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(71) Applicant(s)
Five Prime Therapeutics, Inc.;Bristol-Myers Squibb Company

(72) Inventor(s)
Johnston, Robert J.;Rajpal, Arvind;Sheppard, Paul O.;Borges, Luis;Rankin, Andrew;Bahjat, Keith Sadoon;Korman, Alan;Deng, Andy X.;Su, Lin Hui;Rakestraw, Ginger

(74) Agent / Attorney
AJ PARK, PO Box 949, Wellington, 6140, NZ

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(71) Applicants: **FIVE PRIME THERAPEUTICS, INC.** [US/US]; 111 Oyster Point Blvd., South San Francisco, California 94080 (US). **BRISTOL-MYERS SQUIBB COMPANY** [US/US]; Rte. 206 & Province Line Road, P.O. Box 4000, Princeton, New Jersey 08543 (US).

(72) Inventors: **JOHNSTON, Robert J.**; Rte. 206 & Province Line Road, P.O. Box 4000, Princeton, New Jersey 08543 (US). **RAJPAL, Arvind**; Rte. 206 & Province Line Road, P.O. Box 4000, Princeton, New Jersey 08543 (US). **SHEPPARD, Paul O.**; Rte. 206 & Province Line Road, P.O. Box 4000, Princeton, New Jersey 08543 (US). **BORGES, Luis**; 111 Oyster Point Blvd., South San Francisco, California 94080 (US). **RANKIN, Andrew**; 111 Oyster Point Blvd., South San Francisco, California 94080 (US). **BAHJAT, Keith**; Rte. 206 & Province Line Road, P.O. Box 4000, Princeton, New Jersey 08543 (US). **KORMAN, Alan**; Rte. 206 & Province Line Road, P.O. Box 4000, Princeton, New Jersey 08543 (US). **DENG, Andy X.**; Rte. 206 & Province Line Road, P.O. Box 4000, Princeton, New Jersey 08543 (US). **SU, Linhui Julie**; Rte. 206 & Province Line Road, P.O. Box 4000, Princeton, New Jersey 08543 (US). **RAKESTRAW, Ginger**; Rte. 206 & Province Line Road, P.O. Box 4000, Princeton, New Jersey 08543 (US).

(74) Agent: **DOHERTY, Elizabeth** et al.; McNeill Baur PLLC, 125 Cambridge Park Drive, Suite 301, Cambridge, Massachusetts 02140 (US).

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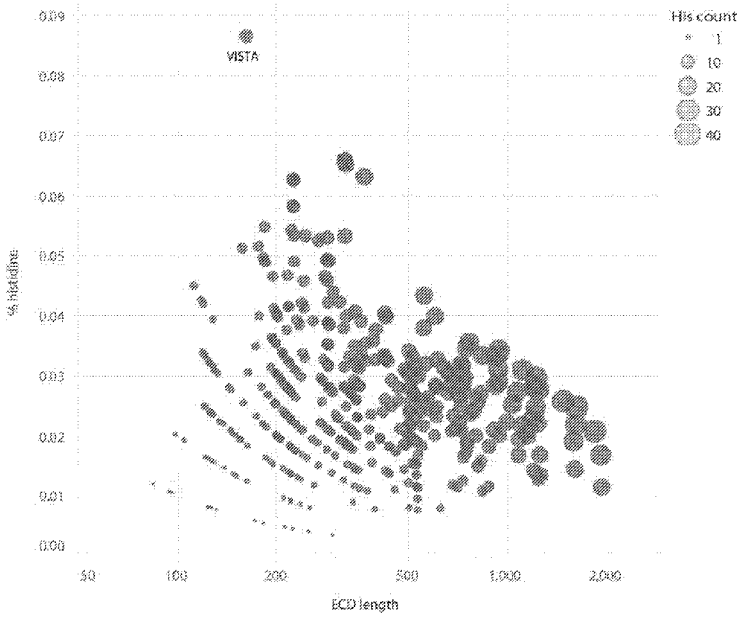


FIG. 1A

(57) Abstract: The present application relates to antibodies specifically binding to the V-domain immunoglobulin-containing suppressor of T-cell activation (VISTA) at acidic pH and their use in cancer treatment. In some embodiments, the antibodies bind specifically to human VISTA at acidic pH, but do not significantly bind to human VISTA at neutral or physiological pH.

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ANTIBODIES BINDING TO VISTA AT ACIDIC pH

FIELD

The present application relates to antibodies specifically binding to the V-domain immunoglobulin-containing suppressor of T-cell activation (VISTA) at acidic pH and their use in cancer treatment.

BACKGROUND AND SUMMARY OF THE DISCLOSURE

The V-domain Ig-containing suppressor of T-cell activation, or VISTA, is a co-inhibitory member of the B7 family of immunoreceptors expressed by myelomonocytic cells and other leukocytes. However, the mechanism by which VISTA suppresses immune responses is poorly understood.

The inventors have found that unlike other known immunoreceptors, VISTA engages its counter-receptors and functions selectively at acidic pH, with little activity at physiological pH (e.g., 7.3 – 7.4). VISTA may thus suppress immune responses in acidic microenvironments, such as tumor beds or sites of inflammation, without perturbing cells circulating in blood or residing in non-inflamed, non-acidic tissues. Additionally, the inventors have found that anti-VISTA antibodies can be engineered to selectively bind to VISTA at acidic pH, with little or no binding at physiological pH, mirroring VISTA's own acidic pH selectivity. These acidic pH selective antibodies may offer desirable properties for treating diseases, such as cancer, relative to antibodies that bind VISTA at physiological pH.

The present disclosure concerns antibodies that specifically bind to the extracellular domain (ECD) of VISTA, such as human VISTA ("hVISTA" or "huVISTA") at acidic pH (e.g., in acidic conditions). The present disclosure also concerns antibodies that specifically bind to the extracellular domain (ECD) of VISTA, such as hVISTA, at acidic pH, with little or no binding at neutral or physiological pH. The inventors have noted herein that the hVISTA-ECD amino acid sequence includes a number of conserved as well as nonconserved histidine residues, and that the frequency of histidine residues in VISTA's ECD is exceptionally high relative to other B7 family members and other Immunoglobulin Superfamily members. (See Figs. 1A and 1B.) In solution, the amino acid histidine has a

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pK_a of about 6.5, meaning that at or below pH 6.5, histidine residues within proteins are often protonated and thus, positively charged, while at pH higher than pH 6.5 they are increasingly unprotonated and neutral in charge. Tumor microenvironments and inflamed tissues are often acidic, and thus, VISTA proteins found in these microenvironments may be at least partially protonated at their histidine residues. The inventors, as discussed herein, have hypothesized that histidine protonation may affect the conformation, surface structure, and/or charge density of VISTA, which, in turn, may create pH-specific or pH-selective epitopes for both receptor-ligand interaction(s) and antibody binding. Targeting VISTA with antibodies that bind at acidic pH but not neutral or physiological pH may prevent target-mediated drug disposition via circulating and lymphoid organ-resident myelomonocytic cells, improving antibody PK, receptor occupancy, and activity in tumor microenvironments. Acidic pH-selective antibodies may also improve the specificity of VISTA antibodies for intratumoral, rather than circulating, target cells in the cases of therapeutic modalities such as antibody-dependent cell-mediated cytotoxicity (ADCC), antibody-dependent cellular phagocytosis (ADCP), complement-dependent cytotoxicity (CDC), and delivery of payloads (antibody-drug conjugates).

It is an object of the present invention to overcome or ameliorate at least one of the disadvantages of the prior art, or at least go some way to provide the public with a useful choice.

In this specification where reference has been made to patent specifications, other external documents, or other sources of information, this is generally for the purpose of providing a context for discussing the features of the invention. Unless specifically stated otherwise, reference to such external documents is not to be construed as an admission that such documents, or such sources of information, in any jurisdiction, are prior art, or form part of the common general knowledge in the art.

BRIEF DESCRIPTION OF THE FIGURES

A color version of several of the figures is provided in priority US provisional application No. 62/636,746, filed Febuary 28, 2018. Should that priority application file

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become available through publication of the present application, it is presumed that copies of the color drawings will be provided by the US Patent and Trademark Office upon request and payment of the necessary fee.

Figs. 1A-C show that VISTA's extracellular domain contains an exceptionally high frequency of histidine residues, that many of these histidine residues are conserved, and that at least some of these histidine residues may participate in receptor-ligand binding. **Fig. 1A** shows a graph of immunoglobulin domain-containing proteins, with the number of extracellular domain amino acid residues for each protein plotted on the x-axis, and the frequency of histidine residues within the extracellular domain for each protein plotted on the y-axis. The size of each data point corresponds to the total number of histidine residues in

[FOLLOWED BY PAGE 3]

each protein's extracellular domain. **Fig. 1B** shows the aligned amino acid sequences of the extracellular domains of human, cynomolgus macaque, and mouse VISTA. Signal peptide (Sig) and transmembrane domain (TMD) sequence locations are marked. Histidine residues conserved across all three species are shown in bold and underlined; histidine residues conserved across human and cynolmogus macaque are shown in bold only. **Fig. 1C** shows a model of the human VISTA immunoglobulindomain's three-dimensional structure. Histidine residues are depicted as ball and stick traces.

Figs. 2A-B show a model in which the histidine residues in VISTA's extracellular domain confer counter-receptor selectivity for acidic pH rather than physiological pH. **Fig. 2A** shows the equilibrium between the lack of, and the presence of, protonation of the pyrrole ammonium group (NH) in a histidine residue. The pKa of histidine in solution is 6.5, indicating that histidine residues are more likely to be protonated at pH 6.5 and lower, and thus, positively charged, than at higher pH. **Fig. 2B** shows shows a model in which VISTA engages P-selectin glycoprotein ligand 1 (PSGL-1) or other counter-receptors and ligands ("VISTA-R") selectively at acidic pH. Accordingly, antibody binding to VISTA's extracellular domainat at acidic pH rather at physiological pH may be critical to inhibiting or modulating VISTA activity.

Fig. 3 shows the level of VISTA surface expression (mean fluorescence intensity (MFI) of anti-VISTA antibody staining) on tumor-infiltrating macrophages, dendritic cells, neutrophils, CD4+ effector T cells, CD4+ regulatory T cells, CD8+ T cells, natural killer (NK) cells, and B cells. VISTA is expressed on many tumor-infiltrating leukocytes, particularly myeloid cells. Tumor microenvironments are often acidic, enabling VISTA to engage counter-receptors and ligands.

Figs. 4A-E show that VISTA selectively binds to leukocytes and to PSGL-1 at acidic pH, with little or no binding at neutral pH, and that this binding can be blocked by an anti-VISTA antibody. **Fig. 4A** on the left shows representative histograms of fluorescently-conjugated recombinant VISTA multimer binding to activated human CD4+ T cells. From darker gray to lighter, the filled histograms depict binding at pH 7.0, 6.5, 6.4, 6.3, 6.1, and 6.0. Some histograms are labeled with their corresponding pH. Non-VISTA control multimer binding at pH 6.0 is shown as the unfilled histogram. On the right, the mean MFI of

VISTA (circles) and control (triangles) multimer binding to activated human CD4+ T cells from two donors at different pH is graphed. **Fig. 4B** shows representative histograms of recombinant VISTA multimer binding to peripheral blood mononuclear cells (PBMC) at pH 6.0 and pH 7.4. From darker gray to lighter, the filled histograms depict binding at pH 6.0 to CD19+ B cells, CD4+ T cells, CD8+ T cells, CD56+ NK cells, and CD14+ monocytes. The unfilled, solid border and dotted border histograms depict binding at pH 7.4 to total PBMC lymphocytes and monocytes respectively. **Fig. 4C** shows representative recombinant VISTA multimer binding to activated human CD4+ T cells in the presence of an anti-VISTA blocking antibody (squares) or a non-VISTA-specific isotype-matched control antibody (circles). Antibody concentrations are plotted on log scale. Non-linear regressions are also shown. The triangle depicts the background signal from activated human CD4+ T cells that were not stained with recombinant VISTA multimers. **Fig. 4D** shows representative two-dimensional flow cytometry plots of recombinant VISTA multimer binding at pH 6.0 to heparan sulfate-deficient Chinese Hamster Ovary (CHO) cells (line pGSD-677, American Type Culture Collection) that were transfected to express human PSGL-1. Multimer binding was performed in the presence and absence of the anti-VISTA blocking antibody shown in Fig. 4C. Cells left unstained by recombinant VISTA multimers are shown as a control. PSGL-1 antibody staining is plotted on the y-axis, and VISTA multimer staining is plotted on the x-axis. **Fig. 4E** shows representative histograms of recombinant mouse VISTA-Fc fusion protein binding to mouse splenocytes at pH 6.0 and pH 7.4. From darker gray to lighter, the filled histograms depict binding at pH 6.0 to CD8+ T cells, CD11b+ myeloid cells, and CD4+ T cells. The unfilled histogram depicts binding at pH 7.4 to total splenocytes.

Figs. 5A-D show that VISTA mediates T cell suppression and cell : cell adhesion preferentially at acidic pH, and that both effects can be reversed with an anti-VISTA blocking antibody. **Fig. 5A** shows representative cell : cell conjugate formation at pH 6.0 and 7.0 between 293T cells expressing hVISTA or vector control (plotted on the y-axes) and CHO cells endogenously expressing cell surface heparan sulfate on the x-axes. **Fig. 5B** is a graph of the frequency of cell conjugates formed at pH 6.0 between the same cells in the presence of an anti-VISTA blocking antibody, an anti-VISTA non-blocking antibody, or isotype-matched non-VISTA-specific control antibodies. **Fig. 5C** shows representative plots

of the luciferase activity generated by Jurkat (human T cell line) cells expressing an NFkB luciferase reporter after co-culture at various pH with 293T cells expressing h VISTA and a single-chain variable fragment of the anti-human T cell receptor agonist antibody OKT3 ("artificial antigen-presenting cells"). An anti-VISTA blocking antibody (squares) or an isotype-matched non-VISTA-specific control antibody (circles) were added to the co-cultured cells. In **Fig. 5D**, the data shown in Fig. 5A are plotted as fold-increase of the luciferase signal with anti-VISTA antibody treatment relative to control ("effect size").

Figs. 6A-G show that VISTA can be found in intracellular endosomes, particularly Rab11+ recycling endosomes, and can recycle to and from the cell surface via endosomal trafficking. **Fig. 6A** shows co-localization of VISTA, Rab5 (early endosome marker), Rab7 (late endosome marker), and Rab11 (recycling endosome marker) within 293T cells expressing human VISTA. **Fig. 6B** shows co-localization of VISTA and Rab11 within human monocytes. Intracellular VISTA is co-localized with Rab11+ recycling endosomes. A non-VISTA-binding control antibody of the same isotype as the VISTA antibody ("cAb") does not detectably bind the monocytes. **Fig. 6C** shows the binding of three anti-VISTA antibodies to recombinant VISTA at pH 7.4 (black), 6.7 (darker gray), and 6. (lighter gray). **Fig. 6D** shows the susceptibility of a VISTA expressing acute myeloid leukemia (AML) cell line to killing by the same anti-VISTA antibodies 1 (inverted triangles), 2 (circles), 3 (squares), or a non-VISTA-specific control antibody (triangles) bearing cathepsin B-sensitive linkers and cytotoxic payloads. Cell viability (CellTiter-Glo LU) is plotted on the y-axis and antibody concentrations are plotted on the x-axis. **Fig. 6E** compares hVISTA binding of anti-VISTA antibody 3 to that of an engineered variant ("VISTA mAb 3c") that does not exhibit impaired binding at acidic pH. **Fig. 6F** shows an antibody drug-conjugate assay comparing the potency of anti-VISTA antibody 3 (squares) and 3c (diamonds). **Fig. 6G** shows a schematic of endosome trafficking, with VISTA recycling to and from and cell surface via early endosomes and recycling endosomes.

Figs. 7A-F show how anti-VISTA antibody variant libraries were designed and screened in order to obtain acidic pH-selective antibodies. **Fig. 7A** shows amino acid substitutions that were made in VH CDR 3 of the anti-human VISTA antibody clone P1-061029 (abbreviated '029) for creating an '029 library for screening. To potentially improve

binding to VISTA's histidine-rich region at acidic pH, the libraries allowed substitutions for the negatively charged amino acids aspartate and glutamate as well as pH-responsive histidine. X=H, D or E. Bracketed sequences were removed from synthesis to avoid introducing liabilities. A total of 647 unique sequences of P1-061029 HCDR3 with 1-2 mutations were synthesized. **Fig. 7B** shows the procedure by which the '029 library is iteratively screened and selected for acidic pH-selective antibody variants. R denotes selection round. **Fig. 7C** shows representative two-dimensional flow cytometry plots data showing the variant pool after 9 rounds of selection. VISTA binding is plotted on the y-axis, and variant antibody expression is plotted on the x-axis. Binding data at various antibody concentrations and pH are shown. **Fig. 7D** shows a diagram of P1-061029 and its progeny clones binding to human VISTA at pH 6.0 and 7.4. **Fig. 7E** shows a diagram of the off-rates of P1-061029 and its progeny clones to human VISTA at pH 6.0. **Fig. 7F** shows SPR binding data of the antibodies P1-068761, P1-068767 and P1-061029 to human VISTA at pH 6.0 and pH 7.4.

Figs. 8A-F show acidic pH-selective cell binding, blocking, and effector activity of the VISTA antibodies P1-068761 and P1-068767. **Fig. 8A** and **Fig. 8B** show the mean fluorescence intensity of the acidic pH-selective antibodies P1-068761 (**Fig. 8A**) and P1-068767 (**Fig. 8B**) binding to Raji cells ectopically expressing human VISTA. The cells were stained at approximately pH 6.0 (circles; highest curve in Fig. 8A), 6.1 (squares; third highest curve), 6.2 (triangles; second highest curve), 6.4 (inverted triangles; fourth highest curve close to the pH 6.1 curve), 6.6 (diamonds; fourth curve from bottom), 7.0 (circles; third curve from bottom), 7.2 (squares; second curve from bottom), and 8.1 (unfilled triangles; bottom curve in Fig. 8A). Binding was detected with a fluorescently conjugated anti-human IgG secondary antibody. **Fig. 8C** shows P1-068767 (circles) and an isotype-matched non-specific control antibody (triangles) binding to Raji cells ectopically expressing human VISTA at 3125 ng/mL at various pH. The "pH_{50}", the pH at which 50% of P1-068767 binding is lost, is approximately 6.6. **Fig. 8D** shows the mean fluorescence intensities (MFI) of an isotype-matched non-specific control antibody (filled and unfilled circles for pH 7.0 and 6.0 respectively), anti-VISTA mAb 2 ("control", see Fig. 6C, filled and unfilled squares at pH 7.0 and 6.0 respectively), P1-068761 (filled and unfilled triangles for pH 7.0 and 6.0

respectively), and P1-068767 (filled and unfilled inverted triangles for pH 7.0 and 6.0 respectively) binding to human monocytes. Binding was detected by a fluorescently conjugated anti-human IgG secondary antibody. **Fig. 8E** shows the comparable blocking of recombinant VISTA multimer binding to activated human CD4+ T cells at pH 6.0 by P1-061029 (squares), P1-068761 (triangles), and P1-068767 (inverted triangles), while a non-VISTA-specific control antibody (circles) did not block VISTA binding. **Fig. 8F** shows the reduced potency of P1-068761 (triangles) and P1-068767 (inverted triangles) in mediating antibody-dependent cell cytotoxicity (ADCC) at physiological pH. P1-061029 (squares), a non-VISTA-specific positive control antibody (circles), and a non-VISTA-specific negative control antibody (diamonds) are also shown. NK cell specific lysis of target cells as a percentage of total target cells is plotted on the y-axis and antibody concentrations are plotted on the x-axis. Non-linear regressions are also shown.

Fig. 9 shows enhanced pharmacokinetics (PK) of acidic pH-selective anti-VISTA antibodies in cynomolgus macaques. The figure shows serum antibody concentrations over time in cynomolgus macaques treated VISTA antibody 2 ("control", circles, see Fig. 6C), VISTA antibody 3 ("acidic pH sensitive", squares, see Fig. 6C), or P1-068767 (triangles).

Figs. 10A and 10B show the binding effects of mutations in the acidic pH-selective anti-VISTA antibodies '761 and '767. **Fig. 10A** shows kinetic binding data of P1-068761 reversion mutants at pH 7.4, pH 6.7 and pH 6.0 and the location of their reversion mutations relative to P1-068761. **Fig. 10B** shows kinetic binding data of P1-068767 reversion mutants at pH 7.4, pH 6.7 and pH 6.0 and the location of their reversion mutations relative to P1-068767.

Figs. 11A-C show epitope binning and mapping of various anti-VISTA antibodies. **Fig. 11A** shows the VISTA epitope competition for P1-068761 and P1-068767 compared to P1-061029 and VISTA antibody controls. **Fig. 11B** and **Fig. 11C** show representations of the epitopes of all the residues for blocking hVISTA antibody (Fig. 11B) as listed in Table 14 compared to a non-blocking hVISTA antibody (mAb1; Fig. 11C). Amino acid residues 66(H) and 162(A) are indicated to denote the orientation of the molecule. Histidine residues are in grey, and epitope residues are in black.

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Figs. 12A-C show imaged capillary isoelectric focusing (icIEF) data for the following: **Fig. 12A**: P1-061029, **Fig. 12B**: P1-068761, and **Fig. 12C**: P1-068767. The isoelectric point of the main species (pI main) as well as pI markers are indicated.

Fig. 13A and B show alignments of variable regions for '029 and '015 progeny clones. **Fig. 13A** shows the alignment of the amino acid sequences of the variable regions of '029 and its progeny clones. **Fig. 13B** shows the alighment of the amino acid sequences of the variable regions of '015 and its progeny clones.

DETAILED DESCRIPTION

According to a first aspect of the invention, there is provided an antibody that binds specifically to human V-domain lg Suppressor of T cell Activation (hVISTA), wherein the antibody comprises

(i) a light chain variable region (VL) comprising VL CDR1, CDR2, and CDR3 comprising positions 24-35, 51-57, and 90-98 of SEQ ID NO: 68 and a heavy chain variable region (VH) comprising VH CDR 1, CDR2 and CDR3 comprising

positions 26-35, 50-66, and 99-112 of SEQ ID NO: 55,
positions 26-35, 50-66, and 99-112 of SEQ ID NO: 51,
positions 26-35, 50-66 and 99-112 of SEQ ID NO: 15,
positions 26-35, 50-66, and 99-112 of SEQ ID NO: 11,
positions 26-35, 50-66, and 99-112 of SEQ ID NO: 59,
positions 26-35, 50-66, and 99-112 of SEQ ID NO: 39,
positions 26-35, 50-66, and 99-112 of SEQ ID NO: 63,
positions 26-35, 50-66, and 99-112 of SEQ ID NO: 71,
positions 26-35, 50-66, and 99-112 of SEQ ID NO: 75,
positions 26-35, 50-66, and 99-112 of SEO ID NO: 83,
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positions 26-35, 50-66, and 99-112 of SEO ID NO: 285,
positions 26-35, 50-66, and 99-112 of SEO ID NO: 265,
positions 26-35, 50-66, and 99-112 of SEO ID NO: 301,
positions 26-35, 50-66, and 99-112 of SEO ID NO: 293,
positions 26-35, 50-66, and 99-112 of SEO ID NO: 313,
positions 26-35, 50-66, and 99-112 of SEO ID NO: 277, or
positions 26-35, 50-66, and 99-112 of SEO ID NO: 305,

or wherein the antibody comprises

(ii) a VL comprising VL CDR1, CDR2, and CDR3 comprising positions 24-35, 51-57, and 90-98 of SEQ ID NO: 96 and a VH comprising VH CDR 1, CDR2 and CDR3 comprising

positions 26-35, 50-66, and 99-110 of SEO ID NO: 99,
positions 26-35, 50-66, and 99-110 of SEO ID NO: 103,
positions 26-35, 50-66, and 99-110 of SEO ID NO: 107, or
positions 26-35, 50-66, and 99-110 of SEO ID NO: 111.

According to a second aspect of the invention, there is provided a nucleic acid encoding an antibody of the first aspect.

According to a third aspect of the invention, there is provided a composition comprising the nucleic acid of the second aspect.

According to a fourth aspect of the invention, there is provided a cell comprising the nucleic acid of the second aspect, or the composition of third aspect.

According to a fifth aspect of the invention, there is provided a method of preparing an antibody, comprising culturing the cell of the fourth aspect in conditions under which the antibody is expressed.

According to a sixth aspect of the invention, there is provided a composition comprising an antibody of the first aspect, the nucleic acid of the second aspect, composition of the third aspect or cell of the fourth aspect and a pharmaceutically acceptable carrier.

According to a seventh aspect of the invention, there is provided a use of an antibody of the first aspect in the preparation of a medicament for treating a subject having cancer.

According to an eighth aspect of the invention, there is provided a use of an antibody of the first aspect in the preparation of a medicament for treating an infectious disease (e.g., viral disease) in a subject.

According to a ninth aspect of the invention, there is provided a method of treating cancer in a subject in need thereof, comprising administering an antibody of the first aspect to the subject.

According to an tenth aspect of the invention, there is provided a method of treating an infectious disease (e.g., viral disease) in a subject in need thereof, comprising administering an antibody of the first aspect to the subject.

In the description in this specification reference may be made to subject matter which is not within the scope of the appended claims. That subject matter should be readily

identifiable by a person skilled in the art and may assist in putting into practice the invention as defined in the appended claims.

Definitions

In this application, the use of "or" means "and/or" unless stated otherwise. In the context of a multiple dependent claim, the use of "or" refers back to more than one preceding independent or dependent claim in the alternative only. The terms "comprising," "including," and "having" can be used interchangeably herein. According to the present invention, an "isolated" molecule is a molecule that has been removed from its natural milieu. As such, the term "isolated" does not necessarily reflect the extent to which the molecule has been purified.

The term "polypeptide" refers to a polymer of amino acid residues, and is not limited to a minimum length. A "protein" may comprise one or more polypeptides. Such polymers of amino acid residues may contain natural or non-natural amino acid residues, and include, but are not limited to, peptides, oligopeptides, dimers, trimers, and multimers of amino acid residues. Both full-length proteins and fragments thereof are encompassed by the definition. The terms also include post-expression modifications of the polypeptide, for example, glycosylation, sialylation, acetylation, phosphorylation, and the like. Furthermore, for purposes of the present invention, a "polypeptide" or "protein" refers to a polypeptide or protein, respectively, which includes modifications, such as deletions, additions, and substitutions (generally conservative in nature), to the native sequence, as long as the protein maintains the desired activity. These modifications may be deliberate, as through site-directed mutagenesis, or may be accidental, such as through mutations of hosts that produce

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the proteins or errors due to PCR amplification. A protein may comprise two or more polypeptides.

"VISTA" is an abbreviation for the V-domain immunoglobulin-containing suppressor of T-cell activation protein, which is a member of the B7 family of immune checkpoint regulators. VISTA is also known as the PD-1 homolog (PD1H), B7-H5, C10orf54, differentiation of ESC-1 (Dies-1), platelet receptor Gi24 precursor, and death domain 1α (DD1α). The term "hVISTA" or "huVISTA" herein refers to the human VISTA protein. The amino acid sequence of hVISTA, including its signal peptide is provided in SEQ ID NO:1, while the sequence without the signal peptide is provided in SEQ ID NO:2. (See the Sequence Table below.) The extracellular domain or "ECD" of VISTA or the "VISTA-ECD" refers to the portion of the VISTA protein that is located in the extracellular space, which, in the case of hVISTA, comprises the amino acids 1-162 of SEQ ID NO:2. (See also Fig. 1B.) The "IgV domain" portion of hVISTA comprises residues 5-135 of SEQ ID NO:2.

The term "leader peptide" or "leader sequence" refers to a sequence of amino acid residues located at the N terminus of a polypeptide that facilitates secretion of a polypeptide from a mammalian cell. A leader sequence may be cleaved upon export of the polypeptide from the mammalian cell, forming a mature protein. Leader sequences may be natural or synthetic, and they may be heterologous or homologous to the protein to which they are attached.

The term "antibody" or "Ab" herein is used in the broadest sense and encompasses various antibody structures, including but not limited to monoclonal antibodies, polyclonal antibodies, multispecific antibodies (*e.g.*, bispecific antibodies), and antibody fragments so long as they exhibit the desired antigen-binding activity. As used herein, the term refers to a molecule comprising at least complementarity-determining region (CDR) 1, CDR2, and CDR3 of a heavy chain and at least CDR1, CDR2, and CDR3 of a light chain, wherein the molecule is capable of binding to antigen. The term antibody includes, but is not limited to, fragments that are capable of binding antigen, such as Fv, single-chain Fv (scFv), Fab, Fab', and $(Fab')_2$. The term antibody also includes, but is not limited to, chimeric antibodies, humanized antibodies, human antibodies, and antibodies of various species such as mouse, cynomolgus monkey, *etc*.

The term "heavy chain" or "HC" refers to a polypeptide comprising at least a heavy chain variable region, with or without a leader sequence. In some embodiments, a heavy chain comprises at least a portion of a heavy chain constant region. The term "full-length heavy chain" refers to a polypeptide comprising a heavy chain variable region and a heavy chain constant region, with or without a leader sequence, and with or without a C-terminal lysine (K).

The term "heavy chain variable region" or "VH" refers to a region comprising a heavy chain complementary determining region (CDR) 1, framework region (FR) 2, CDR2, FR3, and CDR3 of the heavy chain. In some embodiments, a heavy chain variable region also comprises at least a portion of an FR1 and/or at least a portion of an FR4. As specified below, in some embodiments, a heavy chain CDR1 comprises residues 26-35 of a VH SEQ ID NO herein; a heavy chain CDR2 comprises residues 50-66 of a VH SEQ ID NO herein, and a heavy chain CDR3 comprises residues 99-110 of a VH SEQ ID NO herein. In other embodiments, if specified, a heavy chain CDR1 corresponds to Kabat residues 31 to 35; a heavy chain CDR2 corresponds to Kabat residues 50 to 65; and a heavy chain CDR3 corresponds to Kabat residues 95 to 102. *See, e.g.*, Kabat Sequences of Proteins of Immunological Interest (1987 and 1991, NIH, Bethesda, Md.). In some embodiments the heavy chain CDRs are as specified herein, such as in the sequence table below or in Table 2.

The term "light chain" or "LC" refers to a polypeptide comprising at least a light chain variable region, with or without a leader sequence. In some embodiments, a light chain comprises at least a portion of a light chain constant region. The term "full-length light chain" refers to a polypeptide comprising a light chain variable region and a light chain constant region, with or without a leader sequence.

The term "light chain variable region" or "VL" refers to a region comprising a light chain CDR1, FR2, HVR2, FR3, and HVR3. In some embodiments, a light chain variable region also comprises an FR1 and/or an FR4. As specified below, in some embodiments, a light chain CDR1 comprises residues 24-35 of a VL SEQ ID NO herein; a light chain CDR2 comprises residues 51-57 of a VL SEQ ID NO herein, and a light chain CDR3 comprises residues 90-98 of a VL SEQ ID NO herein. In other embodiments, if specified, a light chain CDR1 corresponds to Kabat residues 24 to 34; a light chain CDR2 corresponds to Kabat

residues 50 to 56; and a light chain CDR3 corresponds to Kabat residues 89 to 97. *See, e.g.*, Kabat Sequences of Proteins of Immunological Interest (1987 and 1991, NIH, Bethesda, Md.). In some embodiments, the light chain CDRs are as specified herein such as in the sequence table.

A "chimeric antibody" refers to an antibody in which a portion of the heavy and/or light chain is derived from a particular source or species, while the remainder of the heavy and/or light chain is derived from a different source or species. In some embodiments, a chimeric antibody refers to an antibody comprising at least one variable region from a first species (such as mouse, rat, cynomolgus monkey, *etc.*) and at least one constant region from a second species (such as human, cynomolgus monkey, *etc.*). In some embodiments, a chimeric antibody comprises at least one mouse variable region and at least one human constant region. In some embodiments, a chimeric antibody comprises at least one cynomolgus variable region and at least one human constant region. In some embodiments, all of the variable regions of a chimeric antibody are from a first species and all of the constant regions of the chimeric antibody are from a second species.

A "humanized antibody" refers to an antibody in which at least one amino acid in a framework region of a non-human variable region has been replaced with the corresponding amino acid from a human variable region. In some embodiments, a humanized antibody comprises at least one human constant region or fragment thereof. In some embodiments, a humanized antibody is an Fab, an scFv, a $(Fab')_2$, *etc.*

A "human antibody" as used herein refers to antibodies produced in humans, antibodies produced in non-human animals that comprise human immunoglobulin genes, such as XenoMouse®, and antibodies selected using in vitro methods, such as phage display, wherein the antibody repertoire is based on a human immunoglobulin sequences.

A "VISTA antibody" or "anti-VISTA antibody" as used herein refers to an antibody that specifically binds to VISTA under at least some conditions such as acidic pH. In some embodiments, the antibody may be a "huVISTA antibody" or an "anti-huVISTA antibody" indicting that it specifically binds to the human VISTA protein under at least some conditions such as at acidic pH. A VISTA antibody that specifically binds to the extracellular domain (ECD) of VISTA, for example, may be termed a "VISTA-ECD antibody."

In some embodiments, an antibody may bind with higher affinity to VISTA at acidic pH than at neutral and/or physiological pH. In some embodiments, the antibody may bind with higher affinity to VISTA at acidic pH and may only bind negligibly or nonspecifically at neutral and/or physiological pH.

A "K_D" or "dissociation constant" for binding of an antibody to a protein, e.g., a VISTA-ECD protein is a measure of the affinity or specific binding of the antibody to the protein, e.g., VISTA-ECD protein. A lower K_D indicates improved binding or affinity over a higher K_D. A K_D is composed of a ratio between an "off-rate" or k_{off} or k_d and an "on-rate" or k_{on} or k_a for the antibody and polypeptide. The off-rate and on-rate are the rates at which the two binding partners associate and dissociate in the system. Thus, a slower off-rate, where the on-rate remains roughly constant, leads to higher overall affinity and thus a lower K_D. As used herein, a k_{off} of a particular value "or less" indicates that the k_{off} or "off-rate" is as specified or is slower than the rate specified.

The terms "specific binding" or "specifically binds" or like terms signify that the K_D for the binding of two polypeptides, such as an antibody and its polypeptide target, is less than would be the case between two random polypeptides existing under the same conditions. In other words, the K_D is less than that due to nonspecific aggregation of polypeptides in the system.

In some embodiments, the antibodies specifically bind to a VISTA-ECD protein at a particular pH or pH range. An "acidic" pH herein generally refers to a pH less than 7.0, a "basic" pH generally refers to a pH higher than 7.0 and a "neutral" pH generally refers to a pH of about 7.0. A "physiological pH" herein refers to a pH in normal (i.e., non-cancerous) physiological conditions, e.g., from 7.35 to 7.45, or from 7.3 to 7.4, such as of about 7.4. Phrases such as "binding in acidic conditions" or "binding in physiological conditions" and the like herein, used in the context of binding of two molecules such as VISTA and a VISTA binding partner or VISTA and a T cell, refer to binding in acidic pH and binding in physiological pH, respectively.

When referring to an antibody that "blocks binding of" or "inhibits binding of" a ligand (or receptor) or a competing antibody to a receptor (or ligand) alone or on a cell, binding is blocked if there is an overall decrease that is statistically significant compared to a

control, e.g., an overall decrease of 50% or greater, e.g., an overall decrease of 75%, 80%, 85%, 90%, 95%, or greater. An "anti-VISTA blocking antibody," for example, is one that can block binding of VISTA to PSGL-1 or another VISTA ligand or receptor or heparan sulfate proteoglycans under at least some conditions such as at acidic pH.

A "tumor model," as used herein, refers to an *in vivo* preclinical assay, which may be used for studying the biological activity of a VISTA-ECD antibody, and includes xenograft or native mouse tumor assay systems. In some cases, a tumor model may allow for tracking of tumor size or growth upon treatment with the antibody, and/or tracking of the presence of immune cells in the tumor, such as specific types of T-cells or NK cells, in order to determine whether an antibody has triggered or enhanced an immune response.

The term "immune stimulating agent" as used herein refers to a molecule that stimulates the immune system by either acting as an agonist of an immune-stimulatory molecule, including a co-stimulatory molecule, or acting as an antagonist of an immune inhibitory molecule, including a co-inhibitory molecule. The immune-stimulatory molecule or immune inhibitory molecule may be an immune checkpoint regulator such as VISTA or another B7 family member or another molecule as described further below. An immune stimulating agent may be a biologic, such as an antibody or antibody fragment, other protein, or vaccine, or may be a small molecule drug. An "immune stimulatory molecule" includes a receptor or ligand that acts to enhance, stimulate, induce, or otherwise "turn-on" an immune response. Immune stimulatory molecules as defined herein include co-stimulatory molecules. An "immune inhibitory molecule" includes a receptor or ligand that acts to reduce, inhibit, suppress, or otherwise "turn-off" an immune response. Immune inhibitory molecules as defined herein include co-inhibitory molecules. Such immune stimulatory and immune inhibitory molecules may be, for example, receptors or ligands found on immune cells such as a T cells, or found on cells involved in innate immunity such as NK cells.

"Percent (%) amino acid sequence identity" and "homology" with respect to a peptide, polypeptide or antibody sequence are defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the specific peptide or polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any

conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or MEGALIGNTM (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared.

The terms "trigger" or "enhance" refer to an initiation or increase of any event (such as protein ligand binding) or to an initiation or increase of any biological activity (such as an immune response) or phenotypic characteristic or to the initiation or increase in the incidence, degree, or likelihood of that activity or characteristic. To "trigger" or "enhance" is to begin or increase an activity, function, and/or amount as compared to a reference. It is not necessary that the triggering or enhancement be complete. For example, in certain embodiments, by "enhance" is meant the ability to cause an overall increase of 20% or greater. In another embodiment, by "enhance" is meant the ability to cause an overall increase of 50% or greater. In yet another embodiment, by "enhance" is meant the ability to cause an overall increase of 75%, 85%, 90%, 95%, or greater.

The terms "inhibition" or "inhibit" more generally refer to a decrease or cessation of any event (such as protein ligand binding) or to a decrease or cessation of any phenotypic characteristic or to the decrease or cessation in the incidence, degree, or likelihood of that characteristic. To "reduce" or "inhibit" is to decrease, reduce or arrest an activity, function, and/or amount as compared to a reference. It is not necessary that the inhibition or reduction be complete. For example, in certain embodiments, by "reduce" or "inhibit" is meant the ability to cause an overall decrease of 20% or greater. In another embodiment, by "reduce" or "inhibit" is meant the ability to cause an overall decrease of 50% or greater. In yet another embodiment, by "reduce" or "inhibit" is meant the ability to cause an overall decrease of 75%, 85%, 90%, 95%, or greater.

"Treatment" as used herein, covers any administration or application of a therapeutic for disease in a human, and includes inhibiting the disease or progression of the disease or one or more disease symptoms, inhibiting or slowing the disease or its progression or one or more of its symptoms, arresting its development, partially or fully relieving the disease or

one or more of its symptoms, or preventing a recurrence of one or more symptoms of the disease.

The terms "subject" and "patient" are used interchangeably herein to refer to a human.

The term "effective amount" or "therapeutically effective amount" refers to an amount of a drug effective for treatment of a disease or disorder in a subject, such as to partially or fully relieve one or more symptoms. In some embodiments, an effective amount refers to an amount effective, at dosages and for periods of time necessary, to achieve the desired therapeutic or prophylactic result.

The term "cancer" is used herein to refer to a group of cells that exhibit abnormally high levels of proliferation and growth. A cancer may be benign (also referred to as a benign tumor), pre-malignant, or malignant. Cancer cells may be solid cancer cells or leukemic cancer cells. The term "tumor growth" is used herein to refer to proliferation or growth by a cell or cells that comprise a cancer that leads to a corresponding increase in the size or extent of the cancer.

Examples of cancers applicable to methods of treatment herein include but are not limited to, carcinoma, lymphoma, blastoma, sarcoma, and leukemia. More particular nonlimiting examples of such cancers include squamous cell cancer, small-cell lung cancer, pituitary cancer, esophageal cancer, astrocytoma, soft tissue sarcoma, non-small cell lung cancer (including squamous cell non-small cell lung cancer), adenocarcinoma of the lung, squamous carcinoma of the lung, cancer of the peritoneum, hepatocellular cancer, gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, hepatoma, breast cancer, colon cancer, colorectal cancer, endometrial or uterine carcinoma, salivary gland carcinoma, kidney cancer, renal cell carcinoma, liver cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma, brain cancer, endometrial cancer, testis cancer, cholangiocarcinoma, gallbladder carcinoma, gastric cancer, melanoma, and various types of head and neck cancer (including squamous cell carcinoma of the head and neck).

Administration "in combination with" one or more further therapeutic agents includes simultaneous (concurrent) and consecutive (sequential) administration in any order.

A "pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid, or liquid filler, diluent, encapsulating material, formulation auxiliary, or carrier conventional in the art for use with a therapeutic agent that together comprise a "pharmaceutical composition" for administration to a subject. A pharmaceutically acceptable carrier is non-toxic to recipients at the dosages and concentrations employed and is compatible with other ingredients of the formulation. The pharmaceutically acceptable carrier is appropriate for the formulation employed. For example, if the therapeutic agent is to be administered orally, the carrier may be a gel capsule. If the therapeutic agent is to be administered subcutaneously, the carrier ideally is not irritable to the skin and does not cause injection site reaction.

A "chemotherapeutic agent" is a chemical compound useful in the treatment of cancer. Examples of chemotherapeutic agents that can be administered in methods herein include, but are not limited to, alkylating agents such as thiotepa and Cytoxan® cyclosphosphamide; alkyl sulfonates such as busulfan, improsulfan and piposulfan; aziridines such as benzodopa, carboquone, meturedopa, and uredopa; ethylenimines and methylamelamines including altretamine, triethylenemelamine, trietylenephosphoramide, triethiylenethiophosphoramide and trimethylolomelamine; acetogenins (especially bullatacin and bullatacinone); a camptothecin (including the synthetic analogue topotecan); bryostatin; callystatin; CC-1065 (including its adozelesin, carzelesin and bizelesin synthetic analogues); cryptophycins (particularly cryptophycin 1 and cryptophycin 8); dolastatin; duocarmycin (including the synthetic analogues, KW-2189 and CB1-TM1); eleutherobin; pancratistatin; a sarcodictyin; spongistatin; nitrogen mustards such as chlorambucil, chlornaphazine, cholophosphamide, estramustine, ifosfamide, mechlorethamine, mechlorethamine oxide hydrochloride, melphalan, novembichin, phenesterine, prednimustine, trofosfamide, uracil mustard; nitrosureas such as carmustine, chlorozotocin, fotemustine, lomustine, nimustine, and ranimnustine; antibiotics such as the enediyne antibiotics (*e.g.*, calicheamicin, especially calicheamicin gamma1I and calicheamicin omegaI1 (*see, e.g.*, Agnew, *Chem Intl. Ed. Engl.*, 33: 183-186 (1994)); dynemicin, including dynemicin A; bisphosphonates, such as clodronate; an esperamicin; as well as neocarzinostatin chromophore and related chromoprotein enediyne antiobiotic chromophores), aclacinomysins, actinomycin, authramycin, azaserine, bleomycins, cactinomycin, carabicin, carminomycin, carzinophilin,

chromomycinis, dactinomycin, daunorubicin, detorubicin, 6-diazo-5-oxo-L-norleucine, Adriamycin® doxorubicin (including morpholino-doxorubicin, cyanomorpholino-doxorubicin, 2-pyrrolino-doxorubicin and deoxydoxorubicin), epirubicin, esorubicin, idarubicin, marcellomycin, mitomycins such as mitomycin C, mycophenolic acid, nogalamycin, olivomycins, peplomycin, potfiromycin, puromycin, quelamycin, rodorubicin, streptonigrin, streptozocin, tubercidin, ubenimex, zinostatin, zorubicin; anti-metabolites such as methotrexate and 5-fluorouracil (5-FU); folic acid analogues such as denopterin, methotrexate, pteropterin, trimetrexate; purine analogs such as fludarabine, 6-mercaptopurine, thiamiprine, thioguanine; pyrimidine analogs such as ancitabine, azacitidine, 6-azauridine, carmofur, cytarabine, dideoxyuridine, doxifluridine, enocitabine, floxuridine; androgens such as calusterone, dromostanolone propionate, epitiostanol, mepitiostane, testolactone; anti-adrenals such as aminoglutethimide, mitotane, trilostane; folic acid replenisher such as frolinic acid; aceglatone; aldophosphamide glycoside; aminolevulinic acid; eniluracil; amsacrine; bestrabucil; bisantrene; edatraxate; defofamine; demecolcine; diaziquone; elfornithine; elliptinium acetate; an epothilone; etoglucid; gallium nitrate; hydroxyurea; lentinan; lonidainine; maytansinoids such as maytansine and ansamitocins; mitoguazone; mitoxantrone; mopidanmol; nitraerine; pentostatin; phenamet; pirarubicin; losoxantrone; podophyllinic acid; 2- ethylhydrazide; procarbazine; PSK® polysaccharide complex (JHS Natural Products, Eugene, OR); razoxane; rhizoxin; sizofiran; spirogermanium; tenuazonic acid; triaziquone; 2,2',2"-trichlorotriethylamine; trichothecenes (especially T-2 toxin, verracurin A, roridin A and anguidine); urethan; vindesine; dacarbazine; mannomustine; mitobronitol; mitolactol; pipobroman; gacytosine; arabinoside ("Ara-C"); cyclophosphamide; thiotepa; taxoids, *e.g.*, Taxol® paclitaxel (Bristol- Myers Squibb Oncology, Princeton, N.J.), Abraxane® Cremophor-free, albumin-engineered nanoparticle formulation of paclitaxel (American Pharmaceutical Partners, Schaumberg, Illinois), and Taxotere® doxetaxel (Rhône- Poulenc Rorer, Antony, France); chloranbucil; Gemzar® gemcitabine; 6-thioguanine; mercaptopurine; methotrexate; platinum analogs such as cisplatin, oxaliplatin and carboplatin; vinblastine; platinum; etoposide (VP-16); ifosfamide; mitoxantrone; vincristine; Navelbine® vinorelbine; novantrone; teniposide; edatrexate; daunomycin; aminopterin; xeloda; ibandronate; irinotecan (Camptosar, CPT-11)

(including the treatment regimen of irinotecan with 5-FU and leucovorin); topoisomerase inhibitor RFS 2000; difluorometlhylornithine (DMFO); retinoids such as retinoic acid; capecitabine; combretastatin; leucovorin (LV); oxaliplatin, including the oxaliplatin treatment regimen (FOLFOX); inhibitors of PKC-alpha, Raf, H-Ras, EGFR (*e.g.*, erlotinib (Tarceva®)) and VEGF-A that reduce cell proliferation and pharmaceutically acceptable salts, acids or derivatives of any of the above.

Further nonlimiting exemplary chemotherapeutic agents that can be administered in methods herein include anti-hormonal agents that act to regulate or inhibit hormone action on cancers such as anti-estrogens and selective estrogen receptor modulators (SERMs), including, for example, tamoxifen (including Nolvadex® tamoxifen), raloxifene, droloxifene, 4-hydroxytamoxifen, trioxifene, keoxifene, LY117018, onapristone, and Fareston® toremifene; aromatase inhibitors that inhibit the enzyme aromatase, which regulates estrogen production in the adrenal glands, such as, for example, 4(5)-imidazoles, aminoglutethimide, Megase® megestrol acetate, Aromasin® exemestane, formestanie, fadrozole, Rivisor® vorozole, Femara® letrozole, and Arimidex® anastrozole; and anti-androgens such as flutamide, nilutamide, bicalutamide, leuprolide, and goserelin; as well as troxacitabine (a 1,3-dioxolane nucleoside cytosine analog); antisense oligonucleotides, particularly those which inhibit expression of genes in signaling pathways implicated in abherant cell proliferation, such as, for example, PKC-alpha, Ralf and H-Ras; ribozymes such as a VEGF expression inhibitor (*e.g.*, Angiozyme® ribozyme) and a HER2 expression inhibitor; vaccines such as gene therapy vaccines, for example, Allovectin® vaccine, Leuvectin® vaccine, and Vaxid® vaccine; Proleukin® rIL-2; Lurtotecan® topoisomerase 1 inhibitor; Abarelix® rmRH; and pharmaceutically acceptable salts, acids or derivatives of any of the above.

An “anti-angiogenesis agent” or “angiogenesis inhibitor” refers to a small molecular weight substance, a polynucleotide (including, *e.g.*, an inhibitory RNA (RNAi or siRNA)), a polypeptide, an isolated protein, a recombinant protein, an antibody, or conjugates or fusion proteins thereof, that inhibits angiogenesis, vasculogenesis, or undesirable vascular permeability, either directly or indirectly. It should be understood that the anti-angiogenesis agent includes those agents that bind and block the angiogenic activity of the angiogenic factor or its receptor. For example, an anti-angiogenesis agent that can be administered in

methods herein can include an antibody or other antagonist to an angiogenic agent, *e.g.*, antibodies to VEGF-A (*e.g.*, bevacizumab (Avastin®)) or to the VEGF-A receptor (*e.g.*, KDR receptor or Flt-1 receptor), anti-PDGFR inhibitors such as Gleevec® (Imatinib Mesylate), small molecules that block VEGF receptor signaling (*e.g.*, PTK787/ZK2284, SU6668, Sutent®/SU11248 (sunitinib malate), AMG706, or those described in, *e.g.*, international patent application WO 2004/113304). Anti-angiogensis agents also include native angiogenesis inhibitors , *e.g.*, angiostatin, endostatin, *etc.* *See, e.g.*, Klagsbrun and D'Amore (1991) *Annu. Rev. Physiol.* 53:217-39; Streit and Detmar (2003) *Oncogene* 22:3172-3179 (*e.g.*, Table 3 listing anti-angiogenic therapy in malignant melanoma); Ferrara & Alitalo (1999) *Nature Medicine* 5(12):1359-1364; Tonini *et al.* (2003) *Oncogene* 22:6549-6556 (*e.g.*, Table 2 listing known anti-angiogenic factors); and, Sato (2003) *Int. J. Clin. Oncol.* 8:200-206 (*e.g.*, Table 1 listing anti-angiogenic agents used in clinical trials).

