reduced affinity for inhibitory FcγRs. For some targets and indications, it may be further beneficial to utilize Fc variants that provide differential selectivity for different activating FcγRs; for example, in some cases enhanced binding to FcγRIIa and FcγRIIIa may be desired, but not FcγRI, whereas in other cases, enhanced binding only to FcγRIIa may be preferred. For certain targets and indications, it may be preferable to utilize Fc variants that enhance both FcγR-mediated and complement-mediated effector functions, whereas for other cases it may be advantageous to utilize Fc variants that enhance either FcγR-mediated or complement-mediated effector functions. For some targets or cancer indications, it may be advantageous to reduce or ablate one or more effector functions, for example by knocking out binding to C1q, one or more FcγR's, FcRn, or one or more other Fc ligands. For other targets and indications, it may be preferable to utilize Fc variants that provide enhanced binding to the inhibitory FcγRIIb, yet WT level, reduced, or ablated binding to activating FcγRs. This may be particularly useful, for example, when the goal of an Fc variant is to inhibit inflammation or auto-immune disease, or modulate the immune system in some way.

[136] Clearly an important parameter that determines the most beneficial selectivity of a given Fc variant to treat a given disease is the context of the Fc variant, *e.g.,* what type of Fc variant is being used. Thus the Fc ligand selectivity or specifity of a given Fc variant will provide different properties depending on whether it composes an antibody, Fc fusion, or Fc variants with a coupled fusion or conjugate partner. For example, toxin, radionucleotide, or other conjugates may be less toxic to normal cells if the Fc variant that comprises them has reduced or ablated binding to one or more Fc ligands. As another example, in order to inhibit inflammation or auto-immune disease, it may be preferable to utilize an Fc variant with enhanced affinity for activating FcγRs, such as to bind these FcγRs and prevent their activation. Conversely, an Fc variant that comprises two or more Fc regions

with enhanced FcγRIIb affinity may co-engage this receptor on the surface of immune cells, thereby inhibiting proliferation of these cells. Whereas in some cases an Fc variants may engage its target antigen on one cell type yet engage FcγRs on separate cells from the target antigen, in other cases it may be advantageous to engage FcγRs on the surface of the same cells as the target antigen. For example, if an antibody targets an antigen on a cell that also expresses one or more FcγRs, it may be beneficial to utilize an Fc variant that enhances or reduces binding to the FcγRs on the surface of that cell. This may be the case, for example when the Fc variant is being used as an anti-cancer agent, and co-engagement of target antigen and FcγR on the surface of the same cell promote signaling events within the cell that result in growth inhibition, apoptosis, or other anti-proliferative effect. Alternatively, antigen and FcγR co-engagement on the same cell may be advantageous when the Fc variant is being used to modulate the immune system in some way, wherein co-engagement of target antigen and FcγR provides some proliferative or anti-proliferative effect. Likewise, Fc variants that comprise two or more Fc regions may benefit from Fc variants that modulate FcγR selectivity or specifity to co-engage FcγRs on the surface of the same cell.

[137] The presence of different polymorphic forms of FcγRs provides yet another parameter that impacts the therapeutic utility of the Fc variants of the present invention. Whereas the specificity and selectivity of a given Fc variant for the different classes of FcγRs signficantly affects the capacity of an Fc variant to target a given antigen for treatment of a given disease, the specificity or selectivity of an Fc variant for different polymorphic forms of these receptors may in part determine which research or pre-clinical experiments may be appropriate for testing, and ultimately which patient populations may or may not respond to treatment. Thus the specificity or selecitivty of Fc variants of the present invention to Fc ligand polymorphisms, including but not limited to FcγR, C1q, FcRn, and FcRH polymorphisms, may be used to guide the selection of valid research and pre-clinical experiments, clinical trial design, patient selection, dosing dependence, and/or other aspects concerning clinical trials.

[138] Modification may be made to improve the IgG stability, solubility, function, or clinical use. In a preferred embodiment, the Fc variants of the present invention may comprise modifications to reduce immunogenicity in humans. In a most preferred embodiment, the immunogenicity of an Fc variant of the present invention is reduced using a method described in USSN 11/004,590, filed December 3, 2004, hereby entirely incorporated by reference. In alternate embodiments, the Fc variants of the present invention are humanized (Clark, 2000, *Immunol Today* 21:397-402, hereby entirely incorporated by reference). By "humanized" antibody as used herein is meant an antibody comprising a human framework region (FR) and one or more complementarity determining regions (CDR's) from a non-human (usually mouse or rat) antibody. The non-human antibody providing the CDR's is called the "donor" and the human immunoglobulin providing the framework is called the "acceptor". Humanization relies principally on the grafting of donor CDRs onto acceptor (human) VL and VH frameworks (*e.g.,* Winter et al, US 5225539, hereby entirely incorporated by reference). This strategy is referred to as "CDR grafting". "Backmutation" of selected acceptor framework residues to the corresponding donor residues is often required to regain affinity that is lost in the initial grafted

construct (US 5530101; US 5585089; US 5693761; US 5693762; US 6180370; US 5859205; US 5821337; US 6054297; and US 6407213, all hereby entirely incorporated by reference). The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region, typically that of a human immunoglobulin, and thus will typically comprise a human Fc region. A variety of techniques and methods for humanizing and reshaping non-human antibodies are well known in the art (See Tsurushita & Vasquez, 2004, Humanization of Monoclonal Antibodies, Molecular Biology of B Cells, 533-545, Elsevier Science (USA), and references cited therein, all hereby entirely incorporated by reference). Humanization methods include but are not limited to methods described in Jones *et al.*, 1986, *Nature* 321:522-525; Riechmann *et al.*,1988; *Nature* 332:323-329; Verhoeyen *et al.*, 1988, *Science*, 239:1534-1536; *Queen et al.*, 1989, *Proc Natl Acad Sci*, USA 86:10029-33; He et al., 1998, J. Immunol. 160: 1029-1035; Carter *et al.*, 1992, *Proc Natl Acad Sci USA 89:4285-9*, Presta et al., 1997, Cancer Res.57(20):4593-9; Gorman et al., 1991, Proc. Natl. Acad. Sci. USA 88:4181-4185; O'Connor *et al.*, 1998, *Protein Eng* 11:321-8, all hereby entirely incorporated by reference. Humanization or other methods of reducing the immunogenicity of nonhuman antibody variable regions may include resurfacing methods, as described for example in Roguska et al., 1994, Proc. Natl. Acad. Sci. USA 91:969-973, hereby entirely incorporated by reference. In one embodiment, the parent antibody has been affinity matured, as is well known in the art. Structure-based methods may be employed for humanization and affinity maturation, for example as described in USSN 11/004,590, hereby entirely incorporated by reference. Selection based methods may be employed to humanize and/or affinity mature antibody variable regions, including but not limited to methods described in Wu et al., 1999, J. Mol. Biol. 294:151-162; Baca et al., 1997, J. Biol. Chem. 272(16):10678-10684; Rosok et al., 1996, J. Biol. Chem. 271(37): 22611-22618; Rader et al., 1998, Proc. Natl. Acad. Sci. USA 95: 8910-8915; Krauss et al., 2003, Protein Engineering 16(10):753-759, all hereby entirely incorporated by reference. Other humanization methods may involve the grafting of only parts of the CDRs, including but not limited to methods described in USSN 09/810,502; Tan et al., 2002, J. Immunol. 169:1119-1125; De Pascalis et al., 2002, J. Immunol. 169:3076-3084, all hereby entirely incorporated by reference.

[139] Modifications to reduce immunogenicity may include modifications that reduce binding of processed peptides derived from the parent sequence to MHC proteins. For example, amino acid modifications may be engineered such that there are no or a minimal number of immune epitopes that are predicted to bind, with high affinity, to any prevalent MHC alleles. Several methods of identifying MHC-binding epitopes in protein sequences are known in the art and may be used to score epitopes in an Fc variant of the present invention. See for example WO 98/52976; WO 02/079232; WO 00/3317; USSN 09/903,378; USSN 10/039,170; USSN 60/222,697; USSN 10/754,296; PCT WO 01/21823; and PCT WO 02/00165; Mallios, 1999, *Bioinformatics* 15: 432-439; Mallios, 2001, *Bioinformatics* 17: 942-948; Sturniolo *et al.*, 1999, *Nature Biotech.* 17: 555-561; WO 98/59244; WO 02/069232; WO 02/77187; Marshall *et al.*, 1995, *J. Immunol.* 154: 5927-5933; and Hammer *et al.*, 1994, *J. Exp. Med.* 180: 2353-2358, all hereby entirely incorporated by reference. Sequence-based information can be used to determine a binding score for a given peptide – MHC interaction (see for

example Mallios, 1999, *Bioinformatics* 15: 432-439; Mallios, 2001, *Bioinformatics* 17: p942-948; Sturniolo *et. al.*, 1999, *Nature Biotech.* 17: 555-561, all hereby entirely incorporated by reference).

[140] In one embodiment, the Fc variants of the present invention comprise one or more engineered glycoforms. By "engineered glycoform" as used herein is meant a carbohydrate composition that is covalently attached to an IgG, wherein said carbohydrate composition differs chemically from that of a parent IgG. Engineered glycoforms may be useful for a variety of purposes, including but not limited to enhancing or reducing effector function. Engineered glycoforms may be generated by a variety of methods known in the art (Umaña *et al.*, 1999, *Nat Biotechnol* 17:176-180; Davies *et al.*, 2001, *Biotechnol Bioeng* 74:288-294; Shields *et al.*, 2002, *J Biol Chem* 277:26733-26740; Shinkawa *et al.*, 2003, *J Biol Chem* 278:3466-3473); (US 6,602,684; USSN 10/277,370; USSN 10/113,929; PCT WO 00/61739A1; PCT WO 01/29246A1; PCT WO 02/31140A1; PCT WO 02/30954A1); (Potelligent™ technology [Biowa, Inc., Princeton, NJ]; GlycoMAb® glycosylation engineering technology [GLYCART biotechnology AG, Zürich, Switzerland], all hereby entirely incorporated by reference). Many of these techniques are based on controlling the level of fucosylated and/or bisecting oligosaccharides that are covalently attached to the Fc region, for example by expressing an IgG in various organisms or cell lines, engineered or otherwise (for example Lec-13 CHO cells or rat hybridoma YB2/0 cells), by regulating enzymes involved in the glycosylation pathway (for example FUT8 [α1,6-fucosyltranserase] and/or β1–4- N-acetylglucosaminyltransferase III [GnTIII]), or by modifying carbohydrate(s) after the IgG has been expressed. Engineered glycoform typically refers to the different carbohydrate or oligosaccharide; thus an Fc variant, for example an antibody or Fc fusion, may comprise an engineered glycoform. Alternatively, engineered glycoform may refer to the Fc variant that comprises the different carbohydrate or oligosaccharide.

[141] In an alternate embodiment, the Fc variant of the present invention is conjugated or operably linked to another therapeutic compound. The therapeutic compound may be a cytotoxic agent, a chemotherapeutic agent, a toxin, a radioisotope, a cytokine, or other therapeutically active agent. The IgG may be linked to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, polyoxyalkylenes, or copolymers of polyethylene glycol and polypropylene glycol.

[142] The present invention provides methods for engineering, producing, and screening Fc variants. The described methods are not meant to constrain the present invention to any particular application or theory of operation. Rather, the provided methods are meant to illustrate generally that one or more Fc variants may be engineered, produced, and screened experimentally to obtain Fc variants with optimized effector function. A variety of methods are described for designing, producing, and testing antibody and protein variants in USSN 10/672,280, USSN 10/822,231, USSN 11/124,620, and USSN 11/256,060, all hereby entirely incorporated by reference.

[143] A variety of protein engineering methods may be used to design Fc variants with optimized effector function. In one embodiment, a structure-based engineering method may be used, wherein available structural information is used to guide substitutions. An alignment of sequences may be

used to guide substitutions at the identified positions. Alternatively, random or semi-random mutagenesis methods may be used to make amino acid modifications at the desired positions.

[144] Methods for production and screening of Fc variants are well known in the art. General methods for antibody molecular biology, expression, purification, and screening are described in Antibody Engineering, edited by Duebel & Kontermann, Springer-Verlag, Heidelberg, 2001; and Hayhurst & Georgiou, 2001, *Curr Opin Chem Biol* 5:683-689; Maynard & Georgiou, 2000, *Annu Rev Biomed Eng* 2:339-76, all hereby entirely incorporated by reference. Also see the methods described in USSN 10/672,280, USSN 10/822,231, USSN 11/124,620, and USSN 11/256,060, all hereby entirely incorporated by reference.

[145] In one embodiment of the present invention, the Fc variant sequences are used to create nucleic acids that encode the member sequences, and that may then be cloned into host cells, expressed and assayed, if desired. These practices are carried out using well-known procedures, and a variety of methods that may find use in the present invention are described in Molecular Cloning - A Laboratory Manual, 3rd Ed. (Maniatis, Cold Spring Harbor Laboratory Press, New York, 2001), and Current Protocols in Molecular Biology (John Wiley & Sons), both entirely incorporated by reference. The Fc variants of the present invention may be produced by culturing a host cell transformed with nucleic acid, preferably an expression vector, containing nucleic acid encoding the Fc variants, under the appropriate conditions to induce or cause expression of the protein. A wide variety of appropriate host cells may be used, including but not limited to mammalian cells, bacteria, insect cells, and yeast. For example, a variety of cell lines that may find use in the present invention are described in the ATCC cell line catalog, available from the American Type Culture Collection. The methods of introducing exogenous nucleic acid into host cells are well known in the art, and will vary with the host cell used.

[146] In a preferred embodiment, Fc variants are purified or isolated after expression. Antibodies may be isolated or purified in a variety of ways known to those skilled in the art. Standard purification methods include chromatographic techniques, electrophoretic, immunological, precipitation, dialysis, filtration, concentration, and chromatofocusing techniques. As is well known in the art, a variety of natural proteins bind antibodies, for example bacterial proteins A, G, and L, and these proteins may find use in the present invention for purification. Purification can often be enabled by a particular fusion partner. For example, proteins may be purified using glutathione resin if a GST fusion is employed, Ni^{+2} affinity chromatography if a His-tag is employed, or immobilized anti-flag antibody if a flag-tag is used. For general guidance in suitable purification techniques, see Antibody Purification: Principles and Practice, 3rd Ed., Scopes, Springer-Verlag, NY, 1994, hereby entirely incorporated by reference.

[147] Fc variants may be screened using a variety of methods, including but not limited to those that use *in vitro* assays, *in vivo* and cell-based assays, and selection technologies. Automation and high-throughput screening technologies may be utilized in the screening procedures. Screening may employ the use of a fusion partner or label, for example an immune label, isotopic label, or small molecule label such as a fluorescent or colorimetric dye.

[148] In a preferred embodiment, the functional and/or biophysical properties of Fc variants are screened in an *in vitro* assay. In a preferred embodiment, the protein is screened for functionality, for example its ability to catalyze a reaction or its binding affinity to its target.

[149] As is known in the art, a subset of screening methods are those that select for favorable members of a library. The methods are herein referred to as "selection methods", and these methods find use in the present invention for screening Fc variants. When protein libraries are screened using a selection method, only those members of a library that are favorable, that is which meet some selection criteria, are propagated, isolated, and/or observed. A variety of selection methods are known in the art that may find use in the present invention for screening protein libraries. Other selection methods that may find use in the present invention include methods that do not rely on display, such as *in vivo* methods. A subset of selection methods referred to as "directed evolution" methods are those that include the mating or breading of favorable sequences during selection, sometimes with the incorporation of new mutations.

[150] In a preferred embodiment, Fc variants are screened using one or more cell-based or *in vivo* assays. For such assays, purified or unpurified proteins are typically added exogenously such that cells are exposed to individual variants or pools of variants belonging to a library. These assays are typically, but not always, based on the function of the Fc polypeptide; that is, the ability of the Fc polypeptide to bind to its target and mediate some biochemical event, for example effector function, ligand/receptor binding inhibition, apoptosis, and the like. Such assays often involve monitoring the response of cells to the IgG, for example cell survival, cell death, change in cellular morphology, or transcriptional activation such as cellular expression of a natural gene or reporter gene. For example, such assays may measure the ability of Fc variants to elicit ADCC, ADCP, or CDC. For some assays additional cells or components, that is in addition to the target cells, may need to be added, for example example serum complement, or effector cells such as peripheral blood monocytes (PBMCs), NK cells, macrophages, and the like. Such additional cells may be from any organism, preferably humans, mice, rat, rabbit, and monkey. Antibodies may cause apoptosis of certain cell lines expressing the target, or they may mediate attack on target cells by immune cells which have been added to the assay. Methods for monitoring cell death or viability are known in the art, and include the use of dyes, immunochemical, cytochemical, and radioactive reagents. Transcriptional activation may also serve as a method for assaying function in cell-based assays. Alternatively, cell-based screens are performed using cells that have been transformed or transfected with nucleic acids encoding the variants. That is, Fc variants are not added exogenously to the cells.

[151] In a preferred embodiment, the immunogenicity of the Fc variants is determined experimentally using one or more cell-based assays. Several methods can be used for experimental confirmation of epitopes.

[152] The biological properties of the Fc variants of the present invention may be characterized in cell, tissue, and whole organism experiments. As is known in the art, drugs are often tested in animals, including but not limited to mice, rats, rabbits, dogs, cats, pigs, and monkeys, in order to measure a drug's efficacy for treatment against a disease or disease model, or to measure a drug's

pharmacokinetics, toxicity, and other properties. The animals may be referred to as disease models. Therapeutics are often tested in mice, including but not limited to nude mice, SCID mice, xenograft mice, and transgenic mice (including knockins and knockouts). Such experimentation may provide meaningful data for determination of the potential of the protein to be used as a therapeutic. Any organism, preferably mammals, may be used for testing. For example because of their genetic similarity to humans, monkeys can be suitable therapeutic models, and thus may be used to test the efficacy, toxicity, pharmacokinetics, or other property of the IgGs of the present invention. Tests of the in humans are ultimately required for approval as drugs, and thus of course these experiments are contemplated. Thus the IgGs of the present invention may be tested in humans to determine their therapeutic efficacy, toxicity, immunogenicity, pharmacokinetics, and/or other clinical properties.

[153] The Fc variants of the present invention may find use in a wide range of products. In one embodiment the Fc variant of the present invention is a therapeutic, a diagnostic, or a research reagent, preferably a therapeutic. The Fc variant may find use in an antibody composition that is monoclonal or polyclonal. In a preferred embodiment, the Fc variants of the present invention are used to kill target cells that bear the target antigen, for example cancer cells. In an alternate embodiment, the Fc variants of the present invention are used to block, antagonize, or agonize the target antigen, for example for antagonizing a cytokine or cytokine receptor. In an alternately preferred embodiment, the Fc variants of the present invention are used to block, antagonize, or agonize the target antigen and kill the target cells that bear the target antigen.

[154] The Fc variants of the present invention may be used for various therapeutic purposes. In a preferred embodiment, an antibody comprising the Fc variant is administered to a patient to treat an antibody-related disorder. A "patient" for the purposes of the present invention includes humans and other animals, preferably mammals and most preferably humans. By "antibody related disorder" or "antibody responsive disorder" or "condition" or "disease" herein are meant a disorder that may be ameliorated by the administration of a pharmaceutical composition comprising an Fc variant of the present invention. Antibody related disorders include but are not limited to autoimmune diseases, immunological diseases, infectious diseases, inflammatory diseases, neurological diseases, pain, pulmonary diseases, hematological conditions, fibrotic conditions, and oncological and neoplastic diseases including cancer. By "cancer" and "cancerous" herein refer to or describe the physiological condition in mammals that is typically characterized by unregulated cell growth. Examples of cancer include but are not limited to carcinoma, lymphoma, blastoma, sarcoma (including liposarcoma), neuroendocrine tumors, mesothelioma, schwanoma, meningioma, adenocarcinoma, melanoma, and leukemia and lymphoid malignancies. Other conditions that may be treated include but are not limited to rheumatoid arthritis, juvenile rheumatoid arthritis, crohn's disease, ulcerative colitis, Sjorgren's disease, multiple sclerosis, ankylosing spondylitis, asthma, allergies and allergenic conditions, graft versus host disease, and the like. The term "treatment" as used herein is meant to include therapeutic treatment, as well as prophylactic, or suppressive measures for the disease, condition or disorder. Thus, for example, successful administration of a pharmaceutical composition comprising an Fc variant of the present invention prior to onset of the disease results in "treatment" of the disease. As another example, successful administration of a pharmaceutical composition comprising an Fc variant

of the present invention after clinical manifestation of the disease to combat the symptoms of the disease comprises "treatment" of the disease. "Treatment" also encompasses administration of a pharmaceutical composition comprising an Fc variant of the present invention after the appearance of the disease in order to eradicate the disease. Successful administration of a pharmaceutical composition comprising an Fc variant of the present invention after onset and after clinical symptoms have developed, with possible abatement of clinical symptoms and perhaps amelioration of the disease, comprises "treatment" of the disease. Those "in need of treatment" as used herein include mammals already having the disease or disorder, as well as those prone to having the disease or disorder, including those in which the disease or disorder is to be prevented.

[155] In one embodiment, an Fc variant of the present invention is the only therapeutically active agent administered to a patient. Alternatively, the Fc variant of the present invention is administered in combination with one or more other therapeutic agents, including but not limited to cytotoxic agents, chemotherapeutic agents, cytokines, growth inhibitory agents, anti-hormonal agents, kinase inhibitors, anti-angiogenic agents, cardioprotectants, or other therapeutic agents, as well as pre- or post-surgery. The IgG variants may be administered concomitantly with one or more other therapeutic regimens. For example, an Fc variant of the present invention may be administered to the patient along with surgery, chemotherapy, radiation therapy, or any or all of surgery, chemotherapy and radiation therapy. In one embodiment, the Fc variant of the present invention may be administered in conjunction with one or more antibodies, which may or may not comprise an Fc variant of the present invention. In accordance with another embodiment of the invention, the Fc variant of the present invention and one or more other anti-cancer therapies are employed to treat cancer cells *ex vivo*. It is contemplated that such *ex vivo* treatment may be useful in bone marrow transplantation and particularly, autologous bone marrow transplantation. It is of course contemplated that the Fc variants of the invention can be employed in combination with still other therapeutic techniques such as surgery.

[156] A variety of other therapeutic agents may find use for administration with the Fc variants of the present invention. In one embodiment, the IgG is administered with an anti-angiogenic agent. By "anti-angiogenic agent" as used herein is meant a compound that blocks, or interferes to some degree, the development of blood vessels. The anti-angiogenic factor may, for instance, be a small molecule or a protein, for example an antibody, Fc fusion, or cytokine, that binds to a growth factor or growth factor receptor involved in promoting angiogenesis. The preferred anti-angiogenic factor herein is an antibody that binds to Vascular Endothelial Growth Factor (VEGF). In an alternate embodiment, the IgG is administered with a therapeutic agent that induces or enhances adaptive immune response, for example an antibody that targets CTLA-4. In an alternate embodiment, the IgG is administered with a tyrosine kinase inhibitor. By "tyrosine kinase inhibitor" as used herein is meant a molecule that inhibits to some extent tyrosine kinase activity of a tyrosine kinase. In an alternate embodiment, the Fc variants of the present invention are administered with a cytokine. By "cytokine" as used herein is meant a generic term for proteins released by one cell population that act on another cell as intercellular mediators.

[157] Pharmaceutical compositions are contemplated wherein an Fc variant of the present invention and one or more therapeutically active agents are formulated. Formulations of the Fc variants of the present invention are prepared for storage by mixing said IgG having the desired degree of purity with optional pharmaceutically acceptable carriers, excipients or stabilizers (Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed., 1980, hereby entirely incorporated by reference), in the form of lyophilized formulations or aqueous solutions. The formulations to be used for *in vivo* administration are preferably sterile. This is readily accomplished by filtration through sterile filtration membranes or other methods. The Fc variants and other therapeutically active agents disclosed herein may also be formulated as immunoliposomes, and/or entrapped in microcapsules.

[158] The concentration of the therapeutically active Fc variant in the formulation may vary from about 0.001 to 100 weight %. In a preferred embodiment, the concentration of the IgG is in the range of 0.003 to 1.0 molar. In order to treat a patient, a therapeutically effective dose of the Fc variant of the present invention may be administered. By "therapeutically effective dose" herein is meant a dose that produces the effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques. Dosages may range from 0.001 to 100 mg/kg of body weight or greater, for example 0.1, 1, 10, or 50 mg/kg of body weight, with 1 to 10mg/kg being preferred. As is known in the art, adjustments for protein degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

[159] Administration of the pharmaceutical composition comprising an Fc variant of the present invention, preferably in the form of a sterile aqueous solution, may be done in a variety of ways, including, but not limited to, orally, subcutaneously, intravenously, intranasally, intraotically, transdermally, topically (e.g., gels, salves, lotions, creams, etc.), intraperitoneally, intramuscularly, intrapulmonary (e.g., AERx® inhalable technology commercially available from Aradigm, or Inhance® pulmonary delivery system commercially available from Inhale Therapeutics), vaginally, parenterally, rectally, or intraocularly.

EXAMPLES

[160] Examples are provided below to illustrate the present invention. These examples are not meant to constrain the present invention to any particular application or theory of operation.

Example 1. Fc variants with enhanced FcγR-mediated effector function

[161] Using the methods described in USSN 10/672,280, USSN 10/822,231, USSN 11/124,620, and USSN 11/256,060, all hereby entirely incorporated by reference, additional Fc variants were designed for enhanced binding to Fc ligands and optimized effector function, and for reduced or ablated FcγR binding and effector function. The variants were constructed in the context of the anti-CD20 antibody PRO70769 (PCT/US2003/040426, hereby entirely incorporated by reference), which is known to mediate measurable CDC and ADCC in cell-based assays. Previously characterized

variants were also constructed in PRO70769, in order to further characterize their properties and provide comparators for the current set of new variants. Figure 5 provides a list of these Fc variants. Notably, this variant set comprises a number of insertions. For example, "Insert L > 235-236 / I332E" refers to a double mutant comprising the substitution I332E and an insertion of leucine between residues 235 and 236.

[162] The genes for the variable regions of PRO70769 (Figures 24a and 24b) were constructed using recursive PCR, and subcloned into the mammalian expression vector pcDNA3.1Zeo (Invitrogen) comprising the full length light kappa (Cκ) and heavy chain IgG1 constant regions. Variants were constructed in the variable region of the antibody in the pcDNA3.1Zeo vector using quick-change mutagenesis techniques (Stratagene), expressed in 293T cells. DNA was sequenced to confirm the fidelity of the sequences. Plasmids containing heavy chain gene (VH-CH1-CH2-CH3) (wild-type or variants) were co-transfected with plasmid containing light chain gene (VL-Cκ) into 293T cells. Media were harvested 5 days after transfection, and antibodies were purified from the supernatant using protein A affinity chromatography (Pierce). Select Fc variants were also expressed in the context of alemtuzumab.

[163] Binding affinity to human FcγRs by IgG antibodies was measured using a competitive AlphaScreen™ assay. The AlphaScreen is a bead-based luminescent proximity assay. Laser excitation of a donor bead excites oxygen, which if sufficiently close to the acceptor bead will generate a cascade of chemiluminescent events, ultimately leading to fluorescence emission at 520-620 nm. The AlphaScreen was applied as a competition assay for screening the antibodies. Wild-type IgG1 antibody was biotinylated by standard methods for attachment to streptavidin donor beads, and tagged FcγR was bound to glutathione chelate acceptor beads. In the absence of competing Fc polypeptides, wild-type antibody and FcγR interact and produce a signal at 520-620 nm. Addition of untagged antibody competes with wild-type Fc/FcγR interaction, reducing fluorescence quantitatively to enable determination of relative binding affinities.

[164] Figures 6 provides competitive AlphaScreen data for binding of select PRO70769 Fc variants to the human activating receptors V158 FcγRIIIa (Figure 6a) and F158 FcγRIIIa (Figure 6b). The data were fit to a one site competition model using nonlinear regression, and these fits are represented by the curves in the figure. These fits provide the inhibitory concentration 50% (IC50) (i.e. the concentration required for 50% inhibition) for each antibody, thus enabling the relative binding affinities relative to WT to be determined. Figure 5 provides the IC50's and Fold IC50's relative to WT for fits to these binding curves.

[165] Select Fc variants were reexpressed and reetested using the competition AlphaScreen assay for binding to human V158 FcγRIIIa and F158 FcγRIIIa (Figure 7). Figure 7a shows the binding data for these variants, and Figure 7b provides the IC50's and Fold IC50's relative to WT for fits to these binding curves.

[166] Based on these data, a number of additional Fc variants were constructed in the context of PRO70769 IgG1. Additionally, some Fc variants were constructed in the context of a novel IgG

molecule IgG(1/2) ELLGG described in USSN 11/256,060, filed October 21, 2005, hereby entirely incorporated by reference. These variants were constructed as described above, and expressed and purified along with a number of previously characterized Fc variants. These variants are listed in Figure 8a. Binding of the variant to the human activating receptors V158 FcγRIIIa and F158 FcγRIIIa, and the inhibitory receptor FcγRIIb was measured using the competition AlphaScreen assay. Figure 8b shows data for binding of select variants to these receptors, and Figure 8a provides the IC50's and Folds relative to WT PRO70769 IgG1 for all of this set of Fc variants.

[167] Because of the high avidity nature of the assay, the AlphaScreen provides only relative affinities. True binding constants were obtained using a competition SPR experiment (Nieba et al., 1996, *Anal Biochem* 234:155-65, hereby entirely incorporated by reference) in which unbound antibody in an antibody/FcγR equilibrium was captured to an FcγRIIIa surface. This experiment was carried out with the I332E and S239D/I332E variants in the context of trastuzumab IgG1, constructed and characterized previously (USSN 10/672,280, USSN 10/822,231, and USSN 11/124,620, all hereby entirely incorporated by reference). WT and variant trastuzumab antibodies were expressed and purified as described above. For this experiment, data were acquired on a BIAcore 3000 instrument (BIAcore). V158 FcγRIIIa-His-GST was captured using immobilized anti-GST antibody, blocked with recombinant GST, and binding to antibody/receptor competition analyte was measured. Anti-GST antibody was covalently coupled to a CM5 sensor using the BIAcore GST Capture Kit. Flow cell 1 of every sensor chip was coupled with ethanolamine as a control of unspecific binding and to subtract bulk refractive index changes online. Running buffer was HBS-EP (0.01 M HEPES pH 7.4, 0.15 M NaCl, 3 mM EDTA, 0.005% v/v Surfactant P20, BIAcore), and chip regeneration buffer was Glycine 1.5 (10 mM glycine-HCl, pH 1.5, BIAcore). 1 μM V158 FcγRIIIa-His-GST was bound to the anti-GST CM5 chip in HBS-EP at 1 μl/min for 5 minutes. The surface was blocked with 5 μM recombinant GST (Sigma) injected at 1 μl/minute for 2 minutes. 100 nM wild-type or variant trastuzumab antibody was combined with V158 FcγRIIIa-His-GST in serial dilutions between 4 and 1000 nM and incubated for at least two hours at room temperature. The competition mixture was injected over the V158 FcγRIIIa-His-GST/recombinant GST surface for 30 seconds association in HBS-EP at 50 μl/minute. A cycle with antibody but no competing receptor provided a baseline response.

[168] An earlier described "competition BIAcore" method used fitted kinetic curves to derive on-rates (Nieba et al., 1996, *Anal Biochem* 234:155-65, hereby entirely incorporated by reference). We found this method to be less reliable since the on-rates derived from the kinetic curves showed no linear correlation to the antibody concentration applied. The analysis used in the present study is based on the proportionality of the initial rate R to the free antibody concentration (Holwill et al., 1996, *Process Control and Quality* 8:133-145; Edwards & Leatherbarrow, 1997, *Anal Biochem* 246:1-6, all hereby entirely incorporated by reference). Response units data were exported using BIAevaluation software (BIAcore) and analyzed using Microsoft Excel with Xlfit version 3.0.5 (IDBS). Initial rate (of signal increase) values were determined from the raw data of each sensorgram using the Excel formula for slope. The equilibrium dissociation binding constant (K_D) was determined by plotting the

log of FcγRIIIa concentration against the initial rate obtained at each concentration. GraphPad Prism (GraphPad Software) was used to fit the data to the following formula:

$$R = \frac{R_0}{2[A_0]}([A_0] - 10^x - K_D) + \sqrt{(K_D{}^2 + 2(10^x)(K_D) + (10^x)^2 + 2[A_0]K_D - 2[A_0]10^x + [A_0]^2)}$$

with:

$[A_0]$ = Antibody concentration

R_0 = Initial rate at antibody concentration A_0, with no competing receptor present

$X = \log[L_0]$, where $[L_0]$ = input receptor concentration

K_D = Equilibrium dissociation constant

R_0 reflects the rate of binding between antibody and immobilized receptor (in the absence of competing receptor), and because of their different receptor affinities was calculated separately for WT, I332E, and S239D/I332E antibodies.

The formula for the initial rate R is derived from the definition of K_D for a single binding site:

$$\frac{[A_0][L_0]}{[A_0L_0]} = K_D$$

and the conservation of mass

$$[L_0] = [L] + [A_0L_0]$$

with:

[L] = concentration of free receptor

[169] Initial binding rates were determined from sensorgram raw data (Figure 9a), and K_D's were calculated by plotting the log of receptor concentration against the initial rate obtained at each concentration (Figure 9b, 9c) (Edwards & Leatherbarrow, 1997, *Anal Biochem* 246:1-6, hereby entirely incorporated by reference). The WT K_D (252 nM) agrees well with published data (208 nM from SPR, 535 nM from calorimetry) (Okazaki et al., 2004 *J Mol Biol* 336:1239-49, hereby entirely incorporated by reference). K_D's of the I332E (30 nM) and S239D/I332E (2 nM) variants indicate approximately one- and two- logs greater affinity to V158 FcγRIIIa respectively.

[170] To investigate the capacity of antibodies comprising the Fc variants of the present invention to carry out FcγR-mediated effector function, in vitro cell-based ADCC assays were run using human PBMCs as effector cells. ADCC was measured by the release of lactose dehydrogenase using a LDH Cytotoxicity Detection Kit (Roche Diagnostic). Human PBMCs were purified from leukopacks using a ficoll gradient, and the CD20+ target lymphoma cell line WIL2-S was obtained from ATCC. Target cells were seeded into 96-well plates at 10,000 cells/well, and opsonized using Fc variant or WT antibodies at the indicated final concentration. Triton X100 and PBMCs alone were run as controls. Effector cells were added at 25:1 PBMCs:target cells, and the plate was incubated at 37°C for 4 hrs.

Cells were incubated with the LDH reaction mixture, and fluorescence was measured using a Fusion™ Alpha-FP (Perkin Elmer). Data were normalized to maximal (triton) and minimal (PBMCs alone) lysis, and fit to a sigmoidal dose-response model. Figure 10 provides these data for select Fc variant antibodies in the context of the variable region PRO70769 and either IgG1 or IgG(1/2) ELLGG. The Fc variants provide clear enhancements in FcγR-mediated CD20+ target cell lysis relative to the WT PRO70769 IgG1 antibody.

[171] These in vitro assays suggest that the Fc variants of the present invention may provide enhanced potency and/or efficacy in a clinical setting. In vivo performance may be affected by a number of factors, including some of which are not considered by these in vitro experiments. One such parameter is the high concentration of non-specific IgG in serum, which has been shown to impact antibody clinical potency (Vugmeyster & Howell, 2004, Int Immunopharmacol 4:1117-24; Preithner et al., 2005, Mol Immunol, 43(8):1183-93, all hereby entirely incorporated by reference). In order to investigate how the Fc variants of the present invention perform in a solution more closely mimicking *in vivo* biology, the ADCC assays were repeated in the presence of a biologically relevant (1 mg/ml) concentration of IgG purified from human serum (purchased commercially from Jackson Immunoresearch Lab, Inc.). These data are provided in Figure 11. The efficacy of the WT anti-CD20 antibody is not only reduced, but completely ablated in the presence of serum level IgG. In contrast, the Fc variant antibodies, although significantly reduced, still show substantial capacity to mediate killing against the target cell line.

Example 2. Fc variants with enhanced complement-mediated effector function

[172] A number of variants were designed with the goal of enhancing complement dependant cytotoxicity (CDC). In the same way that Fc/FcγR binding mediates ADCC, Fc/C1q binding mediates complement dependent cytotoxicity (CDC). There is currently no structure available for the Fc/C1q complex; however, mutagenesis studies have mapped the binding site on human IgG for C1q to a region centered on residues D270, K322, P329, and P331 (Idusogie *et al.*, 2000, *J Immunol* 164:4178-4184; Idusogie *et al.*, 2001, *J Immunol* 166:2571-2575, both hereby entirely incorporated by reference). Figure 12 shows a structure of the human IgG1 Fc region with this epicenter mapped. Select amino acid modifications disclosed in USSN 10/672,280, USSN 10/822,231, USSN 11/124,620, and USSN 11/256,060, all hereby entirely incorporated by reference, that are structurally proximal to these four residues were investigated to explore variants that may mediate increased affinity for C1q and and/or provide enhanced CDC. Variants that previously showed enhanced FcγR affinity and FcγR-mediated effector function were included in this set of variants to characterize their complement properties. This variant library is provided in Figure 13.