A "growth inhibitory agent" as used herein refers to a compound or composition that inhibits growth of a cell (such as a cell expressing VEGF) either *in vitro* or *in vivo*. Thus, the growth inhibitory agent that can be administered in methods herein may be one that significantly reduces the percentage of cells (such as a cell expressing VEGF) in S phase. Examples of growth inhibitory agents include, but are not limited to, agents that block cell cycle progression (at a place other than S phase), such as agents that induce G1 arrest and M-phase arrest. Classical M-phase blockers include the vincas (vincristine and vinblastine), taxanes, and topoisomerase II inhibitors such as doxorubicin, epirubicin, daunorubicin, etoposide, and bleomycin. Those agents that arrest G1 also spill over into S-phase arrest, for example, DNA alkylating agents such as tamoxifen, prednisone, dacarbazine, mechlorethamine, cisplatin, methotrexate, 5-fluorouracil, and ara-C. Further information can be found in Mendelsohn and Israel, eds., *The Molecular Basis of Cancer*, Chapter 1, entitled "Cell cycle regulation, oncogenes, and antineoplastic drugs" by Murakami *et al.* (W.B. Saunders, Philadelphia, 1995), *e.g.*, p. 13. The taxanes (paclitaxel and docetaxel) are anticancer drugs both derived from the yew tree. Docetaxel (Taxotere®, Rhone-Poulenc Rorer), derived from the European yew, is a semisynthetic analogue of paclitaxel (Taxol®, Bristol-Myers Squibb). Paclitaxel and docetaxel promote the assembly of microtubules from

tubulin dimers and stabilize microtubules by preventing depolymerization, which results in the inhibition of mitosis in cells.

The term "anti-neoplastic composition" refers to a composition useful in treating cancer comprising at least one active therapeutic agent. Examples of therapeutic agents include, but are not limited to, *e.g.*, chemotherapeutic agents, growth inhibitory agents, cytotoxic agents, agents used in radiation therapy, anti-angiogenesis agents, cancer immunotherapeutic agents, apoptotic agents, anti-tubulin agents, and other-agents to treat cancer, such as anti-HER-2 antibodies, anti-CD20 antibodies, an epidermal growth factor receptor (EGFR) antagonist (*e.g.*, a tyrosine kinase inhibitor), HER1/EGFR inhibitor (*e.g.*, erlotinib (Tarceva®), platelet derived growth factor inhibitors (*e.g.*, Gleevec® (Imatinib Mesylate)), a COX-2 inhibitor (*e.g.*, celecoxib), interferons, CTLA4 inhibitors (*e.g.*, anti-CTLA antibody ipilimumab (YERVOY®)), PD-1 ore PD-L1 inhibitors (e.g., OPDIVO®, KEYTRUDA®, TECENTRIQ®, BAVENCIO®, IMFINZI®), TIM3 inhibitors (*e.g.*, anti-TIM3 antibodies), cytokines, antagonists (*e.g.*, neutralizing antibodies) that bind to one or more of the following targets ErbB2, ErbB3, ErbB4, PDGFR-beta, BlyS, APRIL, BCMA, CTLA4, TIM3, or VEGF receptor(s), TRAIL/Apo2, and other bioactive and organic chemical agents, *etc.* Combinations thereof are also included in this disclosure.

Antibodies Specifically Binding to VISTA-ECD at Acidic pH

Because VISTA has a large number of histidine residues in its ECD, its folding and overall structure, as well as the surface available for the binding of ligands such as antibodies, may differ at acidic pH compared to neutral pH, in particular, near pH 6.5, which is the pK_a for histidine. Since tumor microenvironments are generally acidic, for binding to VISTA in those microenvironments, an antibody may need to bind with specificity to VISTA at acidic pH where at least some of the surface histidine residues are more likely to be protonated.

The Sequence Table below provides the amino acid sequence of human VISTA (hVISTA) with or without signal peptide (SEQ ID NO: 1 and SEQ ID NO: 2 (mature hVISTA)), respectively. The signal peptide constitutes amino acid residues 1-32 of SEQ ID NO: 1. The extracellular domain (ECD) consists of amino acid residues 1-162 of SEQ ID

NO: 2). The IgV domain constitutes amino acids residues 37-167 of SEQ ID NO: 1 and amino acid residues 5- 135 of SEQ ID NO: 2. The stalk region is at amino acid residues 172-194 of SEQ ID NO: 1 and amino acid residues 136-162 of SEQ ID NO: 2; the transmembrane domain is at amino acid residues 195-216 of SEQ ID NO: 1 and amino acid residues 163-184 of SEQ ID NO: 2. Amino acid residue 187 of SEQ ID NO: 1 and 155 of SEQ ID NO: 2 (bold and underlined) can be either D or E, which represents a polymorphism in hVISTA. That residue is shown in bold, underlining. Accordingly, SEQ ID NO:1 and SEQ ID NO:2 encompass both of the human polymorphisms at that residue. The histidine residues in the ECD of VISTA are grey-shaded.

Anti-VISTA antibodies (Abs) may specifically bind to the VISTA-ECD or fragments thereof, e.g., comprising the IgV domain of VISTA or a region from hVISTA comprising, e.g., amino acids 20-95, 20-70 35-70, 35-95, 35-127 or 37-125 of SEQ ID NO: 2 at acidic pH. In certain embodiments, an Ab specifically binds to the VISTA-ECD protein at a pH that is less than pH 7.0. In certain embodiments, an Ab specifically binds to the VISTA-ECD protein at a pH that is less than pH 6.8. In certain embodiments, an Ab specifically binds to the VISTA-ECD protein at a pH that is less than pH 6.5. In certain embodiments, an Ab specifically binds to the VISTA-ECD protein at a pH that is less than pH 6.3. In certain embodiments, an Ab specifically binds to the VISTA-ECD protein at a pH that is less than pH 6.0. In certain embodiments, an Ab specifically binds to the VISTA-ECD protein at a pH that is less than pH 5.8. In certain embodiments, an Ab specifically binds to the VISTA-ECD protein at a pH that is less than pH 5.5. In certain embodiments, an Ab specifically binds to the VISTA-ECD protein at a pH that is less than pH 5.3. In certain embodiments, an Ab specifically binds to the VISTA-ECD protein at a pH that is less than pH 5.0.

Certain Abs specifically bind to a VISTA-ECD protein at a pH within a range of pH 5.0-pH 7.0. Certain Abs specifically bind to the VISTA-ECD protein at a pH within a range of pH 5.0- pH 6.5. Certain Abs specifically bind to the VISTA-ECD protein at a pH within a range of pH 5.0-pH 6.0. Certain Abs specifically bind to the VISTA-ECD protein at a pH within a range of pH 5.5- pH 7.0. Certain Abs specifically bind to the VISTA-ECD protein at a pH within a range of pH 5.5-pH 6.5. Certain Abs specifically bind to the VISTA-ECD protein at a pH within a range of pH 6.0-6.5.

Provided herein are also Abs that bind to a VISTA-ECD protein, such as hVISTA-ECD or fragments thereof comprising the IgV domain of VISTA or a region from hVISTA comprising, e.g., amino acids 20-95, 20-70 35-70, 35-95, 35-127 or 37-125 of SEQ ID NO:2 at a pH of 6.5 or less, with a K_D of 10^{-6} M or less. In some embodiments, the Abs bind with a K_D of 10^{-7} M or less. In some embodiments, the Abs bind with a K_D of 10^{-8} M or less. In some embodiments, the Abs bind with a K_D of 10^{-9} M. In some embodiments, the Abs bind with a K_D of 10^{-10} M or less. For example, an Ab may bind to the VISTA-ECD protein at a pH of 6.5 or less with a K_D of 10^{-8} M or less.

Provided herein are also Abs that bind to the VISTA-ECD protein within a pH range of 6.0-6.5 with a K_D of 10^{-6} M or less. In some embodiments, the Abs bind with a K_D of 10^{-7} M or less. In some embodiments, the Abs bind with a K_D of 10^{-8} M or less. In some embodiments, the Abs bind with a K_D of 10^{-9} M. In some embodiments, the Abs bind with a K_D of 10^{-10} M or less. For example, an Ab may bind to the VISTA-ECD protein at a pH of 6.5 or less, e.g., within a pH range of 6.0-6.5, with a K_D of 10^{-7} M or less. Further, an Ab may bind to the VISTA-ECD protein at a pH of 6.5 or less, e.g., within a pH range of 6.0-6.5, with a K_D of 10^{-8} M or less. An Ab may bind to hVISTA-ECD at a pH of 6.5 or less, e.g., within a pH range of 6.0-6.5, with a K_D of 10^{-9} M or less.

Provided herein are also Abs that specifically bind to a VISTA-ECD protein, such as hVISTA-ECD or fragments thereof comprising the IgV domain of VISTA or a region from hVISTA comprising, e.g., amino acids 20-95, 20-70 35-70, 35-95, 35-127 or 37-125 of SEQ ID NO:2, e.g., at a pH of 6.5 or less, with a k_{off} of 10^{-5} s^{-1} or less at either 25°C or at 37°C. In some embodiments, the Abs have a k_{off} of 10^{-4} s^{-1} or less at either 25°C or at 37°C. In some embodiments, the Abs have a k_{off} of 2 10^{-4} s^{-1} or less at either 25°C or at 37°C. In some embodiments, the Abs have a k_{off} of 5 10^{-4} s^{-1} or less at either 25°C or at 37°C. In some embodiments, the Abs have a k_{off} of 7 10^{-4} s^{-1} or less at either 25°C or at 37°C. In some embodiments, the Abs have a k_{off} of 10^{-3} s^{-1} or less at either 25°C or at 37°C. In some embodiments, the Abs have a k_{off} of 2 10^{-3} s^{-1} or less at either 25°C or at 37°C. In some embodiments, the Abs have a k_{off} of 5 10^{-3} s^{-1} or less at either 25°C or at 37°C. In some embodiments, the Abs have a k_{off} of 7 10^{-3} s^{-1} or less at either 25°C or at 37°C. In some embodiments, the Abs have a k_{off} of 10^{-2} s^{-1} at either 25°C or at 37°C. In some embodiments,

the Abs have a k_{off} of 10^{-1} s^{-1} or less at either 25°C or at 37°C. For example, an Ab may specifically bind to the VISTA-ECD protein at a pH of 6.5 or less with a k_{off} of 10^{-3} s^{-1} or less at either 25°C or at 37°C. An Ab may specifically bind to hVISTA-ECD at a pH of 6.5 or less with a k_{off} of 10^{-3} s^{-1} or less at either 25°C or at 37°C. Further, an Ab may specifically bind to the VISTA-ECD protein at a pH of 6.5 or less with a k_{off} of 10^{-2} s^{-1} or less at either 25°C or at 37°C.

Provided herein are Abs that bind to a VISTA-ECD protein, such as hVISTA-ECD or fragments thereof comprising the IgV domain of VISTA or a region from hVISTA comprising, e.g., amino acids 20-95, 20-70 35-70, or 35-95, 35-95, 35-127 or 37-125 of SEQ ID NO:2, e.g., at a pH of 6.5 or less, with (i) a K_D of 10^{-6} M or less, 10^{-7} M or less, 10^{-8} M or less, 10^{-9} M or less or 10^{-10} M or less and (ii) a k_{off} rate of 10^{-5} s^{-1} or less, 10^{-4} (or 2, 5 or 7 10^{-4}) s^{-1} or less, 10^{-3} (or 2, 5 or 7 10^{-4}) s^{-1} or less, 10^{-2} s^{-1} or less, or 10^{-1} s^{-1} or less, as measured, e.g., at 25°C or at 37°C. For example, an Ab may bind to the VISTA-ECD protein at a pH of 6.5 or less with a K_D of 10^{-7} M or less and a k_{off} rate of 10^{-3} s^{-1} or less, as measured, e.g., at 25°C or at 37°C. An Ab may bind to the VISTA-ECD protein at a pH of 6.5 or less with a K_D of 10^{-8} M or less and a k_{off} rate of 10^{-3} s^{-1} or less, as measured, e.g., at 25°C or at 37°C. An Ab may bind to the VISTA-ECD protein at a pH of 6.5 or less with a K_D of 10^{-8} M or less and a k_{off} rate of 10^{-2} s^{-1} or less, as measured, e.g., at 25°C or at 37°C. For example, an Ab may bind to hVISTA-ECD at a pH of 6.5 or less with a K_D of 10^{-7} M or less and a k_{off} rate of 10^{-3} s^{-1} or less, as measured, e.g., at 25°C or at 37°C. An Ab may bind to hVISTA-ECD at a pH of 6.5 or less with a K_D of 10^{-9} M or less and a k_{off} rate of 10^{-3} s^{-1} or less, as measured, e.g., at 25°C or at 37°C. An Ab may bind to hVISTA-ECD at a pH of 6.5 or less with a K_D of 10^{-9} M or less and a k_{off} rate of 10^{-2} s^{-1} or less, as measured, e.g., at 25°C or at 37°C. An Ab may bind to hVISTA-ECD at a pH of 6.5 or less with a K_D of 10^{-8} M or less and a k_{off} rate of 10^{-4} (or 2, 5 or 7 10^{-4}) s^{-1} or less, as measured, e.g., at 25°C or at 37°C. An Ab may bind to hVISTA-ECD at a pH of 6.5 or less with a K_D of 10^{-8} M or less and a k_{off} rate of 10^{-5} (or 2, 5 or 7 10^{-5}) s^{-1} or less, as measured, e.g., at 25°C or at 37°C. An Ab may bind to hVISTA-ECD at a pH of 6.5 or less with a K_D of 10^{-9} M or less and a k_{off} rate of 10^{-4} (or 2, 5 or 7 10^{-4}) s^{-1} or less, as measured, e.g., at 25°C or at 37°C. An Ab may bind to hVISTA-ECD at a pH of 6.5

or less with a K_D of 10^{-9} M or less and a k_{off} rate of 10^{-5} (or 2, 5 or 7 10^{-5}) s^{-1} or less, as measured, e.g., at 25°C or at 37°C.

Provided herein are Abs that specifically bind to the VISTA-ECD protein, e.g., at a pH of 6.5 or less, with a k_{on} of 10^4 M^{-1} s^{-1} or higher at 25°C or at 37°C. In some such embodiments, the Abs may bind with a k_{on} of 10^5 M^{-1} s^{-1} or higher. In some such embodiments, the Abs may bind with a k_{on} of 10^6 M^{-1} s^{-1} or higher. In some such embodiments, the Abs may bind with a k_{on} of 10^7 M^{-1} s^{-1} or higher. For example, an Ab may bind to the VISTA-ECD protein at a pH of 6.5 or less with a k_{on} of 10^6 M^{-1} s^{-1} or higher, as measured, e.g., at 25°C or at 37°C. For example, an Ab may bind to the ECD of hVISTA at a pH of 6.5 or less with a k_{on} of 10^6 M^{-1} s^{-1} or higher, as measured, e.g., at 25°C or at 37°C.

Provided herein are Abs that bind to the VISTA-ECD protein, e.g., at a pH of 6.5 or less, with (i) a K_D of 10^{-6} M or less, 10^{-7} M or less, 10^{-8} M or less, 10^{-9} M or less or 10^{-10} M or less and (ii) a k_{on} of 10^4 M^{-1} s^{-1} or higher, 10^5 M^{-1} s^{-1} or higher, 10^6 M^{-1} s^{-1} or higher, 10^7 M^{-1} s^{-1} or higher, as measured, e.g., at 25°C or at 37°C. For example, an Ab may bind to the VISTA-ECD protein at a pH of 6.5 or less with a K_D of 10^{-7} M or less and a k_{on} rate of 10^6 M^{-1} s^{-1} or higher, as measured, e.g., at 25°C or at 37°C. For example, an Ab may bind to the VISTA-ECD protein at a pH of 6.5 or less with a K_D of 10^{-8} M or less and a k_{on} rate of 10^6 M^{-1} s^{-1} or higher, as measured, e.g., at 25°C or at 37°C. For example, an Ab may bind to hVISTA-ECD at a pH of 6.5 or less with a K_D of 10^{-7} M or less and a k_{on} rate of 10^6 M^{-1} s^{-1} or higher, as measured, e.g., at 25°C or at 37°C. For example, an Ab may bind to hVISTA-ECD at a pH of 6.5 or less with a K_D of 10^{-8} M or less and a k_{on} rate of 10^6 M^{-1} s^{-1} or higher, as measured, e.g., at 25°C or at 37°C.

In some embodiments, an Ab may bind to the VISTA-ECD protein at a pH of 6.5 or less with a K_D of 10^{-7} M or less as well as with a k_{off} of 10^{-5} s^{-1} or less, 2 10^{-5} s^{-1} or less, 5 10^{-5} s^{-1} or less, 7 10^{-5} s^{-1} or less, 10^{-4} s^{-1} or less, 2 10^{-4} s^{-1} or less, 5 10^{-4} s^{-1} or less, 7 10^{-4} s^{-1} or less, 10^{-3} s^{-1} or less, 2 10^{-3} s^{-1} or less, 5 10^{-3} s^{-1} or less, 7 10^{-3} s^{-1} or less, 10^{-2} s^{-1} or less, or 10^{-1} s^{-1} or less, as measured, e.g., at 25°C or at 37°C. In some embodiments, an Ab may bind to the VISTA-ECD protein at a pH of 6.5 or less with a K_D of 10^{-9} M or less as well as with a k_{off} of 10^{-5} s^{-1} or less, 10^{-4} s^{-1} or less, 10^{-3} s^{-1} or less, 10^{-2} s^{-1} or less, or 10^{-1} s^{-1} or less, as measured, e.g., at 25°C or at 37°C. In some such embodiments, an Ab may bind to the VISTA-ECD

protein at a pH of 6.5 or less with a K_D of 10^{-10} M or less as well as with a k_{off} of 10^{-5} s^{-1} or less, 10^{-4} s^{-1} or less, 10^{-3} s^{-1} or less, 10^{-2} s^{-1} or less, or 10^{-1} s^{-1} or less, as measured, e.g., at 25°C or at 37°C.

In some embodiments, an Ab may bind to the VISTA-ECD protein at a pH of 6.5 or less with a K_D of 10^{-7} M or less as well as with a k_{on} of 10^4 M^{-1} s^{-1} or higher, 10^5 M^{-1} s^{-1} or higher, 10^6 M^{-1} s^{-1} or higher, 10^7 M^{-1} s^{-1} or higher, as measured, e.g., at 25°C or at 37°C. In some embodiments, an Ab may bind to the VISTA-ECD protein at a pH of 6.5 or less with a K_D of 10^{-8} M or less as well as with a k_{on} of 10^4 M^{-1} s^{-1} or higher, 10^5 M^{-1} s^{-1} or higher, 10^6 M^{-1} s^{-1} or higher, 10^7 M^{-1} s^{-1} or higher, as measured, e.g., at 25°C or at 37°C. In some embodiments, an Ab may bind to the VISTA-ECD protein at a pH of 6.5 or less with a K_D of 10^{-9} M or less as well as with a k_{on} of 10^4 M^{-1} s^{-1} or higher, 10^5 M^{-1} s^{-1} or higher, 10^6 M^{-1} s^{-1} or higher, 10^7 M^{-1} s^{-1} or higher, as measured, e.g., at 25°C or at 37°C. In some such embodiments, an Ab may bind to the VISTA-ECD protein at a pH of 6.5 or less with a K_D of 10^{-10} M or less as well as with a k_{on} of 10^4 M^{-1} s^{-1} or higher, 10^5 M^{-1} s^{-1} or higher, 10^6 M^{-1} s^{-1} or higher, 10^7 M^{-1} s^{-1} or higher, as measured, e.g., at 25°C or at 37°C.

In some embodiments, an Ab may bind to the VISTA-ECD protein at a pH of 6.5 or less with a K_D of 10^{-7} M or less as well as with a k_{off} of 10^{-5} s^{-1} or less, 10^{-4} s^{-1} or less, 10^{-3} s^{-1} or less, 10^{-2} s^{-1} or less, or 10^{-1} s^{-1} or less, as measured, e.g., at 25°C or at 37°C, and a k_{on} of 10^4 M^{-1} s^{-1} or higher, 10^5 M^{-1} s^{-1} or higher, 10^6 M^{-1} s^{-1} or higher, 10^7 M^{-1} s^{-1} or higher, as measured, e.g., at 25°C or at 37°C. In some embodiments, an Ab may bind to the VISTA-ECD protein at a pH of 6.5 or less with a K_D of 10^{-8} M or less as well as with a k_{off} of 10^{-5} s^{-1} or less, 10^{-4} s^{-1} or less, 10^{-3} s^{-1} or less, 10^{-2} s^{-1} or less, or 10^{-1} s^{-1} or less, as measured, e.g., at 25°C or at 37°C, and a k_{on} of 10^4 M^{-1} s^{-1} or higher, 10^5 M^{-1} s^{-1} or higher, 10^6 M^{-1} s^{-1} or higher, 10^7 M^{-1} s^{-1} or higher, as measured, e.g., at 25°C or at 37°C. In some embodiments, an Ab may bind to the VISTA-ECD protein at a pH of 6.5 or less with a K_D of 10^{-9} M or less as well as with a k_{off} of 10^{-5} s^{-1} or less, 10^{-4} s^{-1} or less, 10^{-3} s^{-1} or less, 10^{-2} s^{-1} or less, or 10^{-1} s^{-1} or less, as measured, e.g., at 25°C or at 37°C, and a k_{on} of 10^4 M^{-1} s^{-1} or higher, 10^5 M^{-1} s^{-1} or higher, 10^6 M^{-1} s^{-1} or higher, 10^7 M^{-1} s^{-1} or higher, as measured, e.g., at 25°C or at 37°C. In some such embodiments, an Ab may bind to the VISTA-ECD protein at a pH of 6.5 or less with a K_D of 10^{-10} M or less as well as with a k_{off} of 10^{-5} s^{-1} or less, 10^{-4} s^{-1} or less, 10^{-3} s^{-1} or

less, 10^{-2} s^{-1} or less, or 10^{-1} s^{-1} or less, as measured, e.g., at 25°C or at 37°C, and a k_{on} of 10^4 M^{-1} s^{-1} or higher, 10^5 M^{-1} s^{-1} or higher, 10^6 M^{-1} s^{-1} or higher, 10^7 M^{-1} s^{-1} or higher, as measured, e.g., at 25°C or at 37°C.

As noted also above, in some of the above embodiments, the VISTA-ECD protein is hVISTA-ECD or is a portion of hVISTA-ECD such as, for example, the IgV domain. In some of the above embodiments, the Ab may bind specifically to an epitope comprising amino acids 20-95 of SEQ ID NO:2. In some of the above embodiments, the Ab may bind specifically to an epitope comprising amino acids 20-70 of SEQ ID NO:2. In some of the above embodiments, the Ab may bind specifically to an epitope comprising amino acids 35-95 of SEQ ID NO:2. In some of the above embodiments, the Ab may bind specifically to an epitope comprising amino acids 35-70 of SEQ ID NO:2. In some embodiments above, the epitope is a three-dimensional epitope that comprises not only one of the above portions of SEQ ID NO:2 from residues 20-95, 20-70, 35-95, or 35-70, but also another portion of SEQ ID NO:2, such as residues 95-105 of SEQ ID NO:2. In certain embodiments, an Ab binds to the epitope of hVISTA to which an Ab described in WO2015/097536 binds. For example, an Ab may compete or cross-compete for binding to hVISTA with an Ab disclosed in WO2015/097536. In certain embodiments, an Ab binds to a conformational epitope of human VISTA. In certain embodiments, an Ab binds to a conformational epitope that comprises, or is present within, residues 103-111 of SEQ ID NO: 2 and 136-146 of SEQ ID NO:2 for human VISTA. In certain embodiments, an Ab binds to a conformational epitope that comprises, or is present within, residues 24-36, 54-65, and 100-102 of SEQ ID NO:2 for human VISTA. In certain embodiments, an Ab binds to a conformational epitope that comprises amino acid residues in the FG loop of human VISTA. In some embodiments, an Ab binds to a polypeptide comprising amino acid residues 35 to 127 and/or 37-125 of SEQ ID NO: 2. In some embodiments, an Ab binds to a VISTA ECD polypeptide or portion thereof comprising amino acid residues 350-127 of SEQ ID NO: 2, but the antibody does not bind or binds with reduced affinity to the VISTA ECD polyptide or portion thereof comprising an amino acid substitution, wherein the substitution (1) is substitution of one of the following amino acid residues: T35, Y37, K38, T39, Y41, R54, T61, F62, Q63, L65, H66, L67, H68, H69, F97, L115, V117, I119, H121, H122, S124, E125, R127 and SEQ ID

NO: 2 or (2) is a substitution of one of the following amino acid residues: Y37, T39, R54, F62, Q63, H66, L115, V117, I119, S124, or E125. In some embodiments, an anti-VISTA antibody has the same binding characteristics (or significantly the same binding characteristics) as an antibody described herein, e.g., as set forth in the Examples.

Some of the above antibodies may show differential binding affinity for VISTA-ECD proteins depending upon pH. Certain Abs specifically binding to a VISTA-ECD protein in acidic conditions, e.g., at pH 6.5 or less, also specifically bind the VISTA-ECD protein at neutral and/or alkaline pH with similar affinity (i.e. they are "pan binders"). For example, some such Abs may bind to the VISTA-ECD protein with a K_D of 10^{-7} M or less at both pH 6.5 and at pH 7.0 (at a constant temperature, e.g., of 25°C or at 37°C) such that the K_D at pH 6.5 is within 1.5-fold of the K_D at pH 7.0. Some such Abs may bind to the VISTA-ECD protein with a K_D of 10^{-8} M or less at both pH 6.5 and at pH 7.0 (at a constant temperature, e.g., of 25°C or at 37°C) such that the K_D at pH 6.5 is within 1.5-fold of the K_D at pH 7.0. Some such Abs may bind to hVISTA-ECD with a K_D of 10^{-8} M or less at both pH 6.5 and at pH 7.0 (at a constant temperature, e.g., of 25°C or at 37°C) such that the K_D at pH 6.5 is within 1.5-fold of the K_D at pH 7.0.

Certain Abs specifically binding to a VISTA-ECD protein in acidic conditions, e.g., at pH 6.5 or less, may bind the VISTA-ECD protein at neutral, physiological, and/or alkaline conditions with lower affinity ("pH sensitive binders" or "pH sensitive Abs"). Certain Abs specifically binding to a VISTA-ECD protein in acidic conditions, e.g., at pH 6.5 or less, may have non significant, e.g., nearly undetectable, binding to the VISTA-ECD protein in neutral, physiological and/or alkaline conditions. For example, in some embodiments, Abs may bind to the VISTA-ECD protein with a K_D of 10^{-8} M or less at pH 6.5 and with a K_D of more than 10^{-8} M at pH 7.0 and/or pH 7.4. In some such embodiments, Abs may bind to the VISTA-ECD protein with a K_D of 10^{-8} M or less at pH 6.5 and with a K_D at pH 7.0 and/or pH 7.4 that is more than 1.5-fold higher than that at pH 6.5. In certain embodiments, a pH sensitive Ab is provided that specifically binds to the VISTA-ECD protein with a K_D that is at least 1.5 fold, 2 fold, 5 fold, 10 fold, 20 fold, 50 fold, 100 fold, 300 fold, 500 fold, 1000 fold, or 5000 fold lower at pH 6.5 than at pH 7.0 (at a constant temperature, e.g., of 25°C or at 37°C). For example, in some cases an Ab binds to the VISTA-ECD protein with a K_D that

is at least 1.5 fold, 2 fold, 5 fold, 10 fold, 20 fold, 50 fold, 100 fold, 300 fold, 500 fold, 1000 fold, or 5000 fold less at pH 6.0, relative to pH 7.0 and/or pH 7.4 or higher (at a constant temperature, e.g., of 25°C or at 37°C).

In certain embodiments, an Ab specifically binds to a VISTA-ECD protein with a k_{off} that is lower in acidic conditions relative to that in neutral, physiological, or alkaline conditions. In certain embodiments, an Ab is provided that binds to the VISTA-ECD protein in acidic conditions with a k_{off} that is at least 1.5 fold, 2 fold, 5 fold, 10 fold, 20 fold, 50 fold, 100 fold, or 1000 fold lower at pH 6.5 than the k_{off} at pH 7.0 and/or pH 7.4, as measured, e.g., at 25°C or at 37°C. In other words, the off-rate is slower at acidic pH than at neutral pH. For example, in some embodiments, an Ab specifically binds to a VISTA-ECD protein with a k_{off} rate that is at least 1.5 fold, 2 fold, 5 fold, 10 fold, 20 fold, 50 fold, 100 fold or 1000 fold lower at pH 6.0, relative to pH 7.0 and/or pH 7.4, as measured, e.g., at 25°C or at 37°C. In certain embodiments, an Ab is provided that binds to the VISTA-ECD protein with a k_{off} that is at least 1.5 fold, 2 fold, 5 fold, 10 fold, 20 fold, 50 fold, 100 fold or 1000 fold lower at pH 6.5 than the K_{off} at pH 7.4, as measured, e.g., at 25°C or at 37°C. In some embodiments, an Ab specifically binds to a VISTA-ECD protein with a k_{off} rate that is at least 1.5 fold, 2 fold, 5 fold, 10 fold, 20 fold, 50 fold, 100 fold or 1000 fold lower at pH 6.0, relative to pH 7.4, as measured, e.g., at 25°C or at 37°C. In certain embodiments, an Ab is provided that binds to the VISTA-ECD protein with a k_{off} that is at least 1.5 fold, 2 fold, 5 fold, 10 fold, 20 fold, 50 fold, 100 fold or 1000 fold lower at pH 6.0-6.5 than the k_{off} at pH 7.0-7.4, as measured, e.g., at 25°C or at 37°C.

In certain embodiments, an Ab that specifically binds to a VISTA-ECD protein with a k_{on} that is higher in acidic conditions relative to neutral, physiological, or alkaline conditions. In certain embodiments, an Ab is provided that binds to a VISTA-ECD protein in acidic conditions with a k_{on} that is at least 2 fold, 5 fold, 10 fold, 20 fold, 50 fold, 100 fold, or 1000 fold higher at pH 6.5 than the k_{on} at pH 7.0 and/or pH 7.4, as measured, e.g., at 25°C or at 37°C. For example, in some embodiments, an Ab specifically binds to aVISTA-ECD protein with a k_{on} that is at least 2 fold, 5 fold, 10 fold, 20 fold, 50 fold, 100 fold or 1000 fold higher at pH 6.0 than at pH 7.0 and/or pH 7.4, as measured, e.g., at 25°C or at 37°C.

In certain embodiments, an Ab specifically binds to a VISTA-ECD protein at a pH at which at least one histidine residue, e.g., His 98 in SEQ ID NO: 1, is protonated. In certain embodiments, an Ab specifically binds to a VISTA-ECD protein at a pH at which most histidine residues in the ECD are protonated, which is expected to be pH 6.5 or less, e.g., between pH 6.0 and pH 6.5.

Also encompassed herein are Abs that specifically bind to a VISTA-ECD protein with an affinity that is higher at neutral, physiological, or alkaline pH relative to acidic pH, provided that the affinity of binding at acidic pH remains high. For example, Abs may bind to the VISTA-ECD protein with a K_D of 10^{-8} M or less at both pH 6.5 and pH 7.0 even though the Abs bind with a K_D that is at least 1.5 fold, 2 fold, 5 fold, 10 fold, 20 fold, 50 fold, 100 fold, 300 fold, 500 fold, 1000 fold lower at pH 7.0 than at pH 6.5.

Also encompassed herein are Abs that share one or more of the above properties of this section. The above properties, such as particular K_D's, k_{off}'s, k_{on}'s, specific epitopes are not to be treated in isolation. Thus, an Ab may bind to an epitope comprising one of the regions of SEQ ID NO:2 described above, and also may have pan binding or pH sensitive or pH selective binding properties as described above, as shown by one or more of the behaviors of its K_D, k_{off}, or k_{on} at different pH's.

In any of the above embodiments, the Ab may be, for example, a full length antibody (i.e., comprising a full length heavy chain (with or without C-terminal lysine) and a full length light chain), or an antigen binding fragment such as a Fab fragment, a Fab' fragment, $(Fab')_2$ fragment, an scFv fragment, an Fv fragment, or the Ab may be a chimeric, humanized, or human antibody, or the Ab may be a bispecific or multispecific antibody.

Determining how well an Ab binds to a VISTA-ECD protein at a given pH can be conducted using several different methods. For example, by surface plasmon resonance (SPR), such as by BIACORE® assays. An exemplary SPR assay comprises capturing one or several antibodies on a CM4 sensor chip with immobilized capture reagent (e .g., using Biacore® anti-human Fc capture kit, GE Healthcare catalog # BR-1008-39, or Biacore® anti-mouse capture kit, GE Healthcare catalog #BR-1008-39), and flowing VISTA antigen as analyte in a concentration series to determine binding kinetics and affinities in a running buffer with desired pH. In one embodiment, VISTA is injected at two to five concentrations

in the range of 0.1 nM to 500 nM (e.g., 0.1 nM, 1 nM, 10 nM, 100 nM, 500 nM) with a flow rate of 30 uL/min, up to four minutes association time and up to ten minutes dissociation time. Between binding cycles, the capture surface is regenerated following the manufacturer's instructions for the respective capture kit. All data is double-referenced using a reference flow cell and a blank injection. Data with simple 1:1 kinetics are fitted to a Langmuir binding model with mass transfer using the Biacore® T200 evaluation software. The SPR methods described in the Examples may also be used.

The affinity of an Ab for a VISTA ECD polypeptide may be determined using cells expressing a VISTA ECD polypeptide, PSGL-1 or heparan sulfate on their surface, which method comprises flow cytometry, and wherein binding of an Ab to cell bound VISTA-ECD is determined at a given pH, e.g., pH 6.5 or less. An exemplary flow cytometry assay comprises the following: 293T cells or other cells ectopically expressing hVISTA ECD are re-suspended in a buffer consisting of HBSS + 1% BSA adjusted to the desirable pH, e.g., pH 6.0 with MES or pH 7.4 with HEPES. Abs (e.g., human IgG) against hVISTA are serially diluted from approximately 20 μg/mLand incubated with the re-suspended cells for 30 minutes at 4 °C. Cells are then washed twice with the same buffers, maintaining the desired pH, e.g., pH at 6.0 or 7.4, and incubated with a fluorophore-conjugated secondary antibody that recognizes the primary antibody (e.g., human IgG) and is stable at reduced pH. Cells are then washed as before and acquired immediately, without fixation, on a BD Fortessa or other flow cytometer. The affinity of an Ab for a VISTA ECD polypeptide may be determined as described in the Examples.

In certain embodiments, Abs that bind to hVISTA ECD block binding of hVISTA to its binding partner (e.g., a VISTA receptor), e.g., on cells. Inhibition or blocking may be 100% or at least 99%, 95%, 90%, 85%, 80%, 75%, or 50%. In certain embodiments, an Ab binds to a VISTA-ECD protein at acidic pH, e.g., pH 6.5 or less, and inhibits binding of VISTA to its binding partner by at least 50%, such as by at least 75%, 80%, 85%, 90%, 95%, or 100%. In certain embodiments, an Ab specifically binds to the VISTA-ECD protein and inhibits binding of VISTA to its binding partner by at least 50% at a pH that is less than pH 7.0. In certain embodiments, an Ab specifically binds to a VISTA-ECD protein and inhibits binding of VISTA to its binding partner by at least 50% at a pH that is less than pH 6.8. In

certain embodiments, an Ab specifically binds to a VISTA-ECD protein and inhibits binding of VISTA to its binding partner by at least 50% at a pH that is less than pH 6.5. In certain embodiments, an Ab specifically binds to a VISTA-ECD protein and inhibits binding of VISTA to its binding partner by at least 50% at a pH that is less than pH 6.3. In certain embodiments, an Ab specifically binds to a VISTA-ECD protein and inhibits binding of VISTA to its binding partner by at least 50% at a pH that is less than pH 6.0. In certain embodiments, an Ab specifically binds to a VISTA-ECD protein and inhibits binding of VISTA to its binding partner by at least 50% at a pH that is less than pH 5.8. In certain embodiments, an Ab specifically binds to a VISTA-ECD protein and inhibits binding of VISTA to its binding partner by at least 50% at a pH that is less than pH 5.5. In certain embodiments, an Ab specifically binds to a VISTA-ECD protein and inhibits binding of VISTA to its binding partner by at least 50% at a pH that is less than pH 5.3. In certain embodiments, an Ab specifically binds to a VISTA-ECD protein and inhibits binding of VISTA to its binding partner by at least 50% at a pH that is less than pH 5.0.

Certain Abs specifically bind to a VISTA-ECD protein and inhibits binding of VISTA to its binding partner by at least 50% at a pH within a range of pH 5.0-pH 7.0. Certain Abs specifically bind to a VISTA-ECD protein and inhibits binding of VISTA to its binding partner by at least 50% at a pH within a range of pH 5.0- pH 6.5. Certain Abs specifically bind to a VISTA-ECD protein and inhibits binding of VISTA to its binding partner by at least 50% at a pH within a range of pH 5.0-pH 6.0. Certain Abs specifically bind to a VISTA-ECD protein and inhibits binding of VISTA to its binding partner by at least 50% at a pH within a range of pH 5.5- pH 7.0. Certain Abs specifically bind to a VISTA-ECD protein and inhibits binding of VISTA to its binding partner by at least 50% at a pH within a range of pH 5.5-pH 6.5. Certain Abs specifically bind to a VISTA-ECD protein and inhibits binding of VISTA to its binding partner by at least 50% at a pH within a range of pH 6.0-6.5. Inhibition of binding can be determined as described in the Examples.

A VISTA binding partner may be PSGL-1, such as human PSGL-1. Sequences of human PSGL-1 isoforms are provided as SEQ ID NOs: 3-10 herein. It may also be heparan sulfate proteoglycans, e.g., present on certain cells.

Inhibition of binding to a VISTA binding partner can be determined by measuring the inhibition of binding of VISTA (or VISTA ECD or VISTA IgV domain or VISTA positive cells), to cells to which VISTA binds, e.g., T cells (e.g., CD4+T cells, CD8+ T cells, either activated or not), NK cells, or other cells to which VISTA binds, in the presence and absence of the antibody. An exemplary experiment that can be used to determine if an antibody inhibits the binding of VISTA to its binding partner or T cells expressing a binding partner is a flow cytometry assay, e.g., an assay that comprises the following: human peripheral blood mononuclear cells from donor blood, buffy coat, or leukopak are re-suspended in a buffer consisting of HBSS + 1% BSA adjusted to the desirable pH, e.g., pH 6.0 with MES or pH 7.4 with HEPES. The cells are then incubated for 30 minutes at 4 °C with 20 μg/mL recombinant chimeric protein consisting of hVISTA ECD fused to human IgG1 Fc (VISTA-Fc) and with varying concentrations of candidate VISTA blocking antibodies or control antibodies. Cells are then washed twice in the same buffers, maintaining the desired pH, e.g., pH at 6.0 or 7.4, and incubated for another 30 minutes at 4 °C with a fluorophore-conjugated secondary antibody that recognizes VISTA-Fc, but not the candidate blocking antibodies or control antibodies, and is stable at reduced pH. Cells are then washed as before and acquired immediately, without fixation, on a BD Fortessa or other flow cytometer. Inhibition of binding can be determined, e.g., as described in the Examples.

In specific embodiments, the Abs described herein may trigger or enhance an immune response, such as an antigen-specific immune response. In certain embodiments, the Abs stimulate T cell activity, particularly at acidic pH such as is found in tumor microenvironments. Stimulation of T cell activity can be measured, e.g., in a mixed lymphocyte reaction (MLR) or in an in vitro assay with an antigen presenting cell (natural or artificial) and T cells. Stimulation of T cell activity can also be measured using, e.g., the Jurkat assay described in the Examples.

In specific embodiments, the Abs described herein inhbit cell adhesion, which can be measured as described in the Examples.

Activity of anti-VISTA Abs can also be shown in monocyte assays, ADCC assays, and ADCP assays, particularly at acidic pH such as is found in tumor microenvironments.

In certain embodiments, anti-VISTA Abs inhibit tumor growth in a tumor model, e.g., a human VISTA knock-in tumor model.

As shown in the Examples herein, recycling of an anti-VISTA Ab in the endosome such as to enhance the pharmacokinetic (PK) properties, i.e., half-life, of the antibody, requires the anti-VISTA antibody to bind to VISTA in acidic conditions. Thus, anti-VISTA Abs that bind at low pH to VISTA, e.g., a pH of 6.5 or lower, as further described herein, are also expected to have a longer acceptable half-life relative to a VISTA antibody that does not bind to VISTA at acidic pH

Exemplary hVISTA-ECD binding Abs

Provided herein are Abs that bind preferentially to hVISTA (ECD) at acidic pH (e.g., in acidic conditions) relative to physiological pH or neutral pH.

In certain embodiments, an anti-hVISTA Ab comprises a heavy chain variable region ("VH") comprising VH CDR1, CDR2 and/or CDR3 of any of the anti-hVISTA Abs provided herein. In certain embodiments, an anti-hVISTA Ab comprises a VH comprising the VH CDR1, CDR2 and CDR3 of any of the anti-hVISTA Abs provided herein. In certain embodiments, an anti-hVISTA Ab comprises a VH comprising VH CDR1, CDR2 and/or CDR3 of P1-061029 or P1-061015 or progeny thereof, such as P1-061029, P1-068757, P1-068759, P1-068761, P1-068763, P1-068765, P1-068767, P1-068769, P1-068771, P1-068773, P1-068775, P1-069059, P1-069061, P1-069063, P1-069065, P1-069067, P1-069069, P1-069071, P1-069073, P1-069075, P1-069077, P1-061015, P1-068736, P1-068738, P1-068740, P1-068742, P1-068744, P1-068766, P1-068748, P1-068750, P1-068752 P1-068754, P1-068761_E55A, P1-068761_H100G, P1-068761_E56N, P1-068761_E55A_E56N, P1-068761_E30D, P1-068761_E30D_E55A, P1-068761_E56N_H100G, P1-068761_E30D_H100G, P1-068761_E30D_E56N, P1-068761_E100fF, P1-068761_E55A_E100fF, P1-068761_H100G_E100fF, P1-068761_E30D_E100fF, P1-068761_E56N_E100fF, P1-068761_E32Y, P1-068761_E32Y_E55A, P1-068761_E32Y_E56N, P1-068761_E30D_E32Y, P1-068761_E32Y_H100G, P1-068761_E32Y_E100fF, P1-068767_D52N_D102V, P1-068767_D52N, P1-068767_D52N_E55A, P1-068767_E55A_D102V, P1-068767_D102V,

P1-068767_E55A, P1-068767_E30D_D52N, P1-068767_E30D_D102V, P1-068767_E30D, P1-068767_E30D_E55A, P1-068767_E100fF_D102V, P1-068767_E55A_E100fF, P1-068767_D52N_E100fF, P1-068767_E100fF, or P1-068767_E30D_E100fF. The VH CDR1, CDR2, and CDR3 of each of these species comprise amino acid positions 26-35 (VH CDR1), 50-66 (VH CDR2), and 99-110 (VH CDR3), of the VH sequences for each of the above antibody species provided in the sequence table below. The CDRs are also underlined and in bold on each of the VH sequences for the above antibody species provided in the Sequence Table below.

In certain embodiments, an anti-hVISTA Ab comprises a VH comprising VH CDR1, CDR2 and CDR3 of any of the anti-hVISTA Abs provided herein. In certain embodiments, an anti-hVISTA Ab comprises a VH comprising VH CDR1, CDR2 and CDR3 of one of P1-061029, P1-068757, P1-068759, P1-068761, P1-068763, P1-068765, P1-068767, P1-068769, P1-068771, P1-068773, P1-068775, P1-069059, P1-069061, P1-069063, P1-069065, P1-069067, P1-069069, P1-069071, P1-069073, P1-069075, P1-069077, P1-061015, P1-068736, P1-068738, P1-068740, P1-068742, P1-068744, P1-068766, P1-068748, P1-068750, P1-068752 P1-068754, P1-068761_E55A, P1-068761_H100G, P1-068761_E56N, P1-068761_E55A_E56N, P1-068761_E30D, P1-068761_E30D_E55A, P1-068761_E56N_H100G, P1-068761_E30D_H100G, P1-068761_E30D_E56N, P1-068761_E100fF, P1-068761_E55A_E100fF, P1-068761_H100G_E100fF, P1-068761_E30D_E100fF, P1-068761_E56N_E100fF, P1-068761_E32Y, P1-068761_E32Y_E55A, P1-068761_E32Y_E56N, P1-068761_E30D_E32Y, P1-068761_E32Y_H100G, P1-068761_E32Y_E100fF, P1-068767_D52N_D102V, P1-068767_D52N, P1-068767_D52N_E55A, P1-068767_E55A_D102V, P1-068767_D102V, P1-068767_E55A, P1-068767_E30D_D52N, P1-068767_E30D_D102V, P1-068767_E30D, P1-068767_E30D_E55A, P1-068767_E100fF_D102V, P1-068767_E55A_E100fF, P1-068767_D52N_E100fF, P1-068767_E100fF, or P1-068767_E30D_E100fF. The VL CDR1, CDR2, and CDR3 of each of these species comprise amino acid positions 24-35 (VL CDR1), 51-57 (VL CDR2), and 90-98 (VL CDR3), of the VL sequences for each of the above antibody species provided in the Sequence Table below. The CDRs are also underlined and in bold on each of those sequences.

In certain embodiments, an anti-hVISTA Ab comprises a VH comprising VH CDR1, CDR2 and/or CDR3 of any of the anti-hVISTA Abs provided herein and a VL comprising CDR1, CDR2 and/or CDR3 of any of the anti-hVISTA Abs provided herein. In certain embodiments, an anti-hVISTA Ab comprises a VH comprising VH CDR1, CDR2 and CDR3 of any of the anti-hVISTA Abs provided herein and a VLcomprising CDR1, CDR2 and CDR3 of any of the anti-hVISTA Abs provided herein. In certain embodiments, an anti-hVISTA Ab comprises a VH comprising VH CDR1, CDR2 and/or CDR3 of P1-061029 or P1-061015 or progeny thereof, such as P1-061029, P1-068757, P1-068759, P1-068761, P1-068763, P1-068765, P1-068767, P1-068769, P1-068771, P1-068773, P1-068775, P1-069059, P1-069061, P1-069063, P1-069065, P1-069067, P1-069069, P1-069071, P1-069073, P1-069075, P1-069077, P1-061015, P1-068736, P1-068738, P1-068740, P1-068742, P1-068744, P1-068766, P1-068748, P1-068750, P1-068752 P1-068754, P1-068761_E55A, P1-068761_H100G, P1-068761_E56N, P1-068761_E55A_E56N, P1-068761_E30D, P1-068761_E30D_E55A, P1-068761_E56N_H100G, P1-068761_E30D_H100G, P1-068761_E30D_E56N, P1-068761_E100fF, P1-068761_E55A_E100fF, P1-068761_H100G_E100fF, P1-068761_E30D_E100fF, P1-068761_E56N_E100fF, P1-068761_E32Y, P1-068761_E32Y_E55A, P1-068761_E32Y_E56N, P1-068761_E30D_E32Y, P1-068761_E32Y_H100G, P1-068761_E32Y_E100fF, P1-068767_D52N_D102V, P1-068767_D52N, P1-068767_D52N_E55A, P1-068767_E55A_D102V, P1-068767_D102V, P1-068767_E55A, P1-068767_E30D_D52N, P1-068767_E30D_D102V, P1-068767_E30D, P1-068767_E30D_E55A, P1-068767_E100fF_D102V, P1-068767_E55A_E100fF, P1-068767_D52N_E100fF, P1-068767_E100fF, or P1-068767_E30D_E100fF and a VL comprising VL CDR1, CDR2 and CDR3 of P1-061029 or P1-061015 or progeny thereof, such as P1-061029, P1-068757, P1-068759, P1-068761, P1-068763, P1-068765, P1-068767, P1-068769, P1-068771, P1-068773, P1-068775, P1-069059, P1-069061, P1-069063, P1-069065, P1-069067, P1-069069, P1-069071, P1-069073, P1-069075, P1-069077, P1-061015, P1-068736, P1-068738, P1-068740, P1-068742, P1-068744, P1-068766, P1-068748, P1-068750, P1-068752 P1-068754, P1-068761_E55A, P1-068761_H100G, P1-068761_E56N, P1-068761_E55A_E56N, P1-068761_E30D, P1-068761_E30D_E55A, P1-

068761_E56N_H100G, P1-068761_E30D_H100G, P1-068761_E30D_E56N, P1-068761_E100fF, P1-068761_E55A_E100fF, P1-068761_H100G_E100fF, P1-068761_E30D_E100fF, P1-068761_E56N_E100fF, P1-068761_E32Y, P1-068761_E32Y_E55A, P1-068761_E32Y_E56N, P1-068761_E30D_E32Y, P1-068761_E32Y_H100G, P1-068761_E32Y_E100fF, P1-068767_D52N_D102V, P1-068767_D52N, P1-068767_D52N_E55A, P1-068767_E55A_D102V, P1-068767_D102V, P1-068767_E55A, P1-068767_E30D_D52N, P1-068767_E30D_D102V, P1-068767_E30D, P1-068767_E30D_E55A, P1-068767_E100fF_D102V, P1-068767_E55A_E100fF, P1-068767_D52N_E100fF, P1-068767_E100fF, or P1-068767_E30D_E100fF.