[173] The variants were constructed as described above in the context of the anti-CD20 antibody PRO70769 (variable region) and either IgG1 or IgG(1/2) ELLGG as the heavy chain constant region. Variants were expressed and purified as described above. A cell-based assay was used to measure the capacity of the Fc variants to mediate CDC. Lysis was measured using release of Alamar Blue to monitor lysis of Fc variant and WT PRO70769 -opsonized WIL2-S lymphoma cells by human serum complement. Target cells were washed 3x in 10% FBS medium by centrifugation and resuspension,

and WT or variant rituximab antibody was added at the indicated final concentrations. Human serum complement (Quidel) was diluted 50% with medium and added to antibody-opsonized target cells. Final complement concentration was 1/6th original stock. Plates were incubated for 2 hrs at 37 °C, Alamar Blue was added, cells were cultured for two days, and fluorescence was measured. Representative data from this assay are shown in Figure 14. The binding data were normalized to the maximum and minimum luminescence signal for each particular curve, provided by the baselines at low and high antibody concentrations respectively. The data were fit to a sigmoidal dose-response with variable slope model using nonlinear regression, and these fits are represented by the curves in the figure. These fits provide the effective concentration 50% (EC50) (i.e. the concentration required for 50% response) for each antibody, enabling the relative binding affinities of Fc variants to be quantitatively determined. By dividing the EC50 for each variant by that of WT PRO70769, the fold-enhancement or reduction relative to WT PRO70769 (Fold WT) were obtained. These values are provided in Figure 13. Here a fold above 1 indicates an enhancement in CDC EC50, and a fold below 1 indicates a reduction in CDC EC50 relative to WT PRO70769.

[174] The data in Figures 13 and 14 indicate that a number of modifications provide enhanced CDC relative to WT PRO70769 IgG1. For example, greater than 2-fold CDC enhancement is observed for modifications 239D, 267D, 267Q, 268D, 268E, 268F, 268G, 272I, 276D, 276L, 276S, 278R, 282G, 284T, 285Y, 293R, 300T, 324I, 324T, 324V, 326E, 326T, 326W, 327D, 330H, 330S, 332E, 333F, 334T, and 335D (Figure 15). Additionally, the data show that a number of modifications provide reduced CDC relative to WT PRO70769 IgG1. For example, modifications that show 0.5 fold and lower relative CDC include 235D, 239D, 284D, 322H, 322T, 322Y, 327R, 330E, 330I, 330L, 330N, 330V, 331D, and 331L, 332E (Figure 15). These modifications provide further valuable structure activity relationship (SAR) information that may be used to guide further design of variants for enhanced CDC. Together the data suggest that modification at positions 235, 239, 267, 268, 272, 276, 278, 282, 284, 285, 293, 300, 322, 324, 326, 327, 330, 331, 332, 333, 334, and 335 (Figure 15) may provide enhanced CDC relative to a parent Fc polypeptide.

Example 3. Fc variants with reduced FcγR- and complement-mediated effector function

[175] As described above, in contrast antibody therapeutics and indications wherein effector functions contribute to clinical efficacy, for some antibodies and clinical applications it may be favorable to reduce or eliminate binding to one or more FcγRs, or reduce or eliminate one or more FcγR- or complement-mediated effector functions including but not limited to ADCC, ADCP, and/or CDC. This is often the case for therapeutic antibodies whose mechanism of action involves blocking or antagonism but not killing of the cells bearing target antigen. In these cases depletion of target cells is undesirable and can be considered a side effect. Effector function can also be a problem for radiolabeled antibodies, referred to as radioconjugates, and antibodies conjugated to toxins, referred to as immunotoxins. These drugs can be used to destroy cancer cells, but the recruitment of immune cells via Fc interaction with FcγRs brings healthy immune cells in proximity to the deadly payload (radiation or toxin), resulting in depletion of normal lymphoid tissue along with targeted cancer cells.

[176] A previously unconsidered advantage of ablated FcγR- and complement- binding is that in cases where effector function is not needed, binding to FcγR and complement may effectively reduce the active concentration of drug. Binding to Fc ligands may localize an antibody or Fc fusion to cell surfaces or in complex with serum proteins wherein it is less active or inactive relative to when it is free (uncomplexed). This may be due to decreased effective concentration at binding sites where the antibody is desired, or perhaps Fc ligand binding may put the Fc polypeptide in a conformation in which it is less active than it would be if it were unbound. An additional consideration is that FcγR-receptors may be one mechanism of antibody turnover, and can mediate uptake and processing by antigen presenting cells such as dendritic cells and macrophages. This may affect affect the pharmacokinetics (or in vivo half-life) of the antibody or Fc fusion and its immunogenicity, both of which are critical parameters of clinical performance.

[177] Visual inspection of the Fc/FcγR structure (Figure 2) and the aforedescribed Fc/C1q interface (Figure 12), as well as data disclosed above and in USSN 10/672,280, USSN 10/822,231, USSN 11/124,620, and USSN 11/256,060, all hereby entirely incorporated by reference, were used to guide the design of a library to screen for variants with reduced affinity for FcγRs and reduced CDC. This variant library is provided in Figure 16. The variants were constructed in the context of PRO70769 IgG1, and expressed and purified as described above. Relative FcγR affinity was measured using the competition AlphaScreen assay, as described above. Figure 17 shows AlphaScreen data for binding of select Fc variants to human V158 FcγRIIIa, and Figure 16 provides their Fold IC50's relative to WT PRO70769 IgG1. The variants were also investigated for their capacity to mediate complement-mediated lysis against CD20+ WIL2-S lymphoma target cells using the CDC assay described above. Figure 18 provides CDC data for select Fc variants, and Figure 16 provides their Fold EC50's relative to WT PRO70769 IgG1. Based on the results of these experiments, select Fc variants were characterized for their capacity to mediate FcγR-mediated effector function. An ADCC assay using human PBMCs as effector cells and WIL2-S lymphoma cells as target cells was carried out as described above. Figure 19 shows these ADCC data for select variants.

[178] The data indicate that modification at a number of positions provide reduced or ablated FcγR affinity, reduced FcγR-mediated effector function, and reduced complement-mediated effector function. Furthermore, modifications at some positions, including but not limited to 235 and 330, may provide reduced CDC but WT FcγR affinity. For example 235D, 330L, 330N, and 330R display such behavior. Alternatively, modification at some positions, including but not limited to 236 and 299, may provide reduced FcγR affinity but WT level CDC. For example 236I and 299A show these properties.

[179] Based on the results of these experiments, a number of modifications that simultaneously ablate FcγR affinity and CDC were combined in multiple mutations variants in a new library of Fc variants was designed to screen for variants with completely ablated FcγR affinity, FcγR-mediated effector function, and complement-mediated effector function. These variants include modifications at positions 234, 235, 236, 267, 269, 325, and 328, and are provided in Figure 20. Included in the set are the WT IgG1 antibody, as well as IgG2 and IgG4 antibody versions, an aglycosylated variant

N297S, and two variants previously characterized as having reduced effector function: L234A/L235A (Xu et al., 2000, Cellular Immunology 200:16-26; USSN 10/267,286, hereby entirely incorporated by reference) and E233P/L234V/L235A/G236- (Armour et al., 1999, Eur J Immunol 29:2613-2624, hereby entirely incorporated by reference).

[180] These variants were constructed in the context of the anti-CD20 antibody PRO70769, with the heavy chain constant region IgG1 except for the IgG2 and IgG4 antibodies. Antibodies were expressed and purified as described previously. The competition AlphaScreen assay was used as described previously to measure the relative FcγR affinity of the Fc variants. Figure 21 shows AlphaScreen data for binding of select variants to the low affinity human activating receptor V158 FcγRIIIa, as well as the high affinity human activating receptor FcγRI. The fold IC50's relative to WT are provided in Figure 20. Because of its greater binding affinity for the Fc region, FcγRI provides a more stringent test for the variants. The data in Figures 20 and 21 support this, showing that although variants may substantially reduce or completely ablate affinity to FcγRIIIa, FcγRI binding is more modestly affected. The Fc variants were also tested for their capacity to mediate complement-mediated lysis against CD20+ WIL2-S cells using the CDC assay described above. Figure 22 shows CDC data for select Fc variants, and Figure 20 provides the fold EC50's relative to WT PRO70769 IgG1.

[181] In order to investigate the capacity of the Fc variants to mediate ADCC, select variants were subcloned into the anti-Her2/neu antibody trastuzumab (variable region sequences provided in Figures 24c and 24d). Trastuzumab robustly provides a substantial signal in ADCC assays against Her2+ expressing cell lines, and therefore provides a stringent test of the Fc variants for reducing/ablating effector function. Fc variants L235G, G236R, G237K, N325L, N325A, L328R, L235G/G236R, G236R/G237K, G236R/N325L, G236R/L328R, G237K/N325L, L235G/G236R/G237K, and G236R/G237K/L328R were constructed in the context of trastuzumab IgG1. WT IgG1,WT IgG2, and WT IgG4 antibody versions were constructed as well. An ADCC assay was carried out as described above, except the Her2+ breast carcinoma cell line SkBr-3 was used as target cells. Figure 23 provides the results of the ADCC experiments. The data indicate that some of the variants completely ablate ADCC. Additionally, although IgG2 also appears to mediate no ADCC, IgG4 does show a significant level of ADCC.

[182] The results show that amino acid modifications at a number of positions, including but not limited to 232, 234, 235, 236, 237, 238, 239, 265, 267, 269, 270, 297, 299, 325, 327, 328, 329, 330, and 331, provide promising candidates for improving the clinical properties of antibodies and Fc fusions wherein FcγR binding, FcγR-mediated effector functions, and/or complement-mediated effector function are undesired. For example the amino acid modifications 232G, 234G, 234H, 235D, 235G, 235H, 236I, 236N, 236P, 236R, 237K, 237L, 237N, 237P, 238K, 239R, 265G, 267R, 269R, 270H, 297S, 299A, 299I, 299V, 325A, 325L, 327R, 328R, 329K, 330I, 330L, 330N, 330P, 330R, 330S, and 331L provide significantly reduced Fc ligand binding properties and/or effector function. Particularly effective at reducing binding to Fc ligands and effector function are variants 236R/237K, 236R/325L, 236R/328R, 237K/325L, 237K/328R, 325L/328R, 235G/236R, 267R/269R, 234G/235G,

236R/237K/325L, 236R/325L/328R, 235G/236R/237K, and 237K/325L/328R. Notably, the amino acid modifications that compose these variants, including 234G, 235G, 236R, 237K, 267R, 269R, 325L, and 328R, are capable of reducing binding to both FcγRIIIa and FcγRI, and reducing CDC by greater than 10 fold. Additionally, the data show that human IgG2 has significantly reduced FcγR-affinity, FcγR-mediated effector function, and complement-mediated effector function relative to human IgG4.

[183] As discussed above, reduced FcγR affinity and/or effector function may be optimal for Fc polypeptides for which Fc ligand binding or effector function leads to toxicity and/or reduced efficacy. For example, antibodies that target CTLA-4 block inhibition of T-cell activation and are effective at promoting anti-tumor immune response, but destruction of T cells via antibody mediated effector functions may be counterproductive to mechanism of action and/or potentially toxic. Indeed toxicity has been observed with clinical use of the anti-CTLA-4 antibody ipilimumab (Maker et al., 2005, Ann Surg Oncol 12:1005-16, hereby entirely incorporated by reference). The sequences for the anti-CTLA-4 antibody ipilimumab (Mab 10D.1, MDX010) are provided in Figure 24, taken from US 6,984,720 SEQ ID:7 (VL, Figure 24e) and SEQ ID:17 (VH, Figure 24f) , hereby entirely incorporated by reference. For illustration purposes, a number of Fc variants of the present invention have been incorporated into the sequence of an antibody targeting CTLA-4. Because combinations of Fc variants of the present invention have typically resulted in additive or synergistic binding modulations, and accordingly additive or synergistic modulations in effector function, it is anticipated that as yet unexplored combinations of the Fc variants provided in the present invention, or with other previously disclosed modifications, will also provide favorable results. Potential Fc variants are provided in Figure 26a. The optimized antibody sequences sequences comprise at least one non-WT amino acid selected from the group consisting of X_1, X_2, X_3, X_4, X_5, X_6, X_7, and X_8. For example, an improved anti-CTLA-4 antibody sequence comprising the L235G and G236R modifications in the IgG1 constant region are provided in Figures 26b and 26c. Alternatively, as the present invention shows, IgG2 and IgG4 can also be used to reduce Fc ligand binding and Fc-mediated effector function. Figures 26b and 26d provide the sequences of improved anti-CTLA-4 IgG2 antibody sequences. The use of an anti-CTLA-4 here is solely an example, and is not meant to constrain application of the Fc variants to this antibody or any other particular Fc polypeptide. Other exemplary applications for reduced Fc ligand binding and/or effector function include but are not limited to anti-TNFα antibodies, including for example infliximab and adalimumab, anti-VEGF antibodies, including for example bevacizumab, anti-α4-integrin antibodies, including for example natalizumab, and anti-CD32b antibodies, including for example those described in USSN 10/643,857, hereby entirely incorporated by reference.

[184] This list of preferred Fc variants is not meant to constrain the present invention. Indeed all combinations of the any of the Fc variants provided are embodiments of the present invention. Furthermore, combinations of any of the Fc variants of the present invention with other discovered or undiscovered Fc variants may also provide favorable properties, and these combinations are also contemplated as embodiments of the present invention. Finally, it is anticipated from these results that other substitutions at positions mutated in present invention may also provide favorable binding

2006230413 26 Aug 2010

enhancements and specificities, and thus substitutions at all positions disclosed herein are contemplated.

[185] All cited references are herein expressly incorporated by reference in their entirety.

[186] Whereas particular embodiments of the invention have been described above for purposes of illustration, it will be appreciated by those skilled in the art that numerous variations of the details may be made without departing from the invention as described in the appended claims.

[187] The reference in this specification to any prior publication (or information derived from it), or to any matter which is known, is not, and should not be taken as an acknowledgment or admission or any form of suggestion that that prior publication (or information derived from it) or known matter forms part of the common general knowledge in the field of endeavour to which this specification relates.

[188] Throughout this specification and the claims which follow, unless the context requires otherwise, the word "comprise", and variations such as "comprises" and "comprising", will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or group of integers or steps.

THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. A non-naturally occurring Fc variant of a parent Fc polypeptide, wherein said Fc variant exhibits altered binding to at least one FcγR or altered antibody dependent cell-mediated cytotoxicity as compared to said parent Fc polypeptide, wherein said Fc variant comprises at least one amino acid modification in the Fc region of said parent Fc polypeptide, wherein said variant is selected from the group consisting of: 227G/332E, 234D/332E, 234E/332E, 234G/332E, 235I/332E, 235S/332E, 235E/332E, 246H/332E, 255Y/332E, 258H/332E, 260H/332E, 267E/332E, 267D/332E, 268E/330Y, 268D/330Y, 272R/332E, 272H/332E, 283H/332E, 293R/332E, 295E/332E, 304T/332E, 324I/332E, 324G/332E, 324I/332D, 324G/332D, 327D/332E, 328F/332E, 328Y/332E, 328A/332D, 328T/332D, 328V/332D, 328I/332D, 328F/332D, 328Y/332D, 328M/332D, 328D/332D, 328E/332D, 328N/332D, 328Q/332D, 335D/332E, 239D/268E/330Y, 239D/332E/268E/330Y, 239D/332E/327A, 239D/332E/268E/327A, 239D/332E/330Y/327A, 332E/330Y/268E/327A, and 239D/332E/268E/330Y/327A, wherein numbering is according to the EU index.

2. An Fc variant according to claim 1, wherein said Fc polypeptide is a human IgG1 antibody.

3. An Fc variant according to claim 2, wherein said IgG1 antibody comprises the allotypic residues 356D and 358L.

4. An Fc variant according to claim 2, wherein said IgG1 antibody comprises the allotypic residues 356E and 358M.

5. An Fc variant according to claim 1, wherein said Fc polypeptide comprises a IgG(1/2) ELLGG antibody as defined by SEQ ID:12.

6. A non-naturally occurring IgG1 variant of a parent IgG1 polypeptide, wherein said IgG1 variant exhibits improved binding to at least on FcγR, wherein said Fc variant comprises at least one amino acid insertion in the Fc region of said parent IgG1 polypeptide, wherein said insertion occurs between two positions selected from the group consisting of 235 and 236, 297 and 298, and 326 and 327, wherein numbering is according

to the EU index.

7. A non-naturally occurring IgGI variant according to claim 6, wherein said insertion is selected from the group consisting of: an insertion of G between positions 235 and 236, an insertion of A between positions 235 and 236, an insertion of S between positions 235 and 236, an insertion of T between positions 235 and 236, an insertion of N between positions 235 and 236, an insertion of D between positions 235 and 236, an insertion of V between positions 235 and 236, an insertion of L between positions 235 and 236, an insertion of G between positions 297 and 298, an insertion of A between positions 297 and 298, an insertion of S between positions 297 and 298, an insertion of D between positions 297 and 298, an insertion of G between positions 326 and 327, an insertion of A between positions 326 and 327, an insertion of T between positions 326 and 327, an insertion of D between positions 326 and 327, and an insertion of E between positions 326 and 327, wherein numbering is according to the EU index.

8. A non-naturally occurring Fc variant of a parent Fc polypeptide, wherein said Fc variant exhibits altered complement dependent cytotoxicity as compared to said parent Fc polypeptide, wherein said Fc variant comprises at least one amino acid modification in the Fc region of said parent Fc polypeptide, wherein said modification is selected from the group consisting of: 233I, 239D, 267D, 267E, 267Q, 268E, 268F, 268G, 271A, 271D, 271I, 272H, 272I), 272R, 274E, 274R, 274Y, 276D, 276L, 276S, 278E, 278H, 278Q, 278R, 281 D, 282G, 284D, 284E, 284T, 285Y, 293R, 300D, 300T, 320I, 320T, 320Y, 324D, 324H, 324I, 324L, 324T, 324V, 328Q, 330E, 330G, 330H, 330I, 330L, 330N, 330V, 330Y, 332E, 335D, and 335Y, wherein numbering is according to the EU index.

9. A non-naturally occurring Fc variant of a parent Fc polypeptide, wherein said Fc variant exhibits improved complement dependent cytotoxicity as compared to said parent Fc polypeptide, wherein said Fc variant comprises at least one amino acid modification in the Fc region of said parent Fc polypeptide, wherein said modification is at a position selected from the group consisting of: 235, 239, 267, 268, 272, 276, 278, 282, 284, 285, 293, 300, 324, 330, 332, and 335, wherein numbering is according to the EU index.

10. An Fc variant according to claim 9, wherein said Fc variant comprises one or more amino acid modifications selected from the group consisting of: 267D, 267Q, 268D, 268E,

268F, 268G, 272I, 276D, 276L, 276S, 278R, 282G, 284T, 285Y, 293R, 300T, 324I, 324T, 324V, 327D, 330H, 330S, 332E, 335D.

11. A non-naturally occurring Fc variant of a parent Fc polypeptide, wherein said Fc variant exhibits reduced binding to one or more FcγRs, reduced antibody dependent cell-mediated cytotoxicity, or reduced complement dependent cytotoxicity as compared to said parent Fc polypeptide, wherein said Fc variant comprises at least one amino acid modification in the Fc region of said parent Fc polypeptide, wherein said variant is selected from the group consisting of: 236R/237K, 236R/325L, 236R/328R, 237K/325L, 237K/328R, 325L/328R, 235G/236R, 267R/269R, 234G/235G, 236R/237K/325L, 236R/325L/328R, 235G/236R/237K, and 237K/325L/328R.