In some embodiments, an anti-hVISTA Ab may comprise:

(a) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-061029 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-061029;

(b) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-061015 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-061015;

(c) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068757 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068757;

(d) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068759 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068759;

(e) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068761 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068761;

(f) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068763 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068763;

(g) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068765 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068765;

(h) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068767 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068767;

(i) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068769 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068769;

(j) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068771 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068771;

(k) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068773 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068773;

(l) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068775 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068775;

(m) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-069059 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-069059;

(n) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-069061 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-069061;

(o) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-069063 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-069063;

(p) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-069065 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-069065;

(q) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-069067 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-069067;

(r) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-069069 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-069069;

(s) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-069071 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-069071;

(t) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-069073 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-069073;

(u) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-069075 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-069075;

(v) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-069077 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-069077;

(w) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068736 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068736;

(x) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068738 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068738;

(y) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068740 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068740;

(z) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068742 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068742;

(aa) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068744 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068744;

(bb) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068746 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068746;

(cc) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068748 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068748;

(dd) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068750 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068750;

(ee) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068752 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068752;

(ff) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068754 and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068754;

(gg) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068761_E55A and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068761_E55A;

(hh) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068761_H100G and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068761_H100G;

(ii) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068761_E56N and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068761_E56N;

(jj) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068761_E55A_E56N and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068761_E55A_E56N;

(kk) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068761_E30D and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068761_E30D;

(ll) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068761_E30D_E55A and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068761_E30D_E55A;

(mm) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068761_E56N_H100G and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068761_E56N_H100G;

(nn) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068761_E30D_H100G and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068761_E30D_H100G;

(oo) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068761_E30D_E56N and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068761_E30D_E56N;

(pp) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068761_E100fF and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068761_E100fF;

(qq) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068761_E55A_E100fF and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068761_E55A_E100fF;

(rr) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068761_H100G_E100fF and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068761_H100G_E100fF;

(ss) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068761_E30D_E100fF and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068761_E30D_E100fF;

(tt) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068761_E56N_E100fF and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068761_E56N_E100fF;

(uu) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068761_E32Y and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068761_E32Y;

(vv) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068761_E32Y_E55A and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068761_E32Y_E55A;

(ww) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068761_E32Y_E56N and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068761_E32Y_E56N;

(xx) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068761_E30D_E32Y and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068761_E30D_E32Y;

(yy) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068761_E32Y_H100G and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068761_E32Y_H100G;

(zz) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068761_E32Y_E100fF and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068761_E32Y_E100fF;

(aaa) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068767_D52N_D102V and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068767_D52N_D102V;

(bbb) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068767_D52N and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068767_D52N;

(ccc) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068767_D52N_E55A and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068767_D52N_E55A;

(ddd) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068767_E55A_D102V and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068767_E55A_D102V;

(eee) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068767_D102V and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068767_D102V;

(fff) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068767_E55A and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068767_E55A;

(ggg) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068767_E30D_D52N and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068767_E30D_D52N;

(hhh) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068767_E30D_D102V and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068767_E30D_D102V;

(iii)a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068767_E30D and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068767_E30D;

(jjj)a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068767_E30D_E55A and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068767_E30D_E55A;

(kkk) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068767_E100fF_D102V and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068767_E100fF_D102V;

(lll) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068767_E55A_E100fF and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068767_E55A_E100fF;

(mmm) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068767_D52N_E100fF and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068767_D52N_E100fF;

(nnn) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068767_E100fF and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068767_E100fF;

(ooo) a VH comprising the amino acid sequence of the VH CDR1, CDR2 and CDR3 of P1-068767_E30D_E100fF and a VL comprising the VL CDR1, CDR2 and CDR3 of P1-068767_E30D_E100fF.

Again, the Sequence Table below provides the heavy and light chain variable region sequences and full length heavy and light chain sequences of the antibodies listed above with an IgG1.3 heavy chain constant region (unless a different HC constant region is noted in the table) and notes the locations of their VH CDR1, CDR2, and CDR3 and VL CDR1, CDR2, and CDR3 by amino acid residue and with bolding and underlining of the CDRs in each VH and VL sequence. Thus, for example, VH CDR1 of P1-061029 comprises amino acids 26-35 of SEQ ID NO: 67, while VH CDR2 comprises amino acids 50-66 of SEQ ID NO: 67, and VH CDR3 comprises amino acids 99-110 of SEQ ID NO: 67, and so forth, as noted by the bolded and underlined amino acids of SEQ ID NO: 67 shown in the Sequence Table.

In certain embodiments, an anti-hVISTA Ab comprises a VH comprising the amino acid sequence of the VH of any of the anti-hVISTA Abs provided herein. The individual VH sequences for particular antibody species provided herein are listed in the Sequence Table. In certain embodiments, an anti-hVISTA Ab comprises a VH comprising the amino acid sequence of the VH of P1-061029 or P1-061015 or progeny thereof, such as P1-061029, P1-068757, P1-068759, P1-068761, P1-068763, P1-068765, P1-068767, P1-068769, P1-068771, P1-068773, P1-068775, P1-069059, P1-069061, P1-069063, P1-069065, P1-069067, P1-069069, P1-069071, P1-069073, P1-069075, P1-069077, P1-061015, P1-068736, P1-068738, P1-068740, P1-068742, P1-068744, P1-068766, P1-068748, P1-068750, P1-068752 P1-068754, P1-068761_E55A, P1-068761_H100G, P1-068761_E56N, P1-068761_E55A_E56N, P1-068761_E30D, P1-068761_E30D_E55A, P1-068761_E56N_H100G, P1-068761_E30D_H100G, P1-068761_E30D_E56N, P1-068761_E100fF, P1-068761_E55A_E100fF, P1-068761_H100G_E100fF, P1-068761_E30D_E100fF, P1-068761_E56N_E100fF, P1-068761_E32Y, P1-

068761_E32Y_E55A, P1-068761_E32Y_E56N, P1-068761_E30D_E32Y, P1-068761_E32Y_H100G, P1-068761_E32Y_E100fF, P1-068767_D52N_D102V, P1-068767_D52N, P1-068767_D52N_E55A, P1-068767_E55A_D102V, P1-068767_D102V, P1-068767_E55A, P1-068767_E30D_D52N, P1-068767_E30D_D102V, P1-068767_E30D, P1-068767_E30D_E55A, P1-068767_E100fF_D102V, P1-068767_E55A_E100fF, P1-068767_D52N_E100fF, P1-068767_E100fF, or P1-068767_E30D_E100fF. In certain embodiments, an anti-hVISTA Ab comprises a VH CDR1, CDR2, and CDR3 comprising the amino acid sequences of the VH CDRs of any of the anti-hVISTA Abs provided herein and comprises a VH that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH of any of the anti-hVISTA Abs provided herein. In certain embodiments, an anti-hVISTA Ab comprises a VH comprising an amino acid sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of the VH of P1-061029, P1-068757, P1-068759, P1-068761, P1-068763, P1-068765, P1-068767, P1-068769, P1-068771, P1-068773, P1-068775, P1-069059, P1-069061, P1-069063, P1-069065, P1-069067, P1-069069, P1-069071, P1-069073, P1-069075, P1-069077, P1-061015, P1-068736, P1-068738, P1-068740, P1-068742, P1-068744, P1-068766, P1-068748, P1-068750, P1-068752 P1-068754, P1-068761_E55A, P1-068761_H100G, P1-068761_E56N, P1-068761_E55A_E56N, P1-068761_E30D, P1-068761_E30D_E55A, P1-068761_E56N_H100G, P1-068761_E30D_H100G, P1-068761_E30D_E56N, P1-068761_E100fF, P1-068761_E55A_E100fF, P1-068761_H100G_E100fF, P1-068761_E30D_E100fF, P1-068761_E56N_E100fF, P1-068761_E32Y, P1-068761_E32Y_E55A, P1-068761_E32Y_E56N, P1-068761_E30D_E32Y, P1-068761_E32Y_H100G, P1-068761_E32Y_E100fF, P1-068767_D52N_D102V, P1-068767_D52N, P1-068767_D52N_E55A, P1-068767_E55A_D102V, P1-068767_D102V, P1-068767_E55A, P1-068767_E30D_D52N, P1-068767_E30D_D102V, P1-068767_E30D, P1-068767_E30D_E55A, P1-068767_E100fF_D102V, P1-068767_E55A_E100fF, P1-068767_D52N_E100fF, P1-068767_E100fF, or P1-068767_E30D_E100fF. In certain embodiments, an anti-hVISTA Ab comprises a VH consisting of the amino acid sequence of

the VH of any of the anti-hVISTA Abs provided herein. In certain embodiments, an anti-hVISTA Ab comprises a VH that consists of the amino acid sequence of the VH of P1-061029 or P1-061015 or progeny thereof, such as P1-061029, P1-068757, P1-068759, P1-068761, P1-068763, P1-068765, P1-068767, P1-068769, P1-068771, P1-068773, P1-068775, P1-069059, P1-069061, P1-069063, P1-069065, P1-069067, P1-069069, P1-069071, P1-069073, P1-069075, P1-069077, P1-061015, P1-068736, P1-068738, P1-068740, P1-068742, P1-068744, P1-068766, P1-068748, P1-068750, P1-068752 P1-068754, P1-068761_E55A, P1-068761_H100G, P1-068761_E56N, P1-068761_E55A_E56N, P1-068761_E30D, P1-068761_E30D_E55A, P1-068761_E56N_H100G, P1-068761_E30D_H100G, P1-068761_E30D_E56N, P1-068761_E100fF, P1-068761_E55A_E100fF, P1-068761_H100G_E100fF, P1-068761_E30D_E100fF, P1-068761_E56N_E100fF, P1-068761_E32Y, P1-068761_E32Y_E55A, P1-068761_E32Y_E56N, P1-068761_E30D_E32Y, P1-068761_E32Y_H100G, P1-068761_E32Y_E100fF, P1-068767_D52N_D102V, P1-068767_D52N, P1-068767_D52N_E55A, P1-068767_E55A_D102V, P1-068767_D102V, P1-068767_E55A, P1-068767_E30D_D52N, P1-068767_E30D_D102V, P1-068767_E30D, P1-068767_E30D_E55A, P1-068767_E100fF_D102V, P1-068767_E55A_E100fF, P1-068767_D52N_E100fF, P1-068767_E100fF, or P1-068767_E30D_E100fF.

In certain embodiments, an anti-hVISTA Ab comprises a VL comprising the amino acid sequence of the VL of any of the anti-hVISTA Abs provided herein. In certain embodiments, an anti-hVISTA Ab comprises a VL comprising the amino acid sequence of the VL of P1-061029 or P1-061015 or progeny thereof, such as P1-061029, P1-068757, P1-068759, P1-068761, P1-068763, P1-068765, P1-068767, P1-068769, P1-068771, P1-068773, P1-068775, P1-069059, P1-069061, P1-069063, P1-069065, P1-069067, P1-069069, P1-069071, P1-069073, P1-069075, P1-069077, P1-061015, P1-068736, P1-068738, P1-068740, P1-068742, P1-068744, P1-068766, P1-068748, P1-068750, P1-068752 P1-068754, P1-068761_E55A, P1-068761_H100G, P1-068761_E56N, P1-068761_E55A_E56N, P1-068761_E30D, P1-068761_E30D_E55A, P1-068761_E56N_H100G, P1-068761_E30D_H100G, P1-068761_E30D_E56N, P1-068761_E100fF, P1-068761_E55A_E100fF, P1-068761_H100G_E100fF, P1-

068761_E30D_E100fF, P1-068761_E56N_E100fF, P1-068761_E32Y, P1-068761_E32Y_E55A, P1-068761_E32Y_E56N, P1-068761_E30D_E32Y, P1-068761_E32Y_H100G, P1-068761_E32Y_E100fF, P1-068767_D52N_D102V, P1-068767_D52N, P1-068767_D52N_E55A, P1-068767_E55A_D102V, P1-068767_D102V, P1-068767_E55A, P1-068767_E30D_D52N, P1-068767_E30D_D102V, P1-068767_E30D, P1-068767_E30D_E55A, P1-068767_E100fF_D102V, P1-068767_E55A_E100fF, P1-068767_D52N_E100fF, P1-068767_E100fF, or P1-068767_E30D_E100fF. In certain embodiments, an anti-hVISTA Ab comprises a VL CDR1, CDR2, and CDR3 comprising the amino acid sequences of the VL CDRs of any of the anti-hVISTA Abs provided herein and comprises a VL that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VL of any of the anti-hVISTA Abs provided herein. In certain embodiments, an anti-hVISTA Ab comprises a VL comprising an amino acid sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the amino acid sequence of the VL of P1-061029, P1-068757, P1-068759, P1-068761, P1-068763, P1-068765, P1-068767, P1-068769, P1-068771, P1-068773, P1-068775, P1-069059, P1-069061, P1-069063, P1-069065, P1-069067, P1-069069, P1-069071, P1-069073, P1-069075, P1-069077, P1-061015, P1-068736, P1-068738, P1-068740, P1-068742, P1-068744, P1-068766, P1-068748, P1-068750, P1-068752 P1-068754, P1-068761_E55A, P1-068761_H100G, P1-068761_E56N, P1-068761_E55A_E56N, P1-068761_E30D, P1-068761_E30D_E55A, P1-068761_E56N_H100G, P1-068761_E30D_H100G, P1-068761_E30D_E56N, P1-068761_E100fF, P1-068761_E55A_E100fF, P1-068761_H100G_E100fF, P1-068761_E30D_E100fF, P1-068761_E56N_E100fF, P1-068761_E32Y, P1-068761_E32Y_E55A, P1-068761_E32Y_E56N, P1-068761_E30D_E32Y, P1-068761_E32Y_H100G, P1-068761_E32Y_E100fF, P1-068767_D52N_D102V, P1-068767_D52N, P1-068767_D52N_E55A, P1-068767_E55A_D102V, P1-068767_D102V, P1-068767_E55A, P1-068767_E30D_D52N, P1-068767_E30D_D102V, P1-068767_E30D, P1-068767_E30D_E55A, P1-068767_E100fF_D102V, P1-068767_E55A_E100fF, P1-068767_D52N_E100fF, P1-068767_E100fF, or P1-068767_E30D_E100fF. In certain

embodiments, an anti-hVISTA Ab comprises a VL consisting of the amino acid sequence of the VL of any of the anti-hVISTA Abs provided herein. In certain embodiments, an anti-hVISTA Ab comprises a VL that consists of the amino acid sequence of the VL of P1-061029 or P1-061015 or progeny thereof, such as P1-061029, P1-068757, P1-068759, P1-068761, P1-068763, P1-068765, P1-068767, P1-068769, P1-068771, P1-068773, P1-068775, P1-069059, P1-069061, P1-069063, P1-069065, P1-069067, P1-069069, P1-069071, P1-069073, P1-069075, P1-069077, P1-061015, P1-068736, P1-068738, P1-068740, P1-068742, P1-068744, P1-068766, P1-068748, P1-068750, P1-068752 P1-068754, P1-068761_E55A, P1-068761_H100G, P1-068761_E56N, P1-068761_E55A_E56N, P1-068761_E30D, P1-068761_E30D_E55A, P1-068761_E56N_H100G, P1-068761_E30D_H100G, P1-068761_E30D_E56N, P1-068761_E100fF, P1-068761_E55A_E100fF, P1-068761_H100G_E100fF, P1-068761_E30D_E100fF, P1-068761_E56N_E100fF, P1-068761_E32Y, P1-068761_E32Y_E55A, P1-068761_E32Y_E56N, P1-068761_E30D_E32Y, P1-068761_E32Y_H100G, P1-068761_E32Y_E100fF, P1-068767_D52N_D102V, P1-068767_D52N, P1-068767_D52N_E55A, P1-068767_E55A_D102V, P1-068767_D102V, P1-068767_E55A, P1-068767_E30D_D52N, P1-068767_E30D_D102V, P1-068767_E30D, P1-068767_E30D_E55A, P1-068767_E100fF_D102V, P1-068767_E55A_E100fF, P1-068767_D52N_E100fF, P1-068767_E100fF, or P1-068767_E30D_E100fF.

In certain embodiments, an anti-hVISTA Ab comprises a VH comprising the amino acid sequence of the VH of any of the anti-hVISTA Abs provided herein and comprises a VL comprising the amino acid sequence of the VL of any of the anti-hVISTA Abs provided herein. In certain of these embodiments, an anti-hVISTA Ab comprises a VH comprising the amino acid sequence of the VH of P1-061029 or P1-061015 or progeny thereof, such as P1-061029, P1-068757, P1-068759, P1-068761, P1-068763, P1-068765, P1-068767, P1-068769, P1-068771, P1-068773, P1-068775, P1-069059, P1-069061, P1-069063, P1-069065, P1-069067, P1-069069, P1-069071, P1-069073, P1-069075, P1-069077, P1-061015, P1-068736, P1-068738, P1-068740, P1-068742, P1-068744, P1-068766, P1-068748, P1-068750, P1-068752 P1-068754, P1-068761_E55A, P1-068761_H100G, P1-068761_E56N, P1-068761_E55A_E56N, P1-068761_E30D, P1-068761_E30D_E55A, P1-

068761_E56N_H100G, P1-068761_E30D_H100G, P1-068761_E30D_E56N, P1-068761_E100fF, P1-068761_E55A_E100fF, P1-068761_H100G_E100fF, P1-068761_E30D_E100fF, P1-068761_E56N_E100fF, P1-068761_E32Y, P1-068761_E32Y_E55A, P1-068761_E32Y_E56N, P1-068761_E30D_E32Y, P1-068761_E32Y_H100G, P1-068761_E32Y_E100fF, P1-068767_D52N_D102V, P1-068767_D52N, P1-068767_D52N_E55A, P1-068767_E55A_D102V, P1-068767_D102V, P1-068767_E55A, P1-068767_E30D_D52N, P1-068767_E30D_D102V, P1-068767_E30D, P1-068767_E30D_E55A, P1-068767_E100fF_D102V, P1-068767_E55A_E100fF, P1-068767_D52N_E100fF, P1-068767_E100fF, or P1-068767_E30D_E100fF; and a VL comprising the amino acid sequence of the VL of P1-061029 or P1-061015. In certain embodiments, an anti-hVISTA Ab comprises a VH and a VL comprising the amino acid sequences of the VH and VL of P1-061029 or P1-061015 or progeny thereof, such as P1-061029, P1-068757, P1-068759, P1-068761, P1-068763, P1-068765, P1-068767, P1-068769, P1-068771, P1-068773, P1-068775, P1-069059, P1-069061, P1-069063, P1-069065, P1-069067, P1-069069, P1-069071, P1-069073, P1-069075, P1-069077, P1-061015, P1-068736, P1-068738, P1-068740, P1-068742, P1-068744, P1-068766, P1-068748, P1-068750, P1-068752 P1-068754, P1-068761_E55A, P1-068761_H100G, P1-068761_E56N, P1-068761_E55A_E56N, P1-068761_E30D, P1-068761_E30D_E55A, P1-068761_E56N_H100G, P1-068761_E30D_H100G, P1-068761_E30D_E56N, P1-068761_E100fF, P1-068761_E55A_E100fF, P1-068761_H100G_E100fF, P1-068761_E30D_E100fF, P1-068761_E56N_E100fF, P1-068761_E32Y, P1-068761_E32Y_E55A, P1-068761_E32Y_E56N, P1-068761_E30D_E32Y, P1-068761_E32Y_H100G, P1-068761_E32Y_E100fF, P1-068767_D52N_D102V, P1-068767_D52N, P1-068767_D52N_E55A, P1-068767_E55A_D102V, P1-068767_D102V, P1-068767_E55A, P1-068767_E30D_D52N, P1-068767_E30D_D102V, P1-068767_E30D, P1-068767_E30D_E55A, P1-068767_E100fF_D102V, P1-068767_E55A_E100fF, P1-068767_D52N_E100fF, P1-068767_E100fF, or P1-068767_E30D_E100fF.

In certain embodiments, an anti-hVISTA Ab comprises a VH CDR1, CDR2, and CDR3 comprising the amino acid sequences of the VH CDRs of any of the anti-hVISTA Abs provided herein as well as a VL CDR1, CDR2, and CDR3 comprising the amino acid

sequences of the VL CDRs of any of the anti-hVISTA Abs provided herein, and also comprises a VH and a VL that are each at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the corresponding VH and VL of any of the anti-hVISTA Abs provided herein. In certain embodiments, an anti-hVISTA Ab comprises all 6 CDRs of an anti-hVISTA Ab provided herein and also comprises VH and VL amino acid sequences that are each at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the corresponding VH and VL of the anti-hVISTA Ab, such as the VH and VL of P1-061029 or P1-061015 or progeny thereof, such as P1-061029, P1-068757, P1-068759, P1-068761, P1-068763, P1-068765, P1-068767, P1-068769, P1-068771, P1-068773, P1-068775, P1-069059, P1-069061, P1-069063, P1-069065, P1-069067, P1-069069, P1-069071, P1-069073, P1-069075, P1-069077, P1-061015, P1-068736, P1-068738, P1-068740, P1-068742, P1-068744, P1-068766, P1-068748, P1-068750, P1-068752 P1-068754, P1-068761_E55A, P1-068761_H100G, P1-068761_E56N, P1-068761_E55A_E56N, P1-068761_E30D, P1-068761_E30D_E55A, P1-068761_E56N_H100G, P1-068761_E30D_H100G, P1-068761_E30D_E56N, P1-068761_E100fF, P1-068761_E55A_E100fF, P1-068761_H100G_E100fF, P1-068761_E30D_E100fF, P1-068761_E56N_E100fF, P1-068761_E32Y, P1-068761_E32Y_E55A, P1-068761_E32Y_E56N, P1-068761_E30D_E32Y, P1-068761_E32Y_H100G, P1-068761_E32Y_E100fF, P1-068767_D52N_D102V, P1-068767_D52N, P1-068767_D52N_E55A, P1-068767_E55A_D102V, P1-068767_D102V, P1-068767_E55A, P1-068767_E30D_D52N, P1-068767_E30D_D102V, P1-068767_E30D, P1-068767_E30D_E55A, P1-068767_E100fF_D102V, P1-068767_E55A_E100fF, P1-068767_D52N_E100fF, P1-068767_E100fF, or P1-068767_E30D_E100fF. In certain embodiments, an anti-hVISTA Ab comprises a VH and a VL consisting of the amino acid sequence of the VH and VL of any of the anti-hVISTA Abs provided herein. In certain embodiments, an anti-hVISTA Ab comprises a VH and a VL that each consist of the amino acid sequences of the VH and VL of P1-061029 or P1-061015 or progeny thereof, such as P1-061029, P1-068757, P1-068759, P1-068761, P1-068763, P1-068765, P1-068767, P1-068769, P1-068771, P1-068773, P1-068775, P1-069059, P1-069061, P1-069063, P1-

069065, P1-069067, P1-069069, P1-069071, P1-069073, P1-069075, P1-069077, P1-061015, P1-068736, P1-068738, P1-068740, P1-068742, P1-068744, P1-068766, P1-068748, P1-068750, P1-068752 P1-068754, P1-068761_E55A, P1-068761_H100G, P1-068761_E56N, P1-068761_E55A_E56N, P1-068761_E30D, P1-068761_E30D_E55A, P1-068761_E56N_H100G, P1-068761_E30D_H100G, P1-068761_E30D_E56N, P1-068761_E100fF, P1-068761_E55A_E100fF, P1-068761_H100G_E100fF, P1-068761_E30D_E100fF, P1-068761_E56N_E100fF, P1-068761_E32Y, P1-068761_E32Y_E55A, P1-068761_E32Y_E56N, P1-068761_E30D_E32Y, P1-068761_E32Y_H100G, P1-068761_E32Y_E100fF, P1-068767_D52N_D102V, P1-068767_D52N, P1-068767_D52N_E55A, P1-068767_E55A_D102V, P1-068767_D102V, P1-068767_E55A, P1-068767_E30D_D52N, P1-068767_E30D_D102V, P1-068767_E30D, P1-068767_E30D_E55A, P1-068767_E100fF_D102V, P1-068767_E55A_E100fF, P1-068767_D52N_E100fF, P1-068767_E100fF, or P1-068767_E30D_E100fF.

An anti-hVISTA Ab may comprise:

(a) a VH comprising the amino acid sequence of the VH of P1-061029 and a VL comprising the amino acid sequence of the VL of P1-061029;

(b) a VH comprising the amino acid sequence of the VH of P1-061015 and a VL comprising the amino acid sequence of the VL of P1-061015;

(c) a VH comprising the amino acid sequence of the VH of P1-068757 and a VL comprising the amino acid sequence of the VL of P1-068757;

(d) a VH comprising the amino acid sequence of the VH of P1-068759 and a VL comprising the amino acid sequence of the VL of P1-068759;

(e) a VH comprising the amino acid sequence of the VH of P1-068761 and a VL comprising the amino acid sequence of the VL of P1-068761;

(f) a VH comprising the amino acid sequence of the VH of P1-068763 and a VL comprising the amino acid sequence of the VL of P1-068763;

(g) a VH comprising the amino acid sequence of the VH of P1-068765 and a VL comprising the amino acid sequence of the VL of P1-068765;

(h) a VH comprising the amino acid sequence of the VH of P1-068767 and a VL comprising the amino acid sequence of the VL of P1-068767;

(i) a VH comprising the amino acid sequence of the VH of P1-068769 and a VL comprising the amino acid sequence of the VL of P1-068769;

(j) a VH comprising the amino acid sequence of the VH of P1-068771 and a VL comprising the amino acid sequence of the VL of P1-068771;

(k) a VH comprising the amino acid sequence of the VH of P1-068773 and a VL comprising the amino acid sequence of the VL of -068773;

(l) a VH comprising the amino acid sequence of the VH of P1-068775 and a VL comprising the amino acid sequence of the VL of P1-068775;

(m)a VH comprising the amino acid sequence of the VH of P1-069059 and a VL comprising the amino acid sequence of the VL of P1-069059;

(n) a VH comprising the amino acid sequence of the VH of P1-069061 and a VL comprising the amino acid sequence of the VL of P1-069061;

(o) a VH comprising the amino acid sequence of the VH of P1-069063 and a VL comprising the amino acid sequence of the VL of P1-069063;

(p) a VH comprising the amino acid sequence of the VH of P1-069065 and a VL comprising the amino acid sequence of the VL of P1-069065;

(q) a VH comprising the amino acid sequence of the VH of P1-069067 and a VL comprising the amino acid sequence of the VL of P1-069067;

(r) a VH comprising the amino acid sequence of the VH of P1-069069 and a VL comprising the amino acid sequence of the VL of P1-069069;

(s) a VH comprising the amino acid sequence of the VH of P1-069071 and a VL comprising the amino acid sequence of the VL of P1-069071;

(t) a VH comprising the amino acid sequence of the VH of P1-069073 and a VL comprising the amino acid sequence of the VL of P1-069073;

(u) a VH comprising the amino acid sequence of the VH of P1-069075 and a VL comprising the amino acid sequence of the VL of P1-069075;

(v) a VH comprising the amino acid sequence of the VH of P1-069077 and a VL comprising the amino acid sequence of the VL of P1-069077;

(w) a VH comprising the amino acid sequence of the VH of P1-068736 and a VL comprising the amino acid sequence of the VL of P1-068736;

(x) a VH comprising the amino acid sequence of the VH of P1-068738 and a VL comprising the amino acid sequence of the VL of P1-068738;

(y) a VH comprising the amino acid sequence of the VH of P1-068740 and a VL comprising the amino acid sequence of the VL of P1-068740;

(z) a VH comprising the amino acid sequence of the VH of P1-068742 and a VL comprising the amino acid sequence of the VL of P1-068742;

(aa) a VH comprising the amino acid sequence of the VH of P1-068744 and a VL comprising the amino acid sequence of the VL of P1-068744;

(bb) a VH comprising the amino acid sequence of the VH f P1-068746 and a VL comprising the amino acid sequence of the VL of P1-068746;

(cc) a VH comprising the amino acid sequence of the VH of P1-068748 and a VL comprising the amino acid sequence of the VL of P1-068748;

(dd) a VH comprising the amino acid sequence of the VH of P1-068750 and a VL comprising the amino acid sequence of the VL of P1-068750;

(ee) a VH comprising the amino acid sequence of the VH of P1-068752 and a VL comprising the amino acid sequence of the VL of P1-068752;

(ff) a VH comprising the amino acid sequence of the VH of P1-068754 and a VL comprising the amino acid sequence of the VL of P1-068754;

(gg) a VH comprising the amino acid sequence of the VH of P1-068761_E55A and a VL comprising the amino acid sequence of the VL of P1-068761_E55A;

(hh) a VH comprising the amino acid sequence of the VH of P1-068761_H100G and a VL comprising the amino acid sequence of the VL of P1-068761_H100G;

(ii) a VH comprising the amino acid sequence of the VH of P1-068761_E56N and a VL comprising the amino acid sequence of the VL of P1-068761_E56N;

(jj) a VH comprising the amino acid sequence of the VH of P1-068761_E55A_E56N and a VL comprising the amino acid sequence of the VL of P1-068761_E55A_E56N;

(kk) a VH comprising the amino acid sequence of the VH of P1-068761_E30D and a VL comprising the amino acid sequence of the VL of P1-068761_E30D;

(ll) a VH comprising the amino acid sequence of the VH of P1-068761_E30D_E55A and a VL comprising the amino acid sequence of the VL of P1-068761_E30D_E55A;

(mm) a VH comprising the amino acid sequence of the VH of P1-068761_E56N_H100G and a VL comprising the amino acid sequence of the VL of P1-068761_E56N_H100G;

(nn) a VH comprising the amino acid sequence of the VH of P1-068761_E30D_H100G and a VL comprising the amino acid sequence of the VL of P1-068761_E30D_H100G;

(oo) a VH comprising the amino acid sequence of the VH of P1-068761_E30D_E56N and a VL comprising the amino acid sequence of the VL of P1-068761_E30D_E56N;

(pp) a VH comprising the amino acid sequence of the VH of P1-068761_E100fF and a VL comprising the amino acid sequence of the VL of P1-068761_E100fF;

(qq) a VH comprising the amino acid sequence of the VH of P1-068761_E55A_E100fF and a VL comprising the amino acid sequence of the VL of P1-068761_E55A_E100fF;

(rr) a VH comprising the amino acid sequence of the VH of P1-068761_H100G_E100fF and a VL comprising the amino acid sequence of the VL of P1-068761_H100G_E100fF;

(ss) a VH comprising the amino acid sequence of the VH of P1-068761_E30D_E100fF and a VL comprising the amino acid sequence of the VL of P1-068761_E30D_E100fF;

(tt) a VH comprising the amino acid sequence of the VH of P1-068761_E56N_E100fF and a VL comprising the amino acid sequence of the VL of P1-068761_E56N_E100fF;

(uu) a VH comprising the amino acid sequence of the VH of P1-068761_E32Y and a VL comprising the amino acid sequence of the VL of P1-068761_E32Y;

(vv) a VH comprising the amino acid sequence of the VH of P1-068761_E32Y_E55A and a VL comprising the amino acid sequence of the VL of P1-068761_E32Y_E55A;

(ww) a VH comprising the amino acid sequence of the VH of P1-068761_E32Y_E56N and a VL comprising the amino acid sequence of the VL of P1-068761_E32Y_E56N;

(xx) a VH comprising the amino acid sequence of the VH of P1-068761_E30D_E32Y and a VL comprising the amino acid sequence of the VL of P1-068761_E30D_E32Y;

(yy) a VH comprising the amino acid sequence of the VH of P1-068761_E32Y_H100G and a VL comprising the amino acid sequence of the VL of P1-068761_E32Y_H100G;

(zz) a VH comprising the amino acid sequence of the VH of P1-068761_E32Y_E100fF and a VL comprising the amino acid sequence of the VL of P1-068761_E32Y_E100fF;

(aaa) a VH comprising the amino acid sequence of the VH of P1-068767_D52N_D102V and a VL comprising the amino acid sequence of the VL of P1-068767_D52N_D102V;

(bbb) a VH comprising the amino acid sequence of the VH of P1-068767_D52N and a VL comprising the amino acid sequence of the VL of P1-068767_D52N;

(ccc) a VH comprising the amino acid sequence of the VH of P1-068767_D52N_E55A and a VL comprising the amino acid sequence of the VL of P1-068767_D52N_E55A;

(ddd) a VH comprising the amino acid sequence of the VH of P1-068767_E55A_D102V and a VL comprising the amino acid sequence of the VL of P1-068767_E55A_D102V;

(eee) a VH comprising the amino acid sequence of the VH of P1-068767_D102V and a VL comprising the amino acid sequence of the VL of P1-068767_D102V;

(fff) a VH comprising the amino acid sequence of the VH of P1-068767_E55A and a VL comprising the amino acid sequence of the VL of P1-068767_E55A;

(ggg) a VH comprising the amino acid sequence of the VH of P1-068767_E30D_D52N and a VL comprising the amino acid sequence of the VL of P1-068767_E30D_D52N;

(hhh) a VH comprising the amino acid sequence of the VH of P1-068767_E30D_D102V and a VL comprising the amino acid sequence of the VL of P1-068767_E30D_D102V;

(iii) a VH comprising the amino acid sequence of the VH of P1-068767_E30D and a VL comprising the amino acid sequence of the VL of P1-068767_E30D;

(jjj)a VH comprising the amino acid sequence of the VH of P1-068767_E30D_E55A and a VL comprising the amino acid sequence of the VL of P1-068767_E30D_E55A;

(kkk) a VH comprising the amino acid sequence of the VH of P1-068767_E100fF_D102V and a VL comprising the amino acid sequence of the VL of P1-068767_E100fF_D102V;

(lll) a VH comprising the amino acid sequence of the VH of P1-068767_E55A_E100fF and a VL comprising the amino acid sequence of the VL of P1-068767_E55A_E100fF;

(mmm) a VH comprising the amino acid sequence of the VH of P1-068767_D52N_E100fF and a VL comprising the amino acid sequence of the VL of P1-068767_D52N_E100fF;

(nnn) a VH comprising the amino acid sequence of the VH of P1-068767_E100fF and a VL comprising the amino acid sequence of the VL of P1-068767_E100fF; or

(ooo) a VH comprising the amino acid sequence of the VH of P1-068767_E30D_E100fF and a VL comprising the amino acid sequence of the VL of P1-068767_E30D_E100fF.

An anti-hVISTA Ab may comprise:

(a) a VH comprising the VH CDRs of the VH of P1-061029 and a VL comprising the VL CDRs of P1-061029 and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-061029;

(b) a VH comprising the VH CDRs of the VH of P1-061015 and a VL comprising the VL CDRs of P1-061015 and VH and VL amino acid sequences that are at least 90%, at

least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-061015;

(c) a VH comprising the VH CDRs of the VH of P1-068757 and a VL comprising the VL CDRs of P1-068757 and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068757;

(d) a VH comprising the VH CDRs of the VH of P1-068759 and a VL comprising the VL CDRs of P1-068759 and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068759;

(e) a VH comprising the VH CDRs of the VH of P1-068761 and a VL comprising the VL CDRs of P1-068761 and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068761;

(f) a VH comprising the VH CDRs of the VH of P1-068763 and a VL comprising the VL CDRs of P1-068763 and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068763;

(g) a VH comprising the VH CDRs of the VH of P1-068765 and a VL comprising the VL CDRs of P1-068765 and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068765;

(h) a VH comprising the VH CDRs of the VH of P1-068767 and a VL comprising the VL CDRs of P1-068767 and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068767;

(i) a VH comprising the VH CDRs of the VH of P1-068769 and a VL comprising the VL CDRs of P1-068769 and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068769;

(j) a VH comprising the VH CDRs of the VH of P1-068771 and a VL comprising the VL CDRs of P1-068771 and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068771;

(k) a VH comprising the VH CDRs of the VH of P1-068773 and a VL comprising the VL CDRs of P1-068773 and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068773;

(l) a VH comprising the VH CDRs of the VH of P1-068775 and a VL comprising the VL CDRs of P1-068775 and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068775;

(m) a VH comprising the VH CDRs of the VH of P1-069059 and a VL comprising the VL CDRs of P1-069059 and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-069059;

(n) a VH comprising the VH CDRs of the VH of P1-069061 and a VL comprising the VL CDRs of P1-069061 and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-069061;

(o) a VH comprising the VH CDRs of the VH of P1-069063 and a VL comprising the VL CDRs of P1-069063 and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-069063;

(p) a VH comprising the VH CDRs of the VH of P1-069065 and a VL comprising the VL CDRs of P1-069065 and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-069065;

(q) a VH comprising the VH CDRs of the VH of P1-069067 and a VL comprising the VL CDRs of P1-069067 and VH and VL amino acid sequences that are at least 90%, at

least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-069067;

(r) a VH comprising the VH CDRs of the VH of P1-069069 and a VL comprising the VL CDRs of P1-069069 and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-069069;

(s) a VH comprising the VH CDRs of the VH of P1-069071 and a VL comprising the VL CDRs of P1-069071 and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-069071;

(t) a VH comprising the VH CDRs of the VH of P1-069073 and a VL comprising the VL CDRs of P1-069073 and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-069073;

(u) a VH comprising the VH CDRs of the VH of P1-069075 and a VL comprising the VL CDRs of P1-069075 and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-069075;

(v) a VH comprising the VH CDRs of the VH of P1-069077 and a VL comprising the VL CDRs of P1-069077 and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-069077;

(w) a VH comprising the VH CDRs of the VH of P1-068736 and a VL comprising the VL CDRs of P1-068736 and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068736;

(x) a VH comprising the VH CDRs of the VH of P1-068738 and a VL comprising the VL CDRs of P1-068738 and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068738;

(y) a VH comprising the VH CDRs of the VH of P1-068740 and a VL comprising the VL CDRs of P1-068740 and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068740;

(z) a VH comprising the VH CDRs of the VH of P1-068742 and a VL comprising the VL CDRs of P1-068742 and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068742;

(aa) a VH comprising the VH CDRs of the VH of P1-068744 and a VL comprising the VL CDRs of P1-068744 and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068744;

(bb) a VH comprising the VH CDRs of the VH of P1-068746 and a VL comprising the VL CDRs of P1-068746 and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068746;

(cc) a VH comprising the VH CDRs of the VH of P1-068748 and a VL comprising the VL CDRs of P1-068748 and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068748;

(dd) a VH comprising the VH CDRs of the VH of P1-068750 and a VL comprising the VL CDRs of P1-068750 and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068750;

(ee) a VH comprising the VH CDRs of the VH of P1-068752 and a VL comprising the VL CDRs of P1-068752 and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068752;

(ff) a VH comprising the VH CDRs of the VH of P1-068754 and a VL comprising the VL CDRs of P1-068754 and VH and VL amino acid sequences that are at least 90%, at

least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068754;

(gg) a VH comprising the VH CDRs of the VH of P1-068761_E55A and a VL comprising the VL CDRs of P1-068761_E55A and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068761_E55A;

(hh) a VH comprising the VH CDRs of the VH of P1-068761_H100G and a VL comprising the VL CDRs of P1-068761_H100G and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068761_H100G;

(ii) a VH comprising the VH CDRs of the VH of P1-068761_E56N and a VL comprising the VL CDRs of P1-068761_E56N and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068761_E56N;

(jj) a VH comprising the VH CDRs of the VH of P1-068761_E55A_E56N and a VL comprising the VL CDRs of P1-068761_E55A_E56N and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068761_E55A_E56N;

(kk) a VH comprising the VH CDRs of the VH of P1-068761_E30D and a VL comprising the VL CDRs of P1-068761_E30D and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068761_E30D;

(ll) a VH comprising the VH CDRs of the VH of P1-068761_E30D_E55A and a VL comprising the VL CDRs of P1-068761_E30D_E55A and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%,

at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068761_E30D_E55A;

(mm) a VH comprising the VH CDRs of the VH of P1-068761_E56N_H100G and a VL comprising the VL CDRs of P1-068761_E56N_H100G and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068761_E56N_H100G;

(nn) a VH comprising the VH CDRs of the VH of P1-068761_E30D_H100G and a VL comprising the VL CDRs of P1-068761_E30D_H100G and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068761_E30D_H100G;

(oo) a VH comprising the VH CDRs of the VH of P1-068761_E30D_E56N and a VL comprising the VL CDRs of P1-068761_E30D_E56N and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068761_E30D_E56N;

(pp) a VH comprising the VH CDRs of the VH of P1-068761_E100fF and a VL comprising the VL CDRs of P1-068761_E100fF and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068761_E100fF;

(qq) a VH comprising the VH CDRs of the VH of P1-068761_E55A_E100fF and a VL comprising the VL CDRs of P1-068761_E55A_E100fF and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068761_E55A_E100fF;

(rr) a VH comprising the VH CDRs of the VH of P1-068761_H100G_E100fF and a VL comprising the VL CDRs of P1-068761_H100G_E100fF and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%,

at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068761_H100G_E100fF;

(ss)a VH comprising the VH CDRs of the VH of P1-068761_E30D_E100fF and a VL comprising the VL CDRs of P1-068761_E30D_E100fF and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068761_E30D_E100fF;

(tt) a VH comprising the VH CDRs of the VH of P1-068761_E56N_E100fF and a VL comprising the VL CDRs of P1-068761_E56N_E100fF and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068761_E56N_E100fF;

(uu) a VH comprising the VH CDRs of the VH of P1-068761_E32Y and a VL comprising the VL CDRs of P1-068761_E32Y and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068761_E32Y;

(vv) a VH comprising the VH CDRs of the VH of P1-068761_E32Y_E55A and a VL comprising the VL CDRs of P1-068761_E32Y_E55A and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068761_E32Y_E55A;

(ww) a VH comprising the VH CDRs of the VH of P1-068761_E32Y_E56N and a VL comprising the VL CDRs of P1-068761_E32Y_E56N and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068761_E32Y_E56N;

(xx) a VH comprising the VH CDRs of the VH of P1-068761_E30D_E32Y and a VL comprising the VL CDRs of P1-068761_E30D_E32Y and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least

94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068761_E30D_E32Y;

(yy) a VH comprising the VH CDRs of the VH of P1-068761_E32Y_H100G and a VL comprising the VL CDRs of P1-068761_E32Y_H100G and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068761_E32Y_H100G;

(zz) a VH comprising the VH CDRs of the VH of P1-068761_E32Y_E100fF and a VL comprising the VL CDRs of P1-068761_E32Y_E100fF and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068761_E32Y_E100fF;

(aaa) a VH comprising the VH CDRs of the VH of P1-068767_D52N_D102V and a VL comprising the VL CDRs of P1-068767_D52N_D102V and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068767_D52N_D102V;

(bbb) a VH comprising the VH CDRs of the VH of P1-068767_D52N and a VL comprising the VL CDRs of P1-068767_D52N and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068767_D52N;

(ccc) a VH comprising the VH CDRs of the VH of P1-068767_D52N_E55A and a VL comprising the VL CDRs of P1-068767_D52N_E55A and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068767_D52N_E55A;

(ddd) a VH comprising the VH CDRs of the VH of P1-068767_E55A_D102V and a VL comprising the VL CDRs of P1-068767_E55A_D102V and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least

94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068767_E55A_D102V;

(eee) a VH comprising the VH CDRs of the VH of P1-068767_D102V and a VL comprising the VL CDRs of P1-068767_D102V and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068767_D102V;

(fff) a VH comprising the VH CDRs of the VH of P1-068767_E55A and a VL comprising the VL CDRs of P1-068767_E55A and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068767_E55A;

(ggg) a VH comprising the VH CDRs of the VH of P1-068767_E30D_D52N and a VL comprising the VL CDRs of P1-068767_E30D_D52N and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068767_E30D_D52N;

(hhh) a VH comprising the VH CDRs of the VH of P1-068767_E30D_D102V and a VL comprising the VL CDRs of P1-068767_E30D_D102V and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068767_E30D_D102V;

(iii)a VH comprising the VH CDRs of the VH of P1-068767_E30D and a VL comprising the VL CDRs of P1-068767_E30D and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068767_E30D;

(jjj)a VH comprising the VH CDRs of the VH of P1-068767_E30D_E55A and a VL comprising the VL CDRs of P1-068767_E30D_E55A and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%,

at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068767_E30D_E55A;

(kkk) a VH comprising the VH CDRs of the VH of P1-068767_E100fF_D102V and a VL comprising the VL CDRs of P1-068767_E100fF_D102V and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068767_E100fF_D102V;

(lll) a VH comprising the VH CDRs of the VH of P1-068767_E55A_E100fF and a VL comprising the VL CDRs of P1-068767_E55A_E100fF and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068767_E55A_E100fF;

(mmm) a VH comprising the VH CDRs of the VH of P1-068767_D52N_E100fF and a VL comprising the VL CDRs of P1-068767_D52N_E100fF and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068767_D52N_E100fF;

(nnn) a VH comprising the VH CDRs of the VH of P1-068767_E100fF and a VL comprising the VL CDRs of P1-068767_E100fF and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068767_E100fF; or

(ooo) a VH comprising the VH CDRs of the VH of P1-068767_E30D_E100fF and a VL comprising the VL CDRs of P1-068767_E30D_E100fF and VH and VL amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the VH and VL of P1-068767_E30D_E100fF.

An anti-hVISTA Ab may comprise:

(a) a VH consisting of the amino acid sequence of the VH of P1-061029 and a VL consisting of the VL of P1-061029;

(b) a VH consisting of the amino acid sequence of the VH of P1-061015 and a VL consisting of the VL of P1-061015;

(c) a VH consisting of the amino acid sequence of the VH of P1-068757 and a VL consisting of the VL of P1-068757;

(d) a VH consisting of the amino acid sequence of the VH of P1-068759 and a VL consisting of the VL of P1-068759;

(e) a VH consisting of the amino acid sequence of the VH of P1-068761 and a VL consisting of the VL of P1-068761;

(f) a VH consisting of the amino acid sequence of the VH of P1-068763 and a VL consisting of the VL of P1-068763;

(g) a VH consisting of the amino acid sequence of the VH of P1-068765 and a VL consisting of the VL of P1-068765;

(h) a VH consisting of the amino acid sequence of the VH of P1-068767 and a VL consisting of the VL of P1-068767;

(i) a VH consisting of the amino acid sequence of the VH of P1-068769 and a VL consisting of the VL of P1-068769;

(j) a VH consisting of the amino acid sequence of the VH of P1-068771 and a VL consisting of the VL of P1-068771;

(k) a VH consisting of the amino acid sequence of the VH of P1-068773 and a VL consisting of the VL of P1-068773;

(l) a VH consisting of the amino acid sequence of the VH of P1-068775 and a VL consisting of the VL of P1-068775;

(m) a VH consisting of the amino acid sequence of the VH of P1-069059 and a VL consisting of the VL of P1-069059;

(n) a VH consisting of the amino acid sequence of the VH of P1-069061 and a VL consisting of the VL of P1-069061;

(o) a VH consisting of the amino acid sequence of the VH of P1-069063 and a VL consisting of the VL of P1-069063;

(p) a VH consisting of the amino acid sequence of the VH of P1-069065 and a VL consisting of the VL of P1-069065;

(q) a VH consisting of the amino acid sequence of the VH of P1-069067 and a VL consisting of the VL of P1-069067;

(r) a VH consisting of the amino acid sequence of the VH of P1-069069 and a VL consisting of the VL of P1-069069;

(s) a VH consisting of the amino acid sequence of the VH of P1-069071 and a VL consisting of the VL of P1-069071;

(t) a VH consisting of the amino acid sequence of the VH of P1-069073 and a VL consisting of the VL of P1-069073;

(u) a VH consisting of the amino acid sequence of the VH of P1-069075 and a VL consisting of the VL of P1-069075;

(v) a VH consisting of the amino acid sequence of the VH of P1-069077 and a VL consisting of the VL of P1-069077;

(w) a VH consisting of the amino acid sequence of the VH of P1-068736 and a VL consisting of the VL of P1-068736;

(x) a VH consisting of the amino acid sequence of the VH of P1-068738 and a VL consisting of the VL of P1-068738;

(y) a VH consisting of the amino acid sequence of the VH of P1-068740 and a VL consisting of the VL of P1-068740;

(z) a VH consisting of the amino acid sequence of the VH of P1-068742 and a VL consisting of the VL of P1-068742;

(aa) a VH consisting of the amino acid sequence of the VH of P1-068744 and a VL consisting of the VL of P1-068744;

(bb) a VH consisting of the amino acid sequence of the VH f P1-068746 and a VL consisting of the VL of P1-068746;

(cc) a VH consisting of the amino acid sequence of the VH of P1-068748 and a VL consisting of the VL of P1-068748;

(dd) a VH consisting of the amino acid sequence of the VH of P1-068750 and a VL consisting of the VL of P1-068750;

(ee) a VH consisting of the amino acid sequence of the VH of P1-068752 and a VL consisting of the VL of P1-068752;

(ff) a VH consisting of the amino acid sequence of the VH of P1-068754 and a VL consisting of the VL of P1-068754;

(gg) a VH consisting of the amino acid sequence of the VH of P1-068761_E55A and a VL consisting of the amino acid sequence of the VL of P1-068761_E55A;

(hh) a VH consisting of the amino acid sequence of the VH of P1-068761_H100G and a VL consisting of the amino acid sequence of the VL of P1-068761_H100G;

(ii) a VH consisting of the amino acid sequence of the VH of P1-068761_E56N and a VL consisting of the amino acid sequence of the VL of P1-068761_E56N;

(jj) a VH consisting of the amino acid sequence of the VH of P1-068761_E55A_E56N and a VL consisting of the amino acid sequence of the VL of P1-068761_E55A_E56N;

(kk) a VH consisting of the amino acid sequence of the VH of P1-068761_E30D and a VL consisting of the amino acid sequence of the VL of P1-068761_E30D;

(ll) a VH consisting of the amino acid sequence of the VH of P1-068761_E30D_E55A and a VL consisting of the amino acid sequence of the VL of P1-068761_E30D_E55A;

(mm) a VH consisting of the amino acid sequence of the VH of P1-068761_E56N_H100G and a VL consisting of the amino acid sequence of the VL of P1-068761_E56N_H100G;

(nn) a VH consisting of the amino acid sequence of the VH of P1-068761_E30D_H100G and a VL consisting of the amino acid sequence of the VL of P1-068761_E30D_H100G;

(oo) a VH consisting of the amino acid sequence of the VH of P1-068761_E30D_E56N and a VL consisting of the amino acid sequence of the VL of P1-068761_E30D_E56N;

(pp) a VH consisting of the amino acid sequence of the VH of P1-068761_E100fF and a VL consisting of the amino acid sequence of the VL of P1-068761_E100fF;

(qq) a VH consisting of the amino acid sequence of the VH of P1-068761_E55A_E100fF and a VL consisting of the amino acid sequence of the VL of P1-068761_E55A_E100fF;

(rr) a VH consisting of the amino acid sequence of the VH of P1-068761_H100G_E100fF and a VL consisting of the amino acid sequence of the VL of P1-068761_H100G_E100fF;

(ss) a VH consisting of the amino acid sequence of the VH of P1-068761_E30D_E100fF and a VL consisting of the amino acid sequence of the VL of P1-068761_E30D_E100fF;

(tt) a VH consisting of the amino acid sequence of the VH of P1-068761_E56N_E100fF and a VL consisting of the amino acid sequence of the VL of P1-068761_E56N_E100fF;

(uu) a VH consisting of the amino acid sequence of the VH of P1-068761_E32Y and a VL consisting of the amino acid sequence of the VL of P1-068761_E32Y;

(vv) a VH consisting of the amino acid sequence of the VH of P1-068761_E32Y_E55A and a VL consisting of the amino acid sequence of the VL of P1-068761_E32Y_E55A;

(ww) a VH consisting of the amino acid sequence of the VH of P1-068761_E32Y_E56N and a VL consisting of the amino acid sequence of the VL of P1-068761_E32Y_E56N;

(xx) a VH consisting of the amino acid sequence of the VH of P1-068761_E30D_E32Y and a VL consisting of the amino acid sequence of the VL of P1-068761_E30D_E32Y;

(yy) a VH consisting of the amino acid sequence of the VH of P1-068761_E32Y_H100G and a VL consisting of the amino acid sequence of the VL of P1-068761_E32Y_H100G;

(zz) a VH consisting of the amino acid sequence of the VH of P1-068761_E32Y_E100fF and a VL consisting of the amino acid sequence of the VL of P1-068761_E32Y_E100fF;

(aaa) a VH consisting of the amino acid sequence of the VH of P1-068767_D52N_D102V and a VL consisting of the amino acid sequence of the VL of P1-068767_D52N_D102V;

(bbb) a VH consisting of the amino acid sequence of the VH of P1-068767_D52N and a VL consisting of the amino acid sequence of the VL of P1-068767_D52N;

(ccc) a VH consisting of the amino acid sequence of the VH of P1-068767_D52N_E55A and a VL consisting of the amino acid sequence of the VL of P1-068767_D52N_E55A;

(ddd) a VH consisting of the amino acid sequence of the VH of P1-068767_E55A_D102V and a VL consisting of the amino acid sequence of the VL of P1-068767_E55A_D102V;

(eee) a VH consisting of the amino acid sequence of the VH of P1-068767_D102V and a VL consisting of the amino acid sequence of the VL of P1-068767_D102V;

(fff) a VH consisting of the amino acid sequence of the VH of P1-068767_E55A and a VL consisting of the amino acid sequence of the VL of P1-068767_E55A;

(ggg) a VH consisting of the amino acid sequence of the VH of P1-068767_E30D_D52N and a VL consisting of the amino acid sequence of the VL of P1-068767_E30D_D52N;

(hhh) a VH consisting of the amino acid sequence of the VH of P1-068767_E30D_D102V and a VL consisting of the amino acid sequence of the VL of P1-068767_E30D_D102V;

(iii) a VH consisting of the amino acid sequence of the VH of P1-068767_E30D and a VL consisting of the amino acid sequence of the VL of P1-068767_E30D;

(jjj)a VH consisting of the amino acid sequence of the VH of P1-068767_E30D_E55A and a VL consisting of the amino acid sequence of the VL of P1-068767_E30D_E55A;

(kkk) a VH consisting of the amino acid sequence of the VH of P1-068767_E100fF_D102V and a VL consisting of the amino acid sequence of the VL of P1-068767_E100fF_D102V;

(lll) a VH consisting of the amino acid sequence of the VH of P1-068767_E55A_E100fF and a VL consisting of the amino acid sequence of the VL of P1-068767_E55A_E100fF;

(mmm) a VH consisting of the amino acid sequence of the VH of P1-068767_D52N_E100fF and a VL consisting of the amino acid sequence of the VL of P1-068767_D52N_E100fF;

(nnn) a VH consisting of the amino acid sequence of the VH of P1-068767_E100fF and a VL consisting of the amino acid sequence of the VL of P1-068767_E100fF; or

(ooo) a VH consisting of the amino acid sequence of the VH of P1-068767_E30D_E100fF and a VL consisting of the amino acid sequence of the VL of P1-068767_E30D_E100fF.

In certain embodiments, an anti-VISTA Ab comprises any of the variable regions and/or variable region CDRs 1-3 of the antibodies described above and elsewhere herein, such as:

(1) one or more of VH CDR1, CDR2 and CDR3 of:

(2) the VH CDR1, CDR2 and CDR3 of:

(3) the VH of:

(4) one or more of VH CDR1, CDR2 and CDR3 and one or more of VL CDR1, CDR2 and CDR3 of:

(5) the VH CDR1, CDR2 and CDR3 and VL CDR1, CDR2 and CDR3 of:

or

(6) the VH and the VLs of:

P1-061029, P1-068757, P1-068759, P1-068761, P1-068763, P1-068765, P1-068767, P1-068769, P1-068771, P1-068773, P1-068775, P1-069059, P1-069061, P1-069063, P1-069065, P1-069067, P1-069069, P1-069071, P1-069073, P1-069075, P1-069077, P1-061015, P1-068736, P1-068738, P1-068740, P1-068742, P1-068744, P1-068766, P1-068748, P1-068750, P1-068752 P1-068754, P1-068761_E55A, P1-068761_H100G, P1-068761_E56N, P1-068761_E55A_E56N, P1-068761_E30D, P1-068761_E30D_E55A, P1-068761_E56N_H100G, P1-068761_E30D_H100G, P1-068761_E30D_E56N, P1-

068761_E100fF, P1-068761_E55A_E100fF, P1-068761_H100G_E100fF, P1-068761_E30D_E100fF, P1-068761_E56N_E100fF, P1-068761_E32Y, P1-068761_E32Y_E55A, P1-068761_E32Y_E56N, P1-068761_E30D_E32Y, P1-068761_E32Y_H100G, P1-068761_E32Y_E100fF, P1-068767_D52N_D102V, P1-068767_D52N, P1-068767_D52N_E55A, P1-068767_E55A_D102V, P1-068767_D102V, P1-068767_E55A, P1-068767_E30D_D52N, P1-068767_E30D_D102V, P1-068767_E30D, P1-068767_E30D_E55A, P1-068767_E100fF_D102V, P1-068767_E55A_E100fF, P1-068767_D52N_E100fF, P1-068767_E100fF, or P1-068767_E30D_E100fF; and the anti-VISTA Ab

is also an IgG antibody, such as IgG1, IgG2, IgG3 or IgG4 antibody or a modified form thereof as described in the section below. In some embodiments, the constant region has effector function, and in some embodiments, the constant region is effectorless. In certain embodiments, the constant region is that of IgG1.3.

In certain embodiments, an anti-VISTA Ab comprises any of the variable regions and/or variable region CDRs 1-3 of the antibodies described above and elsewhere herein, such as:

(1) one or more of VH CDR1, CDR2 and CDR3 of:

(2) the VH CDR1, CDR2 and CDR3 of:

(3) the VH of:

(4) one or more of VH CDR1, CDR2 and CDR3 and one or more of VL CDR1, CDR2 and CDR3 of:

(5) the VH CDR1, CDR2 and CDR3 and VL CDR1, CDR2 and CDR3 of:

or

(6) the VH and the VLs of:

P1-061029, P1-068757, P1-068759, P1-068761, P1-068763, P1-068765, P1-068767, P1-068769, P1-068771, P1-068773, P1-068775, P1-069059, P1-069061, P1-069063, P1-069065, P1-069067, P1-069069, P1-069071, P1-069073, P1-069075, P1-069077, P1-061015, P1-068736, P1-068738, P1-068740, P1-068742, P1-068744, P1-068766, P1-068748, P1-068750, P1-068752 P1-068754, P1-068761_E55A, P1-068761_H100G, P1-

068761_E56N, P1-068761_E55A_E56N, P1-068761_E30D, P1-068761_E30D_E55A, P1-068761_E56N_H100G, P1-068761_E30D_H100G, P1-068761_E30D_E56N, P1-068761_E100fF, P1-068761_E55A_E100fF, P1-068761_H100G_E100fF, P1-068761_E30D_E100fF, P1-068761_E56N_E100fF, P1-068761_E32Y, P1-068761_E32Y_E55A, P1-068761_E32Y_E56N, P1-068761_E30D_E32Y, P1-068761_E32Y_H100G, P1-068761_E32Y_E100fF, P1-068767_D52N_D102V, P1-068767_D52N, P1-068767_D52N_E55A, P1-068767_E55A_D102V, P1-068767_D102V, P1-068767_E55A, P1-068767_E30D_D52N, P1-068767_E30D_D102V, P1-068767_E30D, P1-068767_E30D_E55A, P1-068767_E100fF_D102V, P1-068767_E55A_E100fF, P1-068767_D52N_E100fF, P1-068767_E100fF, or P1-068767_E30D_E100fF,

and further comprises one or more of the following characteristics:

- specifically binding to hVISTA, e.g., histidine rich region of the ECD or a polypeptide comprising amino acid residues 35-127 of SEQ ID NO: 2, at acidic pH, e.g., pH 6.0 or pH 6.5;
- lacking of significant binding to hVISTA, e.g., histidine rich region of the ECD or a polypeptide comprising amino acid residues 35-127 of SEQ ID NO: 2, at physiological pH or neutral pH, e.g., pH 7.4 or pH 7.0;
- specifically binding to cyno VISTA, e.g., histidine rich region of the ECD, at acidic pH, e.g., pH 6.0 or pH 6.5;
- lacking of significant binding to cyno VISTA, e.g., histidine rich region of the ECD, at physiological pH or neutral pH, e.g., pH 7.4 or pH 7.0;
- having reduced binding to hVISTA-ECD having a substitution at one or more of the following amino acids: T35, Y37, K38, T39, Y41, R54, T61, F62, Q63, L65, H66, L67, H68, H69, F97, L115, V117, I119, H121, H122, S124, E125, R127 relative to hVISTA ECD having SEQ ID NO: 2;
- cross-competiting for binding to hVISTA with P1-061029, P1-068761, P1-068767 and/or P1-061015;
- inhibiting binding of hVISTA to human T cells at acidic pH e.g., pH 6.0 or pH 6.5;
- inhibiting binding of hVISTA to PSGL-1 at acidic pH e.g., pH 6.0 or pH 6.5;
- a mean residence time of at least 350 hours in cynomolgus monkeys;

- stimulating T cell activation;
- inhibiting VISTA mediated cell:cell adhesion; and
- specifically binding to hVISTA in samples of human tumor cells or samples of inflamed human tissue.

In certain embodiments, an anti-hVISTA Ab comprises a heavy chain (HC) comprising the amino acid sequence of the heavy chain of any of the anti-hVISTA Abs provided herein. In certain embodiments, an anti-hVISTA Ab comprises a heavy chain comprising the amino acid sequence of the heavy chain of P1-061029 or P1-061015 or progeny thereof, as shown below in the Sequence Table, comprising an IgG1.3 heavy chain constant region, such as P1-061029.IgG1.3 (SEQ ID NO: 69), P1-068757.IgG1.3, P1-068759.IgG1.3, P1-068761.IgG1.3, P1-068763.IgG1.3, P1-068765.IgG1.3, P1-068767.IgG1.3, P1-068769.IgG1.3, P1-068771.IgG1.3, P1-068773.IgG1.3, P1-068775.IgG1.3, P1-069059.IgG1.3, P1-069061.IgG1.3, P1-069063.IgG1.3, P1-069065.IgG1.3, P1-069067.IgG1.3, P1-069069.IgG1.3, P1-069071.IgG1.3, P1-069073.IgG1.3, P1-069075.IgG1.3, P1-069077.IgG1.3, P1-061015.IgG1.3, P1-068736.IgG1.3, P1-068738.IgG1.3, P1-068740.IgG1.3, P1-068742.IgG1.3, P1-068744.IgG1.3, P1-068766.IgG1.3, P1-068748.IgG1.3, P1-068750.IgG1.3, P1-068752.IgG1.3, P1-068754.IgG1.3, P1-068761_E55A.IgG1.3, P1-068761_H100G.IgG1.3, P1-068761_E56N.IgG1.3, P1-068761_E55A_E56N.IgG1.3, P1-068761_E30D.IgG1.3, P1-068761_E30D_E55A.IgG1.3, P1-068761_E56N_H100G.IgG1.3, P1-068761_E30D_H100G.IgG1.3, P1-068761_E30D_E56N.IgG1.3, P1-068761_E100fF.IgG1.3, P1-068761_E55A_E100fF.IgG1.3, P1-068761_H100G_E100fF.IgG1.3, P1-068761_E30D_E100fF.IgG1.3, P1-068761_E56N_E100fF.IgG1.3, P1-068761_E32Y.IgG1.3, P1-068761_E32Y_E55A.IgG1.3, P1-068761_E32Y_E56N.IgG1.3, P1-068761_E30D_E32Y.IgG1.3, P1-068761_E32Y_H100G.IgG1.3, P1-068761_E32Y_E100fF.IgG1.3, P1-068767_D52N_D102V.IgG1.3, P1-068767_D52N.IgG1.3, P1-068767_D52N_E55A.IgG1.3, P1-068767_E55A_D102V.IgG1.3, P1-068767_D102V.IgG1.3, P1-068767_E55A.IgG1.3, P1-068767_E30D_D52N.IgG1.3, P1-068767_E30D_D102V.IgG1.3, P1-

068767_E30D.IgG1.3, P1-068767_E30D_E55A.IgG1.3, P1-068767_E100fF_D102V.IgG1.3, P1-068767_E55A_E100fF.IgG1.3, P1-068767_D52N_E100fF.IgG1.3, P1-068767_E100fF.IgG1.3, or P1-068767_E30D_E100fF.IgG1.3.

In certain embodiments, an anti-hVISTA Ab comprises a heavy chain comprising the amino acid sequence of the heavy chain of any of the anti-hVISTA Abs provided herein, which comprise an IgG1.3 heavy chain constant region, and the amino acid sequence of the light chain of any of the anti-hVISTA Abs provided herein. In certain embodiments, an anti-hVISTA Ab comprises a heavy chain comprising the amino acid sequence of the VH of P1-061029 or P1-061015 or progeny thereof, which comprise an IgG1.3 HC constant region, such as P1-061029.IgG1.3 (SEQ ID NO: 69), P1-068757.IgG1.3, P1-068759.IgG1.3, P1-068761.IgG1.3, P1-068763.IgG1.3, P1-068765.IgG1.3, P1-068767.IgG1.3, P1-068769.IgG1.3, P1-068771.IgG1.3, P1-068773.IgG1.3, P1-068775.IgG1.3, P1-069059.IgG1.3, P1-069061.IgG1.3, P1-069063.IgG1.3, P1-069065.IgG1.3, P1-069067.IgG1.3, P1-069069.IgG1.3, P1-069071.IgG1.3, P1-069073.IgG1.3, P1-069075.IgG1.3, P1-069077.IgG1.3, P1-061015.IgG1.3, P1-068736.IgG1.3, P1-068738.IgG1.3, P1-068740.IgG1.3, P1-068742.IgG1.3, P1-068744.IgG1.3, P1-068766.IgG1.3, P1-068748.IgG1.3, P1-068750.IgG1.3, P1-068752.IgG1.3, P1-068754.IgG1.3, P1-068761_E55A.IgG1.3, P1-068761_H100G.IgG1.3, P1-068761_E56N.IgG1.3, P1-068761_E55A_E56N.IgG1.3, P1-068761_E30D.IgG1.3, P1-068761_E30D_E55A.IgG1.3, P1-068761_E56N_H100G.IgG1.3, P1-068761_E30D_H100G.IgG1.3, P1-068761_E30D_E56N.IgG1.3, P1-068761_E100fF.IgG1.3, P1-068761_E55A_E100fF.IgG1.3, P1-068761_H100G_E100fF.IgG1.3, P1-068761_E30D_E100fF.IgG1.3, P1-068761_E56N_E100fF.IgG1.3, P1-068761_E32Y.IgG1.3, P1-068761_E32Y_E55A.IgG1.3, P1-068761_E32Y_E56N.IgG1.3, P1-068761_E30D_E32Y.IgG1.3, P1-068761_E32Y_H100G.IgG1.3, P1-068761_E32Y_E100fF.IgG1.3, P1-068767_D52N_D102V.IgG1.3, P1-068767_D52N.IgG1.3, P1-068767_D52N_E55A.IgG1.3, P1-068767_E55A_D102V.IgG1.3, P1-068767_D102V.IgG1.3, P1-068767_E55A.IgG1.3, P1-068767_E30D_D52N.IgG1.3, P1-068767_E30D_D102V.IgG1.3, P1-

068767_E30D.IgG1.3, P1-068767_E30D_E55A.IgG1.3, P1-068767_E100fF_D102V.IgG1.3, P1-068767_E55A_E100fF.IgG1.3, P1-068767_D52N_E100fF.IgG1.3, P1-068767_E100fF.IgG1.3, or P1-068767_E30D_E100fF.IgG1.3; and a light chain comprising the amino acid sequence of the light chain of P1-061029 or P1-061015.

An anti-hVISTA Ab may comprise:

(a) a heavy chain comprising the amino acid sequence of the heavy chain of P1-061029.IgG1.3 (SEQ ID NO: 69) and a light chain comprising the light chain amino acid sequence of P1-061029 (SEQ ID NO: 70);

(b) a heavy chain comprising the amino acid sequence of the heavy chain of P1-061015.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-061015;

(c) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068757.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068757;

(d) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068759.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068759;

(e) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068761.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068761;

(f) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068763.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068763;

(g) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068765.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068765;

(h) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068767.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068767;

(i) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068769.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068769;

(j) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068771.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068771;

(k) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068773.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068773;

(l) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068775.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068775;

(m) a heavy chain comprising the amino acid sequence of the heavy chain of P1-069059.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-069059;

(n) a heavy chain comprising the amino acid sequence of the heavy chain of P1-069061.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-069061;

(o) a heavy chain comprising the amino acid sequence of the heavy chain of P1-069063.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-069063;

(p) a heavy chain comprising the amino acid sequence of the heavy chain of P1-069065.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-069065;

(q) a heavy chain comprising the amino acid sequence of the heavy chain of P1-069067.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-069067;

(r) a heavy chain comprising the amino acid sequence of the heavy chain of P1-069069.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-069069;

(s) a heavy chain comprising the amino acid sequence of the heavy chain of P1-069071.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-069071;

(t) a heavy chain comprising the amino acid sequence of the heavy chain of P1-069073.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-069073;

(u) a heavy chain comprising the amino acid sequence of the heavy chain of P1-069075.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-069075;

(v) a heavy chain comprising the amino acid sequence of the heavy chain of P1-069077.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-069077;

(w) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068736.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068736;

(x) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068738.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068738;

(y) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068740.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068740;

(z) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068742.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068742;

(aa) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068744.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068744;

(bb) a heavy chain comprising the amino acid sequence of the heavy chain f P1-068746.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068746;

(cc) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068748.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068748;

(dd) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068750.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068750;

(ee) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068752.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068752;

(ff) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068754.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068754;

(gg) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068761_E55A.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068761_E55A;

(hh) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068761_H100G.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068761_H100G;

(ii) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068761_E56N.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068761_E56N;

(jj) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068761_E55A_E56N.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068761_E55A_E56N;

(kk) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068761_E30D.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068761_E30D;

(ll) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068761_E30D_E55A.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068761_E30D_E55A;

(mm) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068761_E56N_H100G.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068761_E56N_H100G;

(nn) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068761_E30D_H100G.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068761_E30D_H100G;

(oo) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068761_E30D_E56N.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068761_E30D_E56N;

(pp) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068761_E100fF.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068761_E100fF;

(qq) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068761_E55A_E100fF.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068761_E55A_E100fF;

(rr) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068761_H100G_E100fF.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068761_H100G_E100fF;

(ss) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068761_E30D_E100fF.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068761_E30D_E100fF;

(tt) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068761_E56N_E100fF.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068761_E56N_E100fF;

(uu) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068761_E32Y.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068761_E32Y;

(vv) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068761_E32Y_E55A.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068761_E32Y_E55A;

(ww) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068761_E32Y_E56N.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068761_E32Y_E56N;

(xx) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068761_E30D_E32Y.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068761_E30D_E32Y;

(yy) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068761_E32Y_H100G.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068761_E32Y_H100G;

(zz) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068761_E32Y_E100fF.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068761_E32Y_E100fF;

(aaa) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068767_D52N_D102V.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068767_D52N_D102V;

(bbb) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068767_D52N.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068767_D52N;

(ccc) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068767_D52N_E55A.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068767_D52N_E55A;

(ddd) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068767_E55A_D102V.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068767_E55A_D102V;

(eee) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068767_D102V.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068767_D102V;

(fff) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068767_E55A.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068767_E55A;

(ggg) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068767_E30D_D52N.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068767_E30D_D52N;

(hhh) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068767_E30D_D102V.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068767_E30D_D102V;

(iii)a heavy chain comprising the amino acid sequence of the heavy chain of P1-068767_E30D.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068767_E30D;

(jjj)a heavy chain comprising the amino acid sequence of the heavy chain of P1-068767_E30D_E55A.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068767_E30D_E55A;

(kkk) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068767_E100fF_D102V.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068767_E100fF_D102V;

(lll)a heavy chain comprising the amino acid sequence of the heavy chain of P1-068767_E55A_E100fF.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068767_E55A_E100fF;

(mmm) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068767_D52N_E100fF.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068767_D52N_E100fF;

(nnn) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068767_E100fF.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068767_E100fF; or

(ooo) a heavy chain comprising the amino acid sequence of the heavy chain of P1-068767_E30D_E100fF.IgG1.3 and a light chain comprising the light chain amino acid sequence of P1-068767_E30D_E100fF.

An anti-hVISTA Ab may comprise:

(a) a heavy chain (HC) comprising the HC CDRs of the HC of P1-061029 and a light chain (LC) comprising the LC CDRs of P1-061029 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-061029.IgG1.3, respectively;

(b) a HC comprising the HC CDRs of the HC of P1-061015 and a LC comprising the LC CDRs of P1-061015 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-061015.IgG1.3, respectively;

(c) a HC comprising the HC CDRs of the HC of P1-068757 and a LC comprising the LC CDRs of P1-068757 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068757.IgG1.3, respectively;

(d) a HC comprising the HC CDRs of the HC of P1-068759 and a LC comprising the LC CDRs of P1-068759 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068759.IgG1.3, respectively;

(e) a HC comprising the HC CDRs of the HC of P1-068761 and a LC comprising the LC CDRs of P1-068761 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068761.IgG1.3, respectively;

(f) a HC comprising the HC CDRs of the HC of P1-068763 and a LC comprising the LC CDRs of P1-068763 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068763.IgG1.3, respectively;

(g) a HC comprising the HC CDRs of the HC of P1-068765 and a LC comprising the LC CDRs of P1-068765 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068765.IgG1.3, respectively;

(h) a HC comprising the HC CDRs of the HC of P1-068767 and a LC comprising the LC CDRs of P1-068767 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068767.IgG1.3, respectively;

(i) a HC comprising the HC CDRs of the HC of P1-068769 and a LC comprising the LC CDRs of P1-068769 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068769.IgG1.3, respectively;

(j) a HC comprising the HC CDRs of the HC of P1-068771 and a LC comprising the LC CDRs of P1-068771 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068771.IgG1.3, respectively;

(k) a HC comprising the HC CDRs of the HC of P1-068773 and a LC comprising the LC CDRs of P1-068773 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068773.IgG1.3, respectively;

(l) a HC comprising the HC CDRs of the HC of P1-068775 and a LC comprising the LC CDRs of P1-068775 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068775.IgG1.3, respectively;

(m) a HC comprising the HC CDRs of the HC of P1-069059 and a LC comprising the LC CDRs of P1-069059 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-069059.IgG1.3, respectively;

(n) a HC comprising the HC CDRs of the HC of P1-069061 and a LC comprising the LC CDRs of P1-069061 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-069061.IgG1.3, respectively;

(o) a HC comprising the HC CDRs of the HC of P1-069063 and a LC comprising the LC CDRs of P1-069063 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-069063.IgG1.3, respectively;

(p) a HC comprising the HC CDRs of the HC of P1-069065 and a LC comprising the LC CDRs of P1-069065 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-069065.IgG1.3, respectively;

(q) a HC comprising the HC CDRs of the HC of P1-069067 and a LC comprising the LC CDRs of P1-069067 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-069067.IgG1.3, respectively;

(r) a HC comprising the HC CDRs of the HC of P1-069069 and a LC comprising the LC CDRs of P1-069069 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-069069.IgG1.3, respectively;

(s) a HC comprising the HC CDRs of the HC of P1-069071 and a LC comprising the LC CDRs of P1-069071 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-069071.IgG1.3, respectively;

(t) a HC comprising the HC CDRs of the HC of P1-069073 and a LC comprising the LC CDRs of P1-069073 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-069073.IgG1.3, respectively;

(u) a HC comprising the HC CDRs of the HC of P1-069075 and a LC comprising the LC CDRs of P1-069075 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-069075.IgG1.3, respectively;

(v) a HC comprising the HC CDRs of the HC of P1-069077 and a LC comprising the LC CDRs of P1-069077 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-069077.IgG1.3, respectively;

(w) a HC comprising the HC CDRs of the HC of P1-068736 and a LC comprising the LC CDRs of P1-068736 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068736.IgG1.3, respectively;

(x) a HC comprising the HC CDRs of the HC of P1-068738 and a LC comprising the LC CDRs of P1-068738 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068738.IgG1.3, respectively;

(y) a HC comprising the HC CDRs of the HC of P1-068740 and a LC comprising the LC CDRs of P1-068740 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068740.IgG1.3, respectively;

(z) a HC comprising the HC CDRs of the HC of P1-068742 and a LC comprising the LC CDRs of P1-068742 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068742.IgG1.3, respectively;

(aa) a HC comprising the HC CDRs of the HC of P1-068744 and a LC comprising the LC CDRs of P1-068744 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068744.IgG1.3, respectively;

(bb) a HC comprising the HC CDRs of the HC of P1-068746 and a LC comprising the LC CDRs of P1-068746 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068746.IgG1.3, respectively;

(cc) a HC comprising the HC CDRs of the HC of P1-068748 and a LC comprising the LC CDRs of P1-068748 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068748.IgG1.3, respectively;

(dd) a HC comprising the HC CDRs of the HC of P1-068750 and a LC comprising the LC CDRs of P1-068750 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068750.IgG1.3, respectively;

(ee) a HC comprising the HC CDRs of the HC of P1-068752 and a LC comprising the LC CDRs of P1-068752 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068752.IgG1.3, respectively;

(ff) a HC comprising the HC CDRs of the HC of P1-068754 and a LC comprising the LC CDRs of P1-068754 and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068754.IgG1.3, respectively;

(gg) a HC comprising the HC CDRs of the HC of P1-068761_E55A.IgG1.3 and a LC comprising the LC CDRs of P1-068761_E55A and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068761_E55A.IgG1.3, respectively;

(hh) a HC comprising the HC CDRs of the HC of P1-068761_H100G.IgG1.3 and a LC comprising the LC CDRs of P1-068761_H100G and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068761_H100G.IgG1.3, respectively;

(ii) a HC comprising the HC CDRs of the HC of P1-068761_E56N.IgG1.3 and a LC comprising the LC CDRs of P1-068761_E56N and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068761_E56N.IgG1.3, respectively;

(jj) a HC comprising the HC CDRs of the HC of P1-068761_E55A_E56N.IgG1.3 and a LC comprising the LC CDRs of P1-068761_E55A_E56N and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068761_E55A_E56N.IgG1.3, respectively;

(kk) a HC comprising the HC CDRs of the HC of P1-068761_E30D.IgG1.3 and a LC comprising the LC CDRs of P1-068761_E30D and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068761_E30D.IgG1.3, respectively;

(ll) a HC comprising the HC CDRs of the HC of P1-068761_E30D_E55A.IgG1.3 and a LC comprising the LC CDRs of P1-068761_E30D_E55A and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068761_E30D_E55A.IgG1.3, respectively;

(mm) a HC comprising the HC CDRs of the HC of P1-068761_E56N_H100G.IgG1.3 and a LC comprising the LC CDRs of P1-068761_E56N_H100G and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068761_E56N_H100G.IgG1.3, respectively;

(nn) a HC comprising the HC CDRs of the HC of P1-068761_E30D_H100G.IgG1.3 and a LC comprising the LC CDRs of P1-068761_E30D_H100G and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068761_E30D_H100G.IgG1.3, respectively;

(oo) a HC comprising the HC CDRs of the HC of P1-068761_E30D_E56N.IgG1.3 and a LC comprising the LC CDRs of P1-068761_E30D_E56N and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068761_E30D_E56N.IgG1.3, respectively;

(pp) a HC comprising the HC CDRs of the HC of P1-068761_E100fF.IgG1.3 and a LC comprising the LC CDRs of P1-068761_E100fF and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%,

at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068761_E100fF.IgG1.3, respectively;

(qq) a HC comprising the HC CDRs of the HC of P1-068761_E55A_E100fF.IgG1.3 and a LC comprising the LC CDRs of P1-068761_E55A_E100fF and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068761_E55A_E100fF.IgG1.3, respectively;

(rr) a HC comprising the HC CDRs of the HC of P1-068761_H100G_E100fF.IgG1.3 and a LC comprising the LC CDRs of P1-068761_H100G_E100fF and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068761_H100G_E100fF.IgG1.3, respectively;

(ss) a HC comprising the HC CDRs of the HC of P1-068761_E30D_E100fF.IgG1.3 and a LC comprising the LC CDRs of P1-068761_E30D_E100fF and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068761_E30D_E100fF.IgG1.3, respectively;

(tt) a HC comprising the HC CDRs of the HC of P1-068761_E56N_E100fF.IgG1.3 and a LC comprising the LC CDRs of P1-068761_E56N_E100fF and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068761_E56N_E100fF.IgG1.3, respectively;

(uu) a HC comprising the HC CDRs of the HC of P1-068761_E32Y.IgG1.3 and a LC comprising the LC CDRs of P1-068761_E32Y and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068761_E32Y.IgG1.3, respectively;

(vv) a HC comprising the HC CDRs of the HC of P1-068761_E32Y_E55A.IgG1.3 and a LC comprising the LC CDRs of P1-068761_E32Y_E55A and HC and LC

amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068761_E32Y_E55A.IgG1.3, respectively;

(ww) a HC comprising the HC CDRs of the HC of P1-068761_E32Y_E56N.IgG1.3 and a LC comprising the LC CDRs of P1-068761_E32Y_E56N and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068761_E32Y_E56N.IgG1.3, respectively;

(xx) a HC comprising the HC CDRs of the HC of P1-068761_E30D_E32Y.IgG1.3 and a LC comprising the LC CDRs of P1-068761_E30D_E32Y and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068761_E30D_E32Y.IgG1.3, respectively;

(yy) a HC comprising the HC CDRs of the HC of P1-068761_E32Y_H100G.IgG1.3 and a LC comprising the LC CDRs of P1-068761_E32Y_H100G and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068761_E32Y_H100G.IgG1.3, respectively;

(zz) a HC comprising the HC CDRs of the HC of P1-068761_E32Y_E100fF.IgG1.3 and a LC comprising the LC CDRs of P1-068761_E32Y_E100fF and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068761_E32Y_E100fF.IgG1.3, respectively;

(aaa) a HC comprising the HC CDRs of the HC of P1-068767_D52N_D102V.IgG1.3 and a LC comprising the LC CDRs of P1-068767_D52N_D102V and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least

97%, at least 98%, or at least 99% identical to the HC and LC of P1-068767_D52N_D102V.IgG1.3, respectively;

(bbb) a HC comprising the HC CDRs of the HC of P1-068767_D52N.IgG1.3 and a LC comprising the LC CDRs of P1-068767_D52N and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068767_D52N.IgG1.3, respectively;

(ccc) a HC comprising the HC CDRs of the HC of P1-068767_D52N_E55A.IgG1.3 and a LC comprising the LC CDRs of P1-068767_D52N_E55A and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068767_D52N_E55A.IgG1.3, respectively;

(ddd) a HC comprising the HC CDRs of the HC of P1-068767_E55A_D102V.IgG1.3 and a LC comprising the LC CDRs of P1-068767_E55A_D102V and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068767_E55A_D102V.IgG1.3, respectively;

(eee) a HC comprising the HC CDRs of the HC of P1-068767_D102V.IgG1.3 and a LC comprising the LC CDRs of P1-068767_D102V and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068767_D102V.IgG1.3, respectively;

(fff) a HC comprising the HC CDRs of the HC of P1-068767_E55A.IgG1.3 and a LC comprising the LC CDRs of P1-068767_E55A and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068767_E55A.IgG1.3, respectively;

(ggg) a HC comprising the HC CDRs of the HC of P1-068767_E30D_D52N.IgG1.3 and a LC comprising the LC CDRs of P1-068767_E30D_D52N and HC and LC

amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068767_E30D_D52N.IgG1.3, respectively;

(hhh) a HC comprising the HC CDRs of the HC of P1-068767_E30D_D102V.IgG1.3 and a LC comprising the LC CDRs of P1-068767_E30D_D102V and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068767_E30D_D102V.IgG1.3, respectively;

(iii) a HC comprising the HC CDRs of the HC of P1-068767_E30D.IgG1.3 and a LC comprising the LC CDRs of P1-068767_E30D and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068767_E30D.IgG1.3, respectively;

(jjj) a HC comprising the HC CDRs of the HC of P1-068767_E30D_E55A.IgG1.3 and a LC comprising the LC CDRs of P1-068767_E30D_E55A and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068767_E30D_E55A.IgG1.3, respectively;

(kkk) a HC comprising the HC CDRs of the HC of P1-068767_E100fF_D102V.IgG1.3 and a LC comprising the LC CDRs of P1-068767_E100fF_D102V and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068767_E100fF_D102V.IgG1.3, respectively;

(lll) a HC comprising the HC CDRs of the HC of P1-068767_E55A_E100fF.IgG1.3 and a LC comprising the LC CDRs of P1-068767_E55A_E100fF and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068767_E55A_E100fF.IgG1.3, respectively;

(mmm) a HC comprising the HC CDRs of the HC of P1-068767_D52N_E100fF.IgG1.3 and a LC comprising the LC CDRs of P1-068767_D52N_E100fF and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068767_D52N_E100fF.IgG1.3, respectively;

(nnn) a HC comprising the HC CDRs of the HC of P1-068767_E100fF.IgG1.3 and a LC comprising the LC CDRs of P1-068767_E100fF and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068767_E100fF.IgG1.3, respectively; or

(ooo) a HC comprising the HC CDRs of the HC of P1-068767_E30D_E100fF.IgG1.3 and a LC comprising the LC CDRs of P1-068767_E30D_E100fF and HC and LC amino acid sequences that are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to the HC and LC of P1-068767_E30D_E100fF.IgG1.3, respectively.

In some embodiments, an anti-hVISTA Ab may comprise:

(a) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-061029.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-061029;

(b) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-061015.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-061015;

(c) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068757.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068757;

(d) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068759.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068759;

(e) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068761.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068761;

(f) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068763.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068763;

(g) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068765.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068765;

(h) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068767.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068767;

(i) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068769.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068769;

(j) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068771.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068771;

(k) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068773.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068773;

(l) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068775.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068775;

(m)a heavy chain consisting of the amino acid sequence of the heavy chain of P1-069059.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-069059;

(n) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-069061.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-069061;

(o) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-069063.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-069063;

(p) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-069065.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-069065;

(q) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-069067.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-069067;

(r) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-069069.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-069069;

(s) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-069071.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-069071;

(t) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-069073.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-069073;

(u) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-069075.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-069075;

(v) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-069077.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-069077;

(w) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068736 and a light chain consisting of the amino acid sequence of the light chain of P1-068736;

(x) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068738.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068738;

(y) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068740.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068740;

(z) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068742.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068742;

(aa) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068744.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068744;

(bb) a heavy chain consisting of the amino acid sequence of the heavy chain f P1-068746.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068746;

(cc) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068748.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068748;

(dd) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068750.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068750;

(ee) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068752.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068752;

(ff) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068754 and a light chain consisting of the amino acid sequence of the light chain of P1-068754;

(gg) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068761_E55A.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068761_E55A;

(hh) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068761_H100G.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068761_H100G;

(ii) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068761_E56N.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068761_E56N;

(jj) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068761_E55A_E56N.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068761_E55A_E56N;

(kk) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068761_E30D.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068761_E30D;

(ll) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068761_E30D_E55A.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068761_E30D_E55A;

(mm) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068761_E56N_H100G.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068761_E56N_H100G;

(nn) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068761_E30D_H100G.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068761_E30D_H100G;

(oo) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068761_E30D_E56N.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068761_E30D_E56N;

(pp) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068761_E100fF.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068761_E100fF;

(qq) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068761_E55A_E100fF.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068761_E55A_E100fF;

(rr) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068761_H100G_E100fF.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068761_H100G_E100fF;

(ss) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068761_E30D_E100fF.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068761_E30D_E100fF;

(tt) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068761_E56N_E100fF.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068761_E56N_E100fF;

(uu) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068761_E32Y.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068761_E32Y;

(vv) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068761_E32Y_E55A.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068761_E32Y_E55A;

(ww) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068761_E32Y_E56N.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068761_E32Y_E56N;

(xx) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068761_E30D_E32Y.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068761_E30D_E32Y;

(yy) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068761_E32Y_H100G.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068761_E32Y_H100G;

(zz) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068761_E32Y_E100fF.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068761_E32Y_E100fF;

(aaa) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068767_D52N_D102V.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068767_D52N_D102V;

(bbb) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068767_D52N.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068767_D52N;

(ccc) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068767_D52N_E55A.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068767_D52N_E55A;

(ddd) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068767_E55A_D102V.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068767_E55A_D102V;

(eee) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068767_D102V.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068767_D102V;

(fff) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068767_E55A.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068767_E55A;

(ggg) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068767_E30D_D52N.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068767_E30D_D52N;

(hhh) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068767_E30D_D102V.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068767_E30D_D102V;

(iii)a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068767_E30D.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068767_E30D;

(jjj)a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068767_E30D_E55A.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068767_E30D_E55A;

(kkk) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068767_E100fF_D102V.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068767_E100fF_D102V;

(lll)a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068767_E55A_E100fF.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068767_E55A_E100fF;

(mmm) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068767_D52N_E100fF.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068767_D52N_E100fF;

(nnn) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068767_E100fF.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068767_E100fF; or

(ooo) a heavy chain consisting of the amino acid sequence of the heavy chain of P1-068767_E30D_E100fF.IgG1.3 and a light chain consisting of the amino acid sequence of the light chain of P1-068767_E30D_E100fF.

In some embodiments, the disclosure contemplates anti-VISTA mAbs comprising:

a heavy chain consisting of the amino acid sequences of the heavy chain of (a) to (ooo) listed above followed by a Lys residue; and

a light chain consisting of the light chain amino acid sequence of (a) to (ooo) listed above;

wherein the heavy chain and light chain amino acid sequences are chosen from the same antibody species from among (a) to (ooo) listed above.

In some embodiments, an anti-hVISTA Ab may comprise a heavy chain amino acid sequence comprising the VH amino acid sequence of the antibody species herein, but rather than an IgG1.3 heavy chain constant region, as provided in the HC sequences in the Sequence Table herein (and see SEQ ID NO: 163), the antibody may comprise a different heavy chain constant region sequence, such as a human wild-type IgG1 constant region such as human IgG1 allotype f (IgG1f) (SEQ ID NO: 182), or a modified human IgG1 constant region such as IgG1.1f (SEQ ID NO: 183), or a modified human IgG1 constant region such as IgG1.P238K (SEQ ID NO: 184). Accordingly, embodiments of this disclosure include anti-VISTA Abs comprising:

(a) a heavy chain comprising (i) the amino acid sequence of the VH of P1-061029 (SEQ ID NO: 67) and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-061029 (SEQ ID NO: 70);

(b) a heavy chain comprising (i) the amino acid sequence of the VH of P1-061015 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-061015;

(c) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068757 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068757;

(d) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068759 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068759;

(e) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068761;

(f) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068763 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068763;

(g) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068765 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068765;

(h) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068767;

(i) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068769 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068769;

(j) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068771 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068771;

(k) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068773 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068773;

(l) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068775 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068775;

(m) a heavy chain comprising (i) the amino acid sequence of the VH of P1-069059 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-069059;

(n) a heavy chain comprising (i) the amino acid sequence of the VH of P1-069061 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-069061;

(o) a heavy chain comprising (i) the amino acid sequence of the VH of P1-069063 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-069063;

(p) a heavy chain comprising (i) the amino acid sequence of the VH of P1-069065 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-069065;

(q) a heavy chain comprising (i) the amino acid sequence of the VH of P1-069067 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-069067;

(r) a heavy chain comprising (i) the amino acid sequence of the VH of P1-069069 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-069069;

(s) a heavy chain comprising (i) the amino acid sequence of the VH of P1-069071 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-069071;

(t) a heavy chain comprising (i) the amino acid sequence of the VH of P1-069073 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-069073;

(u) a heavy chain comprising (i) the amino acid sequence of the VH of P1-069075 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-069075;

(v) a heavy chain comprising (i) the amino acid sequence of the VH of P1-069077 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-069077;

(w) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068736 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068736;

(x) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068738 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068738;

(y) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068740 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068740;

(z) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068742 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068742;

(aa) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068744 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068744;

(bb) a heavy chain comprising the amino acid sequence of the heavy chain f P1-068746 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068746;

(cc) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068748 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068748;

(dd) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068750 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068750;

(ee) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068752 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068752;

(ff) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068754 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068754;

(gg) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E55A and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068761_E55A;

(hh) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_H100G and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068761_H100G;

(ii) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E56N and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068761_E56N;

(jj) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E55A_E56N and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068761_E55A_E56N;

(kk) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E30D and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068761_E30D;

(ll) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E30D_E55A and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068761_E30D_E55A;

(mm) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E56N_H100G and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068761_E56N_H100G;

(nn) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E30D_H100G and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068761_E30D_H100G;

(oo) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E30D_E56N and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068761_E30D_E56N;

(pp) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E100fF and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068761_E100fF;

(qq) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E55A_E100fF and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068761_E55A_E100fF;

(rr) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_H100G_E100fF and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068761_H100G_E100fF;

(ss) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E30D_E100fF and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068761_E30D_E100fF;

(tt) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E56N_E100fF and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068761_E56N_E100fF;

(uu) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E32Y and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068761_E32Y;

(vv) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E32Y_E55A and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068761_E32Y_E55A;

(ww) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E32Y_E56N and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068761_E32Y_E56N;

(xx) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E30D_E32Y and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068761_E30D_E32Y;

(yy) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E32Y_H100G and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068761_E32Y_H100G;

(zz) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E32Y_E100fF and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068761_E32Y_E100fF;

(aaa) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_D52N_D102V and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068767_D52N_D102V;

(bbb) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_D52N and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068767_D52N;

(ccc) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_D52N_E55A and (ii) the amino acid sequence of SEQ ID NO: 182, and a

light chain comprising the light chain amino acid sequence of P1-068767_D52N_E55A;

(ddd) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_E55A_D102V and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068767_E55A_D102V;

(eee) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_D102V and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068767_D102V;

(fff) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_E55A and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068767_E55A;

(ggg) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_E30D_D52N and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068767_E30D_D52N;

(hhh) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_E30D_D102V and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068767_E30D_D102V;

(iii)a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_E30D and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068767_E30D;

(jjj)a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_E30D_E55A and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068767_E30D_E55A;

(kkk) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_E100fF_D102V and (ii) the amino acid sequence of SEQ ID NO: 182, and a

light chain comprising the light chain amino acid sequence of P1-068767_E100fF_D102V;

(lll)a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_E55A_E100fF and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068767_E55A_E100fF;

(mmm) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_D52N_E100fF and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068767_D52N_E100fF;

(nnn) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_E100fF and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068767_E100fF; or

(ooo) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_E30D_E100fF and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain comprising the light chain amino acid sequence of P1-068767_E30D_E100fF.

Certain embodiments of this disclosure include anti-VISTA Abs comprising:

(a) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-061029 (SEQ ID NO: 67) and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-061029 (SEQ ID NO: 70);

(b) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-061015 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-061015;

(c) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068757 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068757;

(d) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068759 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068759;

(e) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068761;

(f) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068763 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068763;

(g) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068765 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068765;

(h) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068767;

(i) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068769 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068769;

(j) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068771 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068771;

(k) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068773 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068773;

(l) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068775 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068775;

(m) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-069059 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-069059;

(n) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-069061 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-069061;

(o) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-069063 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-069063;

(p) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-069065 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-069065;

(q) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-069067 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-069067;

(r) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-069069 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-069069;

(s) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-069071 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-069071;

(t) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-069073 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-069073;

(u) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-069075 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-069075;

(v) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-069077 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-069077;

(w) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068736 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068736;

(x) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068738 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068738;

(y) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068740 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068740;

(z) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068742 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068742;

(aa) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068744 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068744;

(bb) a heavy chain consisting of the amino acid sequence of the heavy chain f P1-068746 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068746;

(cc) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068748 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068748;

(dd) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068750 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068750;

(ee) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068752 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068752;

(ff) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068754 and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068754;

(gg) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E55A and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068761_E55A;

(hh) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_H100G and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068761_H100G;

(ii) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E56N and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068761_E56N;

(jj) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E55A_E56N and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068761_E55A_E56N;

(kk) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E30D and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068761_E30D;

(ll) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E30D_E55A and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068761_E30D_E55A;

(mm) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E56N_H100G and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068761_E56N_H100G;

(nn) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E30D_H100G and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068761_E30D_H100G;

(oo) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E30D_E56N and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068761_E30D_E56N;

(pp) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E100fF and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068761_E100fF;

(qq) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E55A_E100fF and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068761_E55A_E100fF;

(rr) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_H100G_E100fF and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068761_H100G_E100fF;

(ss) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E30D_E100fF and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068761_E30D_E100fF;

(tt) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E56N_E100fF and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068761_E56N_E100fF;

(uu) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E32Y and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068761_E32Y;

(vv) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E32Y_E55A and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068761_E32Y_E55A;

(ww) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E32Y_E56N and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068761_E32Y_E56N;

(xx) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E30D_E32Y and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068761_E30D_E32Y;

(yy) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E32Y_H100G and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068761_E32Y_H100G;

(zz) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E32Y_E100fF and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068761_E32Y_E100fF;

(aaa) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_D52N_D102V and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068767_D52N_D102V;

(bbb) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_D52N and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068767_D52N;

(ccc) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_D52N_E55A and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068767_D52N_E55A;

(ddd) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_E55A_D102V and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068767_E55A_D102V;

(eee) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_D102V and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068767_D102V;

(fff) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_E55A and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068767_E55A;

(ggg) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_E30D_D52N and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068767_E30D_D52N;

(hhh) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_E30D_D102V and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068767_E30D_D102V;

(iii)a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_E30D and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068767_E30D;

(jjj)a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_E30D_E55A and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068767_E30D_E55A;

(kkk) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_E100fF_D102V and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068767_E100fF_D102V;

(lll)a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_E55A_E100fF and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068767_E55A_E100fF;

(mmm) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_D52N_E100fF and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068767_D52N_E100fF;

(nnn) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_E100fF and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068767_E100fF; or

(ooo) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_E30D_E100fF and (ii) the amino acid sequence of SEQ ID NO: 182, and a light chain consisting of the light chain amino acid sequence of P1-068767_E30D_E100fF,

wherein the C-terminal amino acid of VH and the N-terminal amino acid of SEQ ID NO: 182 form a peptidic bond.

In some embodiments, the disclosure contemplates anti-VISTA mAbs comprising:

a heavy chain consisting of the amino acid sequences of (i) a VH of (a) to (ooo) listed above, (ii) SEQ ID NO: 182, and (iii) a Lys residue, wherein the C-terminal amino acid of VH and the N-terminal amino acid of SEQ ID NO: 182 form a peptidic bond and wherein the C-terminal amino acid of SEQ ID NO: 182 is joined to the N-terminal of the Lys; and

a light chain consisting of the light chain amino acid sequence of (a) to (ooo) listed above;

wherein the VH and light chain amino acid sequences are chosen from the same antibody species from among (a) to (ooo) listed above.