12. A non-naturally occurring Fc variant of a parent Fc polypeptide comprising at least one modification at a position selected from the group consisting of: 234G, 235G, 236R, 237K, 267R, 325L, 328R, wherein numbering is a according to the EU index, wherein said Fc variant reduces by at least 10 fold relative to said parent Fc polypeptide: affinity to human FcγRIIIa, affinity to human FcγRI, and complement dependent cytotoxicity.

13. A non-naturally occurring IgG antibody that targets CTLA-4, TNFα, VEGF, α4-integrin, or CD32b, wherein said antibody has reduced FcγR affinity, reduced antibody dependent cell-mediated cytotoxicity, or reduced complement dependent cytotoxicity relative to a WT antibody, and wherein said antibody comprises an amino acid modification at a position selected from the group consisting of: 234, 235, 236, 237, 267, and 328, relative to a parent IgG antibody, wherein numbering is according to the EU index.

14. An IgG antibody according to claim 13, wherein said antibody is a human IgG2 or IgG4 antibody.

15. An Fc variant according to claim 1, claim 8, claim 9, claim 11 or claim 12, an IgGI variant according to claim 6, or an IgG antibody according to claim 12, substantially as herein described with reference to the Examples and the accompanying drawings.

Figure 1

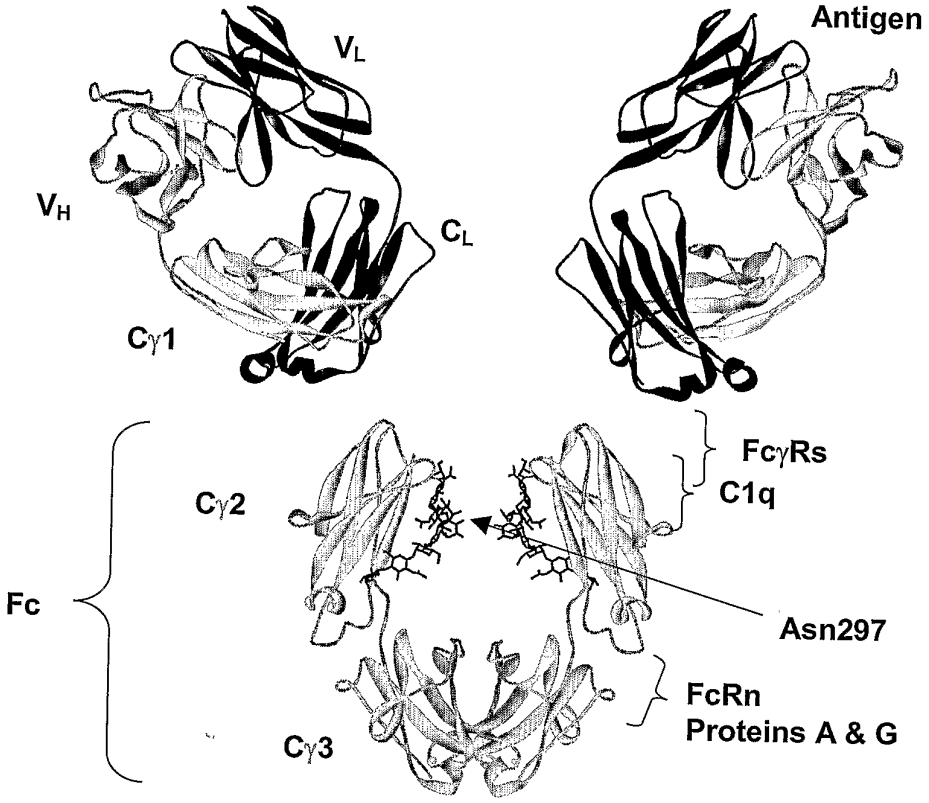

Antigen
V_L
V_H
C_L
$C\gamma1$
$C\gamma2$
Fc
$Fc\gamma Rs$
C1q
Asn297
FcRn
Proteins A & G
$C\gamma3$

Figure 2

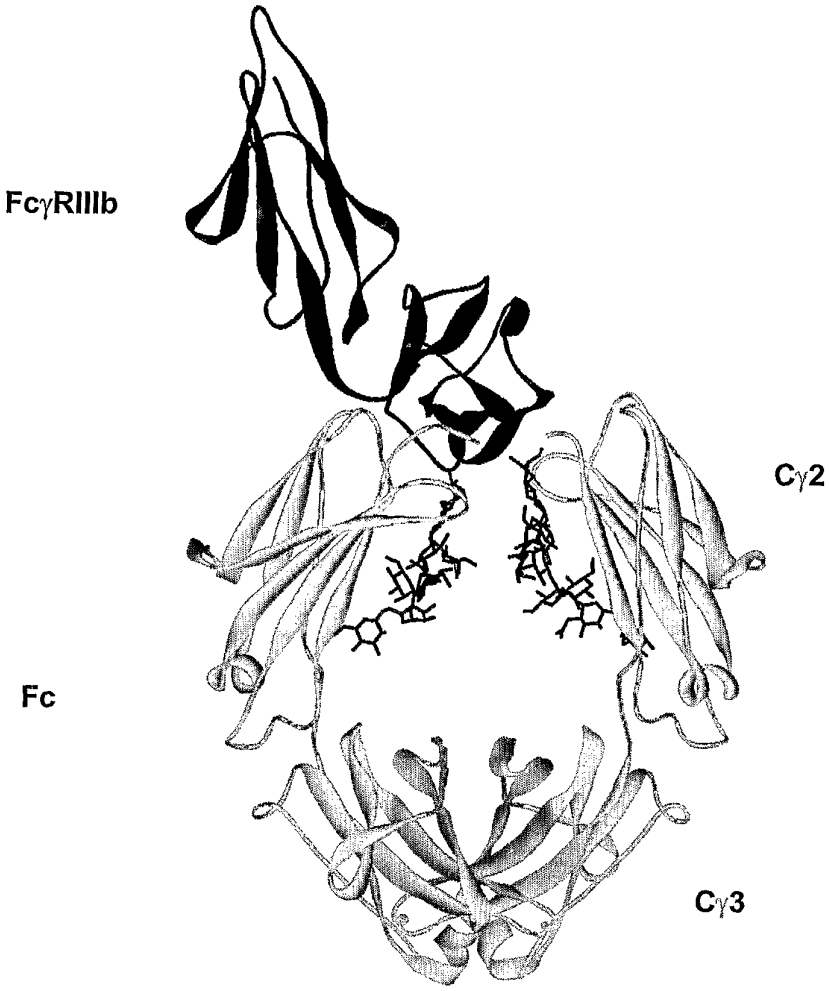


Figure 3a

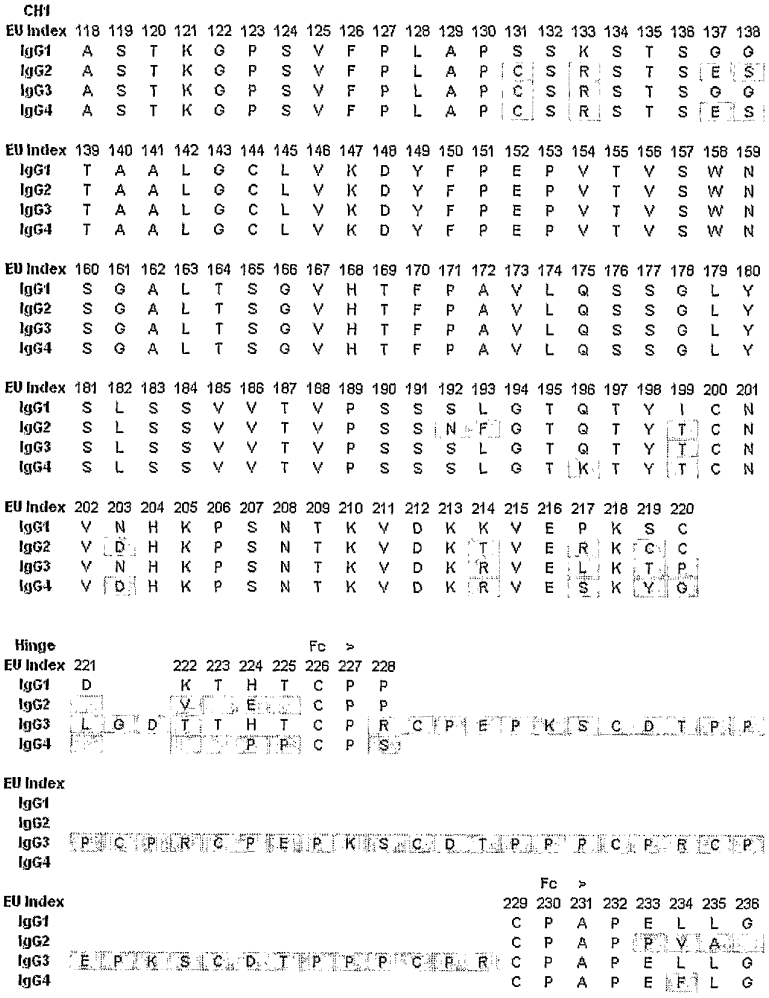
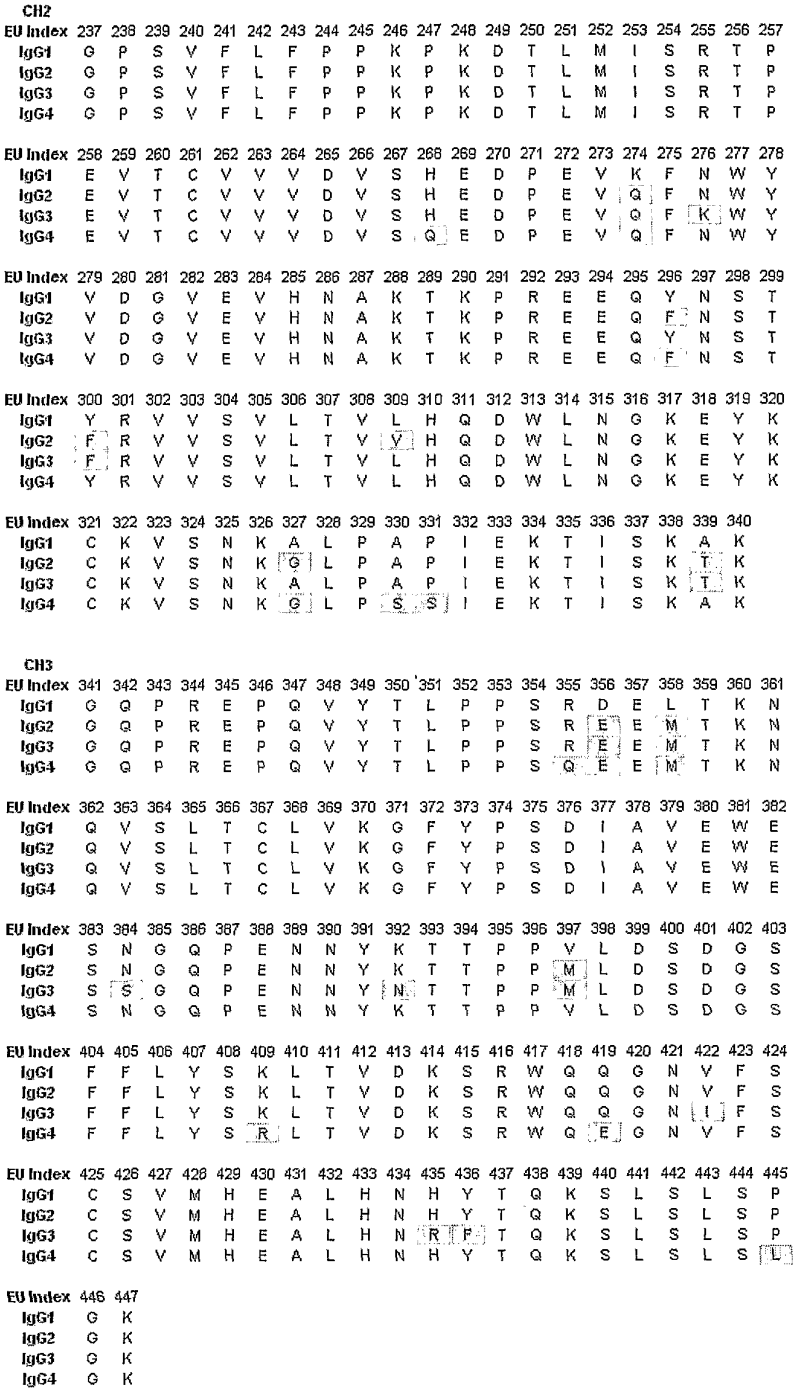

CH1
EU Index 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138
IgG1 A S T K G P S V F P L A P S S K S T S G G
IgG2 A S T K G P S V F P L A P C S R S T S E S
IgG3 A S T K G P S V F P L A P C S R S T S G G
IgG4 A S T K G P S V F P L A P C S R S T S E S
EU Index 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159
IgG1 T A A L G C L V K D Y F P E P V T V S W N
IgG2 T A A L G C L V K D Y F P E P V T V S W N
IgG3 T A A L G C L V K D Y F P E P V T V S W N
IgG4 T A A L G C L V K D Y F P E P V T V S W N
EU Index 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180
IgG1 S G A L T S G V H T F P A V L Q S S G L Y
IgG2 S G A L T S G V H T F P A V L Q S S G L Y
IgG3 S G A L T S G V H T F P A V L Q S S G L Y
IgG4 S G A L T S G V H T F P A V L Q S S G L Y
EU Index 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201
IgG1 S L S S V V T V P S S S L G T Q T Y I C N
IgG2 S L S S V V T V P S S N F G T Q T Y T C N
IgG3 S L S S V V T V P S S S L G T Q T Y T C N
IgG4 S L S S V V T V P S S S L G T K T Y T C N
EU Index 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220
IgG1 V N H K P S N T K V D K K V E P K S C
IgG2 V D H K P S N T K V D K T V E R K C C
IgG3 V N H K P S N T K V D K R V E L K T P
IgG4 V D H K P S N T K V D K R V E S K Y G
Hinge
Fc
EU Index 221 222 223 224 225 226 227 228
IgG1 D K T H T C P P
IgG2 V E C P P
IgG3 L G D T T H T C P R C P E P K S C D T P P
IgG4 P P C P S
EU Index
IgG1
IgG2
IgG3 P C P R C P E P K S C D T P P P C P R C P
IgG4
Fc
EU Index 229 230 231 232 233 234 235 236
IgG1 C P A P E L L G
IgG2 C P A P P V A
IgG3 E P K S C D T P P P C P R C P A P E L L G
IgG4 C P A P E F L G

Figure 3b



CH2

EU Index	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257
IgG1	G	P	S	V	F	L	F	P	P	K	P	K	D	T	L	M	I	S	R	T	P
IgG2	G	P	S	V	F	L	F	P	P	K	P	K	D	T	L	M	I	S	R	T	P
IgG3	G	P	S	V	F	L	F	P	P	K	P	K	D	T	L	M	I	S	R	T	P
IgG4	G	P	S	V	F	L	F	P	P	K	P	K	D	T	L	M	I	S	R	T	P

EU Index	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278
IgG1	E	V	T	C	V	V	V	D	V	S	H	E	D	P	E	V	K	F	N	W	Y
IgG2	E	V	T	C	V	V	V	D	V	S	H	E	D	P	E	V	Q	F	N	W	Y
IgG3	E	V	T	C	V	V	V	D	V	S	H	E	D	P	E	V	Q	F	K	W	Y
IgG4	E	V	T	C	V	V	V	D	V	S	Q	E	D	P	E	V	Q	F	N	W	Y

EU Index	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299
IgG1	V	D	G	V	E	V	H	N	A	K	T	K	P	R	E	E	Q	Y	N	S	T
IgG2	V	D	G	V	E	V	H	N	A	K	T	K	P	R	E	E	Q	F	N	S	T
IgG3	V	D	G	V	E	V	H	N	A	K	T	K	P	R	E	E	Q	Y	N	S	T
IgG4	V	D	G	V	E	V	H	N	A	K	T	K	P	R	E	E	Q	F	N	S	T

EU Index	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320
IgG1	Y	R	V	V	S	V	L	T	V	L	H	Q	D	W	L	N	G	K	E	Y	K
IgG2	F	R	V	V	S	V	L	T	V	V	H	Q	D	W	L	N	G	K	E	Y	K
IgG3	F	R	V	V	S	V	L	T	V	L	H	Q	D	W	L	N	G	K	E	Y	K
IgG4	Y	R	V	V	S	V	L	T	V	L	H	Q	D	W	L	N	G	K	E	Y	K

EU Index	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340
IgG1	C	K	V	S	N	K	A	L	P	A	P	I	E	K	T	I	S	K	A	K
IgG2	C	K	V	S	N	K	G	L	P	A	P	I	E	K	T	I	S	K	T	K
IgG3	C	K	V	S	N	K	A	L	P	A	P	I	E	K	T	I	S	K	T	K
IgG4	C	K	V	S	N	K	G	L	P	S	S	I	E	K	T	I	S	K	A	K

CH3

EU Index	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361
IgG1	G	Q	P	R	E	P	Q	V	Y	T	L	P	P	S	R	D	E	L	T	K	N
IgG2	G	Q	P	R	E	P	Q	V	Y	T	L	P	P	S	R	E	E	M	T	K	N
IgG3	G	Q	P	R	E	P	Q	V	Y	T	L	P	P	S	R	E	E	M	T	K	N
IgG4	G	Q	P	R	E	P	Q	V	Y	T	L	P	P	S	Q	E	E	M	T	K	N

EU Index	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382
IgG1	Q	V	S	L	T	C	L	V	K	G	F	Y	P	S	D	I	A	V	E	W	E
IgG2	Q	V	S	L	T	C	L	V	K	G	F	Y	P	S	D	I	A	V	E	W	E
IgG3	Q	V	S	L	T	C	L	V	K	G	F	Y	P	S	D	I	A	V	E	W	E
IgG4	Q	V	S	L	T	C	L	V	K	G	F	Y	P	S	D	I	A	V	E	W	E

EU Index	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403
IgG1	S	N	G	Q	P	E	N	N	Y	K	T	T	P	P	V	L	D	S	D	G	S
IgG2	S	N	G	Q	P	E	N	N	Y	K	T	T	P	P	M	L	D	S	D	G	S
IgG3	S	S	G	Q	P	E	N	N	Y	N	T	T	P	P	M	L	D	S	D	G	S
IgG4	S	N	G	Q	P	E	N	N	Y	K	T	T	P	P	V	L	D	S	D	G	S