Certain embodiments of this disclosure include anti-VISTA Abs comprising:

(a) a heavy chain comprising (i) the amino acid sequence of the VH of P1-061029 (SEQ ID NO: 67) and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-061029 (SEQ ID NO: 70);

(b) a heavy chain comprising (i) the amino acid sequence of the VH of P1-061015 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-061015;

(c) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068757 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068757;

(d) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068759 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068759;

(e) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068761;

(f) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068763 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068763;

(g) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068765 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068765;

(h) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068767;

(i) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068769 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068769;

(j) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068771 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068771;

(k) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068773 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068773;

(l) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068775 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068775;

(m)a heavy chain comprising (i) the amino acid sequence of the VH of P1-069059 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-069059;

(n) a heavy chain comprising (i) the amino acid sequence of the VH of P1-069061 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-069061;

(o) a heavy chain comprising (i) the amino acid sequence of the VH of P1-069063 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-069063;

(p) a heavy chain comprising (i) the amino acid sequence of the VH of P1-069065 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-069065;

(q) a heavy chain comprising (i) the amino acid sequence of the VH of P1-069067 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-069067;

(r) a heavy chain comprising (i) the amino acid sequence of the VH of P1-069069 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-069069;

(s) a heavy chain comprising (i) the amino acid sequence of the VH of P1-069071 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-069071;

(t) a heavy chain comprising (i) the amino acid sequence of the VH of P1-069073 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-069073;

(u) a heavy chain comprising (i) the amino acid sequence of the VH of P1-069075 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-069075;

(v) a heavy chain comprising (i) the amino acid sequence of the VH of P1-069077 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-069077;

(w) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068736 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068736;

(x) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068738 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068738;

(y) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068740 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068740;

(z) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068742 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068742;

(aa) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068744 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068744;

(bb) a heavy chain comprising the amino acid sequence of the heavy chain f P1-068746 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068746;

(cc) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068748 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068748;

(dd) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068750 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068750;

(ee) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068752 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068752;

(ff) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068754 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068754;

(gg) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E55A and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068761_E55A;

(hh) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_H100G and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068761_H100G;

(ii) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E56N and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068761_E56N;

(jj) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E55A_E56N and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068761_E55A_E56N;

(kk) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E30D and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068761_E30D;

(ll) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E30D_E55A and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068761_E30D_E55A;

(mm) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E56N_H100G and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068761_E56N_H100G;

(nn) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E30D_H100G and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068761_E30D_H100G;

(oo) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E30D_E56N and (ii) the amino acid sequence of SEQ ID NO: 183, and a

light chain comprising the light chain amino acid sequence of P1-068761_E30D_E56N;

(pp) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E100fF and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068761_E100fF;

(qq) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E55A_E100fF and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068761_E55A_E100fF;

(rr) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_H100G_E100fF and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068761_H100G_E100fF;

(ss) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E30D_E100fF and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068761_E30D_E100fF;

(tt) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E56N_E100fF and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068761_E56N_E100fF;

(uu) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E32Y and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068761_E32Y;

(vv) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E32Y_E55A and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068761_E32Y_E55A;

(ww) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E32Y_E56N and (ii) the amino acid sequence of SEQ ID NO: 183, and a

light chain comprising the light chain amino acid sequence of P1-068761_E32Y_E56N;

(xx) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E30D_E32Y and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068761_E30D_E32Y;

(yy) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E32Y_H100G and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068761_E32Y_H100G;

(zz) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E32Y_E100fF and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068761_E32Y_E100fF;

(aaa) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_D52N_D102V and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068767_D52N_D102V;

(bbb) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_D52N and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068767_D52N;

(ccc) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_D52N_E55A and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068767_D52N_E55A;

(ddd) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_E55A_D102V and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068767_E55A_D102V;

(eee) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_D102V and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068767_D102V;

(fff) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_E55A and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068767_E55A;

(ggg) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_E30D_D52N and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068767_E30D_D52N;

(hhh) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_E30D_D102V and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068767_E30D_D102V;

(iii)a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_E30D and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068767_E30D;

(jjj)a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_E30D_E55A and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068767_E30D_E55A;

(kkk) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_E100fF_D102V and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068767_E100fF_D102V;

(lll)a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_E55A_E100fF and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068767_E55A_E100fF;

(mmm) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_D52N_E100fF and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068767_D52N_E100fF;

(nnn) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_E100fF and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068767_E100fF; or

(ooo) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_E30D_E100fF and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain comprising the light chain amino acid sequence of P1-068767_E30D_E100fF.

Certain embodiments of this disclosure include anti-VISTA Abs comprising:

(a) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-061029 (SEQ ID NO: 67) and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-061029 (SEQ ID NO: 70);

(b) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-061015 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-061015;

(c) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068757 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068757;

(d) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068759 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068759;

(e) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068761;

(f) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068763 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068763;

(g) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068765 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068765;

(h) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068767;

(i) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068769 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068769;

(j) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068771 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068771;

(k) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068773 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068773;

(l) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068775 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068775;

(m) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-069059 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-069059;

(n) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-069061 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-069061;

(o) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-069063 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-069063;

(p) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-069065 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-069065;

(q) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-069067 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-069067;

(r) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-069069 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-069069;

(s) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-069071 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-069071;

(t) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-069073 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-069073;

(u) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-069075 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-069075;

(v) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-069077 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-069077;

(w) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068736 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068736;

(x) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068738 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068738;

(y) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068740 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068740;

(z) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068742 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068742;

(aa) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068744 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068744;

(bb) a heavy chain consisting of the amino acid sequence of the heavy chain f P1-068746 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068746;

(cc) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068748 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068748;

(dd) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068750 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068750;

(ee) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068752 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068752;

(ff) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068754 and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068754;

(gg) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E55A and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068761_E55A;

(hh) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_H100G and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068761_H100G;

(ii) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E56N and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068761_E56N;

(jj) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E55A_E56N and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068761_E55A_E56N;

(kk) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E30D and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068761_E30D;

(ll) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E30D_E55A and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068761_E30D_E55A;

(mm) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E56N_H100G and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068761_E56N_H100G;

(nn) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E30D_H100G and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068761_E30D_H100G;

(oo) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E30D_E56N and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068761_E30D_E56N;

(pp) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E100fF and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068761_E100fF;

(qq) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E55A_E100fF and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068761_E55A_E100fF;

(rr) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_H100G_E100fF and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068761_H100G_E100fF;

(ss) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E30D_E100fF and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068761_E30D_E100fF;

(tt) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E56N_E100fF and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068761_E56N_E100fF;

(uu) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E32Y and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068761_E32Y;

(vv) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E32Y_E55A and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068761_E32Y_E55A;

(ww) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E32Y_E56N and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068761_E32Y_E56N;

(xx) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E30D_E32Y and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068761_E30D_E32Y;

(yy) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E32Y_H100G and (ii) the amino acid sequence of SEQ ID NO: 183, and a

light chain consisting of the light chain amino acid sequence of P1-068761_E32Y_H100G;

(zz) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E32Y_E100fF and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068761_E32Y_E100fF;

(aaa) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_D52N_D102V and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068767_D52N_D102V;

(bbb) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_D52N and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068767_D52N;

(ccc) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_D52N_E55A and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068767_D52N_E55A;

(ddd) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_E55A_D102V and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068767_E55A_D102V;

(eee) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_D102V and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068767_D102V;

(fff) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_E55A and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068767_E55A;

(ggg) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_E30D_D52N and (ii) the amino acid sequence of SEQ ID NO: 183, and a

light chain consisting of the light chain amino acid sequence of P1-068767_E30D_D52N;

(hhh) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_E30D_D102V and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068767_E30D_D102V;

(iii)a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_E30D and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068767_E30D;

(jjj)a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_E30D_E55A and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068767_E30D_E55A;

(kkk) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_E100fF_D102V and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068767_E100fF_D102V;

(lll)a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_E55A_E100fF and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068767_E55A_E100fF;

(mmm) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_D52N_E100fF and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068767_D52N_E100fF;

(nnn) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_E100fF and (ii) the amino acid sequence of SEQ ID NO: 183, and a light chain consisting of the light chain amino acid sequence of P1-068767_E100fF; or

(ooo) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_E30D_E100fF and (ii) the amino acid sequence of SEQ ID NO: 183, and a

light chain consisting of the light chain amino acid sequence of P1-068767_E30D_E100fF,

wherein the C-terminal amino acid of VH and the N-terminal amino acid of SEQ ID NO: 183 form a peptidic bond.

In some embodiments, the disclosure contemplates anti-VISTA mAbs comprising:

a heavy chain consisting of the amino acid sequences of (i) a VH of (a) to (ooo) listed above, (ii) SEQ ID NO: 183, and (iii) a Lys residue, wherein the C-terminal amino acid of VH and the N-terminal amino acid of SEQ ID NO: 183 form a peptidic bond and wherein the C-terminal amino acid of SEQ ID NO: 183 is joined to the N-terminal of the Lys; and

a light chain consisting of the light chain amino acid sequence of (a) to (ooo) listed above;

wherein the VH and light chain amino acid sequences are chosen from the same antibody species from among (a) to (ooo) listed above.

Further embodiments of this disclosure include anti-VISTA Abs comprising:

(a) a heavy chain comprising (i) the amino acid sequence of the VH of P1-061029 (SEQ ID NO: 67) and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-061029 (SEQ ID NO: 70);

(b) a heavy chain comprising (i) the amino acid sequence of the VH of P1-061015 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-061015;

(c) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068757 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068757;

(d) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068759 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068759;

(e) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068761;

(f) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068763 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068763;

(g) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068765 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068765;

(h) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068767;

(i) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068769 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068769;

(j) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068771 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068771;

(k) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068773 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068773;

(l) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068775 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068775;

(m) a heavy chain comprising (i) the amino acid sequence of the VH of P1-069059 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-069059;

(n) a heavy chain comprising (i) the amino acid sequence of the VH of P1-069061 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-069061;

(o) a heavy chain comprising (i) the amino acid sequence of the VH of P1-069063 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-069063;

(p) a heavy chain comprising (i) the amino acid sequence of the VH of P1-069065 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-069065;

(q) a heavy chain comprising (i) the amino acid sequence of the VH of P1-069067 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-069067;

(r) a heavy chain comprising (i) the amino acid sequence of the VH of P1-069069 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-069069;

(s) a heavy chain comprising (i) the amino acid sequence of the VH of P1-069071 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-069071;

(t) a heavy chain comprising (i) the amino acid sequence of the VH of P1-069073 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-069073;

(u) a heavy chain comprising (i) the amino acid sequence of the VH of P1-069075 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-069075;

(v) a heavy chain comprising (i) the amino acid sequence of the VH of P1-069077 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-069077;

(w) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068736 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068736;

(x) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068738 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068738;

(y) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068740 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068740;

(z) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068742 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068742;

(aa) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068744 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068744;

(bb) a heavy chain comprising the amino acid sequence of the heavy chain f P1-068746 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068746;

(cc) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068748 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068748;

(dd) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068750 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068750;

(ee) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068752 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068752;

(ff) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068754 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068754;

(gg) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E55A and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068761_E55A;

(hh) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_H100G and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068761_H100G;

(ii) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E56N and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068761_E56N;

(jj) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E55A_E56N and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068761_E55A_E56N;

(kk) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E30D and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068761_E30D;

(ll) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E30D_E55A and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068761_E30D_E55A;

(mm) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E56N_H100G and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068761_E56N_H100G;

(nn) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E30D_H100G and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068761_E30D_H100G;

(oo) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E30D_E56N and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068761_E30D_E56N;

(pp) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E100fF and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068761_E100fF;

(qq) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E55A_E100fF and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068761_E55A_E100fF;

(rr) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_H100G_E100fF and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068761_H100G_E100fF;

(ss) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E30D_E100fF and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068761_E30D_E100fF;

(tt) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E56N_E100fF and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068761_E56N_E100fF;

(uu) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E32Y and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068761_E32Y;

(vv) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E32Y_E55A and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068761_E32Y_E55A;

(ww) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E32Y_E56N and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068761_E32Y_E56N;

(xx) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E30D_E32Y and (ii) the amino acid sequence of SEQ ID NO: 184, and a

light chain comprising the light chain amino acid sequence of P1-068761_E30D_E32Y;

(yy) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E32Y_H100G and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068761_E32Y_H100G;

(zz) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068761_E32Y_E100fF and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068761_E32Y_E100fF;

(aaa) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_D52N_D102V and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068767_D52N_D102V;

(bbb) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_D52N and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068767_D52N;

(ccc) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_D52N_E55A and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068767_D52N_E55A;

(ddd) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_E55A_D102V and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068767_E55A_D102V;

(eee) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_D102V and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068767_D102V;

(fff) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_E55A and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068767_E55A;

(ggg) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_E30D_D52N and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068767_E30D_D52N;

(hhh) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_E30D_D102V and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068767_E30D_D102V;

(iii)a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_E30D and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068767_E30D;

(jjj)a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_E30D_E55A and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068767_E30D_E55A;

(kkk) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_E100fF_D102V and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068767_E100fF_D102V;

(lll)a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_E55A_E100fF and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068767_E55A_E100fF;

(mmm) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_D52N_E100fF and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068767_D52N_E100fF;

(nnn) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_E100fF and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068767_E100fF; or

(ooo) a heavy chain comprising (i) the amino acid sequence of the VH of P1-068767_E30D_E100fF and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain comprising the light chain amino acid sequence of P1-068767_E30D_E100fF.

Yet further embodiments of this disclosure include anti-VISTA Abs comprising:

(a) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-061029 (SEQ ID NO: 67) and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-061029 (SEQ ID NO: 70);

(b) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-061015 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-061015;

(c) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068757 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068757;

(d) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068759 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068759;

(e) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068761;

(f) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068763 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068763;

(g) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068765 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068765;

(h) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068767;

(i) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068769 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068769;

(j) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068771 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068771;

(k) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068773 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068773;

(l) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068775 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068775;

(m) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-069059 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-069059;

(n) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-069061 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-069061;

(o) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-069063 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-069063;

(p) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-069065 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-069065;

(q) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-069067 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-069067;

(r) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-069069 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-069069;

(s) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-069071 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-069071;

(t) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-069073 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-069073;

(u) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-069075 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-069075;

(v) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-069077 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-069077;

(w) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068736 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068736;

(x) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068738 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068738;

(y) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068740 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068740;

(z) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068742 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068742;

(aa) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068744 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068744;

(bb) a heavy chain consisting of the amino acid sequence of the heavy chain f P1-068746 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068746;

(cc) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068748 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068748;

(dd) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068750 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068750;

(ee) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068752 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068752;

(ff) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068754 and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068754;

(gg) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E55A and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068761_E55A;

(hh) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_H100G and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068761_H100G;

(ii) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E56N and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068761_E56N;

(jj) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E55A_E56N and (ii) the amino acid sequence of SEQ ID NO: 184, and a

light chain consisting of the light chain amino acid sequence of P1-068761_E55A_E56N;

(kk) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E30D and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068761_E30D;

(ll) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E30D_E55A and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068761_E30D_E55A;

(mm) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E56N_H100G and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068761_E56N_H100G;

(nn) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E30D_H100G and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068761_E30D_H100G;

(oo) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E30D_E56N and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068761_E30D_E56N;

(pp) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E100fF and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068761_E100fF;

(qq) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E55A_E100fF and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068761_E55A_E100fF;

(rr) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_H100G_E100fF and (ii) the amino acid sequence of SEQ ID NO: 184, and a

light chain consisting of the light chain amino acid sequence of P1-068761_H100G_E100fF;

(ss)a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E30D_E100fF and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068761_E30D_E100fF;

(tt) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E56N_E100fF and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068761_E56N_E100fF;

(uu) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E32Y and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068761_E32Y;

(vv) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E32Y_E55A and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068761_E32Y_E55A;

(ww) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E32Y_E56N and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068761_E32Y_E56N;

(xx) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E30D_E32Y and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068761_E30D_E32Y;

(yy) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E32Y_H100G and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068761_E32Y_H100G;

(zz) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068761_E32Y_E100fF and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068761_E32Y_E100fF;

(aaa) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_D52N_D102V and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068767_D52N_D102V;

(bbb) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_D52N and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068767_D52N;

(ccc) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_D52N_E55A and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068767_D52N_E55A;

(ddd) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_E55A_D102V and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068767_E55A_D102V;

(eee) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_D102V and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068767_D102V;

(fff) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_E55A and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068767_E55A;

(ggg) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_E30D_D52N and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068767_E30D_D52N;

(hhh) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_E30D_D102V and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068767_E30D_D102V;

(iii)a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_E30D and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068767_E30D;

(jjj)a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_E30D_E55A and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068767_E30D_E55A;

(kkk) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_E100fF_D102V and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068767_E100fF_D102V;

(lll)a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_E55A_E100fF and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068767_E55A_E100fF;

(mmm) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_D52N_E100fF and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068767_D52N_E100fF;

(nnn) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_E100fF and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068767_E100fF; or

(ooo) a heavy chain consisting of (i) the amino acid sequence of the VH of P1-068767_E30D_E100fF and (ii) the amino acid sequence of SEQ ID NO: 184, and a light chain consisting of the light chain amino acid sequence of P1-068767_E30D_E100fF,

wherein the C-terminal amino acid of VH and the N-terminal amino acid of SEQ ID NO: 184 form a peptidic bond.

In some embodiments, the disclosure contemplates anti-VISTA mAbs comprising:

a heavy chain consisting of the amino acid sequences of (i) a VH of (a) to (ooo) listed above, (ii) SEQ ID NO: 184, and (iii) a Lys residue, wherein the C-terminal amino acid of VH and the N-terminal amino acid of SEQ ID NO: 184 form a peptidic bond and wherein the C-terminal amino acid of SEQ ID NO: 184 is joined to the N-terminal of the Lys; and

a light chain consisting of the light chain amino acid sequence of (a) to (ooo) listed above;

wherein the VH and light chain amino acid sequences are chosen from the same antibody species from among (a) to (ooo) listed above.

In some embodiments, an anti-hVISTA Ab may comprise an amino acid VH sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to that of P1-061029, wherein the antibody comprises a VH CDR1, CDR2, and/or CDR3 of P1-061029 in which at least one residue has been substituted with a D, an E, or an H. In some embodiments, each of the VH CDR1, CDR2, and CDR3 of P1-061029 contains one, two, or three residues substituted with a D, E, or H. In some embodiments, an anti-hVISTA Ab may comprise an amino acid VH sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to that of P1-061029, wherein the antibody comprises a VH CDR1 comprising one or two D or E residues at amino acid positions 4, 5, or 7 of CDR1, and/or comprises a VH CDR2 with one, two, or three D, E, or H residues at positions 3, 5, 6, or 7 of CDR2, and/or a VH CDR3 with one, two, or three D, E, or H residues at positions 6, 12, or 14 of CDR 3. (See Table 5 below for examples os antibodies falling within these embodiments.) In such cases, the light chain variable region may comprise the CDR1, CDR2, and/or CDR3 of P1-061029 or P1-061015 or progeny thereof, such as P1-061029, P1-068757, P1-068759, P1-068761, P1-068763,

P1-068765, P1-068767, P1-068769, P1-068771, P1-068773, P1-068775, P1-069059, P1-069061, P1-069063, P1-069065, P1-069067, P1-069069, P1-069071, P1-069073, P1-069075, P1-069077, P1-061015, P1-068736, P1-068738, P1-068740, P1-068742, P1-068744, P1-068766, P1-068748, P1-068750, P1-068752 P1-068754, P1-068761_E55A, P1-068761_H100G, P1-068761_E56N, P1-068761_E55A_E56N, P1-068761_E30D, P1-068761_E30D_E55A, P1-068761_E56N_H100G, P1-068761_E30D_H100G, P1-068761_E30D_E56N, P1-068761_E100fF, P1-068761_E55A_E100fF, P1-068761_H100G_E100fF, P1-068761_E30D_E100fF, P1-068761_E56N_E100fF, P1-068761_E32Y, P1-068761_E32Y_E55A, P1-068761_E32Y_E56N, P1-068761_E30D_E32Y, P1-068761_E32Y_H100G, P1-068761_E32Y_E100fF, P1-068767_D52N_D102V, P1-068767_D52N, P1-068767_D52N_E55A, P1-068767_E55A_D102V, P1-068767_D102V, P1-068767_E55A, P1-068767_E30D_D52N, P1-068767_E30D_D102V, P1-068767_E30D, P1-068767_E30D_E55A, P1-068767_E100fF_D102V, P1-068767_E55A_E100fF, P1-068767_D52N_E100fF, P1-068767_E100fF, or P1-068767_E30D_E100fF, and/or the light chain variable region may be at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to that of P1-061029 or P1-061015 or progeny thereof, such as P1-061029, P1-068757, P1-068759, P1-068761, P1-068763, P1-068765, P1-068767, P1-068769, P1-068771, P1-068773, P1-068775, P1-069059, P1-069061, P1-069063, P1-069065, P1-069067, P1-069069, P1-069071, P1-069073, P1-069075, P1-069077, P1-061015, P1-068736, P1-068738, P1-068740, P1-068742, P1-068744, P1-068766, P1-068748, P1-068750, P1-068752 P1-068754, P1-068761_E55A, P1-068761_H100G, P1-068761_E56N, P1-068761_E55A_E56N, P1-068761_E30D, P1-068761_E30D_E55A, P1-068761_E56N_H100G, P1-068761_E30D_H100G, P1-068761_E30D_E56N, P1-068761_E100fF, P1-068761_E55A_E100fF, P1-068761_H100G_E100fF, P1-068761_E30D_E100fF, P1-068761_E56N_E100fF, P1-068761_E32Y, P1-068761_E32Y_E55A, P1-068761_E32Y_E56N, P1-068761_E30D_E32Y, P1-068761_E32Y_H100G, P1-068761_E32Y_E100fF, P1-068767_D52N_D102V, P1-068767_D52N, P1-068767_D52N_E55A, P1-068767_E55A_D102V, P1-068767_D102V, P1-068767_E55A, P1-068767_E30D_D52N,

P1-068767_E30D_D102V, P1-068767_E30D, P1-068767_E30D_E55A, P1-068767_E100fF_D102V, P1-068767_E55A_E100fF, P1-068767_D52N_E100fF, P1-068767_E100fF, or P1-068767_E30D_E100fF.

In some embodiments, an anti-hVISTA Ab may comprise an amino acid VH sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to that of P1-061015, wherein the antibody comprises a VH CDR1, CDR2, and/or CDR3 of P1-061015 in which at least one residue has been substituted with a D, an E, or an H. In some embodiments, each of the VH CDR1, CDR2, and CDR3 of P1-061015 contains one, two, or three residues substituted with a D, E, or H. In some embodiments, an anti-hVISTA Ab may comprise an amino acid VH sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to that of P1-061015, wherein the antibody comprises a VH CDR1 comprising one or two D, E, or H residues at amino acid positions 6, 7, 8, and 9 of CDR1, and/or comprises a VH CDR2 with one, two, or three D, E, or H residues at positions 1, 2, 4, or 8-11 of CDR2, and/or a VH CDR3 with one, two, or three D, E, or H residues at positions 2, 3, 6, 7, or 12 of CDR 3. (See Table 6 below for examples os antibodies falling within these embodiments.) In such cases, the light chain variable region may comprise the CDR1, CDR2, and/or CDR3 of P1-061029 or P1-061015 or progeny thereof, such as P1-061029, P1-068757, P1-068759, P1-068761, P1-068763, P1-068765, P1-068767, P1-068769, P1-068771, P1-068773, P1-068775, P1-069059, P1-069061, P1-069063, P1-069065, P1-069067, P1-069069, P1-069071, P1-069073, P1-069075, P1-069077, P1-061015, P1-068736, P1-068738, P1-068740, P1-068742, P1-068744, P1-068766, P1-068748, P1-068750, P1-068752 P1-068754, P1-068761_E55A, P1-068761_H100G, P1-068761_E56N, P1-068761_E55A_E56N, P1-068761_E30D, P1-068761_E30D_E55A, P1-068761_E56N_H100G, P1-068761_E30D_H100G, P1-068761_E30D_E56N, P1-068761_E100fF, P1-068761_E55A_E100fF, P1-068761_H100G_E100fF, P1-068761_E30D_E100fF, P1-068761_E56N_E100fF, P1-068761_E32Y, P1-068761_E32Y_E55A, P1-068761_E32Y_E56N, P1-068761_E30D_E32Y, P1-068761_E32Y_H100G, P1-068761_E32Y_E100fF, P1-068767_D52N_D102V, P1-068767_D52N, P1-

068767_D52N_E55A, P1-068767_E55A_D102V, P1-068767_D102V, P1-068767_E55A, P1-068767_E30D_D52N, P1-068767_E30D_D102V, P1-068767_E30D, P1-068767_E30D_E55A, P1-068767_E100fF_D102V, P1-068767_E55A_E100fF, P1-068767_D52N_E100fF, P1-068767_E100fF, or P1-068767_E30D_E100fF, and/or the light chain variable region may be at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical to that of P1-061029 or P1-061015 or progeny thereof, such as P1-061029, P1-068757, P1-068759, P1-068761, P1-068763, P1-068765, P1-068767, P1-068769, P1-068771, P1-068773, P1-068775, P1-069059, P1-069061, P1-069063, P1-069065, P1-069067, P1-069069, P1-069071, P1-069073, P1-069075, P1-069077, P1-061015, P1-068736, P1-068738, P1-068740, P1-068742, P1-068744, P1-068766, P1-068748, P1-068750, P1-068752 P1-068754, P1-068761_E55A, P1-068761_H100G, P1-068761_E56N, P1-068761_E55A_E56N, P1-068761_E30D, P1-068761_E30D_E55A, P1-068761_E56N_H100G, P1-068761_E30D_H100G, P1-068761_E30D_E56N, P1-068761_E100fF, P1-068761_E55A_E100fF, P1-068761_H100G_E100fF, P1-068761_E30D_E100fF, P1-068761_E56N_E100fF, P1-068761_E32Y, P1-068761_E32Y_E55A, P1-068761_E32Y_E56N, P1-068761_E30D_E32Y, P1-068761_E32Y_H100G, P1-068761_E32Y_E100fF, P1-068767_D52N_D102V, P1-068767_D52N, P1-068767_D52N_E55A, P1-068767_E55A_D102V, P1-068767_D102V, P1-068767_E55A, P1-068767_E30D_D52N, P1-068767_E30D_D102V, P1-068767_E30D, P1-068767_E30D_E55A, P1-068767_E100fF_D102V, P1-068767_E55A_E100fF, P1-068767_D52N_E100fF, P1-068767_E100fF, or P1-068767_E30D_E100fF.

In some embodiments, such modified anti-hVISTA P1-061029 or P1-061015 progeny possess one or more of the following characteristics:

- specifically binding to hVISTA, e.g., histidine rich region of the ECD or a polypeptide comprising amino acid residues 35-127 of SEQ ID NO: 2, at acidic pH, e.g., pH 6.0 or pH 6.5;
- lacking of significant binding to hVISTA, e.g., histidine rich region of the ECD or a polypeptide comprising amino acid residues 35-127 of SEQ ID NO: 2, at physiological pH or neutral pH, e.g., pH 7.4 or pH 7.0;

- specifically binding to cyno VISTA, e.g., histidine rich region of the ECD, at acidic pH, e.g., pH 6.0 or pH 6.5;
- lacking of significant binding to cyno VISTA, e.g., histidine rich region of the ECD, at physiological pH or neutral pH, e.g., pH 7.4 or pH 7.0;
- having reduced binding to hVISTA-ECD having a substitution at one or more of the following amino acids: T35, Y37, K38, T39, Y41, R54, T61, F62, Q63, L65, H66, L67, H68, H69, F97, L115, V117, I119, H121, H122, S124, E125, R127 relative to hVISTA ECD having SEQ ID NO: 2;
- cross-competiting for binding to hVISTA with P1-061029, P1-068761, P1-068767 and/or P1-061015;
- inhibiting binding of hVISTA to human T cells at acidic pH e.g., pH 6.0 or pH 6.5;
- inhibiting binding of hVISTA to PSGL-1 at acidic pH e.g., pH 6.0 or pH 6.5;
- a mean residence time of at least 350 hours in cynomolgus monkeys;
- stimulating T cell activation;
- inhibiting VISTA mediated cell:cell adhesion; and
- specifically binding to hVISTA in samples of human tumor cells or samples of inflamed human tissue.

Exemplary Antibody Constant Regions

In some embodiments, an antibody described herein comprises one or more human constant regions. In some embodiments, the human heavy chain constant region is of an isotype selected from IgA, IgG, and IgD. In some embodiments, the human light chain constant region is of an isotype selected from κ and λ. In some embodiments, an antibody described herein comprises a human IgG constant region, such as an IgG1, IgG2, IgG3, or IgG4. In some embodiments, an antibody described herein comprises a human IgG4 heavy chain constant region. In some such embodiments, an antibody described herein comprises an S241P mutation in the human IgG4 constant region. In some embodiments, an antibody described herein comprises a human IgG4 constant region and a human κ light chain.

The choice of heavy chain constant region can determine whether or not an antibody will have effector function *in vivo*. Such effector function, in some embodiments, includes

antibody-dependent cell-mediated cytotoxicity (ADCC) and/or complement-dependent cytotoxicity (CDC), and can result in killing of the cell to which the antibody is bound. In some methods of treatment, including methods of treating some cancers, cell killing may be desirable, for example, when the antibody binds to a cell that supports the maintenance or growth of the tumor. Exemplary cells that may support the maintenance or growth of a tumor include, but are not limited to, tumor cells themselves, cells that aid in the recruitment of vasculature to the tumor, and cells that provide ligands, growth factors, or counter-receptors that support or promote tumor growth or tumor survival. In some embodiments, when effector function is desirable, an antibody comprising a human IgG1 heavy chain or a human IgG3 heavy chain is selected.

In certain embodiments, an antibody provided herein is altered to increase or decrease the extent to which the antibody is glycosylated. Addition or deletion of glycosylation sites to an antibody may be conveniently accomplished by altering the amino acid sequence such that one or more glycosylation sites is created or removed.

Where the antibody comprises an Fc region, the carbohydrate attached thereto may be altered. Native antibodies produced by mammalian cells typically comprise a branched, biantennary oligosaccharide that is generally attached by an N-linkage to Asn297 of the CH2 domain of the Fc region. See, *e.g.*, Wright *et al. TIBTECH* 15:26-32 (1997). The oligosaccharide may include various carbohydrates, *e.g.*, mannose, N-acetyl glucosamine (GlcNAc), galactose, and sialic acid, as well as a fucose attached to a GlcNAc in the "stem" of the biantennary oligosaccharide structure. In some embodiments, modifications of the oligosaccharide in an antibody of the invention may be made in order to create antibodies with certain improved properties. For example, in some embodiments an antibody may be afucosylated, for example, by mutating residues such as Asn297 that are normally glycosylated with fucose-containing glycosylations, or through other means. In some embodiments, antibodies herein may comprise an afucosylated human IgG1 constant region.

Antibodies are further provided with bisected oligosaccharides, *e.g.*, in which a biantennary oligosaccharide attached to the Fc region of the antibody is bisected by GlcNAc. Such antibodies may have reduced fucosylation and/or improved ADCC function. Examples of such antibodies are described, *e.g.*, in WO 2003/011878 (Jean-Mairet *et al.*); US Patent

No. 6,602,684 (Umana *et al.*); and US 2005/0123546 (Umana *et al.*). Antibodies with at least one galactose residue in the oligosaccharide attached to the Fc region are also provided. Such antibodies may have improved CDC function. Such antibodies are described, *e.g.*, in WO 1997/30087 (Patel *et al.*); WO 1998/58964 (Raju, S.); and WO 1999/22764 (Raju, S.).

Antibodies are also provided with amino-terminal leader extensions. For example, one or more amino acid residues of the amino-terminal leader sequence are present at the amino-terminus of any one or more heavy or light chains of an antibody. An exemplary amino-terminal leader extension comprises or consists of three amino acid residues, VHS, present on one or both light chains of an antibody.

The *in vivo* or serum half-life of human FcRn high affinity binding polypeptides can be assayed, *e.g.*, in transgenic mice, in humans, or in non-human primates to which the polypeptides with a variant Fc region are administered. See also, *e.g.*, Petkova *et al.* *International Immunology* 18(12):1759-1769 (2006).

In some embodiments of the invention, an afucosylated antibody mediates ADCC in the presence of human effector cells more effectively than a parent antibody that comprises fucose, Generally, ADCC activity may be determined using the *in vitro* ADCC assay as herein disclosed, but other assays or methods for determining ADCC activity, *e.g.* in an animal model *etc.*, are contemplated.

In certain embodiments, the Fc region is altered by replacing at least one amino acid residue with a different amino acid residue to alter the effector function(s) of the antibody. For example, one or more amino acids selected from amino acid residues 234, 235, 236, 237, 297, 318, 320, 322, 330, and/or 331 can be replaced with a different amino acid residue such that the antibody has an altered affinity for an effector ligand but retains the antigen-binding ability of the parent antibody. The effector ligand to which affinity is altered can be, for example, an Fc receptor or the C1 component of complement. This approach is described in further detail in U.S. Patent Nos. 5,624,821 and 5,648,260, both by Winter *et al.*

In some examples, one or more amino acids selected from amino acid residues 329, 331 and 322 can be replaced with a different amino acid residue such that the antibody has altered C1q binding and/or reduced or abolished complement dependent cytotoxicity (CDC). This approach is described in further detail in U.S. Patent Nos. 6,194,551 by Idusogie *et al.*

In some examples, one or more amino acid residues within amino acid positions 231 and 239 are altered to thereby alter the ability of the antibody to fix complement. This approach is described further in PCT Publication WO 94/29351 by Bodmer *et al.* In some examples, the Fc region can be modified to decrease antibody dependent cellular cytotoxicity (ADCC) and/or to decrease the affinity for an Fcγ receptor by modifying one or more amino acids at the following positions: 234, 235, 236, 238, 239, 240, 241 , 243, 244, 245, 247, 248, 249, 252, 254, 255, 256, 258, 262, 263, 264, 265, 267, 268, 269, 270, 272, 276, 278, 280, 283, 285, 286, 289, 290, 292, 293, 294, 295, 296, 298, 299, 301, 303, 305, 307, 309, 312, 313, 315, 320, 322, 324, 325, 326, 327, 329, 330, 331, 332, 333, 334, 335, 337, 338, 340, 360, 373, 376, 378, 382, 388, 389, 398, 414, 416, 419, 430, 433, 434, 435, 436, 437, 438 or 439. Exemplary substitutions include 236A, 239D, 239E, 268D, 267E, 268E, 268F, 324T, 332D, and 332E. Exemplary variants include 239D/332E, 236A/332E, 236A/239D/332E, 268F/324T, 267E/268F, 267E/324T, and 267E/268F7324T. Other Fc modifications that can be made to Fcs are those for reducing or ablating binding to FcγR and/or complement proteins, thereby reducing or ablating Fc-mediated effector functions such as ADCC, ADCP, and CDC. Exemplary modifications include but are not limited substitutions, insertions, and deletions at positions 234, 235, 236, 237, 267, 269, 325, 328, 330, and/or 331 (*e.g.,* 330 and 331), wherein numbering is according to the EU index. Exemplary substitutions include but are not limited to 234A, 235E, 236R, 237A, 267R, 269R, 325L, 328R, 330S, and 331S (*e.g.,* 330S, and 331S), wherein numbering is according to the EU index. An Fc variant can comprise 236R/328R. Other modifications for reducing FcγR and complement interactions include substitutions 297A, 234A, 235A, 237A, 318A, 228P, 236E, 268Q, 309L, 330S, 331 S, 220S, 226S, 229S, 238S, 233P, and 234V, as well as removal of the glycosylation at position 297 by mutational or enzymatic means or by production in organisms such as bacteria that do not glycosylate proteins. These and other modifications are reviewed in Strohl, 2009, *Current Opinion in Biotechnology* 20:685-691. For example, the human IgG1.3 Fc constant region contains L234A, L235E, and G237A substitutions. The IgG1fa.P238K (or IgG1.P238K) contains a P238K substitution. The IgG1.1f omprises L234A, L235E, G237A, A330S, and P331S substitutions.

Fc variants that enhance affinity for an inhibitory receptor FcγRIIb can also be used. Such variants can provide an Fc fusion protein with immunomodulatory activities related to FcγRIIb cells, including for example B cells and monocytes. In one embodiment, the Fc variants provide selectively enhanced affinity to FcγRIIb relative to one or more activating receptors. Modifications for altering binding to FcγRIIb include one or more modifications at a position selected from the group consisting of 234, 235, 236, 237, 239, 266, 267, 268, 325, 326, 327, 328, 330, 331, and 332, according to the EU index. Exemplary substitutions for enhancing FcγRllb affinity include but are not limited to 234A, 234D, 234E, 234F, 234W, 235D, 235E, 235F, 235R, 235Y, 236D, 236N, 237A, 237D, 237N, 239D, 239E, 266M, 267D, 267E, 268D, 268E, 327D, 327E, 328F, 328W, 328Y, 330S, 331S, and 332E. Exemplary substitutions include 235Y, 236D, 239D, 266M, 267E, 268D, 268E, 328F, 328W, and 328Y. Other Fc variants for enhancing binding to FcγRIIb include 235Y/267E, 236D/267E, 239D/268D, 239D/267E, 267E/268D, 267E/268E, and 267E/328F.

Other modifications for enhancing FcγR and complement interactions include but are not limited to substitutions 298 A, 333A, 334A, 326A, 2471, 339D, 339Q, 280H, 290S, 298D, 298V, 243L, 292P, 300L, 396L, 3051, and 396L. These and other modifications are reviewed in Strohl, 2009, Current Opinion in Biotechnology 20:685-691. Fc modifications that increase binding to an Fcγ receptor include amino acid modifications at any one or more of amino acid positions 238, 239, 248, 249, 252, 254, 255, 256, 258, 265, 267, 268, 269, 270, 272, 279, 280, 283, 285, 298, 289, 290, 292, 293, 294, 295, 296, 298, 301, 303, 305, 307, 312, 315, 324, 327, 329, 330, 335, 337, 338, 340, 360, 373, 376, 379, 382, 388, 389, 398, 414, 416, 419, 430, 434, 435, 437, 438 or 439 of the Fc region, wherein the numbering of the residues in the Fc region is that of the EU index as in Patent Publication No. WO 00/42072.

Optionally, the Fc region can comprise a non-naturally occurring amino acid residue at additional and/or alternative positions known to one skilled in the art (see, *e.g.,* U.S. Pat. Nos. 5,624,821; 6,277,375; 6,737,056; 6,194,551; 7,317,091; 8,101,720; PCX Patent Publications WO 00/42072; WO 01/58957; WO 02/06919; WO 04/016750; WO 04/029207; WO 04/035752; WO 04/074455; WO 04/099249; WO 04/063351; WO 05/070963; WO 05/040217, WO 05/092925 and WO 06/0201 14).

The affinities and binding properties of an Fc region for its ligand can be determined by a variety of *in vitro* assay methods (biochemical or immunological based assays) known in the art including but not limited to, equilibrium methods (*e.g.,* enzyme-linked immunoabsorbent assay (ELISA), or radioimmunoassay (RIA)), or kinetics (*e.g.,* BIACORE analysis), and other methods such as indirect binding assays, competitive inhibition assays, fluorescence resonance energy transfer (FRET), gel electrophoresis and chromatography (*e.g.,* gel filtration). These and other methods can utilize a label on one or more of the components being examined and/or employ a variety of detection methods including but not limited to chromogenic, fluorescent, luminescent, or isotopic labels. A detailed description of binding affinities and kinetics can be found in Paul, W. E., ed., Fundamental immunology, 4th Ed., Lippincott-Raven, Philadelphia (1999), which focuses on antibody-immunogen interactions.

In certain embodiments, the antibody is modified to increase its biological half-life. Various approaches are possible. For example, this can be done by increasing the binding affinity of the Fc region for FcRn, For example, one or more of more of following residues can be mutated: 252, 254, 256, 433, 435, 436, as described in U.S. Pat. No. 6,277,375. Specific exemplary substitutions include one or more of the following: T252L, T254S, and/or T256F. Alternatively, to increase the biological half life, the antibody can be altered within the CH1 or CL region to contain a salvage receptor binding epitope taken from two loops of a CH2 domain of an Fc region of an IgG, as described in U.S. Patent Nos. 5,869,046 and 6,121,022 by Presta *et al.* Other exemplary variants that increase binding to FcRn and/or improve pharmacokinetic properties include substitutions at positions 259, 308, 428, and 434, including for example 2591, 308F, 428L, 428M, 434S, 4341 1. 434F, 434Y, and 434X1. Other variants that increase Fc binding to FcRn include: 250E, 250Q, 428 L, 428F, 250Q/428L (Hinton *et al.* 2004, *J. Biol. Chem.* 279(8): 6213-6216, Hinton *et al.* 2006 *Journal of Immunology* 176:346-356), 256A, 272A, 286A, 305A, 307A, 307Q, 31 1A, 312A, 376A, 378Q, 380A, 382A, 434A (Shields *et al.*, *Journal of Biological Chemistry*, 2001, 276(9):6591-6604), 252F, 252T, 252Y, 252W, 254T, 256S, 256R, 256Q, 256E, 256D, 256T, 309P, 31 1 S, 433R, 433S, 4331, 433P, 433Q, 434H, 434F, 434Y, 252Y/254T/256E, 433K/434F/436H, 308T/309P/311S (Dall Acqua *et al. Journal of Immunology*, 2002,

169:5171-5180, Dall'Acqua *et al.*, 2006, *Journal of Biological Chemistry* 281:23514-23524). Other modifications for modulating FcRn binding are described in Yeung *et al.*, 2010, *J Immunol*, 182:7663-7671.

In certain embodiments, hybrid IgG isotypes with particular biological characteristics can be used. For example, an IgG1/IgG3 hybrid variant can be constructed by substituting IgG1 positions in the CH2 and/or CH3 region with the amino acids from IgG3 at positions where the two isotypes differ. Thus a hybrid variant IgG antibody can be constructed that comprises one or more substitutions, *e.g.,* 274Q, 276K, 300F, 339T, 356E, 358M, 384S, 392N, 397M, 4221, 435R, and 436F. In some embodiments described herein, an IgG1/IgG2 hybrid variant can be constructed by substituting IgG2 positions in the CH2 and/or CH3 region with amino acids from IgG1 at positions where the two isotypes differ. Thus a hybrid variant IgG antibody can be constructed that comprises one or more substitutions, *e.g.,* one or more of the following amino acid substitutions: 233E, 234L, 235L, -236G (referring to an insertion of a glycine at position 236), and 327A.

Moreover, the binding sites on human IgG1 for FcγRI, FcγRII, FcγRIII and FcRn have been mapped and variants with improved binding have been described (see Shields, R.L. *et al.* (2001) *J. Biol. Chem.* 276:6591-6604). Specific mutations at positions 256, 290, 298, 333, 334 and 339 were shown to improve binding to FcγRIII. Additionally, the following combination mutants were shown to improve FcγRIII binding: T256A/S298A, S298A/E333A, S298A/K224A and S298A/E333A/K334A, which has been shown to exhibit enhanced FcγRIIIa binding and ADCC activity (Shields *et al.*, 2001). Other IgG1 variants with strongly enhanced binding to FcγRIIIa have been identified, including variants with S239D/I332E and S239D/I332E/A330L mutations which showed the greatest increase in affinity for FcγRIIIa, a decrease in FcγRIIb binding, and strong cytotoxic activity in cynomolgus monkeys (Lazar *et al.*, 2006). Introduction of the triple mutations into antibodies such as alemtuzumab (CD52-specific), trastuzumab (HER2/neu-specific), rituximab (CD20-specific), and cetuximab (EGFR- specific) translated into greatly enhanced ADCC activity *in vitro*, and the S239D/I332E variant showed an enhanced capacity to deplete B cells in monkeys (Lazar *et al.*, 2006). In addition, IgG1 mutants containing L235V, F243L, R292P, Y300L and P396L mutations which exhibited enhanced binding to FcγRIIIa and

concomitantly enhanced ADCC activity in transgenic mice expressing human FcγRIIIa in models of B cell malignancies and breast cancer have been identified (Stavenhagen *et al.*, 2007; Nordstrom *et al.*, 2011). Other Fc mutants that can be used include: S298A/E333A/L334A, S239D/I332E, S239D/I332E/A330L, L235V/F243L/R292P/Y300L/ P396L, and M428L/N434S.

In certain embodiments, an Fc is chosen that has reduced binding to FcγRs. An exemplary Fc, *e.g.,* IgG1 Fc, with reduced FcγR binding comprises the following three amino acid substitutions: L234A, L235E and G237A.

In certain embodiments, an Fc is chosen that has reduced complement fixation. An exemplary Fc, *e.g.,* IgG1 Fc, with reduced complement fixation has the following two amino acid substitutions: A330S and P331S.

In certain embodiments, an Fc is chosen that has essentially no effector function, *i.e.,* it has reduced binding to FcγRs and reduced complement fixation. An exemplary Fc, *e.g.,* IgG1 Fc, that is effectorless comprises the following five mutations: L234A, L235E, G237A, A330S and P331S.

When using an IgG4 constant domain, it can include the substitution S228P, which mimics the hinge sequence in IgG1 and thereby stabilizes IgG4 molecules.

Fc modifications described in WO 2017/087678 or WO2016081746 may also be used.

In certain embodiments, the glycosylation of an antibody is modified. For example, an aglycoslated antibody can be made (*i.e.,* the antibody lacks glycosylation). Glycosylation can be altered to, for example, increase the affinity of the antibody for antigen. Such carbohydrate modifications can be accomplished by, for example, altering one or more sites of glycosylation within the antibody sequence. For example, one or more amino acid substitutions can be made that result in elimination of one or more variable region framework glycosylation sites to thereby eliminate glycosylation at that site. Such aglycosylation can increase the affinity of the antibody for antigen. Such an approach is described in further detail in U.S. Patent Nos. 5,714,350 and 6,350,861 by Co *et al.*

Glycosylation of the constant region on N297 can be prevented by mutating the N297 residue to another residue, *e.g.,* N297A, and/or by mutating an adjacent amino acid, *e.g.,* 298 to thereby reduce glycosylation on N297.

Additionally or alternatively, an antibody can be made that has an altered type of glycosylation, such as a hypofucosylated antibody having reduced amounts of fucosyl residues or an antibody having increased bisecting GlcNac structures. Such altered glycosylation patterns have been demonstrated to increase the ADCC ability of antibodies. Such carbohydrate modifications can be accomplished by, for example, expressing the antibody in a host cell with altered glycosylation machinery. Cells with altered glycosylation machinery have been described in the art and can be used as host cells in which to express recombinant antibodies described herein to thereby produce an antibody with altered glycosylation. For example, EP 1,176,195 by Hanai *et al.* describes a cell line with a functionally disrupted FUT8 gene, which encodes a fucosyl transferase, such that antibodies expressed in such a cell line exhibit hypofucosylation. PCT Publication WO 03/035835 by Presta describes a variant CHO cell line, Led 3 cells, with reduced ability to attach fucose to Asn(297)-linked carbohydrates, also resulting in hypofucosylation of antibodies expressed in that host cell (see also Shields, R.L. *et al.* (2002) *J. Biol. Chem.* 277:26733-26740). PCT Publication WO 99/54342 by Umana *et al.* describes cell lines engineered to express glycoprotein-modifying glycosyl transferases {*e.g.,* beta(l,4)-N-acetylglucosaminyltransferase III (GnTIII)) such that antibodies expressed in the engineered cell lines exhibit increased bisecting GlcNac structures which results in increased ADCC activity of the antibodies (see also Umana *et al.* (1999) *Nat. Biotech.* 17: 176-180).

Another modification of the antibodies described herein is pegylation. An antibody can be pegylated to, for example, increase the biological (*e.g.,* serum) half-life of the antibody. To pegylate an antibody, the antibody, or fragment thereof, typically is reacted with polyethylene glycol (PEG), such as a reactive ester or aldehyde derivative of PEG, under conditions in which one or more PEG groups become attached to the antibody or antibody fragment. In some embodiments, the pegylation is carried out via an acylation reaction or an alkylation reaction with a reactive PEG molecule (or an analogous reactive water-soluble polymer). As used herein, the term "polyethylene glycol" is intended to

encompass any of the forms of PEG that have been used to derivatize other proteins, such as mono (CI-CIO) alkoxy- or aryloxy-polyethylene glycol or polyethylene glycol-maleimide. In certain embodiments, the antibody to be pegylated is an aglycosylated antibody. Methods for pegylating proteins are known in the art and can be applied to the antibodies described herein. See for example, EP 0 154 316 by Nishimura *et al.* and EP 0 401 384 by Ishikawa *et al.*

Nucleic Acids and Host Cells

Also provided are nucleic acids encoding an antibody or a heavy or light chain thereof or a portion thereof. Exemplary nucleic acids are provided in the Sequence Table. Any nucleic acid that is at least 80%, 85%, 90%, 95%, 97%, 98% or 99% to a nucleic acid in the Sequence Table is encompassed herein. Compositions comprising nucleic acids encoding an antibody provided herein are also encompassed, as are cells comprising these and methods for preparing antibodies, comprising culturing a cell transformed with a nucleic acid encoding an anti-VISTA antibody, and isolating the antibody from the medium or the cell.

Methods of Treatment using VISTA-ECD Binding Abs and Related Pharmaceutical Compositions

In certain embodiments, an anti-VISTA antibody that binds to VISTA at low pH and, e.g., lacks significant binding at neutral or physiological pH, can be a VISTA antagonist antibody, i.e., an antibody that inhibits the action of VISTA, such that an immune response is stimulated. Such antibodies may be used for treating diseases in which stimulating the immune system or an immune response is desired, such as proliferative diseases (benign or malignant), cancer, and infectious diseases (e.g., viral infections).

In certain embodiments, an anti-VISTA antibody that binds to VISTA at low pH and, e.g., lacks significant binding at neutral or physiological pH can be a VISTA agonist antibody, i.e., an antibody that increases the action of VISTA, such that an immune response is inhibited. Such antibodies may be used for treating diseases in which inhibition of the immune system or an immune response is desired, such as autoimmune diseases and inflammatory conditions, such as rheumatoid arthritis, systemic lupus erythematosus, celiac

disease, Sjoigren's syndrome, Grave's disease, inflammatory bowel disease, psoriasis, ankylosing spondylitis, graft versus host disease, allergy, and asthma.

The antibodies described herein may be used, for example, for treating cancer. In some embodiments, methods for treating cancer are provided, comprising administering an effective amount of an antibody described herein to a patient. In some embodiments, the Abs may trigger or enhance an immune response in the patient, such as an antigen-specific immune response. In some embodiments, the Abs may stimulate T cell activity. In some embodiments, the Abs may inhibit the growth of at least one tumor in the patient.