EU Index	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424
IgG1	F	F	L	Y	S	K	L	T	V	D	K	S	R	W	Q	Q	G	N	V	F	S
IgG2	F	F	L	Y	S	K	L	T	V	D	K	S	R	W	Q	Q	G	N	V	F	S
IgG3	F	F	L	Y	S	K	L	T	V	D	K	S	R	W	Q	Q	G	N	I	F	S
IgG4	F	F	L	Y	S	R	L	T	V	D	K	S	R	W	Q	E	G	N	V	F	S

EU Index	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445
IgG1	C	S	V	M	H	E	A	L	H	N	H	Y	T	Q	K	S	L	S	L	S	P
IgG2	C	S	V	M	H	E	A	L	H	N	H	Y	T	Q	K	S	L	S	L	S	P
IgG3	C	S	V	M	H	E	A	L	H	N	R	F	T	Q	K	S	L	S	L	S	P
IgG4	C	S	V	M	H	E	A	L	H	N	H	Y	T	Q	K	S	L	S	L	S	L

EU Index	446	447
IgG1	G	K
IgG2	G	K
IgG3	G	K
IgG4	G	K

Figure 4

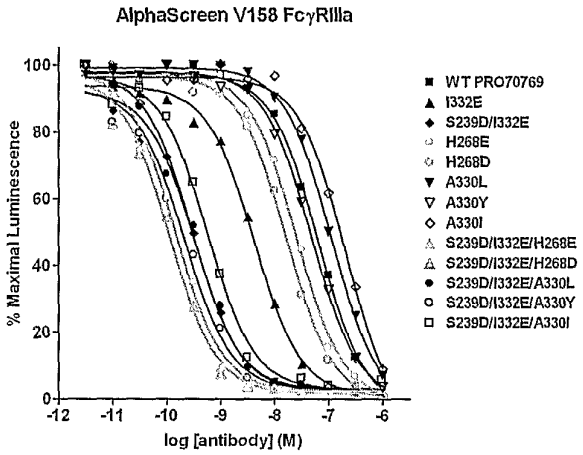
Name	Position	IgG1	IgG2	IgG3	IgG4
Allotypes					
G1m(1)	356	D	E	E	E
	358	L	M	M	M
G1m(2)	431	G	A	A	A
G1m(3)	214	R	T	R	R
G1m(17)	214	K	T	R	R
Isoallotypes					
nG1m(1)	356	E	E	E	E
	358	M	M	M	M
nG1m(2)	431	A	A	A	A
nG1m(17)	214	R	T	R	R

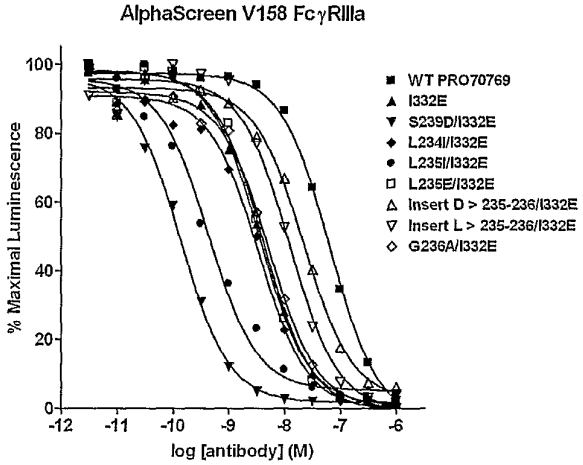
Figure 5

Variant	V158 FcγRIIIa Fold WT IC50	F158 FcγRIIIa Fold WT IC50	Variant	V158 FcγRIIIa Fold WT IC50	F158 FcγRIIIa Fold WT IC50
G236S	0.22	0.21	S324I / I332E	8.17	3.53
G236A	0.36	0.45	S324G / I332E	0.75	1.72
K246H	0.75	0.71	A327D / I332E	0.13	0.36
V264I	1.19	1.03	L328A / I332E	0.99	0.78
H268D	3.90	3.19	L328T / I332E	17.48	18.25
I332D	9.7	9.8	L328V / I332E	6.83	9.17
S267D	8.4		L328I / I332E	25.70	19.59
S267E			L328F / I332E	14.45	10.24
S324I	0.58	0.43	L328Y / I332E	2.96	2.22
L235D	1.68	1.33	L328M / I332E	2.67	1.96
E272I	1.18	2.04	L328D / I332E	3.29	3.29
E272R			L328E / I332E		
E272H	0.85	2.35	L328N / I332E	2.3	
G281D	1.14	1.55	L328Q / I332E	0.71	0.58
V282G	0.90	2.28	A330L / I332E	2.13	1.47
E293R	1.01	1.97	A330Y / I332E	16.09	16.48
A330L	0.57	0.75	A330I / I332E		
A330Y	1.35	1.29	T335D / I332E	17.92	19.78
A330I	0.31	0.83	I332E	15.65	14.10
H268E	2.58	2.09	I332E	18.00	13.50
D221K / I332E	16.57	15.65	I332E	13.90	11.20
H224E / I332E	13.52	10.64	I332E	13.90	12.87
P227G / I332E	13.52	10.15	S239D		
L234D / I332E	1.86	2.20	S239D / I332E	197.31	146.91
L234E / I332E	3.48	5.24	S239D / I332E	475.95	271.59
L234Y / I332E	16.01	12.24	S239D / I332E	146.04	92.08
L234I / I332E	18.98	12.88	S239D / I332E	327.63	229.27
L234G / I332E	1.17	1.08	S239D / I332E / A330Y	309.25	293.30
L235I / I332E	150.49	65.22	S239D / I332E / A330L	220.83	178.24
L235S / I332E	13.39	7.95	S239D / I332E / A330I	115.65	123.50
L235D / I332E	16.46	8.41	S239D / I332E / H268E	461.36	307.87
L235E / I332E	15.74	10.11	S239D / I332E / H268D	590.49	377.89
G236S / I332D	1.11	1.53	S239D / I332E / A327D		
G236A / I332D	1.81	3.94	S239D / I332E / V284E		
G236S / I332E	3.34	5.76	Insert G > 235-236 / I332E	0.70	1.14
G236A / I332E	12.26	18.32	Insert A > 235-236 / I332E	5.25	1.22
K246H / I332E	9.78	8.73	Insert S > 235-236 / I332E	1.08	0.94
R255Y / I332E	20.42	16.44	Insert T > 235-236 / I332E	1.45	1.02
E258H / I332E	391.08	101.46	Insert N > 235-236 / I332E	1.89	1.70
T260H / I332E	16.25	10.16	Insert D > 235-236 / I332E	2.94	5.44
V264I / I332E	20.95	16.08	Insert V > 235-236 / I332E	1.78	0.96
S267E / I332E	4.66	4.19	Insert L > 235-236 / I332E	5.26	3.90
S267D / I332E	21.77	14.11	Insert G > 297-298 / I332E	0.16	0.46
S267D / I332E	26.95	22.93	Insert A > 297-298 / I332E	0.13	0.51
H268E / I332D	25.90	29.12	Insert S > 297-298 / I332E	0.08	0.46
H268D / I332D	25.68	28.26	Insert D > 297-298 / I332E	0.16	0.35

Variant	V158 FcγRIIIa Fold WT IC50	F158 FcγRIIIa Fold WT IC50	Variant	V158 FcγRIIIa Fold WT IC50	F158 FcγRIIIa Fold WT IC50
H268E / I332E	46.3	27.2	Insert G > 326-327 / I332E	1.41	4.57
H268D / I332E	46.6	33.1	Insert A > 326-327 / I332E	15.32	3.56
E272R / I332E	4.79	4.66	Insert T > 326-327 / I332E		
E272H / I332E			Insert D > 326-327 / I332E		
E283H / I332E	11.55	10.07	Insert E > 326-327 / I332E		
V284E / I332E	24.30	14.63	Insert G > 235-236 / I332D	0.25	0.46
E293R / I332E	7.44	7.42	Insert A > 235-236 / I332D	0.78	0.95
Q295E / I332E	9.72	6.91	Insert S > 235-236 / I332D	0.51	0.71
S304T / I332E	2.23	1.97	Insert T > 235-236 / I332D	0.32	0.63
S324I / I332D	3.41	4.98	Insert N > 235-236 / I332D	0.54	0.69
S324G / I332D			Insert D > 235-236 / I332D	5.80	1.35
L328A / I332D	0.29	0.38	Insert V > 235-236 / I332D	0.58	1.36
L328T / I332D			Insert L > 235-236 / I332D	1.19	1.31
L328V / I332D	1.59	1.01			
L328I / I332D	3.04	1.24			
L328F / I332D	0.48	2.02			
L328Y / I332D	0.75	1.15			
L328M / I332D	2.28	2.20			
L328D / I332D					
L328E / I332D					
L328N / I332D					
L328Q / I332D	1.54	1.81			

Figure 6a


AlphaScreen V158 FcγRIIIa
% Maximal Luminescence
log [antibody] (M)
WT PRO70769
I332E
S239D/I332E
H268E
H268D
A330L
A330Y
A330I
S239D/I332E/H268E
S239D/I332E/H268D
S239D/I332E/A330L
S239D/I332E/A330Y
S239D/I332E/A330I


AlphaScreen V158 FcγRIIIa
% Maximal Luminescence
log [antibody] (M)
WT PRO70769
I332E
S239D/I332E
L234I/I332E
L235I/I332E
L235E/I332E
Insert D > 235-236/I332E
Insert L > 235-236/I332E
G236A/I332E

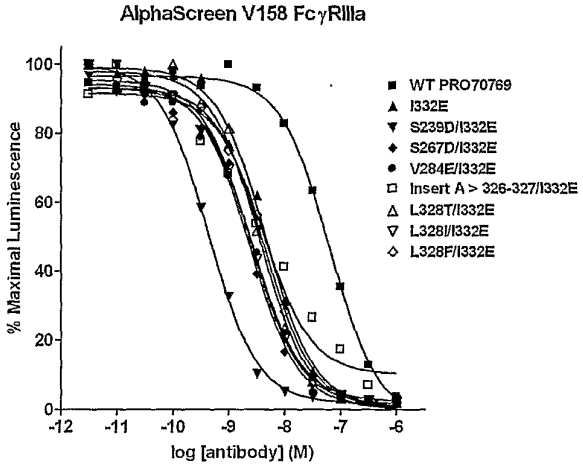

AlphaScreen V158 FcγRIIIa
% Maximal Luminescence
log [antibody] (M)
WT PRO70769
I332E
S239D/I332E
S267D/I332E
V284E/I332E
Insert A > 326-327/I332E
L328T/I332E
L328I/I332E
L328F/I332E

Figure 6b

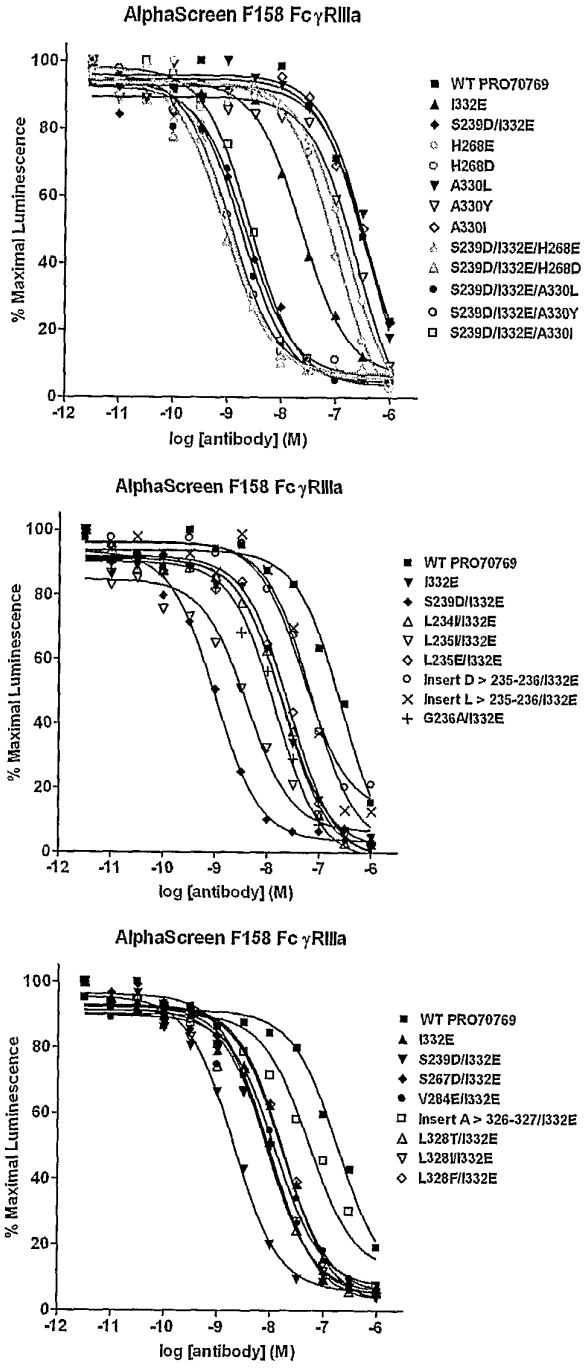

AlphaScreen F158 FcγRIIIa
% Maximal Luminescence
log [antibody] (M)
WT PRO70769
I332E
S239D/I332E
H268E
H268D
A330L
A330Y
A330I
S239D/I332E/H268E
S239D/I332E/H268D
S239D/I332E/A330L
S239D/I332E/A330Y
S239D/I332E/A330I
AlphaScreen F158 FcγRIIIa
% Maximal Luminescence
log [antibody] (M)
WT PRO70769
I332E
S239D/I332E
L234I/I332E
L235I/I332E
L235E/I332E
Insert D > 235-236/I332E
Insert L > 235-236/I332E
G236A/I332E
AlphaScreen F158 FcγRIIIa
% Maximal Luminescence
log [antibody] (M)
WT PRO70769
I332E
S239D/I332E
S267D/I332E
V284E/I332E
Insert A > 326-327/I332E
L328T/I332E
L328I/I332E
L328F/I332E

Figure 7a

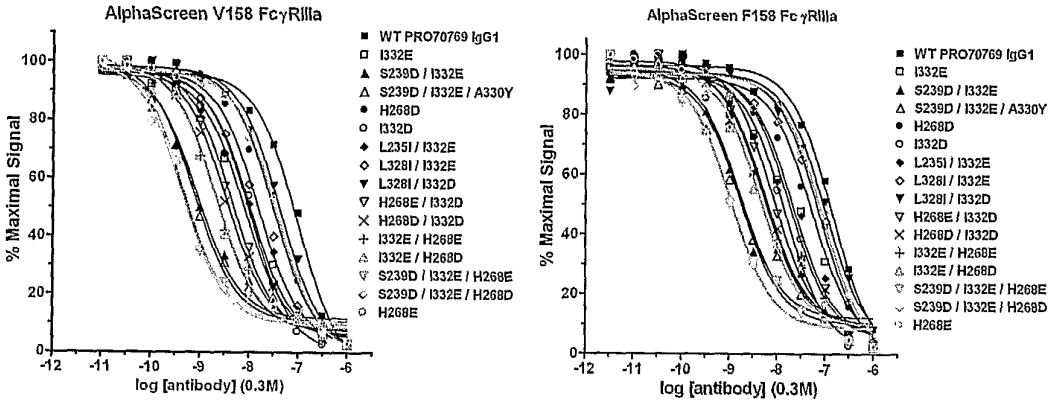


Figure 7b

Substitution(s)	V158 FcγRIIIa		F158 FcγRIIIa	
	IC50 (M)	Fold WT	IC50 (M)	Fold WT
WT PRO70769 IgG1	9.88E-08	1.00	1.42E-07	1.00
I332E	7.82E-09	12.64	2.08E-08	6.81
S239D / I332E	8.62E-10	114.64	1.66E-09	85.40
S239D / I332E / A330Y	7.48E-10	132.16	1.67E-09	84.58
H268D	3.19E-08	3.10	5.25E-08	2.70
I332D	1.02E-08	9.70	1.44E-08	9.81
L235I / I332E	1.03E-08	9.57	1.80E-08	7.86
L328I / I332E	1.53E-08	6.48	7.62E-08	1.86
L328I / I332D	4.34E-08	2.28	9.99E-08	1.42
H268E / I332D	4.35E-09	22.74	7.99E-09	17.72
H268D / I332D	3.39E-09	29.18	5.54E-09	25.54
I332E / H268E	2.14E-09	46.30	5.19E-09	27.24
I332E / H268D	2.12E-09	46.62	4.28E-09	33.08
S239D / I332E / H268E	4.37E-10	225.97	1.05E-09	134.51
S239D / I332E / H268D	4.42E-10	223.67	1.08E-09	131.38
H268E	3.70E-08	2.67	8.53E-08	1.66

Figure 8a

Modification(s)	IgG	V158 FcγRIIIa IC50 (M)	Fold	F158 FcγRIIIa IC50 (M)	Fold	FcγRIIb IC50 (M)	Fold
WT	IgG1	2.3E-08	1.0	1.3E-07	1.0	6.1E-08	1.0
I332E	IgG1	5.8E-09	3.9	1.6E-08	7.9	1.2E-07	0.5
S239D	IgG1	2.9E-09	7.8	1.1E-08	12.0	1.1E-08	5.3
A330Y	IgG1	1.3E-08	1.7	3.7E-08	3.5	2.6E-07	0.2
H268E	IgG1	1.3E-08	1.7	5.4E-08	2.4	5.3E-08	1.1
H268D	IgG1	9.7E-09	2.3	4.6E-08	2.8	3.1E-08	2.0
I332D	IgG1	9.1E-09	2.5	2.1E-08	6.2	1.4E-07	0.4
S239D/I332E	IgG1	4.3E-10	52.1	1.3E-09	98.0	3.1E-09	19.8
A330Y/I332E	IgG1	2.1E-09	10.9	4.8E-09	27.0	7.3E-08	0.8
H268E/I332D	IgG1	2.4E-09	9.3	5.6E-09	23.0	1.3E-08	4.8
I332D/A330Y	IgG1	9.7E-09	2.3	1.7E-08	7.7	2.2E-07	0.3
H268E/A330Y	IgG1	6.6E-09	3.4	2.5E-08	5.2	7.8E-08	0.8
H268D/A330Y	IgG1	1.1E-08	2.0	1.9E-08	6.9	4.2E-08	1.5
I332E/H268E	IgG1	1.8E-09	12.5	5.9E-09	22.0	1.4E-08	4.2
S239D/H268E	IgG1	1.3E-09	17.5	4.5E-09	28.4	9.8E-09	6.2
S239D/I332E/ H268E	IgG1	3.5E-10	64.3	1.2E-09	105.5	5.1E-09	11.9
S239D/I332E/ A330Y	IgG1	5.0E-10	45.3	1.4E-09	92.8	1.2E-08	5.1
S239D/H268E/ A330Y	IgG1	4.4E-10	50.9	1.3E-09	99.6	6.6E-09	9.2
S239D/I332E/ H268E/A330Y	IgG1	1.9E-10	116.8	3.8E-10	335.4	3.4E-09	17.7
S239D/I332E/ G327A	IgG(1/2) ELLGG	1.0E-09	21.6	2.3E-09	55.2	1.5E-08	4.0
S239D/I332E/ H268E/G327A	IgG(1/2) ELLGG	1.8E-10	125.0	4.3E-10	299.4	2.2E-09	27.3
S239D/I332E/ A330Y/G327A	IgG(1/2) ELLGG	2.1E-10	106.7	6.8E-10	189.3	8.2E-09	7.4
I332E/A330Y/ H268E/G327A	IgG(1/2) ELLGG	6.6E-10	33.9	1.7E-09	75.0	8.0E-09	7.7
S239D/I332E/ H268E/A330Y/G327A	IgG(1/2) ELLGG	1.2E-10	187.9	2.5E-10	521.9	2.3E-09	27.0