Provided herein are methods for treating a subject having cancer, comprising administering to the subject a therapeutically effective amount of an anti-VISTA antibody described herein, such that the subject is treated. An anti-VISTA antibody can be used alone. Alternatively, an anti-VISTA antibody can be used in conjunction with another agent, as described further below.

Examples of cancers that may be treated with an Ab specifically binding to a VISTA-ECD protein under acidic conditions as described herein include but are not limited to, carcinoma, lymphoma, blastoma, sarcoma, and leukemia. Cancers that may be treated with an Ab described herein also include cancers typically responsive to immunotherapy and those that are not typically responsive to immunotherapy. Cancers that can be treated also include VISTA positive cancers, e.g., cancers having VISTA positive tumor infiltrating cells, e.g., lymphocytes, myeloid or monocytic cells. Cancers can be cancers with solid tumors or blood malignancies (liquid tumors).

Non-limiting examples of cancers for treatment include squamous cell carcinoma, small-cell lung cancer, non-small cell lung cancer, squamous non-small cell lung cancer (NSCLC), nonsquamous NSCLC, glioma, gastrointestinal cancer, renal cancer (*e.g.,* clear cell carcinoma), ovarian cancer, liver cancer, colorectal cancer, endometrial cancer, kidney cancer (*e.g.,* renal cell carcinoma (RCC)), prostate cancer (*e.g.,* hormone refractory prostate adenocarcinoma), thyroid cancer, neuroblastoma, pancreatic cancer, glioblastoma (glioblastoma multiforme), cervical cancer, stomach cancer, bladder cancer, hepatoma, breast cancer, colon carcinoma, and head and neck cancer (or carcinoma), gastric cancer, germ cell tumor, pediatric sarcoma, sinonasal natural killer, melanoma (*e.g.,* metastatic malignant

melanoma, such as cutaneous or intraocular malignant melanoma), bone cancer, skin cancer, uterine cancer, cancer of the anal region, testicular cancer, carcinoma of the fallopian tubes, carcinoma of the endometrium, carcinoma of the cervix, carcinoma of the vagina, carcinoma of the vulva, cancer of the esophagus, cancer of the small intestine, cancer of the endocrine system, cancer of the parathyroid gland, cancer of the adrenal gland, sarcoma of soft tissue, cancer of the urethra, cancer of the penis, solid tumors of childhood, cancer of the ureter, carcinoma of the renal pelvis, neoplasm of the central nervous system (CNS), primary CNS lymphoma, tumor angiogenesis, spinal axis tumor, brain cancer, brain stem glioma, pituitary adenoma, Kaposi's sarcoma, epidermoid cancer, squamous cell cancer, T-cell lymphoma, environmentally-induced cancers including those induced by asbestos, virus-related cancers or cancers of viral origin (*e.g.,* human papilloma virus (HPV-related or -originating tumors)), and hematologic malignancies derived from either of the two major blood cell lineages, *i.e.,* the myeloid cell line (which produces granulocytes, erythrocytes, thrombocytes, macrophages and mast cells) or lymphoid cell line (which produces B, T, NK and plasma cells), such as all types of leukemias, lymphomas, and myelomas, *e.g.,* acute, chronic, lymphocytic and/or myelogenous leukemias, such as acute leukemia (ALL), acute myelogenous leukemia (AML), chronic lymphocytic leukemia (CLL), and chronic myelogenous leukemia (CML), undifferentiated AML (MO), myeloblastic leukemia (Ml), myeloblastic leukemia (M2; with cell maturation), promyelocytic leukemia (M3 or M3 variant [M3V]), myelomonocytic leukemia (M4 or M4 variant with eosinophilia [M4E]), monocytic leukemia (M5), erythroleukemia (M6), megakaryoblastic leukemia (M7), isolated granulocytic sarcoma, and chloroma; lymphomas, such as Hodgkin's lymphoma (HL), non-Hodgkin's lymphoma (NHL), B cell hematologic malignancy, *e.g.,* B-cell lymphomas, T-cell lymphomas, lymphoplasmacytoid lymphoma, monocytoid B-cell lymphoma, mucosa-associated lymphoid tissue (MALT) lymphoma, anaplastic (*e.g.,* Ki 1+) large-cell lymphoma, adult T-cell lymphoma/leukemia, mantle cell lymphoma, angio immunoblastic T-cell lymphoma, angiocentric lymphoma, intestinal T-cell lymphoma, primary mediastinal B-cell lymphoma, precursor T-lymphoblastic lymphoma, T-lymphoblastic; and lymphoma/leukaemia (T-Lbly/T-ALL), peripheral T- cell lymphoma, lymphoblastic lymphoma, post-transplantation lymphoproliferative disorder, true histiocytic lymphoma,

primary central nervous system lymphoma, primary effusion lymphoma, B cell lymphoma, lymphoblastic lymphoma (LBL), hematopoietic tumors of lymphoid lineage, acute lymphoblastic leukemia, diffuse large B-cell lymphoma, Burkitt's lymphoma, follicular lymphoma, diffuse histiocytic lymphoma (DHL), immunoblastic large cell lymphoma, precursor B -lymphoblastic lymphoma, cutaneous T-cell lymphoma (CTLC) (also called mycosis fungoides or Sezary syndrome), and lymphoplasmacytoid lymphoma (LPL) with Waldenstrom's macroglobulinemia; myelomas, such as IgG myeloma, light chain myeloma, nonsecretory myeloma, smoldering myeloma (also called indolent myeloma), solitary plasmocytoma, and multiple myelomas, chronic lymphocytic leukemia (CLL), hairy cell lymphoma; hematopoietic tumors of myeloid lineage, tumors of mesenchymal origin, including fibrosarcoma and rhabdomyoscarcoma; seminoma, teratocarcinoma, tumors of the central and peripheral nervous, including astrocytoma, schwannomas; tumors of mesenchymal origin, including fibrosarcoma, rhabdomyoscaroma, and osteosarcoma; and other tumors, including melanoma, xeroderma pigmentosum, keratoacanthoma, seminoma, thyroid follicular cancer and teratocarcinoma, hematopoietic tumors of lymphoid lineage, for example T-cell and B-cell tumors, including but not limited to T-cell disorders such as T-prolymphocytic leukemia (T-PLL), including of the small cell and cerebriform cell type; large granular lymphocyte leukemia (LGL) of the T-cell type; a/d T-NHL hepatosplenic lymphoma; peripheral/post-thymic T cell lymphoma (pleomorphic and immunoblastic subtypes); angiocentric (nasal) T-cell lymphoma; cancer of the head or neck, renal cancer, rectal cancer, cancer of the thyroid gland; acute myeloid lymphoma, as well as any combinations of said cancers. The methods described herein can also be used for treatment of metastatic cancers, unresectable, refractory cancers (*e.g.,* cancers refractory to previous immunotherapy, *e.g.,* with a blocking CTLA-4 or PD-1 antibody), and/or recurrent cancers.

In some embodiments, methods of treating cancer are provided, wherein the methods comprise administering an isolated antibody that binds specifically to huVISTA in acidic conditions as described herein to a subject with cancer. In some embodiments, use of an antibody described herein for treating cancer is provided.

In certain embodiments, an antibody described herein is administered to patients having a cancer that has exhibited an inadequate response to, or progressed on, a prior

treatment, *e.g.*, a prior treatment with an immuno-oncology or immunotherapy drug. In some embodiments, the cancer is refractory or resistant to a prior treatment, either intrinsically refractory or resistant (*e.g.*, refractory to a PD-1 pathway antagonist), or a resistance or refractory state is acquired. For example, an antibody described herein may be administered to subjects who are not responsive or not sufficiently responsive to a first therapy or who have disease progression following treatment, *e.g.*, anti-PD-1 pathway antagonist treatment, either alone or in combination with another therapy (*e.g.*, with an anti-PD-1 pathway antagonist therapy). In other embodiments, an antibody described herein is administered to patients who have not previously received (*i.e.*, been treated with) an immuno-oncology agent, *e.g.*, a PD-1 pathway antagonist.

In certain embodiments, a method of treating cancer in a subject comprises first determining the tumor mutational burden (TMB) of a tumor in a subject, and administering an anti-VISTA antibody based on the results, e.g., to subjects found to have a high TMB.

Combinations with Immune Stimulating Agents

In some embodiments, an antibody as described herein, e.g., an antagonist VISTA antibody described herein, is administered in combination with and at least one immune stimulating agent. For example, the therapeutics may be infused together or injected at roughly the same time. In some embodiments, the antibody and the at least one immune stimulating agent are administered sequentially. For example, in some embodiments the antibody is administered sequentially before or after at least one immune stimulating agent such that the two therapeutics are administered 30 minutes, 60 minutes, 90 minutes, 120 minutes, 3 hours, 6 hours, 12 hours, 24 hours, 36 hours, 48 hours, 3 days, 5 days, 7 days, or two weeks apart.

In some embodiments, at least one, at least two, at least three doses, at least five doses, or at least ten doses of the antibody is administered prior to administration of at least one immune stimulating agent. In some embodiments, at least one, at least two, at least three doses, at least five doses, or at least ten doses of at least one immune stimulating agent is administered prior to administration of the antibody. In some embodiments, the last dose of immune stimulating agent is administered at least one, two, three, five, days or ten, or one,

two, three, five, twelve, or twenty four weeks prior to the first dose of the antibody. In some embodiments, the last dose of the antibody is administered at least one, two, three, five, days or ten, or one, two, three, five, twelve, or twenty four weeks prior to the first dose of at least one immune stimulating agent. In some embodiments, a subject has received, or is receiving, therapy with at least one immune stimulating agent and a VISTA-ECD-binding antibody is added to the therapeutic regimen.

In some embodiments, the at least one immune stimulating agent comprises an antagonist of an inhibitor of the activation of T cells, while in some embodiments, the at least one immune stimulating agent comprises an agonist of a stimulator of the activation of T cells. In some embodiments, the at least one immune stimulating agent comprises an antagonist of CTLA4, LAG-3, PD-1, PD-L1, Galectin 1, Galectin 9, CEACAM-1, BTLA, CD25, CD69, TIGIT, CD113, GPR56, VISTA, B7-H3, B7-H4, 2B4, CD48, GARP, PD1H, LAIR1, TIM1, TIM3, TIM4, ILT4, IL-6, IL-10, TGFβ, VEGF, KIR, LAG-3, adenosine A2A receptor, PI3Kdelta, or IDO. In some embodiments, the at least one immune stimulating agent comprises an agonist of B7-1, B7-2, CD28, 4-1BB (CD137), 4-1BBL, ICOS, ICOS-L, OX40, OX40L, GITR, GITRL, CD27, CD40, CD40L, DR3, CD28H, IL-2, IL-7, IL-12, IL-15, IL-21, IFNα, STING, or a Toll-like receptor agonist such as a TLR2/4 agonist. In some embodiments, the at least one immune stimulating agent comprises an agent that binds to another member of the B7 family of membrane-bound proteins such as B7-1, B7-2, B7-H2 (ICOS-L), B7-H3, B7-H4, and B7-H6. In some embodiments, the at least one immune stimulating agent comprises an agent that binds to a member of the TNF receptor family or a co-stimulatory or co-inhibitory molecule binding to a member of the TNF receptor family such as CD40, CD40L, OX40, OX40L, GITR, GITRL, CD70, CD27L, CD30, CD30L, 4-1BBL, CD137 (4-1BB), TRAIL/Apo2-L, TRAILR1/DR4, TRAILR2/DR5, TRAILR3, TRAILR4, OPG, RANK, RANKL, TWEAKR/Fn14, TWEAK, BAFFR, EDAR, XEDAR, EDA1, EDA2, TACI, APRIL, BCMA, LTβR, LIGHT, DeR3, HVEM, VEGL/TL1A, TRAMP/DR3, TNFR1, TNFβ, TNFR2, TNFα, 1β2, FAS, FASL, RELT, DR6, TROY, or NGFβ. In some embodiments, the at least one immune stimulating agent comprises an agent that antagonizes or inhibits a cytokine that inhibits T cell activation such as IL-6, IL-10, TGFβ, VEGF. In some embodiments, the at least one immune stimulating agent comprises

an agonist of a cytokine that stimulates T cell activation such as IL-2, IL-7, IL-12, IL-15, IL-21, and IFNα. In some embodiments, the at least one immune stimulating agent comprises an antagonist of a chemokine, such as CXCR2, CXCR4, CCR2, or CCR4. In some embodiments, the at least one immune stimulating agent comprises an antibody. In some embodiments, the at least one immune stimulating agent may comprise a vaccine, such as a mesothelin-targeting vaccine or attenuated listeria cancer vaccine such as CRS-207.

For example, an anti-VISTA antibody described herein could be administered with one or more of the following agents:

(1) An antagonist (inhibitor or blocking agent) of a protein that inhibits T cell activation (*e.g.,* immune checkpoint inhibitors), such as CTLA-4, PD-1, PD-L1, PD-L2, and LAG-3, Galectin 9, CEACAM-1, BTLA, CD69, Galectin-1, TIGIT, CD113, GPR56, B7-H3, B7-H4, 2B4, CD48, GARP, PD1H, LAIR1, TIM-1,TIM-3 and TIM-4; and/or (2) An agonist of a protein that stimulates T cell activation, such as B7-1, B7-2, CD28, 4-1BB (CD137), 4-1BBL, GITR, ICOS, ICOS-L, OX40, OX40L, CD70, CD27, CD40, DR3 and CD28H.

Exemplary agents that can be combined with anti-VISTA antibodies described herein for treating cancer include: YERVOY® (ipilimumab) or Tremelimumab (to CTLA-4), galiximab (to B7.1), BMS-936558 (to PD-1), MK-3475 (to PD-1), atezolizumab (TECENTRIQ®), Avelumab, Durvalumab, AMP224 (to B7DC), BMS-936559 (to B7-H1), MPDL3280A (to B7-H1), MEDI-570 (to ICOS), AMG557 (to B7H2), MGA271 (to B7H3), IMP321 (to LAG-3), BMS-663513 (to CD137), PF-05082566 (to CD137), CDX-1127 (to CD27), anti-OX40 (Providence Health Services), huMAbOX40L (to OX40L), Atacicept (to TACI), CP-870893 (to CD40), Lucatumumab (to CD40), Dacetuzumab (to CD40), Muromonab-CD3 (to CD3); anti-GITR antibodies MK4166, TRX518, Medi1873, INBRX-110, LK2-145, GWN-323, GITRL-Fc, or any combination thereof.

Other molecules that can be combined with anti-VISTA antibodies for the treatment of cancer include antagonists of inhibitory receptors on NK cells or agonists of activating receptors on NK cells, for example, antagonists of KIR (*e.g.,* lirilumab).

T cell activation may also be regulated by soluble cytokines. In some embodiments, anti-VISTA antibodies can be administered in combination with antagonists of cytokines that are intended to inhibit T cell activation or agonists of cytokines that stimulate T cell

activation. For example, anti-VISTA antibodies can be used in combination with (i) antagonists (or inhibitors or blocking agents) of proteins of the IgSF family or B7 family or the TNF family that inhibit T cell activation or antagonists of cytokines that inhibit T cell activation (*e.g.*, IL-6, IL-10, TGF-β, VEGF; "immunosuppressive cytokines") and/or (ii) agonists of stimulatory receptors of the IgSF family, B7 family or the TNF family or of cytokines that stimulate T cell activation.

Yet other agents for combination therapies include agents that inhibit or deplete macrophages or monocytes, including but not limited to CSF-1R antagonists such as CSF-1R antagonist antibodies including RG7155 (WO11/70024, WO11/107553, WO11/131407, W013/87699, W013/119716, WO13/132044) or FPA-008 (WO11/140249; W013169264; WO14/036357).

Anti-VISTA antibodies can also be administered with agents that inhibit TGF-β signaling.

Additional agents that can be combined with an anti-VISTA antibody include agents that enhance tumor antigen presentation, *e.g.*, dendritic cell vaccines, GM-CSF secreting cellular vaccines, CpG oligonucleotides, and imiquimod, or therapies that enhance the immunogenicity of tumor cells (*e.g.*, anthracyclines).

Yet other therapies that can be combined with an anti-VISTA antibody include therapies that deplete or block Treg cells, *e.g.*, an agent that specifically binds to CD25.

Another therapy that can be combined with an anti-VISTA antibody is a therapy that inhibits a metabolic enzyme such as indoleamine dioxigenase (IDO), dioxigenase, arginase, or nitric oxide synthetase.

Another class of agents that can be used with an anti-VISTA antibody includes agents that inhibit the formation of adenosine, *e.g.*, CD73 inhibitors, or inhibit the adenosine A2A receptor.

Other therapies that can be combined with an anti-VISTA antibody for treating cancer include therapies that reverse/prevent T cell anergy or exhaustion and therapies that trigger an innate immune activation and/or inflammation at a tumor site.

Other therapies that can be combined with an anti-VISTA antibody for treating cancer include therapies that block IL-8, *e.g.*, with HuMax®-IL8.

An anti-VISTA antibody can be combined with more than one immuno-oncology agent, and can be, *e.g.,* combined with a combinatorial approach that is intended to target multiple elements of the immune pathway, such as one or more of the following: a therapy that enhances tumor antigen presentation (*e.g.,* dendritic cell vaccine, GM-CSF secreting cellular vaccines, CpG oligonucleotides, imiquimod); a therapy that inhibits negative immune regulation *e.g.,* by inhibiting CTLA-4 and/or PD1/PD-L1/PD-L2 pathway and/or depleting or blocking Tregs or other immune suppressing cells; a therapy that stimulates positive immune regulation, *e.g.,* with agonists that stimulate the CD-137, OX-40, and/or CD40 or GITR pathway and/or stimulate T cell effector function; a therapy that increases systemically the frequency of anti-tumor T cells; a therapy that depletes or inhibits Tregs, such as Tregs in the tumor, *e.g.,* using an antagonist of CD25 (*e.g.,* daclizumab) or by *ex vivo* anti-CD25 bead depletion; a therapy that impacts the function of suppressor myeloid cells in the tumor; a therapy that enhances immunogenicity of tumor cells (*e.g.,* anthracyclines); adoptive T cell or NK cell transfer including genetically modified cells, *e.g.,* cells modified by chimeric antigen receptors (CAR-T therapy); a therapy that inhibits a metabolic enzyme such as indoleamine dioxigenase (IDO), dioxigenase, arginase, or nitric oxide synthetase; a therapy that reverses/prevents T cell anergy or exhaustion; a therapy that triggers an innate immune activation and/or inflammation at a tumor site; administration of immune stimulatory cytokines; or blocking of immuno repressive cytokines.

Anti-VISTA antibodies described herein can be used together with one or more of agonistic agents that ligate positive costimulatory receptors, blocking agents that attenuate signaling through inhibitory receptors, antagonists, and one or more agents that increase systemically the frequency of anti-tumor T cells, agents that overcome distinct immune suppressive pathways within the tumor microenvironment (*e.g.,* block inhibitory receptor engagement (*e.g.,* PD-L1/PD-1 interactions), deplete or inhibit Tregs (*e.g.,* using an anti-CD25 monoclonal antibody (*e.g.,* daclizumab) or by *ex vivo* anti-CD25 bead depletion), inhibit metabolic enzymes such as IDO, or reverse/prevent T cell anergy or exhaustion) and agents that trigger innate immune activation and/or inflammation at tumor sites.

In certain embodiments, an anti-VISTA antibody is administered to a subject together with a BRAF inhibitor if the subject is BRAF V600 mutation positive.

Suitable PD-1 antagonists for use in the combination therapy described herein, include, without limitation, ligands, antibodies (*e.g.,* monoclonal antibodies and bispecific antibodies), and multivalent agents. In one embodiment, the PD-1 antagonist is a fusion protein, *e.g.,* an Fc fusion protein, such as AMP-244. In one embodiment, the PD-1 antagonist is an anti-PD-1 or anti-PD-L1 antibody.

An exemplary anti-PD-1 antibody is nivolumab (BMS-936558) or an antibody that comprises the CDRs or variable regions of one of antibodies 17D8, 2D3, 4H1, 5C4, 7D3, 5F4 and 4A11 described in WO 2006/121168. In certain embodiments, an anti-PD-l antibody is MK-3475 (Lambrolizumab) described in WO2012/ 145493; AMP-514 described in WO 2012/145493; or PDR001. Further known PD-1 antibodies and other PD-1 inhibitors include those described in WO 2009/014708, WO 03/099196, WO 2009/114335, WO 2011/066389, WO 2011/161699, WO 2012/145493, U.S. Patent Nos. 7,635,757 and 8,217,149, and U.S. Patent Publication No. 2009/0317368. Any of the anti-PD-1 antibodies disclosed in WO2013/173223 can also be used. An anti-PD-1 antibody that competes for binding with, and/or binds to the same epitope on PD-1 as, as one of these antibodies can also be used in combination treatments.

In some embodiments, the anti-PD-L1 antibody useful for the combination therapy is BMS-936559 (referred to as 12A4 in WO 2007/005874 and US Patent No. 7,943,743), or an antibody that comprises the CDRs or variable regions of 3G10, 12A4, 10A5, 5F8, 10H10, 1B12, 7H1, 11E6, 12B7 and 13G4, which are described in PCT Publication WO 07/005874 and US Patent No. 7,943,743. In certain embodiment an anti-PD-L1 antibody is MEDI4736 (also known as durvalumab and Anti-B7-H1), MPDL3280A (also known as atezolizumab and RG7446), MSB0010718C (also known as avelumab; WO2013/79174), or rHigM12B7. Any of the anti-PD-L1 antibodies disclosed in WO2013/173223, WO2011/066389, WO2012/ 145493, U.S. Patent Nos. 7,635,757 and 8,217,149 and U.S. Publication No. 2009/145493 can also be used. Anti-PD-L1 antibodies that compete with and/or bind to the same epitope as that of any of these antibodies can also be used in combination treatments.

In certain embodiments, the anti-VISTA antibody of the disclosure can be used with a CTLA-4 antagonist, *e.g.,* an anti-CTLA-4 antibody. In one embodiment, an anti-CTLA-4 antibody is an antibody selected from the group of: YERVOY® (ipilimumab or antibody

10D1, described in PCT Publication WO 01/14424), tremelimumab (formerly ticilimumab, CP-675,206), monoclonal or an anti-CTLA-4 antibody described in any of the following publications: WO 98/42752; WO 00/37504; U.S. Pat. No. 6,207,156; Hurwitz *et al.* (1998) *Pro. Natl. Acad. Sci. USA* 95(17): 10067-10071; Camacho *et al.* (2004) *J. Clin. Oncology* 22(145): Abstract No. 2505 (antibody CP-675206); and Mokyr *et al.* (1998) *Cancer Res.* 58:5301-5304. Any of the anti-CTLA-4 antibodies disclosed in WO2013/173223 can also be used.

In some embodiments, an anti-VISTA antibody of the disclosure is used in combination with a LAG3 antagonist. Examples of anti-LAG3 antibodies include antibodies comprising the CDRs or variable regions of antibodies 25F7, 26H10, 25E3, 8B7, 11F2 or 17E5, which are described in U.S. Patent Publication No. US2011/0150892, WO10/19570 and WO2014/008218. In one embodiment, an anti-LAG-3 antibody is BMS-986016. Other art recognized anti-LAG-3 antibodies that can be used include IMP731 and IMP-321, described in US 2011/007023, WO08/132601, and WO09/44273. Anti-LAG-3 antibodies that compete with and/or bind to the same epitope as that of any of these antibodies can also be used in combination treatments.

In some embodiments, an anti-VISTA antibody of the disclosure can be administered in combination with a CD137 (4-1BB) agonist, such as an agonistic CD137 antibody. Suitable CD137 antibodies include, for example, urelumab or PF-05082566 (W012/32433).

In some embodiments, an anti-VISTA antibody can be administered in combination with an OX40 agonist, such as an agonistic OX40 antibody. Suitable OX40 antibodies include, for example, MEDI-6383, MEDI-6469 or MOXR0916 (RG7888; WO06/029879).

In one embodiment, an anti-VISTA antibody is administered in combination with a CD40 agonist, such as an agonistic CD40 antibody. In certain embodiments, the immuno-oncology agent is a CD40 antagonist, such as an antagonistic CD40 antibody. Suitable CD40 antibodies include, for example, lucatumumab (HCD122), dacetuzumab (SGN-40), CP-870,893 or Chi Lob 7/4.

In one embodiment, an anti-VISTA antibody is administered in combination with a CD27 agonist, such as an agonistic CD27 antibody. Suitable CD27 antibodies include, for example, varlilumab (CDX-1127).

In certain embodiments, the anti-VISTA antibody is administered together with an anti-GITR antibody, *e.g.,* an antibody having the CDR sequences of 6C8, *e.g.,* a humanized antibody having the CDRs of 6C8, as described, *e.g.,* in WO2006/105021; an antibody comprising the CDRs of an anti-GITR antibody described in WO2011/028683; an antibody comprising the CDRs of an anti-GITR antibody described in JP2008278814, an antibody comprising the CDRs of an anti- GITR antibody described in WO2015/031667, WO2015/187835, WO2015/184099, WO2016/054638, WO2016/057841 or WO2016/057846 or other anti- GITR antibody described or referred to herein.

In some embodiments, an anti-VISTA antibody is administered in combination with MGA271 (to B7H3) (WO11/109400).

In some embodiments, an anti-VISTA antibody is administered in combination with a KIR antagonist, such as lirilumab.

In some embodiments, an anti-VISTA antibody is administered in combination with an IDO antagonist. Suitable IDO antagonists include, for example, INCB-024360 (WO2006/122150, WO07/75598, WO08/36653, WO08/36642), indoximod, NLG-919 (WO09/73620, WO09/1156652, WO11/56652, WO12/142237) or F001287.

In some embodiments, an anti-VISTA antibody is administered in combination with a Toll-like receptor agonist, *e.g.,* a TLR2/4 agonist (*e.g.,* Bacillus Calmette-Guerin); a TLR7 agonist (*e.g.,* Hiltonol or Imiquimod); a TLR7/8 agonist (*e.g.,* Resiquimod); or a TLR9 agonist (*e.g.,* CpG7909).

In one embodiment, an anti-VISTA is administered in combination with a TGF-β inhibitor, *e.g.,* GC1008, LY2157299, TEW7197, or IMC-TR1.

Additional Combination Therapy

The Abs herein may also be provided before, substantially contemporaneous with, or after other modes of treatment, for example, surgery, chemotherapy, radiation therapy, or the administration of a biologic, such as another therapeutic antibody. In some embodiments, the cancer has recurred or progressed following a therapy selected from surgery, chemotherapy, and radiation therapy, or a combination thereof. For example, an anti-VISTA antibody as

described herein could be administered as adjunctive therapy when there is a risk that micrometastases can be present and/or in order to reduce the risk of a relapse.

For treatment of cancer, the combinations may be administered in conjunction with one or more additional anti-cancer agents, such as a chemotherapeutic agent, growth inhibitory agent, anti-cancer vaccine such as a gene therapy vaccine, anti-angiogenesis agent and/or anti-neoplastic composition. Nonlimiting examples of chemotherapeutic agent, growth inhibitory agent, anti-cancer vaccine, anti-angiogenesis agent and anti-neoplastic composition that can be used in combination with the antibodies of the present invention are provided herein under "Definitions."

In some embodiments, an anti-inflammatory drug may be administered with the combination, such as a steroid or a non-steroidal anti-inflammatory drug (NSAID). In cases where it is desirable to render aberrantly proliferative cells quiescent in conjunction with or prior to treatment with anti-VISTA antibodies described herein, hormones and steroids (including synthetic analogs), such as 17a-Ethinylestradiol, Diethylstilbestrol,Testosterone, Prednisone, Fluoxymesterone, Dromostanolone propionate, Testolactone, Megestrolacetate, Methylprednisolone, Methyl-testosterone, Prednisolone, Triamcinolone, Chlorotrianisene, Hydroxyprogesterone, Aminoglutethimide, Estramustine, Medroxyprogesteroneacetate, Leuprolide, Flutamide, Toremifene, ZOLADEX®, can also be administered to the patient. When employing the methods or compositions described herein, other agents used in the modulation of tumor growth or metastasis in a clinical setting, such as antimimetics, can also be administered as desired.

Antibodies described herein can also be combined with an immunogenic agent, such as cancerous cells, purified tumor antigens (including recombinant proteins, peptides, and carbohydrate molecules), cells, and cells transfected with genes encoding immune stimulating cytokines (He *et al.*,(2004) *J. Immunol.* 173:4919-28). Non-limiting examples of tumor vaccines that can be used include peptides of melanoma antigens, such as peptides of gp100, MAGE antigens, Trp-2, MART1 and/or tyrosinase, or tumor cells transfected to express the cytokine GM-CSF (discussed further below).

In humans, some tumors have been shown to be immunogenic such as melanomas. By lowering the threshold of T cell activation via VISTA inhibition, the tumor responses in

the host can be activated, allowing treatment of non-immunogenic tumors or those having limited immunogenicity.

An anti-VISTA antibody described herein, can also be combined with a vaccination protocol. Many experimental strategies for vaccination against tumors have been devised (*see* Rosenberg, S., 2000, Development of Cancer Vaccines, ASCO Educational Book Spring: 60-62; Logothetis, C, 2000, ASCO Educational Book Spring: 300-302; Khayat, D. 2000, ASCO Educational Book Spring: 414-428; Foon, K. 2000, ASCO Educational Book Spring: 730-738; *see also* Restifo, N. and Sznol, M., Cancer Vaccines, Ch. 61, pp. 3023-3043 in DeVita *et al.* (eds.), 1997, Cancer: Principles and Practice of Oncology, Fifth Edition). In one of these strategies, a vaccine is prepared using autologous or allogeneic tumor cells. These cellular vaccines have been shown to be most effective when the tumor cells are transduced to express GM-CSF. GM-CSF has been shown to be a potent activator of antigen presentation for tumor vaccination (Dranoff *et al.* (1993) *Proc. Natl. Acad. Sci U.S.A.* 90: 3539-43).

The study of gene expression and large scale gene expression patterns in various tumors has led to the definition of so called tumor specific antigens (Rosenberg, S A (1999) *Immunity* 10: 281-7). In many cases, these tumor specific antigens are differentiation antigens expressed in the tumors and in the cell from which the tumor arose, for example melanocyte antigens gp100, MAGE antigens, and Trp-2. More importantly, many of these antigens can be shown to be the targets of tumor specific T cells found in the host. VISTA inhibition can be used in conjunction with a collection of recombinant proteins and/or peptides expressed in a tumor in order to generate an immune response to these proteins. These proteins are normally viewed by the immune system as self antigens and are therefore tolerant to them. The tumor antigen can include the protein telomerase, which is required for the synthesis of telomeres of chromosomes and which is expressed in more than 85% of human cancers and in only a limited number of somatic tissues (Kim *et al.* (1994) *Science* 266: 2011-2013). Tumor antigen can also be "neo-antigens" expressed in cancer cells because of somatic mutations that alter protein sequence or create fusion proteins between two unrelated sequences (*i.e.,* bcr-abl in the Philadelphia chromosome), or idiotype from B cell tumors.

Other tumor vaccines can include the proteins from viruses implicated in human cancers such a Human Papilloma Viruses (HPV), Hepatitis Viruses (HBV and HCV) and Kaposi's Herpes Sarcoma Virus (KHSV). Another form of tumor specific antigen which can be used in conjunction with VISTA inhibition is purified heat shock proteins (HSP) isolated from the tumor tissue itself. These heat shock proteins contain fragments of proteins from the tumor cells and these HSPs are highly efficient at delivery to antigen presenting cells for eliciting tumor immunity (Suot & Srivastava (1995) *Science* 269: 1585-1588; Tamura *et al.* (1997) *Science* 278: 117-120).

Dendritic cells (DC) are potent antigen presenting cells that can be used to prime antigen-specific responses. DCs can be produced *ex vivo* and loaded with various protein and peptide antigens as well as tumor cell extracts (Nestle *et al.* (1998) *Nature Medicine* 4: 328-332). DCs can also be transduced by genetic means to express these tumor antigens as well. DCs have also been fused directly to tumor cells for the purposes of immunization (Kugler *et al.* (2000) *Nature Medicine* 6:332-336). As a method of vaccination, DC immunization can be effectively combined with VISTA inhibition to activate more potent anti-tumor responses.

Infectious Disease Treatments

Methods described herein can also be used to treat patients that have been exposed to particular toxins or pathogens. Accordingly, this disclosure also contemplates methods of treating an infectious disease in a subject comprising administering to the subject an antibody as described herein, e.g., an antagonist VISTA antibody, such that the subject is treated for the infectious disease. Similar to its application to tumors as discussed above, antibody-mediated VISTA inhibition can be used alone, or as an adjuvant, in combination with vaccines, to stimulate the immune response to pathogens, toxins, and self-antigens. Examples of pathogens for which this therapeutic approach might be particularly useful, include pathogens for which there is currently no effective vaccine, or pathogens for which conventional vaccines are less than completely effective. These include, but are not limited to HIV, Hepatitis (A, B, & C), Influenza, Herpes, Giardia, Malaria, Leishmania, Staphylococcus aureus, Pseudomonas aeruginosa. VISTA inhibition can be useful against

established infections by agents such as HIV that present altered antigens over the course of the infections.

Some examples of pathogenic viruses causing infections that may be treatable by methods described herein include HIV, hepatitis (A, B, or C), herpes virus (*e.g.,* VZV, HSV-1, HAV-6, HSV-II, and CMV, Epstein Barr virus), adenovirus, influenza virus, flaviviruses, echovirus, rhinovirus, coxsackie virus, coronavirus, respiratory syncytial virus, mumps virus, rotavirus, measles virus, rubella virus, parvovirus, vaccinia virus, HTLV virus, dengue virus, papillomavirus, molluscum virus, poliovirus, rabies virus, JC virus and arboviral encephalitis virus.

Some examples of pathogenic bacteria causing infections that may be treatable by methods described herein include chlamydia, rickettsial bacteria, mycobacteria, staphylococci, streptococci, pneumonococci, meningococci and gonococci, klebsiella, proteus, serratia, pseudomonas, legionella, diphtheria, salmonella, bacilli, cholera, tetanus, botulism, anthrax, plague, leptospirosis, and Lymes disease bacteria.

Some examples of pathogenic fungi causing infections that may be treatable by methods described herein include Candida (albicans, krusei, glabrata, tropicalis, etc.), Cryptococcus neoformans, Aspergillus (fumigatus, niger, etc.), Genus Mucorales (mucor, absidia, rhizopus), *Sporothrix schenkii*, *Blastomyces dermatitidis*, *Paracoccidioides brasiliensis*, *Coccidioides immitis* and *Histoplasma capsulatum*.

Some examples of pathogenic parasites causing infections that may be treatable by methods described herein include *Entamoeba histolytica*, *Balantidium coli*, Naegleriafowleri, *Acanthamoeba sp.*, *Giardia lambia*, *Cryptosporidium sp.*, *Pneumocystis carinii*, *Plasmodium vivax*, *Babesia microti*, *Trypanosoma brucei*, *Trypanosoma cruzi*, *Leishmania donovani*, *Toxoplasma gondii*, and *Nippostrongylus brasiliensis*.

In all of the above methods, VISTA inhibition can be combined with other forms of immunotherapy, *e.g.,* those described herein, such as cytokine treatment (*e.g.,* interferons, GM-CSF, G-CSF, IL-2), or bispecific antibody therapy, which may provide for enhanced presentation of tumor antigens (see, *e.g.,* Holliger (1993) *Proc. Natl. Acad. Sci. USA* 90:6444-6448; Poljak (1994) *Structure* 2: 1121-1123).

Routes of Administration and Carriers

In various embodiments, antibodies may be administered *in vivo* by various routes, including, but not limited to, oral, intra-arterial, parenteral, intranasal, intramuscular, intracardiac, intraventricular, intratracheal, buccal, rectal, intraperitoneal, intradermal, topical, transdermal, and intrathecal, or otherwise by implantation or inhalation. The subject compositions may be formulated into preparations in solid, semi-solid, liquid, or gaseous forms; including, but not limited to, tablets, capsules, powders, granules, ointments, solutions, suppositories, enemas, injections, inhalants, and aerosols. A nucleic acid molecule encoding an antibody may be coated onto gold microparticles and delivered intradermally by a particle bombardment device, or "gene gun," as described in the literature (see, e.g., Tang et al., *Nature* 356:152-154 (1992)). The appropriate formulation and route of administration may be selected according to the intended application.

In various embodiments, compositions comprising antibodies are provided in formulations with a wide variety of pharmaceutically acceptable carriers (see, e.g., Gennaro, *Remington: The Science and Practice of Pharmacy with Facts and Comparisons: Drugfacts Plus*, 20th ed. (2003); Ansel et al., *Pharmaceutical Dosage Forms and Drug Delivery Systems,* 7th ed., Lippencott Williams and Wilkins (2004); Kibbe et al., *Handbook of Pharmaceutical Excipients,* 3rd ed., Pharmaceutical Press (2000)). Various pharmaceutically acceptable carriers, which include vehicles, adjuvants, and diluents, are available. Moreover, various pharmaceutically acceptable auxiliary substances, such as pH adjusting and buffering agents, tonicity adjusting agents, stabilizers, wetting agents and the like, are also available. Non-limiting exemplary carriers include saline, buffered saline, dextrose, water, glycerol, ethanol, and combinations thereof.

In various embodiments, compositions comprising antibodies may be formulated for injection, including subcutaneous administration, by dissolving, suspending, or emulsifying them in an aqueous or nonaqueous solvent, such as vegetable or other oils, synthetic aliphatic acid glycerides, esters of higher aliphatic acids, or propylene glycol; and if desired, with conventional additives such as solubilizers, isotonic agents, suspending agents, emulsifying agents, stabilizers and preservatives. In various embodiments, the compositions may be formulated for inhalation, for example, using pressurized acceptable propellants such as

dichlorodifluoromethane, propane, nitrogen, and the like. The compositions may also be formulated, in various embodiments, into sustained release microcapsules, such as with biodegradable or non-biodegradable polymers. A non-limiting exemplary biodegradable formulation includes poly lactic acid-glycolic acid polymer. A non-limiting exemplary non-biodegradable formulation includes a polyglycerin fatty acid ester. Certain methods of making such formulations are described, for example, in EP 1 125 584 A1.

Pharmaceutical packs and kits comprising one or more containers, each containing one or more doses of an antibody or combination of antibodiesare also provided. In some embodiments, a unit dosage is provided wherein the unit dosage contains a predetermined amount of a composition comprising an antibody or combination of antibodies, with or without one or more additional agents. In some embodiments, such a unit dosage is supplied in single-use prefilled syringe for injection. In various embodiments, the composition contained in the unit dosage may comprise saline, sucrose, or the like; a buffer, such as phosphate, or the like; and/or be formulated within a stable and effective Ph range. Alternatively, in some embodiments, the composition may be provided as a lyophilized powder that may be reconstituted upon addition of an appropriate liquid, for example, sterile water. In some embodiments, the composition comprises one or more substances that inhibit protein aggregation, including, but not limited to, sucrose and arginine. In some embodiments, a composition of the invention comprises heparin and/or a proteoglycan.

Pharmaceutical compositions are administered in an amount effective for treatment or prophylaxis of the specific indication. The therapeutically effective amount is typically dependent on the weight of the subject being treated, his or her physical or health condition, the extensiveness of the condition to be treated, or the age of the subject being treated. In general, antibodies may be administered in an amount in the range of about 10 μg/kg body weight to about 100 mg/kg body weight per dose. In some embodiments, antibodies may be administered in an amount in the range of about 50 μg/kg body weight to about 5 mg/kg body weight per dose. In some embodiments, antibodies may be administered in an amount in the range of about 100 μg/kg body weight to about 10 mg/kg body weight per dose. In some embodiments, antibodies may be administered in an amount in the range of about 100 μg/kg body weight to about 20 mg/kg body weight per dose. In some embodiments,

antibodies may be administered in an amount in the range of about 0.5 mg/kg body weight to about 20 mg/kg body weight per dose.

The antibody compositions may be administered as needed to subjects. Determination of the frequency of administration may be made by persons skilled in the art, such as an attending physician based on considerations of the condition being treated, age of the subject being treated, severity of the condition being treated, general state of health of the subject being treated and the like. In some embodiments, an effective dose of an antibody is administered to a subject one or more times. In various embodiments, an effective dose of an antibody is administered to the subject once a month, less than once a month, such as, for example, every two months or every three months. In other embodiments, an effective dose of an antibody is administered more than once a month, such as, for example, every three weeks, every two weeks or every week. In some embodiments, an effective dose of an antibody is administered once per 1, 2, 3, 4, or 5 weeks. In some embodiments, an effective dose of an antibody is administered twice or three times per week. An effective dose of an antibody is administered to the subject at least once. In some embodiments, the effective dose of an antibody may be administered multiple times, including for periods of at least a month, at least six months, or at least a year.

In certain embodiments, the combination of the anti-VISTA antibody and a second agent discussed herein can be administered concurrently as a single composition in a pharmaceutically acceptable carrier, or concurrently as separate compositions with the anti-VISTA antibody and the second agent in a pharmaceutically acceptable carrier. In one embodiment, the combination of the anti-VISTA antibody and the second agent can be administered sequentially. The administration of the two agents can start at times that are, *e.g.,* 30 minutes, 60 minutes, 90 minutes, 120 minutes, 3 hours, 6 hours, 12 hours, 24 hours, 36 hours, 48 hours, 3 days, 5 days, 7 days, or one or more weeks apart, or administration of the second agent can start, *e.g.,* 30 minutes, 60 minutes, 90 minutes, 120 minutes, 3 hours, 6 hours, 12 hours, 24 hours, 36 hours, 48 hours, 3 days, 5 days, 7 days, or one or more weeks after the first agent has been administered.

Methods of Identifying Low pH Binding hVISTA-ECD Abs

Also provided herein are methods for identifying Abs that specifically bind to a VISTA-ECD protein in acidic (or low pH) conditions. In certain embodiments, a method for identifying an Ab that binds specifically to a VISTA-ECD protein at pH 6.5 or less comprises contacting a test Ab or plurality of test Abs with a VISTA-ECD protein at pH 6.5 or less, and selecting the test Ab if it binds to the ECD of the VISTA protein with a K_D of 10^{-7} M, 10^{-8} M, 10^{-9} M or less. In some embodiments, the method is performed at pH 6.5, while in others it is performed at pH 6.0, or at pH 5.5, or at pH 5.0. In some embodiments, the VISTA-ECD protein is a hVISTA-ECD protein, or comprises the hVISTA IgV domain, or is a polypeptide comprising amino acids 20-95 of SEQ ID NO:2, or amino acids 20-70, 35-95, or 35-70 of SEQ ID NO:2. In some embodiments, the polypeptide also comprises amino acids 95-105 of SEQ ID NO:2. In some embodiments, the polypeptide comprises amino acids 35-127 or 37-125 of SEQ ID NO: 2.

In some embodiments, the method further comprises testing binding of the test Ab or plurality of test Abs at neutral, physiological or alkaline pH, such as at pH 7.0 or pH 7.4. In some embodiments, the method further comprises selecting an antibody if it not only binds to the VISTA-ECD protein with a K_D of 10^{-7} M, 10^{-8} M, 10^{-9} M or less at pH 6.5 or lower, but also if it binds specifically to the polypeptide at pH 7.0 or pH 7.4. In some embodiments, test Abs are selected if they specifically bind to the VISTA-ECD protein in acidic conditions, e.g., at pH 6.5 or less, also specifically bind the VISTA-ECD protein at neutral and/or alkaline pH with similar affinity (i.e. they are "pan binders"). For example, some such Abs may bind to the VISTA-ECD protein with a K_D of 10^{-7} M, 10^{-8} M, 10^{-9} M or less at both pH 6.5 and at pH 7.0 or pH 7.4 (at a constant temperature, e.g., of 25°C or at 37°C) such that the K_D at pH 6.5 is within 1.5-fold of the K_D at pH 7.0.

Certain Abs may be selected if they specifically bind to the VISTA-ECD protein in acidic conditions, e.g., at pH 6.5 or less with higher affinity than at neutral or alkaline pH ("pH sensitive binders" or "pH sensitive Abs"). For example, in some embodiments, Abs may bind to the VISTA-ECD protein with a K_D of 10^{-8} M or less at pH 6.5 and with a K_D of more than 10^{-8} M at pH 7.0 or pH 7.4. In some such embodiments, Abs may bind to the VISTA-ECD protein with a K_D of 10^{-8} M or less at pH 6.5 and with a K_D at pH 7.0 or pH 7.4

that is more than 1.5-fold higher than that at pH 6.5 In certain embodiments, a pH sensitive Ab is selected if it specifically binds to the VISTA-ECD protein with a K_D that is at least 1.5 fold, 2 fold, 5 fold, 10 fold, 20 fold, 50 fold, 100 fold, 300 fold, 500 fold, 1000 fold, or 5000 fold lower at pH 6.5 than at pH 7.0 or pH 7.4 (at a constant temperature, e.g., of 25°C or at 37°C). For example, in some cases an Ab is selected if it binds to the VISTA-ECD protein with a K_D that is at least 1.5 fold, 2 fold, 5 fold, 10 fold, 20 fold, 50 fold, 100 fold, 300 fold, 500 fold, 1000 fold, or 5000 fold less at pH 6.0, relative to pH 7.0 or pH 7.4 or higher (at a constant temperature, e.g., of 25°C or at 37°C).

In certain embodiments, an Ab is selected if it specifically binds to the VISTA-ECD protein with a k_{off} that is lower in acidic conditions relative to that in neutral, physiological or alkaline conditions. In certain embodiments, an Ab is selected if it binds to the VISTA-ECD protein in acidic conditions with a k_{off} that is at least 1.5 fold, 2 fold, 5 fold, 10 fold, 20 fold, 50 fold or 100 fold lower at pH 6.5 than the k_{off} at pH 7.0 or pH 7.4, as measured, e.g., at 25°C or at 37°C. For example, in some embodiments, an Ab is selected if it binds to the VISTA-ECD protein with a k_{off} rate that is at least 1.5 fold, 2 fold, 5 fold, 10 fold, 20 fold, 50 fold or 100 fold lower at pH 6.0, relative to pH 7.0 or pH 7.4, as measured, e.g., at 25°C or at 37°C.

In certain embodiments, an Ab is selected if it binds to the VISTA-ECD protein with a k_{on} that is higher in acidic conditions relative to neutral or alkaline conditions. In certain embodiments, an Ab is selected if it binds to the VISTA-ECD protein in acidic conditions with a k_{on} that is at least 2 fold, 5 fold, 10 fold, 20 fold, 50 fold or 100 fold higher at pH 6.5 than the k_{on} at pH 7.0 or pH 7.4, as measured, e.g., at 25°C or at 37°C. For example, in some embodiments, an Ab is selected if it binds to the VISTA-ECD protein with a k_{on} that is at least 2 fold, 5 fold, 10 fold, 20 fold, 50 fold or 100 fold higher at pH 6.0 than at pH 7.0 or pH 7.4, as measured, e.g., at 25°C or at 37°C.

Methods of Modifying the pH Sensitivity of VISTA-ECD Binding Abs

An Ab that binds to a VISTA-ECD protein, but does not do so at pH 6.5 or less, or does not do so with a high affinity at pH 6.5 or less, can be engineered to increase its affinity of binding at pH 6.5 or lower. For example, the paratope of an Ab may be mutated, e.g., by

the substitution of one or more amino acid residues. For example, in some embodiments, 1 to 8, e.g., 1 to 6, 1 to 4, 1 to 3, 1 to 2 or 1 amino acid residues in the heavy or light chain of the Ab that are contact residues with VISTA-ECD (e.g. residues in one or more of the CDRs) may be replaced with a different amino acid residue. Then, the mutated Ab may be tested for binding to the VISTA-ECD protein at pH 6.5 or less and Ab species binding with higher affinity than the parent antibody may be selected. If desired, the steps above may be repeated so that two or more rounds of mutagenesis and selection are performed on the Abs and the highest affinity binders at the acidic pH are selected. In some embodiments, such selections may improve the anti-tumor efficacy of the resulting antibody over its parent.

The above selection method may also be designed to follow the previously described general selection for VISTA-ECD protein specifically binding antibodies. Namely, in certain embodiments, the improved Ab is selected if it binds to the ECD of the VISTA protein with a K_D of 10^{-8} M or less at pH 6.5. In some embodiments, the selection is performed at pH 6.0, or at pH 5.5, or at pH 5.0 instead of at pH 6.5. In some embodiments, the VISTA-ECD protein used for the selection process is a complete hVISTA-ECD protein, or is a polypeptide that comprises the hVISTA IgV domain, or is a polypeptide comprising amino acids 20-95 of SEQ ID NO:2, or amino acids 20-70, 35-95, or 35-70 of SEQ ID NO:2. In some embodiments, the polypeptide also comprises amino acids 95-105 of SEQ ID NO:2. In some embodiment a polypeptide comprising amino acid residues 35-127of SEQ ID NO: 2 is used.

In some embodiments, a method for improving the binding of a VISTA antibody to VISTA ECD at acidic pH comprises increasing the number of glutamic acid, aspartic acid and histidine residues in one or more VH CDRs, e.g., VH CDR1, CDR2 and CDR3.

In some embodiments, the method further comprises testing binding of the selected Ab at neutral, alkaline or physiological pH, such as at pH 7.0 or 7.4. In some embodiments, the method further comprises selecting an antibody if it not only binds to the VISTA-ECD protein with a K_D of 10^{-8} M or less at pH 6.5 or lower, but also if it binds specifically to the polypeptide at pH 7.0 or 7.4. In some such embodiments, Abs are selected if they specifically bind to the VISTA-ECD protein in acidic conditions, e.g., at pH 6.5 or less, and also specifically bind the VISTA-ECD protein at neutral and/or alkaline or physiological pH with at similar affinity (i.e. they are "pan binders"). For example, some such Abs may bind

to the VISTA-ECD protein with a K_D of 10^{-8} M or less at both pH 6.5 and at pH 7.0 (at a constant temperature, e.g., of 25°C or at 37°C) such that the K_D at pH 6.5 is within 1.5-fold of the K_D at pH 7.0 or at pH 7.4.