Figure 8b

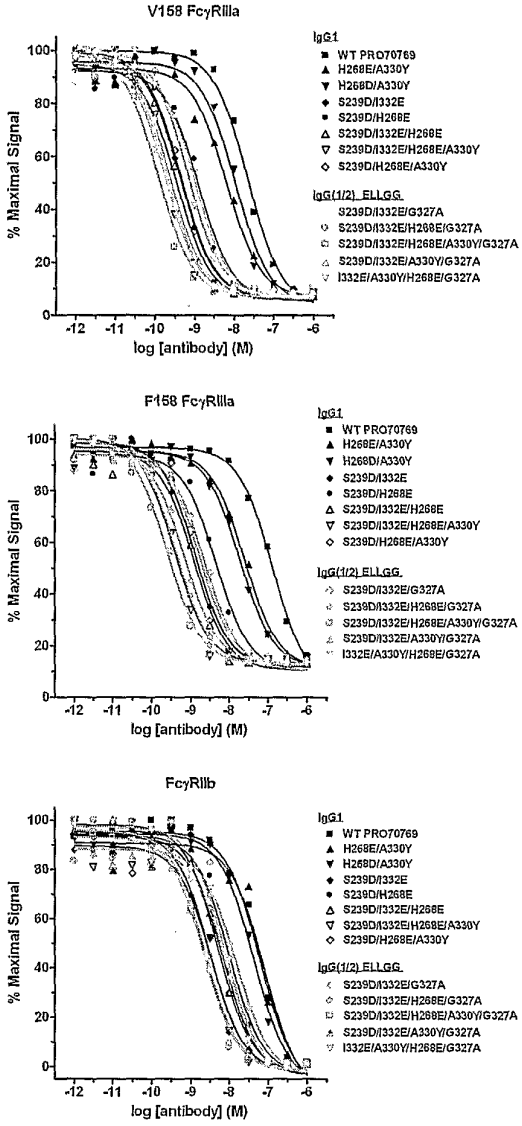

V158 FcγRIIIa
% Maximal Signal
log [antibody] (M)
IgG1
WT PRO70769
H268E/A330Y
H268D/A330Y
S239D/I332E
S239D/H268E
S239D/I332E/H268E
S239D/I332E/H268E/A330Y
S239D/H268E/A330Y
IgG(1/2) ELLGG
S239D/I332E/G327A
S239D/I332E/H268E/G327A
S239D/I332E/H268E/A330Y/G327A
S239D/I332E/A330Y/G327A
I332E/A330Y/H268E/G327A
F158 FcγRIIIa
% Maximal Signal
log [antibody] (M)
IgG1
WT PRO70769
H268E/A330Y
H268D/A330Y
S239D/I332E
S239D/H268E
S239D/I332E/H268E
S239D/I332E/H268E/A330Y
S239D/H268E/A330Y
IgG(1/2) ELLGG
S239D/I332E/G327A
S239D/I332E/H268E/G327A
S239D/I332E/H268E/A330Y/G327A
S239D/I332E/A330Y/G327A
I332E/A330Y/H268E/G327A
FcγRIIb
% Maximal Signal
log [antibody] (M)
IgG1
WT PRO70769
H268E/A330Y
H268D/A330Y
S239D/I332E
S239D/H268E
S239D/I332E/H268E
S239D/I332E/H268E/A330Y
S239D/H268E/A330Y
IgG(1/2) ELLGG
S239D/I332E/G327A
S239D/I332E/H268E/G327A
S239D/I332E/H268E/A330Y/G327A
S239D/I332E/A330Y/G327A
I332E/A330Y/H268E/G327A

Figure 9a

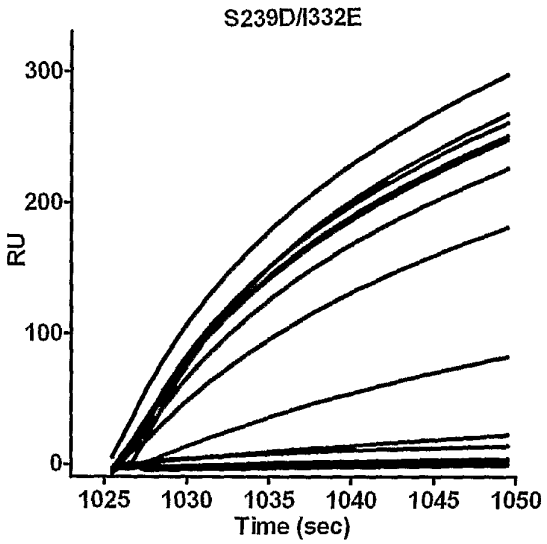


Figure 9b

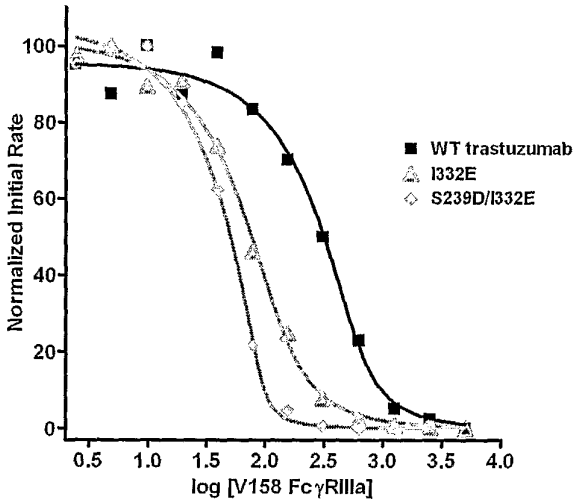
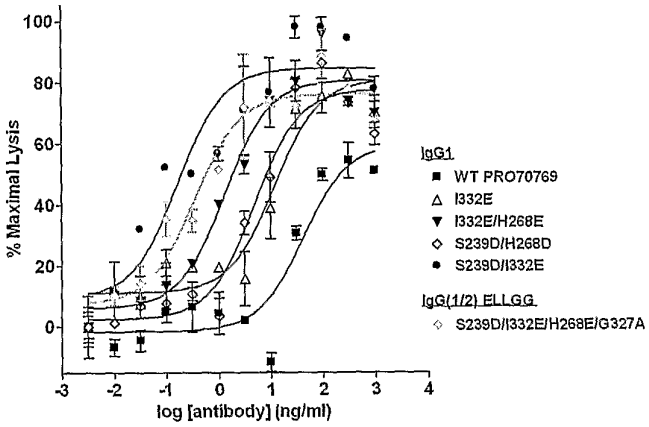


Figure 9c

Variant	V158 FcγRIIIa K_D (nM)	Fold WT
WT trastuzumab	252 ± 89	1.0
I332E	30 ± 7	8
S239D/I332E	2 ± 2	126

Figure 10


% Maximal Lysis
log [antibody] (ng/ml)
IgG1
WT PRO70769
I332E
I332E/H268E
S239D/H268D
S239D/I332E
IgG(1/2) ELLGG
S239D/I332E/H268E/G327A

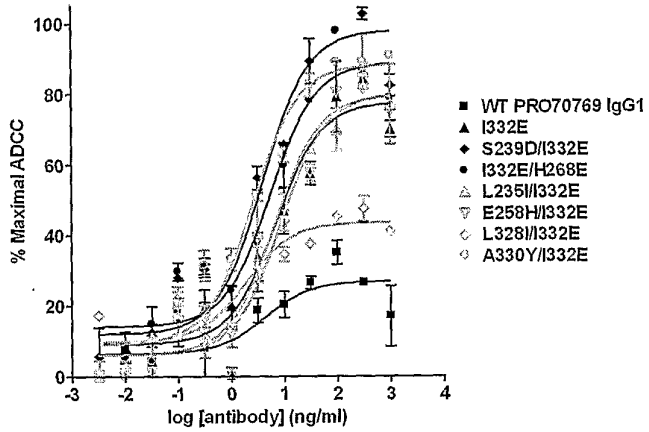

% Maximal ADCC
log [antibody] (ng/ml)
WT PRO70769 IgG1
I332E
S239D/I332E
I332E/H268E
L235I/I332E
E258H/I332E
L328I/I332E
A330Y/I332E

Figure 11

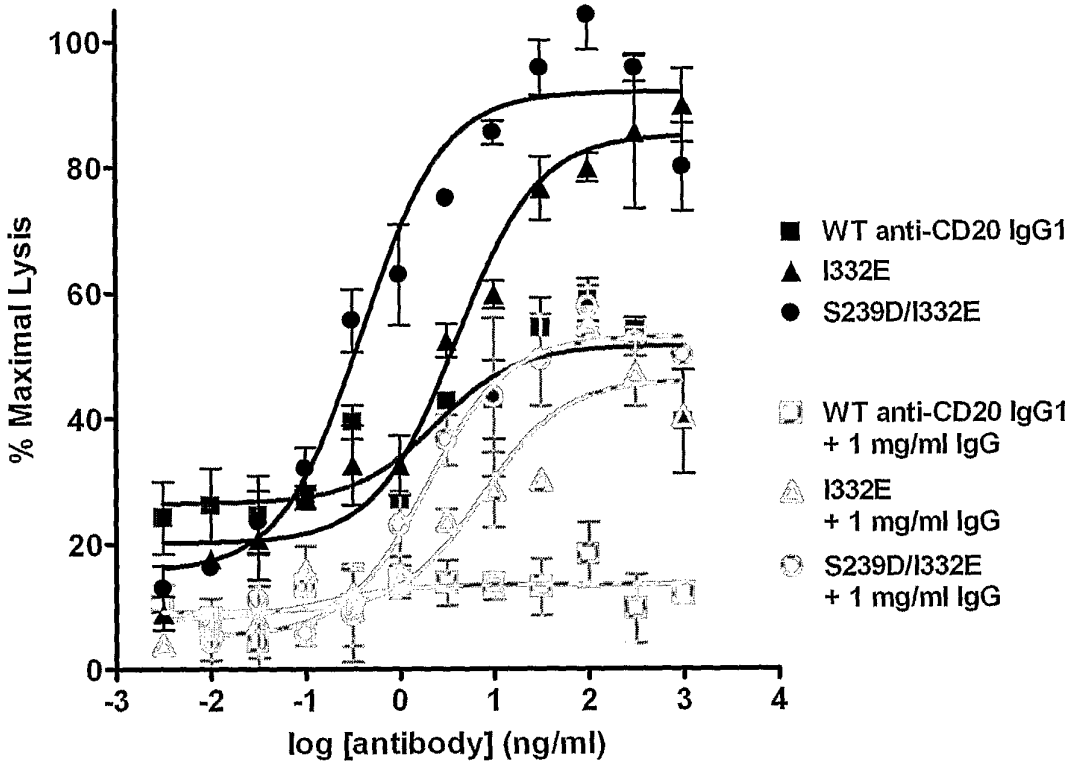

% Maximal Lysis
100
80
60
40
20
0
-3
-2
-1
0
1
2
3
4
log [antibody] (ng/ml)
WT anti-CD20 IgG1
I332E
S239D/I332E
WT anti-CD20 IgG1 + 1 mg/ml IgG
I332E + 1 mg/ml IgG
S239D/I332E + 1 mg/ml IgG

Figure 12

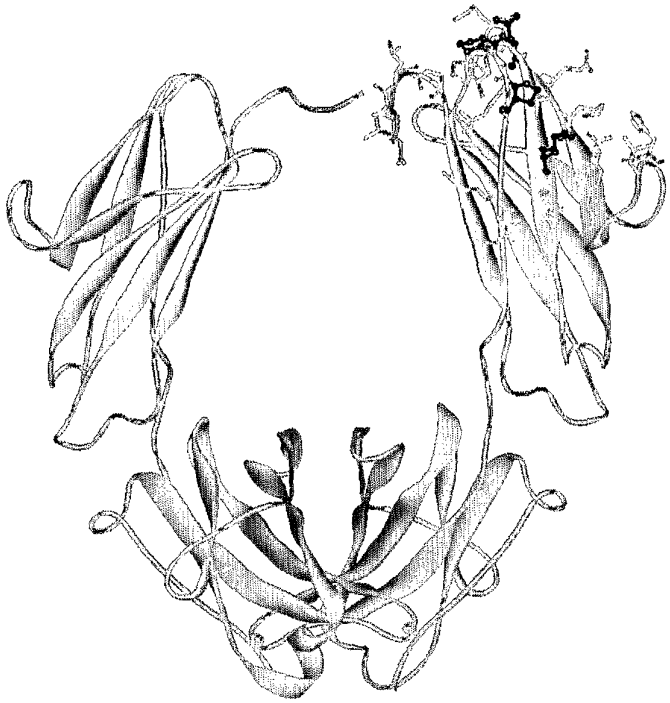


Figure 13

Variant	Fold CDC	Variant	Fold CDC
WT PRO70769 IgG1	1.00	N276L	5.43
I332E	1.74	N276D	3.63
S239D	1.32	Y278E	1.01
S239D/I332E	1.20	Y278Q	0.99
S239D/I332E/A330Y	1.41	Y278R	2.24
S239D/I332E/A330L	0.35	Y278H	
S239D/I332E/A330I	< 0.1	G281D	1.53
S239D/I332E/S298A	1.81	V282G	31.49
S239D/I332E/K326T	2.06	V284T	23.63
S239D/I332E/K326E/A330Y	1.95	H285Y	4.39
S239D/I332E/S298A/K326E	1.58	E293R	2.42
S298A/E333A/K334A	2.45	Y300D	1.27
I332E/H268E	1.72	Y300T	4.36
I332E/H268D	1.71	K320T	1.28
S239D/H268E	1.84	K320I	1.35
S239D/H268D	2.75	K320Y	1.09
S239D/I332E/H268E	1.91	K322T	0.23
S239D/I332E/H268D	2.35	K322H	0.22
S239D/I332E/A327D	2.28	K322Y	0.12
S239D/I332E/V284D	1.41	K326L	1.71
S239D/I332E/V284E	1.09	L328Q	0.51
S298A/E333A/K334A/K326A	3.80	A330V	0.15
K326W	4.89	A330H	2.01
S267D	2.03	A330S	4.94
S267E	0.74	A330E	0.28
S267Q	2.10	A330N	< 0.1
P271D	1.15	A330G	0.65
P271A	1.03	P331D	< 0.1
P271I	1.35	P331L	< 0.1
S324T	3.47	E333F	2.17
S324D	1.94	K334T	2.14
S324I	2.38	T335D	2.68
S324V	2.36	T335Y	1.79
S324L	1.83	A330L	< 0.1
S324H	1.55	A330Y	0.87
A327R	0.25	A330I	< 0.1
A327H	1.19	H268E	3.20
E233I	1.22	K326E	2.44
L234Y	0.82	K326T	3.75
L235D	0.28	S239D/I332E/K326E	
L235Y	1.61	WT PRO70769 IgG(1/2) ELLGG	2.08
H268F	4.23	S239D/I332E IgG(1/2) ELLGG	0.91
H268G	4.80	S239D/I332E/H268D IgG(1/2) ELLGG	0.67
E272I	2.02	S239D/I332E/H268E IgG(1/2) ELLGG	0.57
E272R	1.42	S239D/I332E/G327D IgG(1/2) ELLGG	0.22
E272H	0.92	S239D/I332E/G327A IgG(1/2) ELLGG	1.91
K274E	1.10	S239D/I332E/V284D IgG(1/2) ELLGG	< 0.1
K274R	1.55	S239D/I332E/V284E IgG(1/2) ELLGG	1.11

Variant	Fold CDC	Variant	Fold CDC
K274Y	1.65	S239D/I332E/H268E/G327D IgG(1/2) ELLGG	2.08
N276S	2.38	S239D/I332E/H268E/G327A IgG(1/2) ELLGG	1.32

Figure 14

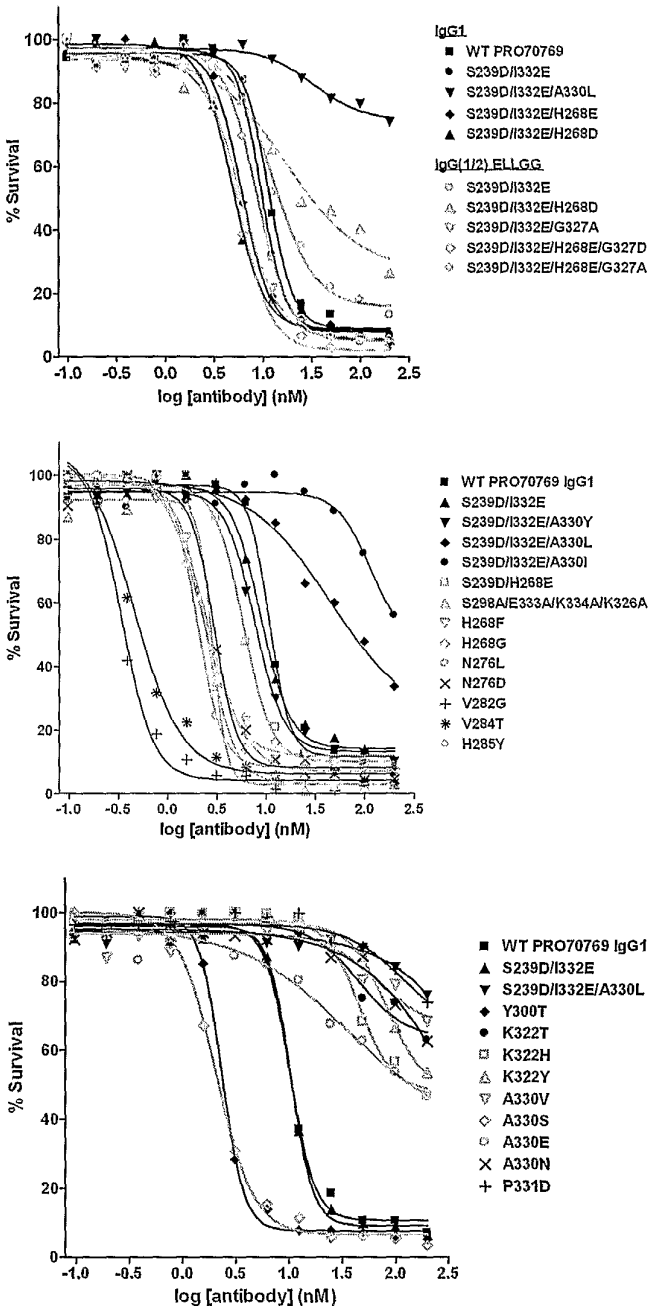

% Survival
log [antibody] (nM)
IgG1
WT PRO70769
S239D/I332E
S239D/I332E/A330L
S239D/I332E/H268E
S239D/I332E/H268D
IgG(1/2) ELLGG
S239D/I332E
S239D/I332E/H268D
S239D/I332E/G327A
S239D/I332E/H268E/G327D
S239D/I332E/H268E/G327A
WT PRO70769 IgG1
S239D/I332E
S239D/I332E/A330Y
S239D/I332E/A330L
S239D/I332E/A330I
S239D/H268E
S298A/E333A/K334A/K326A
H268F
H268G
N276L
N276D
V282G
V284T
H285Y
WT PRO70769 IgG1
S239D/I332E
S239D/I332E/A330L
Y300T
K322T
K322H
K322Y
A330V
A330S
A330E
A330N
P331D