Certain Abs may be selected if they specifically bind to the VISTA-ECD protein in acidic conditions, e.g., at pH 6.5 or less with higher affinity than at neutral, physiological, or alkaline pH ("pH sensitive binders" or "pH sensitive Abs"). For example, in some embodiments, Abs may bind to the VISTA-ECD protein with a K_D of 10^{-8} M or less at pH 6.5 and with a K_D of more than 10^{-8} M at pH 7.0. In some such embodiments, Abs may bind to the VISTA-ECD protein with a K_D of 10^{-8} M or less at pH 6.5 and with a K_D at pH 7.0 that is more than 1.5-fold higher than that at pH 6.5. In certain embodiments, a pH sensitive Ab is selected if it specifically binds to the VISTA-ECD protein with a K_D that is at least 1.5 fold, 2 fold, 5 fold, 10 fold, 20 fold, 50 fold, 100 fold, 300 fold, 500 fold, 1000 fold, or 5000 fold lower at pH 6.5 than at pH 7.0 or pH 7.4 (at a constant temperature, e.g., of 25°C or at 37°C). For example, in some cases an Ab is selected if it binds to the VISTA-ECD protein with a K_D that is at least 1.5 fold, 2 fold, 5 fold, 10 fold, 20 fold, 50 fold, 100 fold, 300 fold, 500 fold, 1000 fold, or 5000 fold less at pH 6.0, relative to pH 7.0 or pH 7.4 or higher (at a constant temperature, e.g., of 25°C or at 37°C).

In certain embodiments, the method further comprises determining k_{off} at two pH values. In some such embodiments, an Ab is selected if it specifically binds to the VISTA-ECD protein with a k_{off} that is lower in acidic conditions relative to that in neutral, physiological, or alkaline conditions. In certain embodiments, an Ab is selected if it binds to the VISTA-ECD protein in acidic conditions with a k_{off} that is at least 1.5 fold, 2 fold, 5 fold, 10 fold, 20 fold, 50 fold or 100 fold lower at pH 6.5 than the k_{off} at pH 7.0 or pH 7.4, as measured, e.g., at 25°C or at 37°C. For example, in some embodiments, an Ab is selected if it binds to the VISTA-ECD protein with a k_{off} rate that is at least 1.5 fold, 2 fold, 5 fold, 10 fold, 20 fold, 50 fold or 100 fold lower at pH 6.0, relative to pH 7.0, as measured, e.g., at 25°C or at 37°C.

In certain embodiments, the method further comprises determining k_{on} at two pH values. In some such embodiments, an Ab is selected if it binds to the VISTA-ECD protein with a k_{on} that is higher in acidic conditions relative to neutral, physiological, or alkaline

conditions. In certain embodiments, an Ab is selected if it binds to the VISTA-ECD protein in acidic conditions with a k_{on} that is at least 2 fold, 5 fold, 10 fold, 20 fold, 50 fold or 100 fold higher at pH 6.5 than the k_{on} at pH 7.0 or pH 7.4, as measured, e.g., at 25°C or at 37°C. For example, in some embodiments, an Ab is selected if it binds to the VISTA-ECD protein with a k_{on} that is at least 2 fold, 5 fold, 10 fold, 20 fold, 50 fold or 100 fold higher at pH 6.0 than at pH 7.0 or pH 7.4, as measured, e.g., at 25°C or at 37°C.

Antibodies that bind preferentially to huVISTA at acidic pH, versus neutral or physiological pH can be identified by positively screening a library of VISTA antibodies or Fabs or scFvs for binding at acidic pH, e.g., pH 6.0 or 6.5, and negatively screening the library for the lack of binding at neutral pH, e.g., pH 7.0 or physiological pH, e.g., pH 7.4. A library may be enriched in glutamic acid, aspartic acid and histidine residues, such as to select binding domains that are positively charged and more likely to bind to VISTA at acidic pH. The screening may involve positive selection at acidic pH and negative selections at neutal or physiological pH. The positive and negative selections may be alternated.

Alternatively, an antibody binding at neutral pH and/or lacking binding at acidic pH to VISTA can be engineered to lack binding at neutral pH and binding at acidic pH.

Specific embodiments

Additional embodiments of this disclosure include the following:

1. An isolated antibody (Ab) that specifically binds to human V-domain immunoglobulin-containing suppressor of T-cell activation (hVISTA) extracellular domain (ECD), wherein the Ab:
    a. Binds to hVISTA-ECD at pH 6.5 or less with an affinity constant (K_D) of 10^{-7} M or less;
    b. Binds to hVISTA-ECD at pH 6.5 or less with an off rate constant (k_{off}) of 10^{-3} sec^{-1} or less; or
    c. Binds to hVISTA-ECD at pH 6.5 or less with a K_D of 10^{-7} M or less and a k_{off} of 10^{-3} sec^{-1} or less.

2. The isolated Ab of embodiment 1, wherein the Ab binds to hVISTA-ECD at pH 6.5 or less with a K_D of 10^{-8} M or less.
3. The isolated Ab of embodiment 2, wherein the Ab binds to hVISTA-ECD at pH 6.5 or less with a K_D of 10^{-9} M or less.
4. The isolated Ab of any one of embodiments 1-3, wherein the Ab binds to hVISTA-ECD at pH 6.5 or less with a k_{off} of 10^{-4} sec^{-1} or less.
5. The isolated Ab of any one of embodiments 1-4, wherein the Ab binds to hVISTA-ECD at pH 7.0 or higher with:
    a. a K_D of 10^{-7} M or less;
    b. a k_{off} of 10^{-3} sec^{-1} or less; or
    c. a K_D of 10^{-7} M or less and a k_{off} of 10^{-3} sec^{-1} or less.
6. The isolated Ab of embodiment 5, wherein the Ab binds to hVISTA-ECD at pH 7.0 or higher with a K_D of 10^{-8} M or less.
7. The isolated Ab of embodiment 6, wherein the Ab binds to hVISTA-ECD at pH 7.0 or higher with a K_D of 10^{-9} M or less.
8. The isolated Ab of any one of embodiments 5-7, wherein the Ab binds to hVISTA-ECD at pH 7.0 or higher with a k_{off} of 10^{-4} sec^{-1} or less.
9. The isolated Ab of any one of embodiments 5-8, wherein the Ab binds to hVISTA-ECD at pH 6.5 with similar affinity as at pH 7.0.
10. The isolated Ab of embodiment 9, wherein the Ab binds to hVISTA-ECD at pH 6.5 with higher affinity than at pH 7.0.
11. The isolated Ab of embodiment 10, wherein the Ab binds to hVISTA-ECD at pH 6.5 with a K_D that is at least 1.5 fold lower than that at pH 7.0.
12. The isolated Ab of embodiment 11, wherein the Ab binds to hVISTA-ECD at pH 6.5 with a K_D that is at least 2 fold lower than that at pH 7.0.
13. The isolated Ab of embodiment 11, wherein the Ab binds to hVISTA-ECD at pH 6.5 with a K_D that is at least 5 fold lower than that at pH 7.0.
14. The isolated Ab of any one of embodiments 10-13, wherein the Ab binds to hVISTA-ECD at pH 6.5 with a k_{off} that is lower than that at pH 7.0.

15. The isolated Ab of embodiment 14, wherein the Ab binds to hVISTA-ECD at pH 6.5 with a k_{off} that is at least 1.5 fold lower than that at pH 7.0.
16. The isolated Ab of embodiment 15, wherein the Ab binds to hVISTA-ECD at pH 6.5 with a k_{off} that is at least 2 fold lower than that at pH 7.0.
17. The isolated Ab of embodiment 16, wherein the Ab binds to hVISTA-ECD at pH 6.5 with a k_{off} that is at least 5 fold lower than that at pH 7.0.
18. The isolated Ab of any one of embodiments 1-17, wherein the Ab specifically binds to hVISTA-ECD under conditions in which at least one histidine residue of hVISTA-ECD is protonated.
19. The isolated Ab of embodiment 18, wherein the Ab binds to the IgV domain of hVISTA-ECD.
20. The isolated Ab of embodiment 19, wherein the Ab binds to a region located within amino acids 20 and 95 of SEQ ID NO: 2.
21. The isolated Ab of embodiment 20, wherein the Ab binds to a region located within amino acids 20 and 70 of SEQ ID NO: 2.
22. The isolated Ab of embodiment 21, wherein the Ab binds to a region located within amino acids 35 and 70 of SEQ ID NO: 2.
23. The isolated Ab of any one of embodiments 20-22, wherein the Ab further binds to another region of the ECD of hVISTA.
24. The isolated Ab of embodiment 23, wherein the other region is located within amino acids 95 and 105 of SEQ ID NO: 2.
25. The isolated Ab of any one of embodiments 18-24, wherein binding is determined by hydrogen-deuterium exchange mass spectrometry (HDX-MS).
26. The isolated Ab of any one of embodiments 1-25, wherein the Ab inhibits binding of hVISTA to a cell to which hVISTA would otherwise bind.
27. The isolated Ab of any one of embodiments 1-26, wherein the Ab triggers or enhances an immune response in a tumor model.
28. The isolated Ab of embodiment 27, wherein the Ab triggers or enhances T cell activity in a tumor model.

29. The isolated Ab of any one of embodiments 1-28, wherein the Ab inhibits tumor growth in a tumor model.
30. The isolated Ab of any one of embodiments 1-29, wherein the Ab inhibits binding of hVISTA to T cells.
31. The Ab of embodiment 30, wherein the Ab more strongly inhibits binding of hVISTA to T cells at pH 6.5 or less than at pH 7.0 or higher, such as wherein the antibody more strongly inhibits binding of hVISTA to T cells a pH 6.5 than at pH 7.0.
32. A composition comprising an isolated Ab of any one of embodiments 1-31 and a pharmaceutically acceptable carrier.
33. A method of treating a subject having cancer, comprising administering to the subject a composition of embodiment 32.
34. A method for identifying an Ab that binds to hVISTA-ECD at pH 6.5 or less with a K_D of 10^{-7} M or less, comprising contacting a test Ab or a plurality of test Abs with a polypeptide comprising hVISTA-ECD or a fragment thereof comprising the IgV domain of hVISTA-ECD or comprising amino acids 20-95, 20-70, or 35-70 of SEQ ID NO:2 at pH 6.5 or less, and selecting the test Ab or Abs that bind to the polypeptide with a K_D of 10^{-7} M or less.
35. A method for identifying an Ab that binds to hVISTA-ECD at pH 6.5 or less with a k_{off} of 10^{-3} sec^{-1} or less, comprising contacting a test Ab or a plurality of test Abs with a polypeptide comprising hVISTA-ECD or a fragment thereof comprising the IgV domain of hVISTA-ECD or comprising amino acids 20-95, 20-70, or 35-70 of SEQ ID NO:2 at pH 6.5 or less, and selecting the test Ab or Abs that bind to the polypeptide with a k_{off} of 10^{-3} sec^{-1} or less.
36. A method for identifying an Ab that specifically binds to hVISTA-ECD at pH 6.5 with similar affinity at pH 7.0 comprising:
    a. contacting a test Ab or plurality of test Abs at pH 6.5 with a polypeptide comprising hVISTA-ECD or a fragment thereof comprising the IgV domain of hVISTA-ECD or comprising amino acids 20-95, 20-70, or 35-70 of SEQ ID NO:2;

b. contacting the test Ab or plurality of test Abs at pH 7.0 with the polypeptide of (a); and

c. selecting a test Ab if it binds to the polypeptide with a K_D of 10^{-7} M or less at pH 6.5 and at pH 7.0.

37. A method for identifying an Ab that binds with higher affinity to hVISTA-ECD at pH 6.5 than at pH 7.0 comprising:

a. contacting a test Ab or plurality of test Abs at pH 6.5 with a polypeptide comprising hVISTA-ECD or a fragment thereof comprising the IgV domain of hVISTA-ECD or comprising amino acids 20-95, 20-70, or 35-70 of SEQ ID NO:2;

b. contacting the test Ab or plurality of test Abs at pH 7.0 with the polypeptide of (a); and

c. selecting a test Ab if it binds to the polypeptide with a K_D at least 2-fold lower at pH 6.5 than at pH 7.0.

38. A method for identifying an Ab that specifically binds to hVISTA-ECD for use in treating cancer, comprising

a. identifying Abs that specifically bind to hVISTA-ECD at pH 6.5 or less, such as according to the methods of embodiments 32-35; and

b. selecting the Abs of (a) that trigger or enhance an immune response in a tumor model or that inhibit tumor growth at pH 6.5 or less.

39. The method of embodiment 38, wherein step (b) comprises measuring T cell activity.

40. The method of embodiment 38 or 39, further comprising measuring the anti-tumor effect of the Ab.

41. A method for improving the anti-tumor efficacy of an Ab that binds to hVISTA-ECD, comprising

a. Providing an Ab that binds to hVISTA-ECD at pH 6.5 or less with an affinity that is less than a desired value;

b. Replacing 1 to 5 amino acid residues in the heavy or light chain of the Ab with a different amino acid residue, wherein the 1 to 5 amino acid residues are contact residues with hVISTA-ECD;

c. Determining if the Ab obtained in (b) has higher affinity for hVISTA-ECD at pH 6.5 or less relative to the Ab of (a); and

d. Repeating steps (a) - (c), for a number of rounds sufficient to obtain an Ab that binds to hVISTA-ECD at pH 6.5 or less with a K_D of 10^{-7} M or less.

42. A method for improving the anti-tumor efficacy of an Ab that binds to hVISTA-ECD, comprising:

a. Providing an Ab that binds to hVISTA-ECD at pH 6.5 or less with an affinity that is less than a desired value;

b. Preparing a library of variants of the Ab of (a), wherein each variant comprises a substitution of 1 to 5 amino acid residues in the heavy or light chain of the Ab with a different amino acid residue, wherein the 1 to 5 amino acid residues are contact residues with hVISTA-ECD;

c. Selecting Abs of the library of variants of (b) that bind to hVISTA-ECD at pH 6.5 or less with a K_D of 10^{-7} M or less; and

d. Testing the anti-tumor efficacy of the Abs of (c) in a tumor model.

43. A method for improving the pharmacokinetics of an antibody that binds to human VISTA ECD, comprising enhancing the ability of the antibody to bind to human VISTA in acidic conditions, e.g., equal to or lower than pH 6.5.

44. A method for selecting an antibody that binds to human VISTA and having an extended half-life (good pharmacokinetic properties), wherein the method comprises selecting an antibody that binds to human VISTA in acidic conditions, e.g., equal to or lower than pH 6.5.

EXAMPLES

The examples discussed below are intended to be purely exemplary of the invention and should not be considered to limit the invention in any way. The examples are not intended to represent that the experiments below are all or the only experiments performed. Efforts have been made to ensure accuracy with respect to numbers used (for example, amounts, temperature, *etc.*) but some experimental errors and deviations should be accounted

for. Unless indicated otherwise, parts are parts by weight, molecular weight is average molecular weight, temperature is in degrees Centigrade, and pressure is at or near atmospheric.

Example 1: VISTA's extracellular domain is exceptionally rich in histidines

This example shows that VISTA's extracellular domain is exceptionally rich in histidine residues, that these histidine residues are evolutionarily conserved, and that they may contribute to receptor-ligand interactions involving VISTA.

The amino acid sequences of the extracellular domains (ECDs) of immunoglobulin domain-containing proteins were extracted from the uniprot and swiss-prot databases and analyzed for histidine content. Fig. 1A depicts the results of this analysis as a graph. For each protein, the frequency of histidine residues as a percentage of all extracellular domain amino acid residues is plotted on the y-axis, and the total number of extracellular domain amino acid residues is plotted on the x-axis. The diameter of each data point corresponds to the total number of histidine residues in the extracellular domain of each protein. VISTA (labeled) contains an exceptionally high frequency of histidine residues in its extracellular domain.

The evolutionary conservation of histidine residues in VISTA was then assessed. Fig. 1B shows the amino acid reference sequences of human, cynomolgus macaque, and mouse VISTA were aligned, excluding the signal peptides ("Sig"), transmembrane domains ("TMD") and intracellular domains. Histidine residues that are conserved across all three species are bolded and underlined. Histidine residues that are conserved across human and cyno VISTA are bolded without underlining. Many of VISTA's extracellular domain histidine residues are evolutionarily conserved, suggesting an important biological role for VISTA's high histidine content.

A three-dimensional model of the hVISTA IgV domain was created based on sequence homology analysis to available solved structures in the PDB database. The model, shown in Fig. 1C, indicates that many histidines in VISTA's ECD are exposed at the surface of the molecule, where they may play a role in ligand binding as well as in antibody recognition. Histidine residues are depicted as balls and sticks.

Example 2: Histidine protonation may regulate VISTA receptor-ligand engagement and immunosuppressive activity in tumors and other acidic microenvironments

This Example describes histidine protonation in response to physiologically relevant acidic pH, as well as a model in which VISTA extracellular domain histidines confer counter-receptor or ligand selectivity for acidic pH rather than physiological pH.

Fig. 2A shows the equilibrium between the lack of, and the presence of, protonation of the pyrrole ammonium group (NH) in a histidine residue. The pKa of histidine in solution is 6.5, indicating that histidine residues are more likely to be protonated at pH 6.5 and lower, and thus, positively charged, than at higher pH. The increase in positive charge at the surface of the VISTA ECD as a result of protonation may affect receptor or ligand binding as well as VISTA structure and/or function. Thus, changes in pH may also modify antibody binding epitopes and/or result in varied antibody affinities.

Fig. 2B shows a model in which VISTA engages PSGL-1 or other counter-receptors and ligands ("VISTA-R") selectively at acidic pH. At physiological pH, such as in the blood, histidine residues on VISTA's ECD are expected to be non-protonated. As a result, VISTA binding to PSGL-1 or other counter-receptors and ligands is neglible at physiological pH. In contrast, in locations that tend to have an acidic extracellular pH, such as tumor microenvironments or sites of inflammation, acidic pH may partially or fully drive VISTA ECD histidine protonation and thus enable VISTA engagement with PSGL-1 or other counter-receptors and ligands. Accordingly, antibodies that bind strongly to VISTA-ECD proteins at acidic pH ranges may be more effective in inhibiting VISTA activity in tumors.

Example 3: VISTA is expressed by myelomonocytic cells in tumors

This Example shows that VISTA is frequently expressed by myelomonocytic cells in tumors, including macrophages, dendritic cells, and granulocytes.

Surgically resected non-small cell lung carcincoma, renal clear cell carcinoma, melanoma, colorectal carcinoma, and other tumor samples were washed in ice-cold PBS, cut into approximately 15 mm^3-sized pieces, and suspended in ice-cold RPMI-1640 media (Fisher Scientific catalog number 11875093) supplemented with 2% heat-inactivated FBS and 2 mM EDTA (Fisher Scientific 15575020). Each sample was transferred to a large

clearance glass dounce (Tenbroeck Tissue Grinders) and ground until the tissue pieces were visually disassociated. The suspensions were filtered through 70 μM nylon mesh and centrifuged. The supernatants were discarded and the cell pellets were re-suspended in room-temperature PBS supplemented with 0.1% bovine serum albumin and 250 mg/mL sterile-filtered DNase 1 (grade II, from bovine pancreas, Roche catalog number 10104159001) for 3 minutes at room temperature. The cells were then washed in ice-cold supplemented RPMI and re-suspended in ice-cold PBS. A cell viability dye was added and the cells were incubated on ice in the dark. After 20 minutes, non-specific antibody staining was blocked by adding 4% normal rat serum, 4% normal mouse serum, 20% human serum from AB plasma, and 1:125 diluted Human TruStain FcX™ (Biolegend catalog number 422302). The cells were stained with fluorophore-conjugated antibodies against HLA-DR (BD Biosciences catalog number 564040), CD8 (Fisher Scientific catalog number 46-0087-42), CD14 (Biolegend catalog number 325620), CD45 (Biolegend catalog number 304017), CD4 (BD Biosciences catalog number 563875), CD11c (BD Biosciences catalog number 744439), CD15 (BD Biosciences catalog number 563142), PD-1 (BD Biosciences catalog number 565299), CD3 (BD Biosciences catalog number 565515), CD56 (Fisher Scientific catalog number 61-0567-42), CD19 (BD Biosciences catalog number 564977), and VISTA (VISTA antibody 3 conjugated to AlexaFluor™ 647, Fisher Scientific catalog number A20186) suspended in Brilliant Stain Buffer (BD Biosciences catalog number 562794) for 30 minutes on ice in the dark. The stained cells were washed in ice-cold PBS, fixed (Fisher Scientific catalog number 00-5523-00), and acquired on a flow cytometer. Data were analyzed using FlowJo™ software (BD Biosciences). As shown in Fig. 3, VISTA cell surface expression was highest on macrophages and granulocytes, moderate on dendritic cells, and low on T cells, natural killer cells, and B cells.

Example 4: VISTA cell binding exhibits acidic pH selectivity

This Example shows that multimerized human VISTA ECD binds more efficiently to stimulated human CD4+ T cells and human peripheral blood mononuclear cells at acidic pH than at neutral or physiological pH, and that this binding can be blocked by an anti-human

VISTA locking antibody. Acidic pH-selective-dimerized mouse VISTA ECD binding to mouse splenocytes is also shown.

Human CD4+ T cells were enriched from healthy donor blood by RosetteSep™ (Stemcell catalog number 15062) and stimulated *in vitro* for approximately four days with Human T-Activator CD3/CD28 Dynabeads™ (Fisher Scientific catalog number 111.32D) and recombinant human IL-2 (Peprotech catalog number 200-02) in RPMI-1640 supplemented with 10% heat-inactivated FBS, Glutamax™ (Fisher Scientific catalog number 35050061), non-essential amino acids (Fisher Scientific 11140050), sodium pyruvate (Fisher Scientific catalog number 11360070), and 2-mercaptoethanol (Fisher Scientific 21985023). The activated CD4+ T cells were stained with monobiotinylated hVISTA ECD molecules (Phe 33 - Ala 194 (Accession # AAH20568)-polyhistidine; AcroBiosystems, Inc. B75-H82F3) loaded at a 28:1 molar ratio onto Phycoerythrin (PE)-conjugated streptavidin dextramers (catalog number DX01-PE) diluted into Hank's Buffered Salt Solution (HBSS, Fisher Scientific catalog number 14025134) acidified to various pH with mM MES (Sigma, 1317-100ML) for 30 minutes at room temperature. As a control, activated CD4+ T cells were stained with PE-conjugated streptavidin dextramers that were not loaded with hVISTA. The stained cells were washed with HBSS + MES and acquired on a flow cytometer. Data were analyzed using FlowJo™ software (BD Biosciences). The results, depicted in Fig. 4A, show that hVISTA did not bind CD4+ T cells better than the control at pH > 6.5. In contrast, hVISTA exhibited progressively stronger binding to CD4+ T cells at pH < 6.5. Left, from darker gray to lighter, the filled histograms depict binding at pH 7.0, 6.5, 6.4, 6.3, 6.1, and 6.0. Some histograms are labeled with their corresponding pH. Non-VISTA control multimer binding at pH 6.0 is shown as the unfilled histogram. Right, graphed PE mean fluorescence intensities (MFI) of CD4+ T cells stained with hVISTA-loaded dextramers (blue circles) or with non-loaded dextramers (triangles) at various pH.

Peripheral blood mononuclear cells (PBMC) were enriched from healthy donor blood by ficoll gradient centrifugation (Ficoll-Paque Plus, GE Life Sciences catalog number 17144003) and stained with hVISTA-loaded dextramers (also referred to as multimers) and fluorophore-conjugated diluted in HBSS + MES buffers as described above. Fig. 4B shows filled histograms that depict, from darker gray to lighter, binding at pH 6.0 to CD19+ B cells,

CD4+ T cells, CD8+ T cells, CD56+ NK cells, and CD14+ monocytes. The unfilled, solid border and dotted border histograms depict binding at pH 7.4 to total PBMC lymphocytes and monocytes respectively. The results show that hVISTA can bind many leukocytes at acidic pH but not significantly at physiological pH.

Activated human CD4+ T cells were stained with hVISTA multimers at pH 6 in the presence of titrated anti-human VISTA antibody or an isotype-matched non-VISTA-specific antibody. The results, graphed in Fig. 4C, show VISTA multimer MFI relative to antibody concentration. Anti-hVISTA antibody (VISTA antibody 3; squares), but not the non-VISTA-specific control antibody (circles), blocked hVISTA binding to activated CD4+ T cells in a concentration-dependent manner. The PE MFI of CD4+ T cells that were not stained with hVISTA-loaded multimers is included as a control (single triangle).

Fig. 4D shows representative two-dimensional flow cytometry plots of VISTA multimer staining at pH 6.0 to heparan sulfate-mutant Chinese Hamster Ovary (CHO) cells (line pGSD-677, American Type Culture Collection) that were transfected to express full length human PSGL-1 (SEQ ID NO: 3; nucleic acid NM_003006.4). Staining was performed in the presence or absence of a titrated anti-VISTA blocking antibody (mAb 3). Cells left unstained by VISTA multimers are shown as a control. PSGL-1 antibody (BD Biosciences catalog number 562758) staining is plotted on the y-axis, and VISTA multimer staining is plotted on the x-axis.

Splenocytes were collected from C57BL6/J mice (Jackson Laboratory catalog number 000664) and stained with mVISTA ECD / human IgG Fc (Fragment, crystallizable) chimeric fusion proteins followed by fluorophore-conjugated anti-human IgG Fc secondary antibodies (Jackson Immunoresearch catalog number 109-065-098) at pH 6.0 or 7.4. The results, depicted by histogram in Fig. 4E, show that mVISTA binds murine splenocytes more efficiently at pH 6.0 than at physiological pH (approximately pH 7.4). From darker gray to lighter, the filled histograms depict binding at pH 6.0 to CD8+ T cells, CD11b+ myeloid cells, and CD4+ T cells. The unfilled histogram depicts binding at pH 7.4 to total splenocytes.

Example 5: VISTA mediates cell : cell adhesion and immune suppression selectively at acidic pH

This Example shows that VISTA mediates cell : cell adhesion and suppresses T cell activation more potently at acidic pH than at neutral or physiological pH.

An acidic pH-compatible flow cytometry-based cell/cell conjugate assay was established. 293T cells (an immortalized human embryonic kidney cell line, ATCC catalog number CRL-3216) ectopically expressing full-length human VISTA or vector were labeled with CFSE (Carboxyfluorescein succinimidyl ester; Fisher Scientific catalog number C34554). CHO cells were labeled with CellTrace™ Far Red (Fisher Scientific catalog number C34564). The Vector or VISTA 293T cells were then mixed at a 1:1 ratio with CHO cells in pH7.0 or pH6.0 buffers and incubated for 1 hour at room temperature. The formation of CHO and 293T cell/cell conjugates was assessed by flow cytometry. The results shown in Figs. 5A-B demonstrate that VISTA-expressing 293T cells preferentially adhere to CHO cells at acidic pH and that inclusion of an anti-VISTA blocking antibody (VISTA mAb 3; red bars) inhibits VISTA mediated cell/cell adhesion.

An acidic pH-compatible T cell suppression assay was established. Jurkat cells (an immortalized human T cell line, ATCC catalog number TIB-152) expressing an NFkB promoter driven luciferase reporter were co-cultured in HBSS + MES buffers of various pH with 293T cells (an immortalized human embryonic kidney cell line, ATCC catalog number CRL-3216) ectopically expressing full-length human VISTA and a single-chain variable fragment of the anti-human T cell receptor agonist antibody clone OKT3 at a 10 : 1 Jurkat : 293T cell ratio. An anti-VISTA blocking antibody (VISTA mAb 3) or an isotype-matched non-VISTA-specific control antibody were added at 10 μg/mL to the co-cultures. After incubation, Jurkat T cell activation was quantified by measuring luciferase activity (1 second interval Promega catalog number G7940). The results are shown in Fig. 5C-D. Fig. 5C shows a plot of luciferase units in Jurkats treated with anti-VISTA (red squares) or control antibody (blue circles) at different pH. Fig. 5D shows a plot of the luciferase signal in anti-VISTA antibody-treated co-cultures divided by the luciferase signal in control antibody-treated co-cultures at each pH tested. The results show that VISTA-mediated T cell suppression is most potent at acidic pH.

Example 6: VISTA trafficks through intracellular recycling endosomes

This Example shows that VISTA can be found in intracellular endosomes, particularly Rab11+ recycling endosomes, and can recycle to and from the cell surface via endosomal trafficking. The strength with which an anti-VISTA antibody binds VISTA at acidic pH influences its capacity to remain bound to VISTA during endosomal trafficking.

Monocytes were isolated from PBMCs by magnetic activated cell sorting. Both monocytes and 293T cells were then fixed in 4% paraformaldehyde and stained intracellularly for Rab5, Rab7 or Rab11, and with an anti-VISTA or control antibody. The control antibody ("cAb"), which is a non-VISTA-binding antibody of the same isotype as the anti-VISTA antibody, does not detectably bind monocytes or 293T cells expressing human VISTA. Anti-VISTA and control antibodies were directly labeled with Alexa488. Rab antibodies were detected using an Alexa594 anti-rabbit Ig secondary antibody. Hoescht 33342 staining was performed to identify cell nuclei. Images were captured using a spinning disk confocal microscope. **Fig. 6A** shows co-localization of VISTA, Rab5 (early endosome marker), Rab7 (late endosome marker), and Rab11 (recycling endosome marker) within 293T cells expressing human VISTA. **Fig. 6B** shows co-localization of VISTA and Rab11 within human monocytes. Intracellular VISTA is co-localized with Rab11+ recycling endosomes.

To assess VISTA's capacity to recycle through endosomes, an endolysosome-dependent antibody drug conjugate killing assay was performed with three anti-hVISTA antibodies (VISTA mAb 1, 2 and 3) with varying VISTA binding properties at physiological and acidic pH. An SPR assay was performed first to compare hVISTA binding profiles for all three VISTA antibodies at pH 7.4, 6.7 and 6.0. VISTA antibodies were captured on a Biacore® T100 (GE Healthcare) CM5 biosensor containing immobilized Protein A, then 100nM hVISTA-ECD (amino acids 32-193 of SEQ ID NO: 1 with a 7xHis tail, i.e., AFKVATPYSL YVCPEGQNVT LTCRLLGPVD KGHDVTFYKT WYRSSRGEVQ TCSERRPIRN LTFQDLHLHH GGHQAANTSH DLAQRHGLES ASDHHGNFSI TMRNLTLLDS GLYCCLVVEI RHHHSEHRVH GAMELQVQTG KDAPSNCVVY PSSSQESENI TAHHHHHHH; SEQ ID NO: 325) was flowed in PBST running buffer at the

indicated pH at 37°C. Reference-subtracted sensorgrams were normalized to the 'binding' report point and plotted. VISTA antibody 3, "mAb 3", (Fig. 6C, top) exhibited the greatest degree of VISTA binding impairment at acidic pH, followed by VISTA antibody 2 , "mAb 2," (Fig. 6C, middle), which was only moderately impaired. VISTA antibody 1, "mAb 1," maintained strong VISTA binding at acidic and physiological pH conditions (Fig. 6C, bottom).

The endolysosome-dependent antibody drug conjugate killing assay was performed as follows. AML3 cells (an immortalized human monocyte cell line, ATCC CRL-9589), which endogenously express human VISTA, were cultured with titrated anti-VISTA antibodies or a non-VISTA-specific control antibody and an anti-human IgG secondary antibody that was conjugated to a cathepsin B-sensitive linker and a cytotoxic tubulysin payload. Because Cathepsin B is predominantly active in late endosomes and lysosomes, anti-VISTA antibodies that recycle with VISTA through early endosomes and recycling endosomes will experience low levels of linker cleavage and as a result low levels of the cytotoxic payload release and cell death. Anti-VISTA antibodies which become disassociated from VISTA in acidic endosomes and sorted into late endosomes and lysosomes will experience higher levels of linker cleavage. Cell viability was measured by Cell Titer Glo® (Promega catalog number G7573) after five days in culture. Fig. 6D shows the results of this assay, with AML3 viability (Cell Titer Glo) plotted on the y-axis and primary antibody concentrations plotted on the x-axis. Calculated EC50s for primary antibodies: VISTA antibody 1, inverted triangles, 0.485 μg/mL; VISTA antibody 2, circles, 0.092 μg/mL; VISTA antibody 3, squares, 0.006 μg/mL; Control, triangles, 1.085 μg/mL. Antibody potency was inversely correlated with anti-VISTA antibody binding at acidic pH.

To confirm that binding at acidic pH was responsible for the differences in potency, VISTA antibody 3 was affinity optimized such that its ability to bind VISTA at acidic pH was improved. Fig. 6E shows an SPR assay comparing the hVISTA antibody binding profiles of VISTA antibody 3 with this variant, VISTA antibody 3c, using the assay conditions described for Fig. 6C. VISTA antibody 3 again exhibited VISTA binding impairment at acidic pH, whereas the variant VISTA antibody 3c exhibited comparable VISTA binding at acidic and physiological pH. Fig. 6F shows the activity of VISTA

antibody 3c (diamonds) in the killing assay described for Fig. 6D. The acidic pH-optimized variant of VISTA antibody 3 exhibited a 31-fold lower potency than that of the original antibody, indicating that impaired anti-VISTA antibody binding at acidic pH results in a loss of antibody binding during VISTA recycling.

Based on these findings, a recycling model is proposed in which VISTA gets recycled to and from the cell surface via early endosomes and recycling endosomes. This model is depicted in Fig. 6G. Anti-VISTA antibodies can recycle with VISTA through these endosomes, maintaining target engagement. However, VISTA antibodies with impaired VISTA binding at acidic pH, particularly those with a fast off-rate at acidic pH, may disassociate from VISTA during recycling and become trapped or degraded inside cells, resulting in poor target engagement and continual consumption of circulating antibodies. In contrast, antibodies which bind and remain bound to VISTA at acidic pH may maintain higher levels of target engagement, particularly in acidic microenvironments such as tumors, and exhibit longer mean residence times *in vivo*.

Example 7: Superiority of VISTA antibodies lacking binding at physiological pH

The inventors have shown that VISTA is an acidic pH-selective immunoreceptor, demonstrating the importance and utility of targeting VISTA with antibodies that bind well at acidic pH. Additionally, antibodies that do not bind or negligibly bind to VISTA at physiological pH are advantageous for several reasons. First, due to the relatively abundant expression of VISTA on circulating myelomonocytic cells, particularly monocytes and neutrophils, antibodies that bind VISTA at physiological pH are subject to high levels of target-mediated drug disposition (TMDD) in blood. This effect is exacerbated by the propensity of VISTA to recycle through intracellular endosomes, leading to anti-VISTA antibody internalization and degradation. This secondary effect is particularly problematic for antibodies which have impaired binding at acidic pH, as can be observed for antibodies that bind VISTA's histidine-rich ligand interface. Both effects will reduce the amount of anti-VISTA antibody in circulation, reducing the amount of antibody that will reach the tumor and thus the intended biology activity of the antibody. Second, antibodies that bind VISTA at

physiological pH and which possess effector functions such as induction of antibody-dependent cell cytotoxicity (ADCC), antibody-dependent cell phagocytosis (ADCP), or delivery of an immunomodulatory payload will subject circulating myelomonocytic cells to those effector functions, potentially resulting in undesirable effects such as circulating neutrophil depletion or activation. Thus, the inventors discovered that antibodies binding to huVISTA at acidic pH, but negligibly at physiological pH, have the double advantage of (1) better exposure in relevant sites such as tumors and (2) reduced toxicities in the case of antibodies with effector functions such as ADCC, ADCP, or delivery of an immunomodulatory payload. Additionally, because VISTA itself is an acidic pH-selective immunoreceptor, blockade of VISTA's ligand interface at physiological pH is likely unnecessary to modulate VISTA receptor-ligand activity. Therefore, antibodies that bind to huVISTA at acidic pH, but not significantly at physiological pH were generated as described below.

Example 8: Isolation of anti-VISTA antibodies binding preferentially to human VISTA at acidic pH over physiological pH

This Example describes the generation of antibodies that bind preferentially to human VISTA at low (acidic) pH relative to neutral or physiological pH.

A library of anti-VISTA antigen binding fragments of antibodies was constructed and screened as follows. Antibody libraries were created using genetic material isolated from HuMab mice immunized with full length human VISTA (hVISTA). These antibodies were formatted as scFv and were selected against full length hVISTA binding at low pH (pH 6.0) via mRNA display (Xu L et al. (2002) *Chemistry & Biology* 9: 933; Roberts RW and JW Szostak (1997) *Proc. Natl. Acad. Sci. USA* 94:12297; Kurz et al. (2000) *Nucleic Acids Res.* 28(18):E83). Selection output was analyzed via next generation sequencing (NGS), and library members that demonstrated an enrichment to VISTA binding at low pH were identified, reformatted as IgG 1.3 (an effectorless IgG1 constant region consisting of an IgG1 Fc having amino acid mutations L234A, L235E, and G237A), and screened for binding to VISTA by SPR.

Surface plasmon resonance (SPR) analysis was performed to measure the association rates (defined as ka or k_{on}, 1/Ms units), dissociation rates (defined as kd or k_{off}, s^{-1} units) and affinity constants (defined as K_D, M units) for VISTA Abs at acidic and physiological pHs using a Biacore® T200 instrument (GE Healthcare). Protein A (Fisher Scientific catalog #21181) was diluted to 20 ug/ml in 10mM sodium acetate pH 4.5 and immobilized onto flow cells of a CM5 biosensor following the manufacturer's amine coupling protocol (GE Healthcare), targeting 6,000 RU immobilization density of Protein A per flow cell. SPR experiments were conducted at 37°C using PBST (137 mM sodium chloride, 2.7 mM potassium chloride, 10 mM phosphate buffer, 0.05% Tween 20) running buffer at pH 7.4 and 6.0. Antibodies were diluted to 20 nM in PBST pH 7.4, and were captured across active biosensor flow cells at 5 ul/min for 50 seconds. A concentration series of 50 – 0.2 nM monovalent hVISTA-ECD (SEQ ID NO: 325) was prepared in pH 7.4 and 6.0 running buffers, and was injected over the captured antibodies at 40 ul/min to measure association and dissociation. Two 15 second injections of 10 mM glycine pH 1.5 were used to regenerate the Protein A capture surface between assay cycles. Rate constants k_a (k_{on}) and k_d (k_{off}) were derived from reference flow cell and 0 nM blank-subtracted sensorgrams, and were fit to a 1:1 binding model in Biacore® T200 Evaluation Software v.2.0. For each VISTA antibody, the ratio of k_{off} at pH 6 / k_{off} at pH 7.4 was calculated to identify antibodies exhibiting slow off-rates at acidic pH and fast off-rates at physiological pH.

Six antibodies, reformatted as IgG1.3 antibodies, demonstrated near equivalent affinity at both pH 6 and pH 7.4. In particular, two antibodies had a slower off rate at pH 6.0 than at pH 7.4 (i.e., faster k_{off} at pH 7.4 than pH 6.0). The variable regions of these two huVISTA antibodies are referred to as P1-061015 and P1-061029 and the antibodies comprising these variable regions and formatted as IgG1.3 antibodies are referred to as P1-061015.IgG1.3 and P1-061029.IgG1.3, respectively. The k_{off} rates of P1-061015.IgG1.3 and P1-061029.IgG1.3 are provided in Table 1.

Table 1: k_{off} of selected antibodies at pH 6.0 and pH 7.0

Antibody name	pH 6 k_{off} (s^{-1})	pH 7 k_{off} (s^{-1})	pH 6/pH 7 k_{off}
P1-061015.lgG1.3	1.4×10^{-3}	2.3×10^{-3}	0.6
P1-061029.lgG1.3	4.8×10^{-3}	9.1×10^{-3}	0.5

The heavy and light chain CDR1, CDR2 and CDR3 sequences of P1-061015 and P1-061029 are provided in Table 2 below and are also shown in the Sequence Table following the Examples section of the disclosure.

Table 2: Amino acid sequences of huVISTA antibodies binding to huVISTA preferentially at pH 6.0 than pH 7.4

P1 ID	VH-gene	VH CDR1	VH CDR2	VH CDR3
P1-061015.lgG1.3	3-33	GFTFSSYAMH (SEQ ID NO: 95 Residues 26-35)	IIWYDGSNKYYADSVKG (SEQ ID NO: 95 Residues 50-66)	DSGFYSSYYFDY (SEQ ID NO: 95 Residues 99-110)
P1-061029.lgG1.3	3-09	GFTLDDYAMH (SEQ ID NO: 67 Residues 26-35)	GINWNSANIGYADSVKG (SEQ ID NO: 67 Residues 50-66)	VPGYSGGWIDAFDV (SEQ ID NO: 67 Residues 99-112)
	VL-gene	VL CDR1	VL CDR2	VL CDR3
P1-061015.lgG1.3	L6	RASQSVSSSYLA (SEQ ID NO: 96 Residues 24-35)	DASNRAT (SEQ ID NO: 96 Residues 51-57)	QQYNSYPYT (SEQ ID NO: 96 Residues 90-98)
P1-061029.lgG1.3	A27	RASQSVSSSYLA (SEQ ID NO: 68 Residues 24-35)	GASSRAT (SEQ ID NO: 68 Residues 51-57)	QQYGSSPFT (SEQ ID NO: 68 Residues 90-98)

Example 9: Further engineering of the P1-061015 and P1-061029 anti-VISTA Abs to develop acidic pH-selective antibodies

This Example describes the further engineering of variable regions P1-061015 and P1-061029 identified in Example 2 to obtain anti-huVISTA variable regions that have a higher k_{off} ratio between binding at pH 6.0 relative to pH 7.4.

Two libraries were built by introducing specific mutations in the VH CDRs of P1-061015 and P1-061029, respectively. The libraries allowed only for amino acid substitutions that were the most likely to improve binding at low pH, i.e., aspartate, glutamate and histidine. The library also allowed for single and double amino acid substitutions in each CDR and for recombinations across CDRs (maximum of 6 amino acid substitutions per

chain). Fig. 7A shows the mutations that were introduced into the heavy chain CDR3 amino acid sequences of P1-061029 to form the P1-061029 library. The figure indicates that specific sequences were excluded to avoid introducing liabilities (e.g., DG).

The '029 and '015 libraries were screened by several rounds of binding to full length hVISTA at pH 6.0 via yeast surface display. Further rounds of selection were conducted by toggling between positive (pH 6.0 binding to huVISTA) and negative (pH 7.4 binding to huVISTA) (shown in Fig. 7B) selections, where library members that did not bind to VISTA at pH 7.4 were collected in the negative selection rounds. The selection output was analyzed by NGS. The '029 library members that bound to huVISTA at pH 6.0 after round 9 of selection were analyzed for binding to human VISTA at pH 6.0 and pH 7.4 via flow cytometry. Fig. 7C shows representative two-dimensional flow cytometry plots showing the variant pool after 9 rounds of selection. VISTA binding is plotted on the y-axis, and variant antibody expression is plotted on the x-axis. Binding data at various antibody concentrations and pH are shown. The results demonstrated very strong pH 6-selective binding to human VISTA, particularly at 20 nM.

Additional progeny clones of the '029 were isolated from the '029 library using a different method. Some clones were the same as those identified by the first method, and nine additional clones were isolated.

The 19 clones isolated from the '029 library selected for further analysis were reformatted as IgG1.3 antibodies. The amino acid differences in the heavy chain CDRs of these clones relative to those of the '029 VH CDRs are shown in Table 5.

Table 5: VH CDR1, CDR2 and CDR3 amino acid sequences (separated by an underscore) of antibodies derived from the '029 parent antibody

NAME	CDR1 (pos 26-35)	CDR2 (pos 50-66)	CDR3 (pos 99-110)	SEQ ID NO
P1-061029	GFT**LD**D**Y**AMH_GI**N**WNS**AN**IGYADSVKG_VPGYS**G**GWIDA**F**D**V**			67
P1-068757	----E-E---_------EE---------_----------E-D			71
P1-068759	----E-E---_--D---E----------_----------E-D			87
P1-068761	----E-E---_------EE---------_-----H-----E--			51
P1-068763	----E-----_--D---E----------_-----H-----E--			91
P1-068765	---DE-----_------EE---------_----------E-D			63
P1-068767	----E-----_--D---E----------_----------E-D			55
P1-068769	----E-E---_------DH---------_----------E-D			83
P1-068771	----E-E---_------HE---------_----------E-D			75
P1-068773	----E-----_--D---D----------_----------E-D			59
P1-068775	----E-E---_--D---EE---------_-----H-----E-D			79
P1-069059	----E-----_------DH---------_----------E-D			11
P1-069061	----E-----_-------E---------_----------E-D			15
P1-069063	----E-----_-------E---------_----------D-E			19
P1-069065	----E-E---_------DD---------_----------			23
P1-069067	----------_------EE---------_----------D-E			27
P1-069069	----------_------EE---------_----------D--			31
P1-069071	----E-E---_-------D---------_-----E--------			35
P1-069073	----E-----_--D---D----------_----------E-D			39
P1-069075	----E-----_----D--E---------_-----H-----E--			43
P1-069077	----E-E---_------DE---------_----------			47

Binding of several preparations of each of the '029 progeny clones and of the parent '029 antibodies, formatted as IgG1.3 antibodies, to human VISTA at pH 6.0 and 7.4 was measured by Surface plasmon resonance (SPR). SPR analysis was performed to measure koff and K_D binding affinity measurements for VISTA Abs at acidic and neutral pHs using a Biacore® T100 instrument (GE Healthcare). Protein A (ThermoFisher Scientific catalog #21181) was diluted to 20 ug/ml in 10mM sodium acetate pH 4.5 and immobilized onto flow cells of a CM5 biosensor following the manufacturer's amine coupling protocol (GE Healthcare), targeting 2,000 RU immobilization density of Protein A per flow cell. SPR

experiments were conducted at 37°C using PBST (137 mM sodium chloride, 2.7 mM potassium chloride, 10 mM phosphate buffer, 0.05% Tween® 20) running buffer at pH 7.4 and 6.0. Antibodies were diluted to 25 nM in PBST pH 7.4, and were captured across active biosensor flow cells at 5 ul/min for 60 seconds. A concentration series of 50 – 5 nM monovalent hVISTA-ECD (SEQ ID NO: 325) was prepared in pH 7.4 and 6.0 running buffers, and was injected over the captured antibodies at 40 ul/min to measure association and dissociation. Two 15 second injections of 10 mM glycine pH 1.5 were used to regenerate the Protein A capture surface between assay cycles. Rate constants ka (k_{on}) and kd (k_{off}) were derived from reference flow cell and 0 nM blank-subtracted sensorgrams, and were fit to a 1:1 binding model in Biacore® T200 Evaluation Software v.2.0. The affinity constant, K_D was calculated as the ratio of rate constants k_{off}/k_{on} for each VISTA antibody.

The maximal (or magnitude) human VISTA binding response is defined as the reference-subtracted 'binding' report point response at the end of the 50nM VISTA injection for each antibody, and is reported in response units (RUs). The maximal human VISTA binding response (RUs) to each antibody is plotted in Fig. 7D. The mean average binding response (between two to four replicate antibodies) is plotted, and error bars represent the standard deviation. The results indicate that the selected progeny clones of '029 bind to hVISTA at pH 6.0, but not at pH 7.4 (empty circles representing binding at pH 7.4 are all located at the bottom of the graph except for the parent '029 clone).

The k_{off} rates at pH 6.0 of the '029 and its progeny was determined by SPR using the method described above, and are represented in Fig. 7E. The dashed line in the figure represent the k_{off} rate of '029, and clones to the left of the dashed line have a slower k_{off} rate at pH 6.0 relative to that of the parental '029 antibody, whereas those on the right side have a faster k_{off} rate at pH 6.0 relative to that of the parental '029 antibody.

Representative hVISTA SPR binding sensorgrams to the '029, '761 and '767 antibodies at neutral and acidic pH are shown in Fig. 7F. Reference-subtracted 50 nM and 5 nM huVISTA sensorgrams are plotted. At neutral pH, <10 RU VISTA binding signal was observed for '761 and '767, thus in order to adequately measure and compare the k_{off} and K_D for '761 and '767 to '029, a SPR kinetics assay utilizing μM VISTA concentrations at physiological pH was required.

For this assay, '029, '761 and '767 were reformatted as hIgG1f isotype and were expressed as both standard hIgG1f and in hIgG1f afucosylated formats to compare against the hIgG1.3f Fc. An SPR kinetics assay was conducted to measure koff and K_D binding affinity measurements for VISTA Abs at acidic and physiological pH using a Biacore® T100 instrument (GE Healthcare). Protein A (ThermoFisher Scientific catalog #21181) was diluted to 20 μg/ml in 10mM sodium acetate pH 4.5 and immobilized onto flow cells of a CM5 biosensor following the manufacturer's amine coupling protocol (GE Healthcare), targeting 2,000 RU immobilization density of Protein A per flow cell. SPR experiments were conducted at 37°C using PBST (137 mM sodium chloride, 2.7 mM potassium chloride, 10 mM phosphate buffer, 0.05% Tween 20) running buffer at pH 7.4 and 6.0. Antibodies were diluted to 25 nM in PBST pH 7.4, and were captured across active biosensor flow cells at 5 ul/min for 45 seconds. A concentration series of 1600 – 0.78 nM (pH 7.4) and 100 – 0.78 nM (pH 6.0) monovalent hVISTA-ECD (SEQ ID NO: 325) was prepared running buffer, and was injected over the captured antibodies at 40 ul/min to measure association and dissociation. Two 15 second injections of 10 mM glycine pH 1.5 were used to regenerate the Protein A capture surface between assay cycles. Rate constants ka (k_{on}) and kd (k_{off}) were derived from reference flow cell and 0 nM blank-subtracted sensorgrams, and were fit to a 1:1 binding model in Biacore® T200 Evaluation Software v.2.0. The affinity constant, K_D was calculated as the ratio of rate constants k_{off}/k_{on} for each VISTA antibody. Ratios of k_{off} and K_D at pH 7.4 / pH 6.0 were calculated to compare off-rate and affinity improvement at acidic pH relative to physiological pH. While the neutral pH binding rate constants were not previously able to be determined for '761 and '767 using 50 nM hVISTA (Figs. 7D and 7F), inceasing the neutral pH VISTA concentration range to 1.6 μM resulted in binding responses (> 10 RU) for these clones that fit to a 1:1 binding model. Kinetic data for these acidic-selective VISTA antibodies is shown in Table 6. The '029 parent exhibits equivalent k_{off} at both pHs, while '761 and '767 exhibit over 10-fold selectivity for pH 6 over pH 7.4 in k_{off} and over 2000-fold selectivity for pH 6 over pH 7.4 in K_D. Human VISTA binding rate constants are conserved across hIgG1.3f, hIgG1f and afucosylated hIgG1f isotype variants.