Figure 15

Modifications Enhanced CDC	Modifications Reduced CDC	Positions Enhanced or Reduced CDC
239D	235D	235
267D	239D	239
267Q	284D	267
268D	322H	268
268E	322T	272
268F	322Y	276
268G	327R	278
272I	330E	282
276D	330I	284
276L	330L	285
276S	330N	293
278R	330V	300
282G	331D	322
284T	331L	324
285Y	332E	326
293R		327
300T		330
324I		331
324T		332
324V		333
326E		334
326T		335
326W		
327D		
330H		
330S		
332E		
333F		
334T		
335D		

Figure 16

Variant	AScreen V158 FcγRIIIa Fold IC50	CDC Fold EC50	Variant	AScreen V158 FcγRIIIa Fold IC50	CDC Fold EC50
P232G	0.32	0.53	T299A	0.20	3.88
L234H	0.23	0.24	T299I	0.10	0.59
L235H	0.39	0.22	T299V	0.18	0.52
L235D	1.10	0.09	N325L	0.10	0.03
G236N			N325A	0.29	0.04
G236R	0.29	0.21	A327R	0.13	
G236I	0.26	1.15	L328R	0.56	0.00
G236P	0.19	0.10	P329K	0.33	0.00
G237N	0.00		A330R	0.59	0.16
G237K	0.31	0.15	A330P	0.19	0.04
G237L	0.00		A330S	0.58	1.18
G237P	0.38	0.16	A330N	0.68	0.03
P238K	0.11	0.00	A330L	0.57	<0.1
S239R			A330Y	1.35	1.00
D265G	0.30	0.14	A330I	0.31	<0.1
S267R	0.29	0.00	P331L	0.05	0.19
E269R	0.44	0.02			
D270H	0.16	0.00			

Figure 17

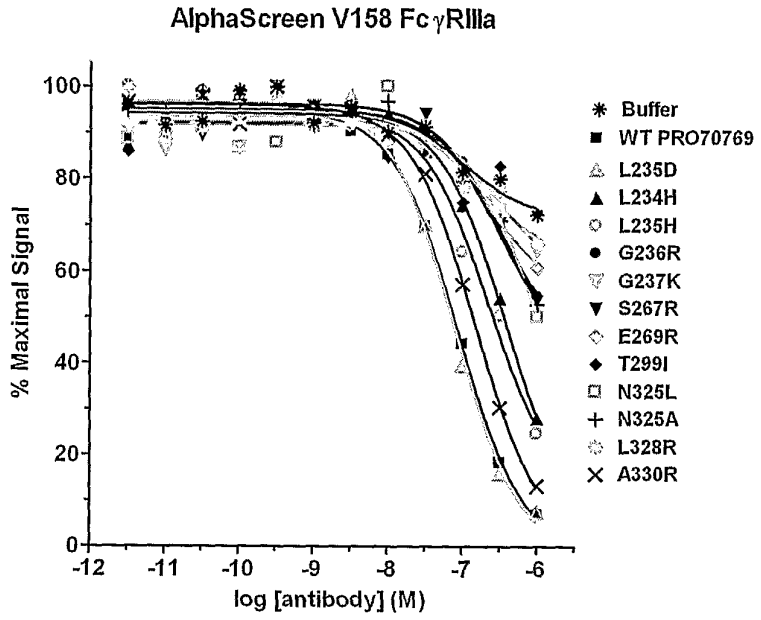
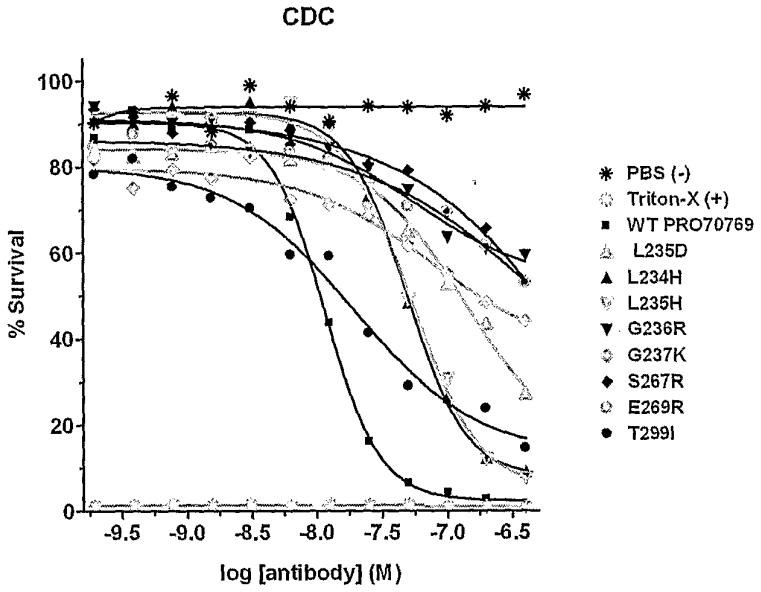

AlphaScreen V158 FcγRIIIa
% Maximal Signal
100
80
60
40
20
0
-12
-11
-10
-9
-8
-7
-6
log [antibody] (M)
Buffer
WT PRO70769
L235D
L234H
L235H
G236R
G237K
S267R
E269R
T299I
N325L
N325A
L328R
A330R

Figure 18


CDC
% Survival
log [antibody] (M)
PBS (-)
Triton-X (+)
WT PRO70769
L235D
L234H
L235H
G236R
G237K
S267R
E269R
T299I

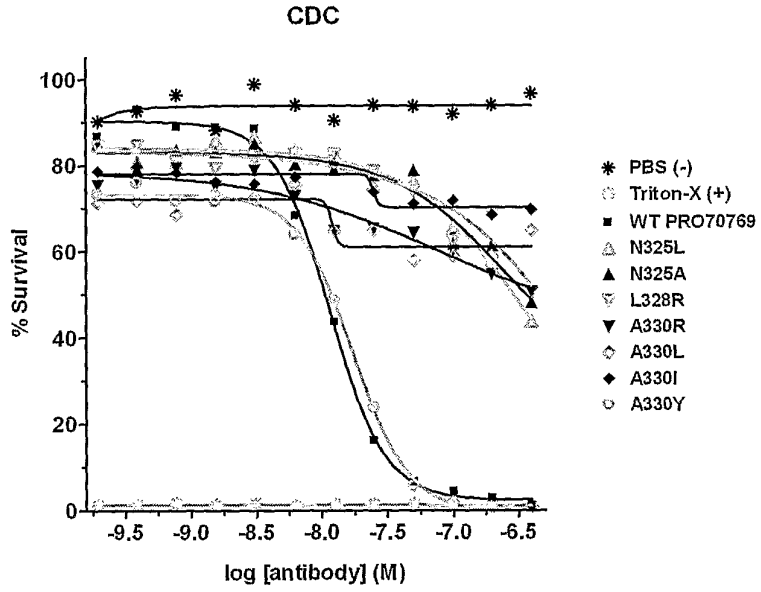

CDC
% Survival
log [antibody] (M)
PBS (-)
Triton-X (+)
WT PRO70769
N325L
N325A
L328R
A330R
A330L
A330I
A330Y

Figure 19

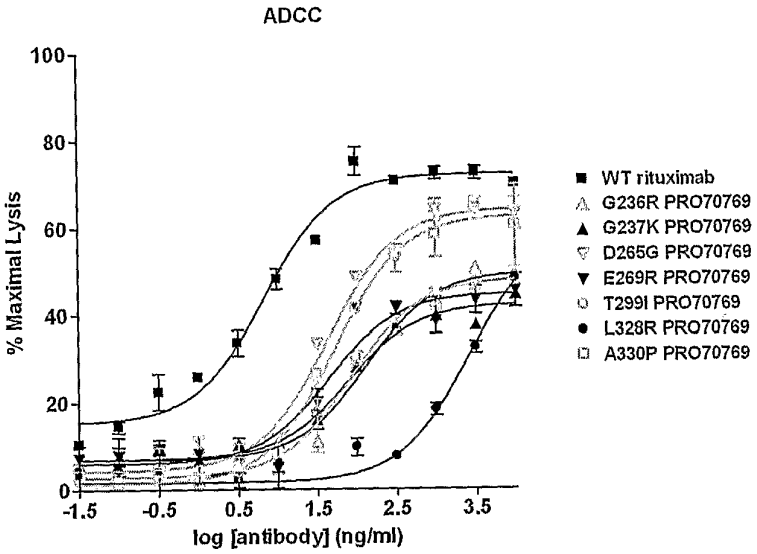

ADCC
% Maximal Lysis
100
80
60
40
20
0
-1.5
-0.5
0.5
1.5
2.5
3.5
log [antibody] (ng/ml)
WT rituximab
G236R PRO70769
G237K PRO70769
D265G PRO70769
E269R PRO70769
T299I PRO70769
L328R PRO70769
A330P PRO70769

Figure 20

	V158 FcγRIIIa Fold	CDC Fold	V158 FcγRIIIa Fold	FcγRI Fold
WT IgG1 PRO70769	1.00	1.00	1.00	1.0000
WT IgG2	0.01	< 0.01	0.01	0.0004
WT IgG4	0.02	< 0.01	0.01	0.3194
G236R/G237K	< 0.01	< 0.01	0.02	0.0054
G236R/N325L	< 0.01	< 0.01	< 0.01	0.0065
G236R/L328R	< 0.01	< 0.01	< 0.01	< 0.01
G237K/N325L	< 0.01		0.01	0.0204
G237K/L328R	< 0.01		< 0.01	0.0004
N325L/L328R	< 0.01		< 0.01	0.0042
L235G/G236R	< 0.01	< 0.01	< 0.01	0.0006
S267R/E269R	0.04	< 0.01		
L234A/L235A	1.01	0.74		
L234G/L235G	0.08	0.08		
G236R/G237K/N325L	< 0.01		< 0.01	0.0017
G236R/N325L/L328R	< 0.01		< 0.01	0.0041
L235G/G236R/G237K	< 0.01	< 0.01	< 0.01	0.0006
G237K/N325L/L328R	0.09	< 0.01	0.03	0.0435
E233P/L234V/L235A/G236-	0.06	0.18		
L234G	0.16	0.28		
L235G	0.06	0.18		
N297S		0.23		
G236R			0.06	0.0254
G237K			0.02	0.0074
N325L			0.05	0.3720
N325A			0.02	0.1252
L328R			1.33	0.0472

Figure 21

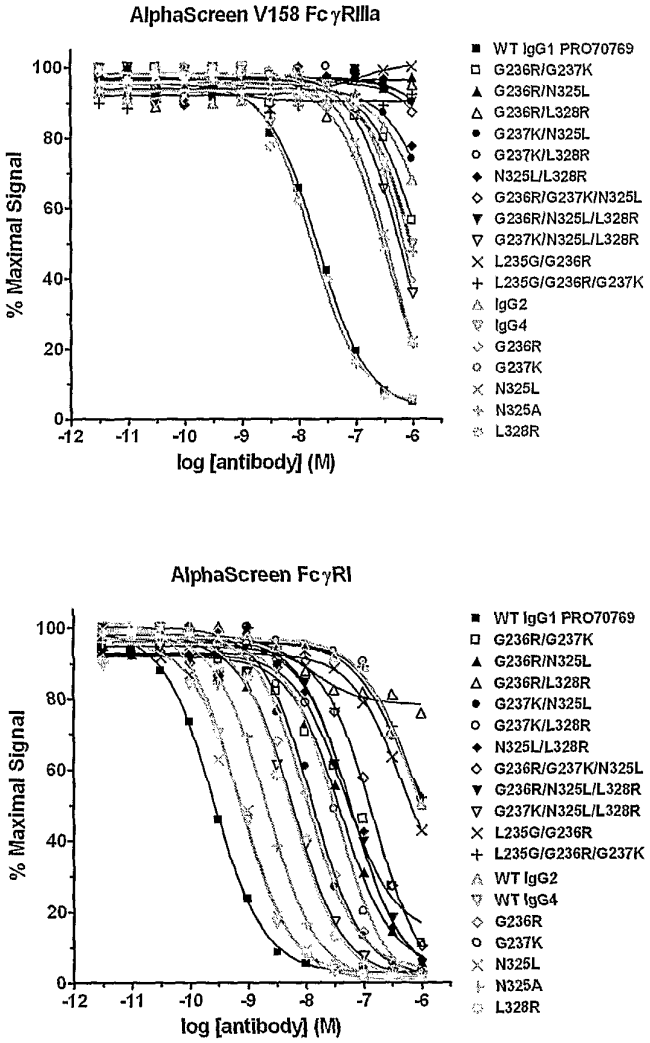

AlphaScreen V158 FcγRIIIa
% Maximal Signal
log [antibody] (M)
WT IgG1 PRO70769
G236R/G237K
G236R/N325L
G236R/L328R
G237K/N325L
G237K/L328R
N325L/L328R
G236R/G237K/N325L
G236R/N325L/L328R
G237K/N325L/L328R
L235G/G236R
L235G/G236R/G237K
IgG2
IgG4
G236R
G237K
N325L
N325A
L328R
AlphaScreen FcγRI
% Maximal Signal
log [antibody] (M)
WT IgG1 PRO70769
G236R/G237K
G236R/N325L
G236R/L328R
G237K/N325L
G237K/L328R
N325L/L328R
G236R/G237K/N325L
G236R/N325L/L328R
G237K/N325L/L328R
L235G/G236R
L235G/G236R/G237K
WT IgG2
WT IgG4
G236R
G237K
N325L
N325A
L328R

Figure 22

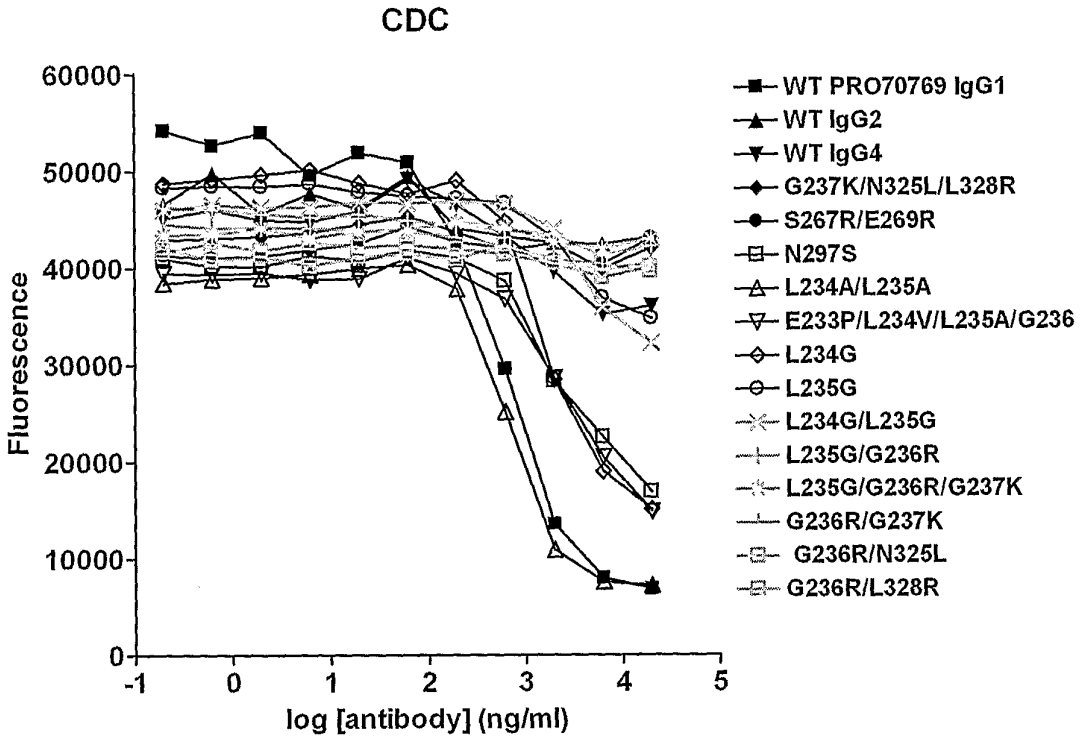

CDC
Fluorescence
60000
50000
40000
30000
20000
10000
0
-1
0
1
2
3
4
5
log [antibody] (ng/ml)
WT PRO70769 IgG1
WT IgG2
WT IgG4
G237K/N325L/L328R
S267R/E269R
N297S
L234A/L235A
E233P/L234V/L235A/G236
L234G
L235G
L234G/L235G
L235G/G236R
L235G/G236R/G237K
G236R/G237K
G236R/N325L
G236R/L328R

Figure 23

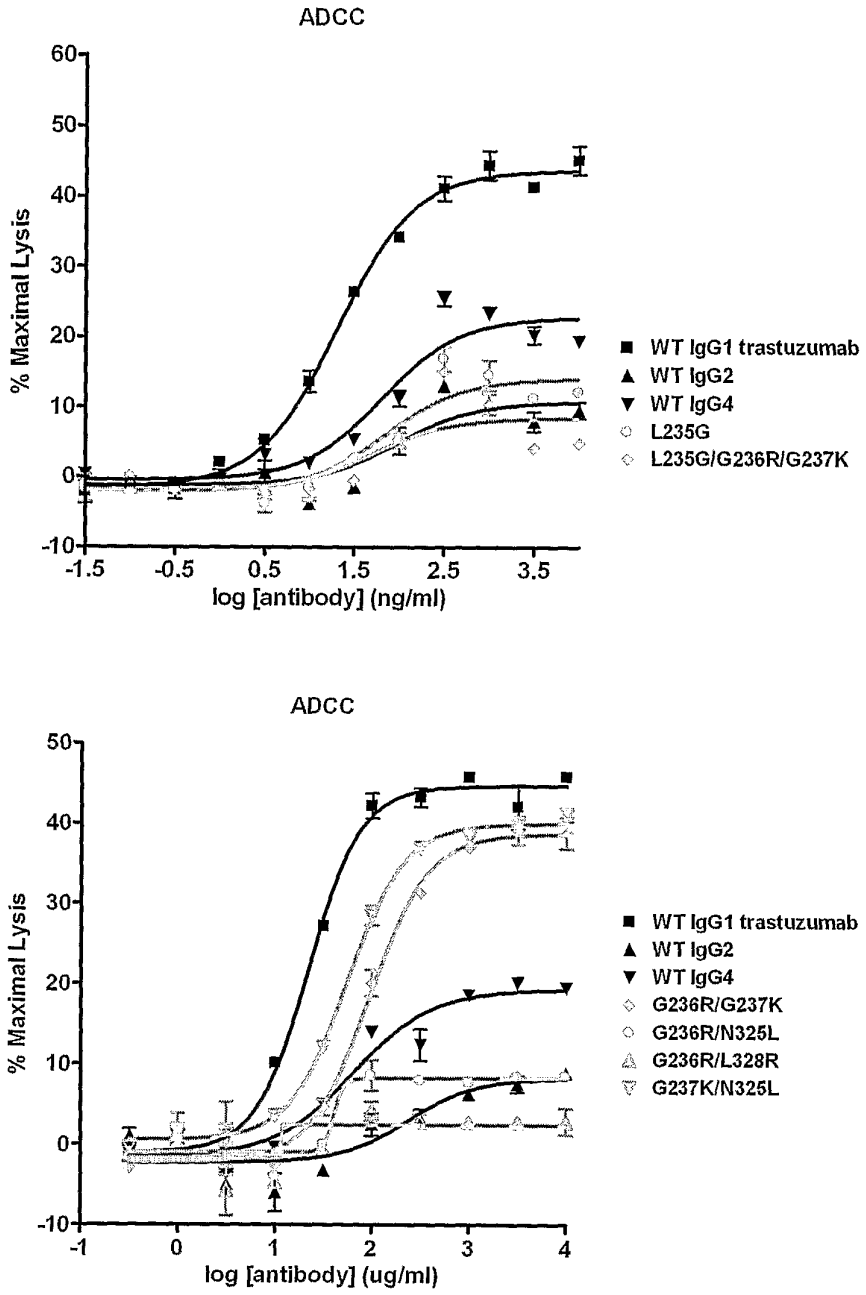

ADCC
% Maximal Lysis
log [antibody] (ng/ml)
WT IgG1 trastuzumab
WT IgG2
WT IgG4
L235G
L235G/G236R/G237K
ADCC
% Maximal Lysis
log [antibody] (ug/ml)
WT IgG1 trastuzumab
WT IgG2
WT IgG4
G236R/G237K
G236R/N325L
G236R/L328R
G237K/N325L

Figure 23 (continued)

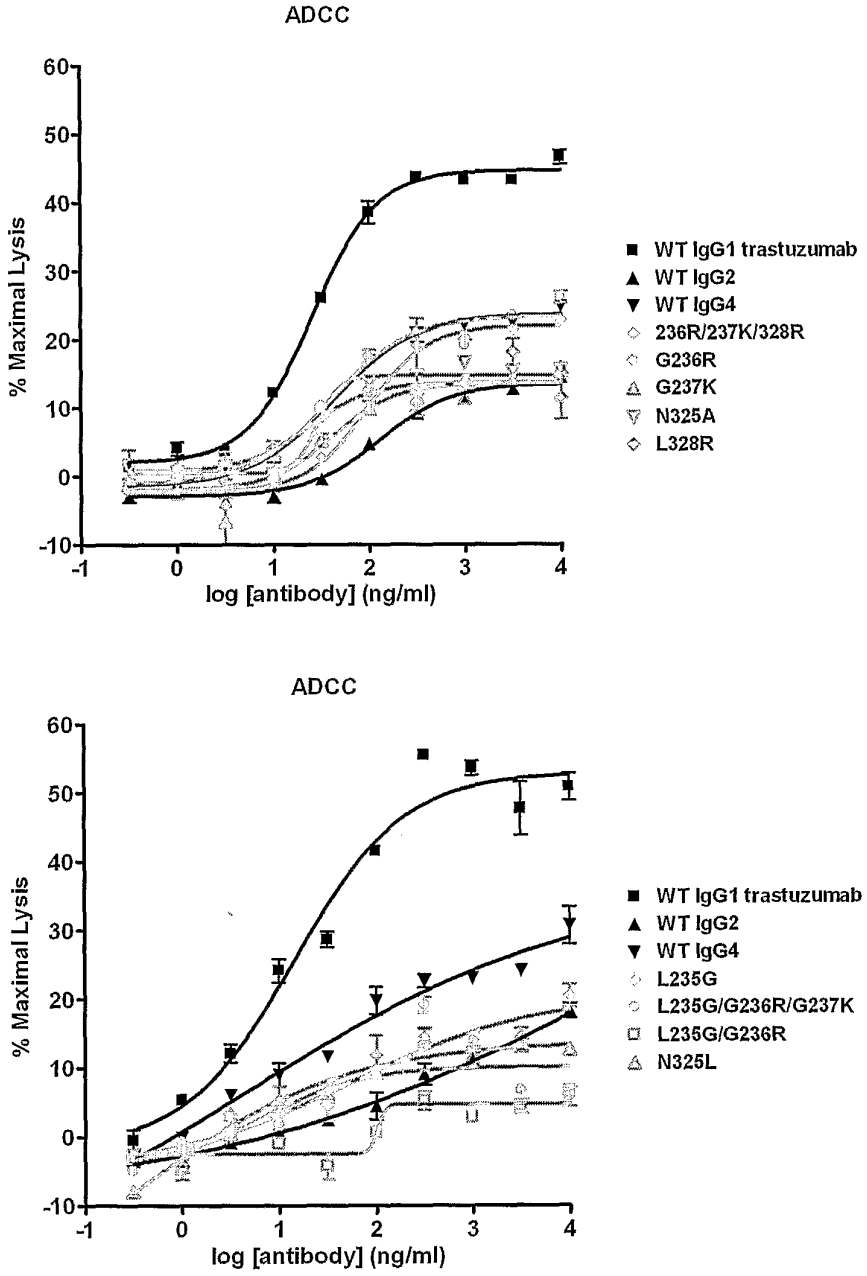


Figure 24a (SEQ ID NO:1)

Anti-CD20 PRO70769 variable light chain (VL)

DIQMTQSPSSLSASVGDRVTITCRASSSVSYMHWYQQKPGKAPKPLIYAPSNLASGVPSRF
SGSGSGTDFTLTISSLQPEDFATYYCQQWSFNPPTFGQGTKVEIK

Figure 24b (SEQ ID NO:2)

Anti-CD20 PRO70769 variable heavy chain (VH)

EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHWVRQAPGKGLEWVGAIYPGNGDTS
YNQKFKGRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARVVYYSNSYWYFDVWGQGTLVT
VSS

Figure 24c (SEQ ID NO:3)

Anti-Her2 trastuzumab variable light chain (VL)

DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSR
FSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIK

Figure 24d (SEQ ID NO:4)

Anti-Her2 trastuzumab heavy chain (VH)

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRY
ADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVS
S

Figure 24e (SEQ ID NO:5)

Anti-CTLA-4 variable light chain (VL)

EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDR
FSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK

Figure 24f (SEQ ID NO:6)

Anti-CTLA-4 variable heavy chain (VH)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKY
YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLVTVSS

Figure 25a (SEQ ID NO:7)

Kappa constant light chain (Cκ)
RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD
SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 25b (SEQ ID NO:8)

IgG1 constant heavy chain (CH1-hinge-CH2-CH3)
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS
VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN
QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
VFSCSVMHEALHNHYTQKSLSLSPGK

Figure 25c (SEQ ID NO:9)

IgG2 constant heavy chain (CH1-hinge-CH2-CH3)
ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
LYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLF
PPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVV
SVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVS
LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFS
CSVMHEALHNHYTQKSLSLSPGK

Figure 25d (SEQ ID NO:10)

IgG3 constant heavy chain (CH1-hinge-CH2-CH3)
ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
GLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVELKTPLGDTTHTCPRCPEPKSCD
TPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDTL
MISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNSTFRVVSVLTVLHQ
DWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
YPSDIAVEWESSGQPENNYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEAL
HNRFTQKSLSLSPGK

Figure 25e (SEQ ID NO:11)

IgG4 constant heavy chain (CH1-hinge-CH2-CH3)
ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
LYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPSCPAPEFLGGPSVFL
FPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRV
VSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQV
SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVF
SCSVMHEALHNHYTQKSLSLSLGK

Figure 25f (SEQ ID NO:12)

IgG(1/2) ELLGG constant heavy chain (CH1-hinge-CH2-CH3)
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPS
VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTF
RVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN
QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGN
VFSCSVMHEALHNHYTQKSLSLSPGK

Figure 26a

IgG1 constant heavy chain (CH1-hinge-CH2-CH3) comprising possible Fc variants

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE**$X_1X_2X_3X_4$**
PSVFLFPPKPKDTLMISRTPEVTCVVVDV**X_5**H**X_6**DPEVKFNWYVDGVEVHNAKTKPREEQY
NSTYRVVSVLTVLHQDWLNGKEYKCKVS**X_7**KA**X_8**PAPIEKTISKAKGQPREPQVYTLPPSRD
ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
QQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Position (EU)	Position	WT IgG1	Possible Substitutions
234	X_1	L	G H
235	X_2	L	D G H
236	X_3	G	I N P R
237	X_4	G	K L
267	X_5	S	R
269	X_6	E	R
325	X_7	N	A L
328	X_8	L	R

Figure 26b (SEQ ID NO:13)

Anti-CTLA-4 light chain (VL-CL)

EIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDR
FSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSK
ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

Figure 26c (SEQ ID NO:14)

Anti-CTLA-4 L235G/G236R IgG1 heavy chain (VH-CH1-hinge-CH2-CH3)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKY
YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLVTVSSA
STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL
YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL**GR**GPSV
FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ
VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV
FSCSVMHEALHNHYTQKSLSLSPGK

Figure 26d (SEQ ID NO:15)

Anti-CTLA-4 IgG2 heavy chain (VH-CH1-hinge-CH2-CH3)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKY
YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLVTVSSA
STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL
YSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFP
PKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVS
VLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSL
TCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSC
SVMHEALHNHYTQKSLSLSPGK

SEQUENCE LISTING

(10) XENCOR, INC.
Lazar, Gregory Alan
Dang, Wei
Desjarlais, John R.
Karki, Sher Bahadur

(20) FC VARIANTS WITH OPTIMIZED PROPERTIES

(30) 187426/PCT

(40) PCT/US 2006/011752
(41) 2006-03-31

(50) US 60/667,197
(51) 2005-03-31

(50) US 60/705,378
(51) 2005-08-03

(50) US 60/723,294
(51) 2005-10-03

(50) US 60/723,335
(51) 2005-10-03

(50) US 11/124,620
(51) 2005-05-05

(60) 20

(70) PatentIn version 3.3

(210) 1
(211) 106
(212) PRT
(213) Artificial

(220)
(223) Synthetic

(400) 1

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Leu Ile Tyr
35 40 45

Ala Pro Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
65 70 75 80

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Phe Asn Pro Pro Thr
85 90 95

ıe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

:10> 2
:11> 122
:12> PRT
:13> Artificial

:20>
:23> Synthetic

400> 2

lu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
5 10 15

er Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

sn Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

ly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
50 55 60

ys Gly Arg Phe Thr Ile Ser Val Asp Lys Ser Lys Asn Thr Leu Tyr
5 70 75 80

eu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

la Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 3
<211> 107
<212> PRT
<213> Artificial

<220>
<223> Synthetic

<400> 3

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

'r Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

;r Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

lu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
85 90 95

hr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

210> 4
211> 120
212> PRT
213> Artificial

220>
223> Synthetic

400> 4

;lu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
5 10 15

;er Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

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

Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 5
<211> 108
<212> PRT
<213> Artificial

<220>
<223> Synthetic

<400> 5

u Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
5 10 15

lu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser
20 25 30

yr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

le Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

ly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
5 70 75 80

ro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

rp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

:210> 6
:211> 118
:212> PRT
:213> Artificial

:220>
:223> Synthetic

<400> 6

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Thr Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

:10> 7
:11> 107
:12> PRT
:13> Artificial

:20>
:23> Synthetic

400> 7

rg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
5 10 15

ln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
20 25 30

yr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

er Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60

hr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
5 70 75 80

ys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

ro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 8
<211> 330
<212> PRT
<213> Artificial

<220>
<223> Synthetic

<400> 8

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

yr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

ys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

ro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

ys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

al Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
45 150 155 160

yr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

lu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

is Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

ys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 9
<211> 326

?12> PRT
?13> Artificial

?20>
?23> Synthetic

400> 9

la Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
5 10 15

er Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

he Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

ly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

eu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
5 70 75 80

yr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

hr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
100 105 110

ro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
115 120 125

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
130 135 140

Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
145 150 155 160

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
165 170 175

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
180 185 190

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
195 200 205

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
210 215 220

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
225 230 235 240

n Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
245 250 255

la Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
260 265 270

ır Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
275 280 285

eu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
290 295 300

er Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
05 310 315 320

er Leu Ser Pro Gly Lys
325

:210> 10
:211> 377
:212> PRT
:213> Artificial

:220>
:223> Synthetic

:400> 10

ıla Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
L 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro
100 105 110

Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg
115 120 125

Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys
130 135 140

ro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
45 150 155 160

la Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
165 170 175

ro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
180 185 190

al Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr
195 200 205

'al Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
210 215 220

;ln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His
!25 230 235 240

;ln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
245 250 255

\la Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
260 265 270

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
275 280 285

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
290 295 300

Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn
305 310 315 320

Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
325 330 335

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
340 345 350

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
355 360 365

Lys Ser Leu Ser Leu Ser Pro Gly Lys
370 375

<210> 11
<211> 327
<212> PRT
<213> Artificial

<220>

:23> Synthetic

:00> 11

la Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
5 10 15

er Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

he Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

ly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

eu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
5 70 75 80

yr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

rg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro
100 105 110

lu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
115 120 125

sp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
130 135 140

sp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
145 150 155 160

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
165 170 175

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
180 185 190

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
195 200 205

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
210 215 220

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
225 230 235 240

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
245 250 255

le Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
260 265 270

ır Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
275 280 285

rg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
290 295 300

ys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
05 310 315 320

eu Ser Leu Ser Leu Gly Lys
325

:210> 12
:211> 330
:212> PRT
:213> Artificial

:220>
:223> Synthetic

:400> 12

\la Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
L 5 10 15

ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

?he Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp
145 150 155 160

yr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

lu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val
180 185 190

is Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

ys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly
210 215 220

ln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
225 230 235 240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 13
<211> 215
<212> PRT
<213> Artificial

<220>
<223> Synthetic

<400> 13

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

e Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

y Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
70 75 80

o Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

rp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
100 105 110

la Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

ly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

la Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
45 150 155 160

ln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

er Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

yr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 14
<211> 448
<212> PRT
<213> Artificial

<220>
<223> Synthetic

<400> 14

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Thr Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

/s Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
70 75 80

:u Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

la Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

eu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

eu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

ys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
45 150 155 160

:er Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

;er Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

;er Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Gly Arg Gly Pro Ser
225 230 235 240

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

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

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

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

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
340 345 350

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 15
<211> 444
<212> PRT
<213> Artificial

<220>
<223> Synthetic

<400> 15

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Thr Phe Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

Ala Arg Thr Gly Trp Leu Gly Pro Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

u Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

u Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

s Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

r Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

r Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

sn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

sn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys
210 215 220

ro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe
225 230 235 240

ro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
245 250 255

hr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe
260 265 270

sn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
275 280 285

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr
290 295 300

Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305 310 315 320

Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
325 330 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
340 345 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
355 360 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
370 375 380

u Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser
5 390 395 400

ıe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
405 410 415

ly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
420 425 430

/r Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

210> 16
211> 330
212> PRT
213> Artificial

220>
223> Synthetic

220>
221> MISC_FEATURE
222> (117)..(117)
223> Xaa can be Leucine, Glycine or Histidine

220>
221> MISC_FEATURE
222> (118)..(118)
223> Xaa can be Leucine, Aspartic Acid, Glycine or Histidine

220>
221> MISC_FEATURE
222> (119)..(119)
223> Xaa can be Glycine, Isoleucine, Asparagine, Proline or Arginine

<220>
<221> MISC_FEATURE
<222> (120)..(120)
<223> Xaa can be Glycine, Lysine or Leucine

<220>
<221> MISC_FEATURE
<222> (150)..(150)
<223> Xaa can be Serine or Arginine

<220>
<221> MISC_FEATURE
<222> (152)..(152)
<223> Xaa can be Glutamic Acid or Arginine

<220>
<221> MISC_FEATURE
<222> (208)..(208)
<223> Xaa can be Asparagine, Alanine or Leucine

<220>
<221> MISC_FEATURE
<222> (211)..(211)
<223> Xaa can be Leucine or Arginine

<400> 16

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys

5 10 15

er Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

he Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

ly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

eu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

yr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

ys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Xaa Xaa Xaa Xaa Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Xaa His Xaa Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Xaa
195 200 205

Lys Ala Xaa Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe

275 280 285

eu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

al Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
05 310 315 320

ln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

210> 17
211> 330
212> PRT
213> Homo sapiens

400> 17

la Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
5 10 15

er Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

he Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

ly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

eu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
5 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190

is Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

ys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220

ln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
25 230 235 240

eu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255

ro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270

sn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285

eu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300

/al Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320

;ln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 18
<211> 326
<212> PRT
<213> Homo sapiens

<400> 18

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1 5 10 15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

r Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
100 105 110

o Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
115 120 125

ır Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
130 135 140

al Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
45 150 155 160

al Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
165 170 175

er Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
180 185 190

eu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
195 200 205

la Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
210 215 220

ro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
25 230 235 240

ln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
245 250 255

la Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
260 265 270

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
275 280 285

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
290 295 300

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
305 310 315 320

Ser Leu Ser Pro Gly Lys
325

<210> 19
<211> 377
<212> PRT
<213> Homo sapiens

<400> 19

la Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
5 10 15

er Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

ne Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

ly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

eu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
5 70 75 80

yr Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

rg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr Thr His Thr Cys Pro
100 105 110

rg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg
115 120 125

ys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys
130 135 140

ro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro Cys Pro Arg Cys Pro
145 150 155 160

la Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
165 170 175

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
180 185 190

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Lys Trp Tyr
195 200 205

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
210 215 220

Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Leu His
225 230 235 240

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
245 250 255

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
260 265 270

'o Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
275 280 285

ır Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
290 295 300

er Asp Ile Ala Val Glu Trp Glu Ser Ser Gly Gln Pro Glu Asn Asn
)5 310 315 320

yr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
325 330 335

yr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Ile
340 345 350

he Ser Cys Ser Val Met His Glu Ala Leu His Asn Arg Phe Thr Gln
355 360 365

ys Ser Leu Ser Leu Ser Pro Gly Lys
370 375

:210> 20
:211> 327
:212> PRT
:213> Homo sapiens

:400> 20

\la Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
L 5 10 15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr
65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro
100 105 110

Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
115 120 125

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val

130 135 140

ip Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
i5 150 155 160

ly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe
165 170 175

sn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
180 185 190

rp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
195 200 205

ro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
210 215 220

lu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
25 230 235 240

sn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
245 250 255

le Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
260 265 270

hr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
275 280 285

rg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
290 295 300

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
305 310 315 320

Leu Ser Leu Ser Leu Gly Lys
325