Table 6: Binding characteristics of VISTA antibodies as determined by SPR

Antibody	Isotype	pH 7.4			pH 6.0			kd ratio (7.4/6)	KD ratio (7.4/6)
		ka (1/Ms)	kd (1/s)	KD (M)	ka (1/Ms)	kd (1/s)	KD (M)		
P1-061029	hIgG1.3f	1.6E+05	6.8E-03	4.2E-08	1.1E+06	7.9E-03	7.2E-09	0.9	5.8
	hIgG1f	1.7E+05	7.4E-03	4.2E-08	1.1E+06	8.0E-03	7.1E-09	0.9	5.9
	hIgG1f afucosylated	1.7E+05	7.2E-03	4.1E-08	1.1E+06	7.8E-03	6.9E-09	0.9	5.9
P1-068761	hIgG1.3f	3.8E+03	4.2E-02	1.1E-05	3.7E+05	1.6E-03	4.3E-09	26.3	2558.1
	hIgG1f	1.2E+03	4.2E-02	3.5E-05	3.6E+05	1.5E-03	4.2E-09	28.0	8333.3
	hIgG1f afucosylated	5.1E+03	4.2E-02	8.2E-06	3.7E+05	1.5E-03	4.1E-09	28.0	2000.0
P1-068767	hIgG1.3f	1.9E+03	3.6E-02	1.9E-05	3.3E+05	2.6E-03	7.8E-09	13.8	2435.9
	hIgG1f	1.5E+03	3.2E-02	2.2E-05	3.2E+05	2.6E-03	8.0E-09	12.3	2750.0
	hIgG1f afucosylated	1.3E+03	3.3E-02	2.4E-05	3.3E+05	2.6E-03	7.9E-09	12.7	3038.0
α-VISTA acidic pH sensitive	hIgG1.3f	2.2E+05	7.8E-04	3.6E-09	2.8E+06	9.0E-02	3.2E-08	0.01	0.1

Human VISTA binding kinetics of '029, '761 and '767 (as IgG1.3 antibodies) were measured at pH values between pH 7.4 and pH 6.0, i.e., at pH 6.9 and pH 6.45 using a Biacore® T100 instrument (GE Healthcare). Protein A (ThermoFisher Scientific catalog #21181) was diluted to 20 ug/ml in 10mM sodium acetate pH 4.5 and immobilized onto flow cells of a CM5 biosensor following the manufacturer's amine coupling protocol (GE Healthcare), targeting 2,000 RU immobilization density of Protein A per flow cell. The assay

was conducted at 37°C using PBST (137 mM sodium chloride, 2.7 mM potassium chloride, 10 mM phosphate buffer, 0.05% Tween 20) running buffer at pH 7.4, 6.9, 6.45 and 6.0. Antibodies were diluted to 25 nM in PBST pH 7.4, and were captured across active biosensor flow cells at 5 ul/min for 45 seconds. A concentration series of 100 – 0.78 nM monovalent hVISTA-ECD (SEQ ID NO: 325) was prepared pH 7.4, 6.9, 6.45 and 6.0 running buffers, and was injected over the captured antibodies at 40 ul/min to measure association and dissociation. Two 15 second injections of 10 mM glycine pH 1.5 were used to regenerate the Protein A capture surface between assay cycles. Rate constants ka (k_{on}) and kd (k_{off}) were derived from reference flow cell and 0 nM blank-subtracted sensorgrams, and were fit to a 1:1 binding model in Biacore® T200 Evaluation Software v.2.0. The affinity constant, K_D was calculated as the ratio of rate constants k_{off}/k_{on} for each VISTA antibody. Ratios of k_{off} and K_D at each pH relative to pH 6.0 were calculated to evaluate how the VISTA k_{off} and K_D change as the buffer pH shifts to physiological, and are shown in Table 7. The '029 parent exhibited consistent k_{off} at each pH tested, while the '761 and '767 progeny exhibited at least 10-fold faster VISTA k_{off} and 100-fold weaker VISTA K_D at pH 6.9 compared to pH 6.0. As the buffer pH shifts from acidic to physiological, VISTA k_{off} and K_D both weaken for '761 and '767. Physiological pH data for '761 and '767 for comparison is referenced from Table 7 and noted with an asterisk (*).

Table 7: Kinetic binding characteristics of '029, '761 and '767 antibodies at different pH values

Antibody	pH	ka (1/Ms)	kd (1/s)	KD (M)	koff ratio to pH 6.0	KD ratio to pH 6.0
P1-061029 (parent)	6.0	2.9E+06	5.7E-03	2.0E-09	1.0	1.0
	6.45	7.4E+05	4.0E-03	5.3E-09	0.7	2.7
	6.9	4.1E+05	5.7E-03	1.4E-08	1.0	7.1
	7.4	2.5E+05	6.4E-03	2.6E-08	1.1	13.2
P1-068761	6.0	6.0E+05	6.6E-04	1.1E-09	1.0	1.0
	6.45	1.1E+05	2.1E-03	2.0E-08	3.2	18.4
	6.9	4.8E+04	8.9E-03	1.9E-07	13.4	170
	7.4 *	3.8E+03	4.2E-02	1.1E-05	~ 63.6	~10000
P1-068768	6.0	5.6E+05	1.9E-03	3.4E-09	1.0	1.0
	6.45	1.3E+05	4.8E-03	3.8E-08	2.5	11.0
	6.9	7.4E+04	2.9E-02	4.0E-07	15.3	115.1
	7.4 *	1.9E+03	3.6E-02	1.9E-05	~ 19.0	~5000

The data in Table 7 indicates that an at least 10 fold lower affinity of binding of '761 and '767 to hVISTA at pH 6.45 compared to pH 6.0; an at least 100 fold lower affinity of binding of '761 and '767 to hVISTA at pH 6.9 compared to pH 6.0; and an at least 1000 fold lower affinity of binding of '761 and '767 to hVISTA at pH 7.4 compared to pH 6.0.

The '015 library also demonstrated a slight preference for pH 6-selective binding to VISTA. The amino acid differences of the progeny clones relative to the '015 VH CDRs is shown in Table 8. Binding of several preparations of each of the '015 progeny clones and of the parent '015 (all as IgG1.3 antibodies) to human VISTA at pH 6.0 and 7.4 was measured via SPR using the identical method described for the '029 analysis above, and is shown in Table 8.

Table 8: VH CDR1, CDR2 and CDR3 amino acid sequences of antibodies (separated by underscore) derived from the '015 parent antibody

NAME	CDR1 (pos 26-35)	CDR2 (pos 50-66)	CDR3 (pos 99-110)	SEQ ID NO
P1-061015	GFTFS**S**YA**M**H	IIW**Y**DGS**NKYY**ADSVKG	DSGFY**SS**YYFDY	95
P1-068736	-----E-----	-D-------	D-------	-----D-----D	107
P1-068738	-----E--H-	---D----H--------	-----------	-----ED-----	131
P1-068740	-----D----	-------	D-D-------	-----D-----D	115
P1-068742	-----D----	-------	D-D-------	-----ED-----	119
P1-068744	-----E----	H---------	E------	-----E-----E	103
P1-068746	----------	--------	HH-------	-----D------	123
P1-068748	-----HH---	--------	DD-------	-----D------	99
P1-068750	-----D-D--	E--D----------	-EE---------	127
P1-068752	----------	E--------	D-------	-----D-----E	111
P1-068754	-----D-D--	E--D----------	----H-D-----	135

A summary of the kinetics of binding of '029 and '015 and their progeny clones to huVISTA at pH 6.0 and 7.4, as determined by SPR, is shown in Tables 9 and 10.

Table 9: huVISTA kinetics summary and VH CDR sequences of the ‘029 clone and their progeny

ID	Avg 7.4 ka (1/Ms)	Avg 7.4 kd (1/s)	Avg 7.4 KD (M)	Avg 6.0 ka (1/Ms)	Avg 6.0 kd (1/s)	Avg 6.0 KD (M)	VH CDR 1 (pos 26-35)	VH CDR 2 (pos 50-66)	VH CDR 3 (pos 99-110)	SEQ ID NO
P1-069077	6.0E+04	1.9E-03	3.1E-08	6.3E+05	1.2E-04	1.9E-10	....E.E...	......DE.....	.....	47
P1-069065	5.9E+04	2.3E-03	3.9E-08	5.7E+05	2.2E-04	3.8E-10	....E.E...	......DD.....	.....	23
P1-069075	1.3E+05	2.3E-03	1.8E-08	1.3E+06	2.9E-04	2.2E-10	....E.....	....D..E.....	.....H.....E..	43
P1-069071	4.3E+04	4.0E-03	9.3E-08	7.0E+05	5.1E-04	7.3E-10	....E.E...	.......D.....	.....E.....	35
P1-069061	Weak, fast kd			4.3E+05	1.1E-03	2.5E-09	....E.....	.......E.....	.....E.D	15
P1-069069	9.0E+04	7.5E-03	8.4E-08	1.4E+06	1.2E-03	8.6E-10	.....	......EE.....	.....D..	31
P1-068761	Weak, fast kd			3.8E+05	1.4E-03	3.8E-09	....E.E...	......EE.....	.....H.....E..	51
P1-069059	Weak, fast kd			3.4E+05	1.6E-03	4.8E-09	....E.....	......DH.....	.....E.D	11
P1-068767	Weak, fast kd			3.4E+05	2.6E-03	7.6E-09	....E.....	..D...E.....	.....E.D	55
P1-068773	Weak, fast kd			3.0E+05	2.9E-03	9.4E-09	....E.....	..D...D.....	.....E.D	59
P1-069063	1.2E+05	2.7E-02	2.3E-07	1.9E+06	4.4E-03	2.4E-09	....E.....	.......E.....	.....D.E	19
P1-069067	1.0E+05	2.7E-02	2.9E-07	1.7E+06	4.5E-03	2.7E-09	.....	......EE.....	.....D.E	27
P1-069073	Weak, fast kd			6.1E+05	5.8E-03	9.4E-09	....E.E...	.......E.....	.....E..	39
P1-061029	2.9E+05	5.6E-03	1.9E-08	1.6E+06	5.8E-03	3.6E-09	GFTLDDYAMH	GINWNSANIGYADSVKG	VPGYSGGWIDAFDV	67
P1-068765	No binding			3.7E+05	7.0E-03	1.9E-08	...DE.....	......EE.....	.....E.D	63
P1-068757	No binding			8.9E+05	1.7E-02	1.9E-08	....E.E...	......EE.....	.....E.D	71

ID	Avg 7.4 ka (1/Ms)	Avg 7.4 kd (1/s)	Avg 7.4 KD (M)	Avg 6.0 ka (1/Ms)	Avg 6.0 kd (1/s)	Avg 6.0 KD (M)	VH CDR 1 (pos 26-35)	VH CDR 2 (pos 50-66)	VH CDR 3 (pos 99-110)	SEQ ID NO
P1-068771	No binding			7.6E+05	1.8E-02	2.5E-08	....E.E....	.......HE..........	..............E.D	75
P1-068769	No binding			8.1E+05	4.0E-02	5.5E-08	....E.E....	.......DH..........	..............E.D	83
P1-068775	No binding			1.8E+06	4.7E-02	2.3E-08	....E.E....	..D...EE..........	.....H.....E.D	79
P1-068759	No binding			1.3E+06	8.0E-02	6.0E-08	....E.E....	..D...E..........	..............E.D	87

Table 10: huVISTA kinetics summary and VH CDR sequences of the ‘015 clone and their progeny

Clone	Avg 7.4 ka (1/Ms)	Avg 7.4 kd (1/s)	Avg 7.4 KD (M)	Avg 6.0 ka (1/Ms)	Avg 6.0 kd (1/s)	Avg 6.0 KD (M)	HCDR Sequence (pos 26-35) (pos 50-66) (pos 99-110)	SEQ ID NO
P1-061015	2.3E+05	2.0E-03	8.8E-09	1.8E+06	9.5E-04	5.4E-10	GFTFSSYAMH_IIWYDGSNKYYADSVKG_DSGFYSSYYFDY	95
P1-068748	No binding			1.4E+06	1.5E-03	1.0E-09	.....HH..._........DD....._.....D.....	99
P1-068744				1.3E+06	1.8E-03	1.3E-09	.....E...._H.........E....._.....E.....E	103
P1-068736				8.4E+06	9.5E-03	1.1E-09	.....E...._.D.......D....._.....D.....D	107
P1-068752				6.1E+06	3.4E-02	5.6E-09	..........E........D....._.....D.....E	111
P1-068740				Too fast	4.7E-02	ND	.....D...._.......D.D....._.....D.....D	115
P1-068742				Too fast	>1E-02	ND	.....D...._.......D.D....._.....ED.....	119
P1-068746				Too fast	>1E-02	ND	..........._........HH....._.....D.....	123
P1-068750				Weak			.....D.D.._E..D.............._.EE.........	127

Thus, several '029 progeny clones were identified which either maintained or improved k_{off} to VISTA-ECD at pH 6.0 compared to the '029 parent, and also demonstrated weaker k_{off} or a loss of binding to VISTA at physiologic pH. The '015 progeny exhibited acidic pH selective binding to VISTA-ECD, with no binding detected to VISTA at neutral pH, but all '015 progeny assayed yielded a faster k_{off} at pH 6.0 compared to the '015 parent.

Example 10: Acidic pH-selective '029 progeny demonstrate acidic pH-dependent cell binding and effector function while maintaining VISTA blocking activity

pH-dependent binding of clones '761 and '767 to Raji cells engineered to ectopically express full length human VISTA (SEQ ID NO: 1 with D187E substitution) was measured. For this experiment, '761 and '767 were formatted as IgG1.3 antibodies, and binding was measured by an anti-human IgG secondary antibody (Jackson Immunoresearch catalog number 109-065-098). The results, which are shown in Figs. 8A-8B, indicate that the '761 (Fig. 8A) and '767 clones (Fig. 8B) bind poorly at pH 7.2 and 8.1, but better at acidic pH, particularly at pH 6.0, 6.1, 6.2, and 6.4. Binding MFIs are plotted on the y-axis and primary antibody concentrations are plotted on the x-axis in log scale. Non-linear regressions are also shown.

Fig. 8C shows data from the experiment described in Figs. 8A-B measuring P1-068767 (circles) and an isotype-matched non-specific control antibody (triangles) binding to Raji cells expressing human VISTA at 3125 ng/mL at different pH. The "pH50", the pH at which 50% of P1-068767 binding is lost, is approximately 6.6. Binding MFIs are plotted on the y-axis, and buffer pH is plotted on the x-axis. Non-linear regressions are also shown.

Fig. 8D shows the MFI of an isotype-matched non-specific control antibody (filled and unfilled circles for pH 7.0 and 6.0 respectively), anti-VISTA mAb 2 ("control", see Fig. 6C, filled and unfilled squares at pH 7.0 and 6.0 respectively), P1-068761 (filled and unfilled triangles for pH 7.0 and 6.0 respectively), and P1-068767 (filled and unfilled inverted triangles for pH 7.0 and 6.0 respectively) binding to human monocytes.. Binding was detected as described in Figs. 8A-B. The non-pH-selective VISTA control antibody (mAb 2) bound monocytes at both pH. Both engineered acidic pH-selective antibodies bound monocytes well at pH 6.0, but did not bind better than the non-specific isotype-matched

control at pH 7.0. Thus, clones '761 and '767 have weak binding or no binding to VISTA at neutral pH, and instead bind VISTA on cells selectively at acidic pH.

Fig. 8E shows the comparable blocking of recombinant VISTA multimer binding to activated human CD4+ T cells at pH 6.0 by '029 (squares), '761 (triangles), and '767 (inverted triangles), while a non-VISTA-specific control antibody (circles) did not block VISTA binding. This blocking assay was performed as described in Example 4. These data show that engineered acidic pH-selective VISTA antibodies are still capable of blocking VISTA receptor-ligand binding at acidic pH.

NK cell specific lysis of target cells (the same Raji cells expressing human VISTA described in Figs. 8A-B) via antibody-dependent cell cytotoxicity (ADCC) at physiological pH was measured for the P1-061029.IgG1f, P1-068761.IgG1f, P1-068767.IgG1f antibodies, a non-VISTA-specific antibody and a non-VISTA-specific negative control antibody, all expressed as afucosylated IgG1 antibodies. NK cells were enriched from PBMC via negative bead selection (StemCell Technologies catalog number 19055) and cultured overnight in Myelocult™ media (StemCell Technologies catalog number 05150) supplemented with 1 μM hydrocortisone (StemCell Technologies catalog number 07904) and 500 U/mL recombinant human IL-2 (Peprotech catalog number 200-02). On the day of the assay, Raji cells ectopically expressing human VISTA (described in Fig. 8A-B) were labeled with Calcein AM (Life Technologies catalog number C3100MP) and co-cultured with the cultured NK cells at a 10:1 NK : target cell ratio and with P1-061029.IgG1f, P1-068761.IgG1f, P1-068767.IgG1f antibodies, a non-VISTA-specific antibody and a non-VISTA-specific negative control antibody for 2 hours at physiological pH. Specific lysis was interpolated from the supernatant fluorescence signal (EnVision™ plate reader). The spontaneous lysis signal obtained from co-culture without antibodies, and the maximal lysis signal was determined by lysis of target cells with Delfia® lysis buffer (PerkinElmer catalog number 4005-0010). Antibody-specific lysis was calculated to be the percentage of lysis observed divided by (the maximal lysis signal minus the spontaneous lysis signal).

The results, which are provided in Fig. 8F, show the reduced potency of P1-068761.IgG1f and P1-068767.IgG1f, relative to P1-061029 and the positive control in mediating antibody-dependent cell cytotoxicity (ADCC) at physiological pH.

Example 11: Cyno PK of VISTA antibodies

Human antibody-naïve cynomolgus macaques were injected intravenously with a single 5 mpk dose of either a VISTA antibody which binds comparably at acidic and neutral pH ("control"; mAb2), a VISTA antibody with impaired binding at acidic pH ("acidic pH sensitive", mAb3), or acidic pH-selective antibody '767, to determine the cyno PK of these antibodies.

The SPR binding kinetics of the antibodies used in this Example are provided in Table 11, and were determined as follows. Cyno VISTA cross-reactivity for acidic pH-selective and control anti-VISTA antibodies was evaluated at acidic and neutral pH. Binding affinity measurements for VISTA Abs were conducted using a Biacore® T100 instrument (GE Healthcare). Protein A (ThermoFisher Scientific catalog number #21181) was diluted to 20 ug/ml in 10mM sodium acetate pH 4.5 and immobilized onto flow cells of a CM5 biosensor following the manufacturer's amine coupling protocol (GE Healthcare), targeting 2,000 RU immobilization density of Protein A per flow cell. The assay was run at 37°C using PBST (137 mM sodium chloride, 2.7 mM potassium chloride, 10 mM phosphate buffer, 0.05% Tween 20) running buffer at pH 7.4 and 6.0. Antibodies (formatted as IgG1.3 antibodies) were diluted to 25 nM in PBST pH 7.4, and were captured across active biosensor flow cells at 5 ul/min for 45 seconds. Concentration series of 1600 – 0.78 nM (pH 7.4) and 100 – 0.78 nM (pH 6.0) monovalent hVISTA-ECD (SEQ ID NO: 325) and cyno VISTA-ECD (AFKVATLYSL YVCPEGQNVT LTCRVFGPVD KGHDVTFYKT WYRSSRGEVQ TCSERRPIRN LTFQDLHLHH GGHQAANTSH DLAQRHGLES ASDHHGNFSI TMRNLTLLDS GLYCCLVVEIRHHHSEHRVH GAMELQVQTG KDAPSSCVAY PSSSQESENI TAHHHHHHH; (SEQ ID NO: 326) were prepared running buffer, and were injected over the captured antibodies at 40 ul/min to measure association and dissociation. Two 15 second injections of 10 mM glycine pH 1.5 were used to regenerate the Protein A capture surface between assay cycles. Rate constants ka (k_{on}) and kd (k_{off}) were derived from reference flow cell and 0 nM blank-subtracted sensorgrams, and were fit to a 1:1 binding model in Biacore® T200 Evaluation Software v.2.0. The affinity constant, K_D was calculated as the ratio of rate

constants koff/kon for each VISTA antibody. Ratios of k_{off} and K_D at pH 7.4 / pH 6.0 were calculated to compare off-rate and affinity differences at acidic pH relative to neutral pH, and are shown in Table 11. All anti-VISTA antibodies tested exhibited comparable (within 2-fold) human and cyno VISTA kinetic binding parameters at both pHs tested, confirming cross-reactivity with cyno VISTA. Both anti-VISTA control antibodies exhibited improved kd and stronger K_Ds at physiological pH compared to acidic pH, and the acidic pH-sensitive control exhibited a faster VISTA kd at acidic pH compared to the control antibody.

Table 11: SPR binding kinetics of VISTA antibodies to cyno VISTA

Antibody	VISTA	pH 7.4			pH 6.0			kd ratio (7.4/6)	KD ratio (7.4/6)
		ka (1/Ms)	kd (1/s)	KD (M)	ka (1/Ms)	kd (1/s)	KD (M)		
P1-061029	human	1.2E+05	7.5E-03	6.2E-08	9.8E+05	6.6E-03	6.8E-09	1.1	9.1
	cyno	1.4E+05	6.7E-03	4.7E-08	6.2E+05	6.2E-03	1.0E-08	1.1	4.7
P1-068761	human	4.3E+03	3.7E-02	8.7E-06	3.5E+05	1.4E-03	4.1E-09	26.4	2122.0
	cyno	6.5E+03	3.6E-02	5.5E-06	2.1E+05	1.7E-03	7.9E-09	21.2	696.2
P1-068767	human	1.6E+03	3.5E-02	2.3E-05	3.2E+05	2.4E-03	7.5E-09	14.6	3066.7
	cyno	1.3E+03	3.4E-02	2.6E-05	1.9E+05	2.5E-03	1.3E-08	13.6	2000.0
α-VISTA control (mAb 3)	human	4.4E+05	1.3E-03	3.0E-09	9.6E+05	6.0E-03	6.2E-09	0.2	0.5
	cyno	4.9E+05	1.7E-03	3.4E-09	5.5E+05	7.1E-03	1.3E-08	0.2	0.3
α-VISTA acidic pH sensitive (mAb 2)	human	1.8E+05	7.8E-04	4.3E-09	1.8E+06	5.0E-02	2.8E-08	0.02	0.2
	cyno	1.9E+05	6.8E-04	3.5E-09	1.2E+06	5.2E-02	4.4E-08	0.01	0.08

Human antibody-naïve cynomolgus macaques were injected intravenously with a single 5 mpk dose of either VISTA mAb2 ("control"), VISTA mAb3 ("acidic pH sensitive"), or P1-068767.IgG1.3. The serum concentration of each antibody following injection is shown in Fig. 9. Mean residence times for P1-068767.IgG1.3 and the control anti-VISTA antibody were 717 and 22 hours respectively, indicating that acidic pH selectivity greatly reduced VISTA antibody TMDD. Although the control antibody (mAb 2) and the acidic pH sensitive antibody (mAb 3) bind VISTA comparably at physiological pH, the acidic pH sensitive antibody had a lower mean residence time of 7.6 hours, demonstrating the importance of acidic pH binding to VISTA antibody recycling as described in Examples 6

and 7. The results show that acidic pH selective antibodies have superior PK and will thus more easily achieve target engagement in tumors or other microenvironments.

Example 12: pH selective '029 progeny do not bind non-specifically to high pI proteins

The binding specificity of the '029, '761 and '767 clones to VISTA and to other high pI proteins was evaluated by SPR at neutral and acidic pH using a Biacore® T100 instrument (GE Healthcare). Protein A (ThermoFisher Scientific catalog #21181) was diluted to 20 ug/ml in 10mM sodium acetate pH 4.5 and immobilized onto flow cells of a CM3 biosensor following the manufacturer's amine coupling protocol (GE Healthcare), targeting 800 RU immobilization density of Protein A per flow cell. SPR experiments were conducted at 25°C using PBST (137 mM sodium chloride, 2.7 mM potassium chloride, 10 mM phosphate buffer, 0.05% Tween 20) running buffer at pH 7.4 and 6.0. Antibodies (formatted as IgG1.3 antibodies) were diluted to 50 nM in PBST pH 7.4, and were captured across active biosensor flow cells at 5 ul/min for 60 seconds. A concentration series of 100 – 10 nM monovalent hVISTA-ECD (SEQ ID NO: 325), avidin (ThermoFisher Scientific catalog #21128), cytochrome C (Sigma catalog #C2867), BSA (Calbiochem catalog #126593), and monovalent control antigen ("Ag") were prepared in pH 7.4 and 6.0 running buffers, and were injected over the captured antibodies at 50 ul/min to evaluate binding specificity. Two 15 second injections of 10 mM glycine pH 1.5 were used to regenerate the Protein A capture surface between assay cycles. Reference flow cell and 0 nM blank-subtracted sensorgrams were inspected using Biacore® T200 Evaluation Software v.2.0. The results are shown in Table 12.

Table 12: Binding of VISTA clones to proteins having a high pI

Sample	Isoel. pt (pI)	'029		'761		'767		Anti-Ag		PBS (no Ab)	
		pH 6	pH 7.4	pH 6	pH 7.4	pH 6	pH 7.4	pH 6	pH 7.4	pH 6	pH 7.4
huVISTA -His	6.9										
Avidin	10										
Cyto-Chrome C	10.7										
BSA	4.7										
Ag-His	6.5										

In Table 12, specific binding, defined as >10 RU SPR binding responses at the end of the sample injection is indicated by filled gray boxes. "Anti-Ag" is an VISTA binding control Ab. The '029 clone was specific for VISTA at acidic and neutral pH. The '029 progeny clones '761 and '767 were specific for VISTA at acidic pH, while the control antibody also maintained antigen specificity. Non-specific binding ("NSB") of the pI control proteins to the Protein A reference surface was not observed in this assay.

Thus, the charged amino acids introduced to the VH CDRs of '761 and '767 do not cause these antibodies to bind electrostatically to other high pI proteins, such as avidin and cytochrome C, or low pI proteins, such as BSA.

Example 13: Inhibition of T cell activation by antibodies '761 and '767

This Example describes an assay that can be conducted to determine the ability of antibodies '761 and '767 to block hVISTA inhibition of Jurkat T cell activation.

The same assay as described in Example 5 is used. Briefly, Jurkat (human T cell line) cells expressing an NFkB luciferase reporter are co-cultured at various pH with 293T cells expressing human VISTA and a single-chain variable fragment of the anti-human T cell receptor agonist antibody OKT3. Anti-VISTA antibodies '761 and '767 or an isotype-matched non-VISTA-specific control antibody are added to the co-cultured cells. Jurkat activation is shown as luciferase units and as the fold-increase of the luciferase signal with anti-VISTA treatment relative to control.

Example 14: Mutational analysis identified key residues conferring pH dependent binding properties to VISTA antibodies

Antibodies P1-068761.IgG1.3 and P1-068767.IgG1.3 contain 5-6 mutations from P1-061029 (Table 7). A mutational analysis was conducted in order to identify key residues important for conferring the pH dependent properties of the VISTA antibodies. As such, a panel of N-1 (1 amino acid reversion to P1-061029) and N-2 (2 amino acid reversion to P1-061029) variants of P1-068761 and P1-068767 were synthesized, expressed as IgG1.3, and analyzed for their binding to huVISTA at pH 6, pH 6.7, and pH 7.4.

Binding kinetics were measured using a Biacore® T100 instrument (GE Healthcare). Protein A (ThermoFisher Scientific catalog #21181) was diluted to 20 ug/ml in 10mM sodium acetate pH 4.5 and immobilized onto flow cells of a CM5 biosensor following the manufacturer's amine coupling protocol (GE Healthcare), targeting 2,000 RU immobilization density of Protein A per flow cell. The assay was conducted at 37°C using PBST (137 mM sodium chloride, 2.7 mM potassium chloride, 10 mM phosphate buffer, 0.05% Tween 20) running buffer at pH 7.4, 6.7 and 6.0. Antibodies were diluted to 25 nM in PBST pH 7.4, and were captured across active biosensor flow cells at 5 ul/min for 40 seconds. A concentration series of 100 – 10 nM monovalent hVISTA-ECD (SEQ ID NO: 325) was prepared in pH 7.4, 6.7 and 6.0 running buffers, and was injected over the captured antibodies at 40 ul/min to measure association and dissociation. Two 15 second injections of 10 mM glycine pH 1.5 were used to regenerate the Protein A capture surface between assay cycles. Rate constants ka (kon) and kd (koff) were derived from reference flow cell and 0 nM blank-subtracted sensorgrams, and were fit to a 1:1 binding model in Biacore® T200 Evaluation Software v.2.0.

The affinity constant, K_D was calculated as the ratio of rate constants k_{off}/k_{on} for each VISTA antibody. The %Rmax was calculated to compare how pH affects an antibody's binding capacity for VISTA, and represents the measured maximal VISTA binding response relative to the expected maximal VISTA binding response. The %Rmax is defined as the ratio of the reference-subtracted 'binding' report point response at the end of the 100 nM VISTA injection for each antibody (Rmax) relative to the expected VISTA binding response (Rexp). Rexp is calculated as Rexp = [(VISTA-ECD molecular weight / mAb molecular weight) x (mAb 'capture' report point response (RUs)] x 2 binding sites per mAb.

The SPR results obtained for P1-068761 reversion variants are shown in Fig. 10A, which is ranked by the pH 6.0 k_{off}, slowest to fastest. In the table, antibodies that exhibited weak or no binding response (< 10 RU) to 100 nM hVISTA were categorized as non-binding (NB). The results indicate that E at positions 32 (i.e., amino acid residue 7 in VH CDR1 of '761) and 100f (amino acid residue 12 in VH CDR3 of '761) are both required for maintaining acidic pH selectivity, since these reversions to P1-061029 parent sequence allowed for significant hVISTA binding at physiological pH (%Rmax > 10). Further analysis

revealed that variants with E55A (amino acid residue 6 in VH CDR2 of '761) reversion maintained acidic pH-selectivity and exhibited comparable binding kinetics within 2-fold of P1-068761. In contrast, while variants with H100G, E56N and E30D (amino acid residues 12 of VH CDR3, 7 of VH CDR2 and 4 of VH CDR1 of '761, respectively) reversions maintained acidic pH selectivity, these mAbs also exhibited ~3-fold faster k_{off} at acidic pHs compared to P1-068761, bringing the off-rates of these mutants at acidic pH closer to the P1-061029 parent. Thus, adding G100H, N56E and/or D30E mutations to the original P1-061029 clone contributed to acidic pH VISTA affinity improvements observed in the acidic selective P1-068761 clone.

The SPR results obtained for P1-068767 reversion variants are shown in Fig. 10B, which is ranked by the pH 6.0 k_{off}, slowest to fastest. The results indicate that D at position 102 (amino acid residue 14 in VH CDR3 of '767) was required for maintaining acidic pH selectivity, and D102V reversion back to P1-061029 parent sequence allowed for significant hVISTA binding at neutral pH (%Rmax > 10). Further analysis revealed that variants with E30D, D52N and E55A (amino acid residues 4 of VH CDR1, 3 of VH CDR2 and 6 of VH CDR3 of '767, respectively) reversions maintained acidic pH-selectivity and exhibited comparable pH 6.0 binding kinetics within 2-fold of P1-068767. In contrast, variants with E100fF (amino acid residue 12 of VH CDR3 of '767) reversion maintained acidic pH selectivity, albeit with > 3-fold faster k_{off} at acidic pH compared to P1-068767. Notably, variants with E100fF reversion exhibited even faster k_{off} at acidic pH compared to the parent mAb P1-061029.

Thus, a summary of the reversion mutants of P1-068761 and P1-068767 (acidic pH-selective) relative to P1-061029 (pH-tolerant) is as follows in Table 13 (HCDR1, HCDR2, and HCDR3 are separated by an underscore).

Table 13:

		Seq Id.
P1-061029	GFTLDDYAMH_GINWNSANIGYADSVKG_VPGYSGGWIDAFDV	67
P1-068761	....E.E..._......EE........._.....H.....E..	51
P1-068767	....E....._..D...E........._..........E.D	55
aa pos.	26-35 50-66 99-110	

The above VH CDR sequences for P1-061029, P1-068761, and P1-068767 in Table 13 are at amino acids ("aa pos.") 26-35, 50-66, and 99-110 of SEQ ID NOs: 67, 51, 55, respectively. Key mutations required for acid pH-selectivity are indicated in bold, and mutations with over 3 fold impact on pH 6.0 k_d compared to P1-068761 and P1-068767 are underlined.

Example 15: Mapping of VISTA antibody epitopes

The hVISTA epitopes of '015, '029, '761 and '767, formatted as IgG1.3 antibodies, were determined by 2 different methods: BLI (bio-layer interferometry) competition and yeast surface display.

Competitive BLI epitope binning assays were conducted to evaluate whether acidic pH-selective VISTA antibodies P1-068761 and P1-068767 retained similar or overlapping epitopes on VISTA compared to the P1-061029 parent, P1-061015 and relevant VISTA control antibodies 1, 2 and 3. Sandwich and tandem format binning assays were performed on an OctetRed384 BLI instrument (PALL/ForteBio). All assay steps were performed at 30°C at 1000 rpm shake speed, and the buffer used was acidic (pH 6.0) or neutral (pH 7.4) PBST (137 mM sodium chloride, 2.7 mM potassium chloride, 10 mM phosphate buffer, 0.05% Tween 20). For the sandwich format, anti-human IgG-Fc sensors (AHC, PALL/ForteBio) first captured the VISTA antibody panel at pH 7.4, then the anti-human capture sensors were blocked with total human IgG (Jackson #009-000-002). Human VISTA-ECD was captured next at pH 6.0, and finally competition for all possible antibody combinations was assessed at pH 6.0. In the tandem format assay, streptavidin-coated biosensors (SAX, PALL/ForteBio) first captured biotinylated hVISTA-ECD at pH 7.4, then the sensors captured the full VISTA antibody panel at pH 6.0, ensuring complete binding saturation of each antibody on VISTA before evaluating competition with all possible antibody combinations at pH 6.0.

The results of the Competitive BLI epitope binning assays are summarized by a competition matrix, Figure 11A. In this figure, the first antibody captured is listed by row, and its binding or blocking activity to the (second) competitor antibodies are shown in each column. The competition matrix was identical for both assay formats. For the sandwich assay, binding (light gray) of the competitor antibody was defined by a signal ranging

between 0.4 – 1.2 nm, and blocked antibodies (black) exhibited non-binding signal < 0.1 nm. For the tandem assay, binding of the competitor antibody was defined by a signal ranging between 0.3 – 0.8 nm, and blocked antibodies exhibited non-binding signal < 0.2 nm. While 'VISTA mAb 3' exhibited a fast acidic pH dissociation from hVISTA-ECD by SPR at 37°C (Figure 6C), it did not rapidly dissociate in either BLI assay format (conducted at 30°C). These competitive assays indicated that P1-061015, P1-061029, acidic-pH selective antibodies P1-068761 and P1-068767 and VISTA antibodies 2 and 3 all compete with one another for similar or overlapping epitopes on VISTA. However, VISTA antibody 1 binds to a separate and distinct epitope. Thus, the charged amino acid mutations introduced to the VH CDRs of P1-061029 to generate the acidic-selective clones P1-068761 and P1-068767 have not signigicantly altered the VISTA binding epitope.

The epitopes of antibodies '029, '015, '761, and '767 were also mapped using yeast surface display and NGS according to the method of Chao *et al.* (2004) *J. Mol. Biol.* 342:539-550, Oliphant *et al.* (2006) *J. Virol.* 80:12149–12159, and Kowalsky *et al.* (2015) *J. Biol. Chem.* 290:26457–26470. Briefly, a saturation mutagenesis library of single point mutants of the VISTA ECD was generated and displayed on the surface of yeast. VISTA mutants that lost binding to the antibody being mapped but retained binding to a non-blocking antibody (mAb1) were sorted and sequenced. Since they retained binding to mAb1, these mutants were likely correctly folded, and the loss of binding seen to the antibody being mapped was likely due to the loss of an energetically important contact residue. The positions of these mutations were designated as energetically important residues in the antibody's epitope and are shown in Table 14.

Table 14: Residues of huVISTA that are identified as epitope residues of anti-VISTA mAbs

mAb	T 29	Y 37	K 38	T 39	Y 40	R 54	T 55	F 62	Q 63	L 66	H 68	L 87	H 88	H 89	F 97	L 118	V 117	I 119	H 121	H 122	S 124	E 126	R 127
Pt. 0810113		x	x	x		x		x	x	x	x				x	x	x	x			x	x	
Pt. 0810229		x		x	x	x	x	x	x	x	x		x	x		x	x	x			x	x	x
Pt. 0687761	x	x		x		x	x	x	x		x	x	x	x		x	x	x			x	x	x
Pt. 0687767		x		x	x	x	x	x	x	x	x					x	x	x		x	x	x	x

Table 15 includes detailed data from Table 14, and lists the amino acid residues of hVISTA that are likely to reduce binding of each antibody listed, based on residue frequency observed in the yeast surface display/NGS method

Table 15: VISTA amino acid substitutions likely to reduce binding of the listed antiobodies

	P1-061015 pH 6	P1-061015 pH 7	P1-061029 pH 6	P1-061029 pH 7	P1-068761 pH 6	P1-068767 pH 6
T35					P, Y, W	
Y37	P, G, A, S, T, K, R, H, N, D, E, Q	P, G, S, N, D, E Q	Y, S, T, V, L, I, M, K, R, N, D, Q	P, G, S, T, V, L, I, M, K, R, N, D, E, Q	P, G, A, S, T, V, L, I, M, K, R, N, D, E, Q	G, T, V, L, I, M, K, R, N, Q
K38	P, G, A, S, V					
T39	G, M, R, H, F, Y, W, N, D, E, Q	M, K, R, H, F, Y, W, D, E, Q	G, A, S, M, Y, W, N, D, E, Q	G, A, S, V, L, M, R, H, F, Y, W, N, D, E, Q	G, Y, D, E	G, A, S, H, Y, W, N, D, E, Q
Y41				A, S, T, I, M		P, I, M, H
R54	L, M, F, Y, E	M, E	P, A, T, V, I, M, F, Y, N, D, E, Q	P, G, A, S, T, V, L, I, M, H, F, Y, W, N, D, E, Q	A, T, V, L, I, M, K, F, Y, E, Q	P, A, S, T, V, L, I, M, F, Y, W, D, E, Q
T61			G, L, R, H, F, Y, D, E, Q	V, L, K, R, H, F, Y	G, V, H, Y, D	L, R, H, F, Y, D, E
F62	G, A, S, M, K, R, N, D, E, Q	G, K, R, D, E, Q	P, G, A, S, T, V, I, M, H, Y, W, D, E, Q	P, G, A, S, T, V, L, I, M, K, R, H, Y, W, N, D, E, Q	P, G, A, S, T, V, M, H, Y, W, D, E, Q	P, G, A, S, T, V, L, M, H, Y, W, N, D, E, Q
Q63	G, R, W, D, E	W, D, E	G, A, S, T, V, K, R, H, Y, W, N, D, E	P, G, S, T, L, M, K, R, H, F, Y, W, N, D, E	G, S, T, K, H, Y, N, D, E	P, G, A, S, T, V, L, I, M, K, H, F, Y, W, N, D, E
L65	P, G, A, S, T, K, R, H, W, N, D, E, Q	P, G, S, K, W, D, E, Q	G, T, Y, D, E, Q	P, G, A, S, T, H, Y, W, N, D, E, Q,		P, G, S, H, D, E, Q
H66	P, T, V, L, I, M, K, R, F, Y, W	P, T, V, L, I, M, K, R, F, Y, W	T, V, L, I, Y, D, E, Q	G, S, T, V, L, I, M, K, R, W, N, D, E, Q	T, I, K, W, D	T, V, I, K, W, D, E
L67					G, A	
H68			L, I, M, F, E	L, I, E	G, T, V, L, I, Y, W, D,	

	P1-061015 pH 6	P1-061015 pH 7	P1-061029 pH 6	P1-061029 pH 7	P1-068761 pH 6	P1-068767 pH 6
					E, Q	
F97	G, D, E					
L115	R, W		A, T, K, N, Q	A, T, K, F, N, Q	A, T, M, K, F, N	A, T, K, F, N, Q
V117	M, K, N, D	M, K, R, W, E	T, M, K, R, W, E	T, L, I, M, K, R, W, E	T, I, M, K, W	T, L, I, M, K, R, W, E
I119	F, P	P, N	P, M, E	P, M, E	M, H	P, M, H, F, N, E
H121						V, E, Q
H122						P, Y, N, D
S124	P, V, L, I, K, F, D, E	L, I, M, H, W, Q	L, I, M, H, W, Q		L, I, M, Q	L, I, M
E125	A, S, T, L, M, K, H, Y, D	A, T, V, I, M, K, H, F, Y, W, N, D	T, V, I, M, H, F, Y, W	G, T, K, H, Y, W, N, D	V, I, H, N	T, V, I, F, Y, W, N
R127			S, V, M, H	P, S, V, M, K, H, N	P, V, M, N	P, S, V, M, H, N

Fig. 11B and Fig. 11C show a representation of an epitope encompassing all the residues for blocking hVISTA antibody as listed in Table 14 (Fig. 11B) compared to the epitope of a non-blocking hVISTA antibody (mAb1; Fig. 11C). Amino acid residues 66(H) and 162(A) are indicated to denote the orientation of the molecule. Histidine residues are in grey, and epitope residues are in black. Notably, all blocking anti-VISTA mAbs occupy the same epitope region, in agreement with the octet binning data (showing that they competed with each other), with subtle residue differences among the queried antibodies. In contrast, the non-blocking hVISTA antibody (mAb1) occupies a distinct epitope region on the hVISTA molecule, and this is further supported by the octet binning data shows that none of the blocking mAbs competed with mAb1.

Example 16: Biophysical properties of '761 and '767

The physical and chemical properties of the P1-068761 and P1-068767 were compared to that of the parent P1-061029 (all with an IgG1.3 constant region) by the following analytical and biophysical techniques.

Analytical SEC data were acquired using an Agilent 1260 HPLC instrument using a Shodex™ KW403-4F column (4.6mmID X 300mmL), in buffer containing 100mM Sodium Phosphate, 150mM Sodium Chloride, pH7.3(0.2 um filtered) running at a flow rate of 0.30 mL/min. Data were collected by an Agilent 1260 Infinity Diode Array Detector set to collect at 280nm and analyzed by Agilent Chemstation software (Agilent, Santa Clara, CA).

Imaged capillary isoelectric focusing (icIEF) data were acquired on a ProteinSimple iCE3 Instrument with Alcott 720NV Autosampler. Antibody samples were mixed with a separation mixture to yield final concentrations of 0.2 mg/ml antibody, 0.35% methyl cellulose, 2.0 M Urea, 1% v/v pharmalyte pI 5-8, and 3% v/v pharmalyte pI 8-10.5. These samples were analyzed using a pre-focus time of 1min at 1500V, and focusing time of 10min at 3000V, in a ProteinSimple cIEF cartridge FC-coated (product # 101701). Data were analyzed using iCE CFR Software V4.3.1.5352.

Antibody hydrodynamic size was determined by dynamic light scattering (DLS) and thermal stability was characterized by fluorescence spectroscopy and static light scattering

(SLS) using an UNcle molecular characterization instrument (Unchained Labs). Antibodies P1-061029, P1-068761, and P1-068767 were prepared at a concentration of 2mg/ml in 1X PBS buffer, and then diluted 1:1 with either 40 mM Tris in 1X PBS, or 40 mM citrate in 1X PBS, at different pH to yield final samples of 1mg/ml antibody in either 20mM Tris / 1X PBS, or 20mM citrate / 1X PBS at pH 3.0, 4.0, 5.0, 6.0, 7.0, 8.0 or 9.0. These samples were loaded into a UNi cuvette cartridge and analyzed within 1 hour of dilution into the different pH formulations. DLS data were collected at 25oC, using 4 acquisitions of 5 s each. Intensity autocorrelation functions were fitted using UNcle analysis software version V2.0. Thermal denaturation data was obtained by scanning samples from 25oC to 90oC at a scan rate of 0.5o/min, with excitation at 266 nm and 473 nm. Fluorescence data was acquired over a range of 250 nm – 720 nm. Fluorescence and SLS data were analyzed using UNcle analysis software version V2.0.

The apparent viscosity of antibodies P1-061029, P1-068761, and P1-068767 was measured on an UNcle molecular characterization instrument (Unchained Labs), using a bead-based DLS method which measures the diffusion rate of polystyrene beads in the presence of formulated antibody solutions, as per Unchained Labs recommended protocol. Briefly, a 10% solution of 100 nm polystyrene beads (Thermo Scientific cat#3100A) was prepared in formulation buffer containing 0.5% tween 80. 3ul of this polystyrene bead mixture was added to 30ul of formulated antibody (various Ab concentrations in 20 mM histidine, 260 mM sucrose pH 6.0,) and the resulting protein/bead mixture was loaded into 3 separate lanes of a UNi cuvette cartridge (9 ul each lane) for triplicate analysis. Data were analyzed using UNcle analysis software version V2.0, using a reference viscosity of 1.3 cP.

The physical stability of antibodies P1-061029, P1-068761, and P1-068767 was studied under accelerated stress conditions by preparing 50 mg/ml antibody samples in 20 mM histidine, 260 mM sucrose pH 6.0 and exposing to 40oC thermal stress for 4 weeks. Aliquots were removed immediately prior to 40oC incubation (time zero = t0), as well as after 1 week (1 w) and 4 weeks (4 w) of thermal stress, and samples were diluted to 2 mg/ml using formulation buffer and analyzed by aSEC. The aSEC data was acquired using an Agilent 1260 HPLC instrument using a Shodex KW403-4F column (4.6mmID X 300mmL), in buffer containing 100mM Sodium Phosphate, 150mM Sodium Chloride, pH7.3(0.2 um

filtered) running at a flow rate of 0.30 mL/min. Data were collected by an Agilent 1260 Infinity Diode Array Detector set to collect at 280nm and analyzed by Agilent Chemstation software (Agilent, Santa Clara, CA).

The resuts are as follows. Analytical size exclusion chromatography (aSEC) data showed that all three antibodies could be purified to high purity, with each antibody sample consisting of more than 99.3% monomer (main peak), less than 0.7% high molecular weight (HMW) species, and undetectable levels of low molecular weight (LMW) species, Table 16.

Table 16: Analytical SEC data for anti-VISTA antibodies, showing the percentage of high molecular weight species (%HMW), percentage of monomeric/main species (%Main) and percentage of low molecular weight species (%LMW).

Sample Name	%HMW	%Main	%LMW
P1-061029	0.4	99.6	0.0
P1-068761	0.6	99.4	0.0
P1-068767	0.5	99.5	0.0

The charge variant profile as determined by imaged capillary isoelectric focusing (icIEF) for antibody P1-061029 showed the presence of a main species (69.4%) with isoelectric point (pI) of 8.56, and 30.6% acidic species. (Fig. 12A-C.) P1-068761 demonstrated a main species (66.4%) with pI of 6.69 and 33.6% acidic species. P1-068767 demonstrated a main species (61.4%) with pI of 6.63 and 38.6% acidic species. Therefore, the distribution of acidic, basic and main species is similar for the three antibodies but the engineered antibodies P1-068761 and P1-068767 have significantly lower isoelectric point than the parental P1-061029 antibody.

The oligomeric state of P1-061029, P1-068761, and P1-068767 wasere determined over the pH range of 3-9 using dynamic light scattering (DLS) in buffers of different pH. All hydrodynamic radius (Rh) values for each antibody were in the range of 4.8 – 5.7 nM, which is typical for monomeric antibody samples, Table 17. This suggests that these antibodies do not form detectable levels of high molecular weight aggregated species at 1 mg/ml within the first hour after dilution into formulations having pH between 3 – 9.

Table 17: The hydrodynamic radius as determined by DLS for 1 mg/ml samples of anti-VISTA antibodies across the pH range of pH3 – pH9.

pH	Buffer	Rh (nm) P1-061029	Rh (nm) P1-068761	Rh (nm) P1-068767
9	20mM Tris / 1 X PBS	5.2	4.8	5.2
8	20mM Tris / 1 X PBS	5.2	5.2	5.2
7	20mM Tris / 1 X PBS	4.8	5.2	5.2
7	20mM citrate / 1 X PBS	4.8	5.2	5.7
6	20mM citrate / 1 X PBS	5.2	5.2	4.8
5	20mM citrate / 1 X PBS	5.2	4.8	5.2
4	20mM citrate / 1 X PBS	4.8	4.8	5.2
3	20mM citrate / 1 X PBS	5.2	5.2	5.2

The thermal stability of P1-061029, P1-068761, and P1-068767 was measured over the pH range of 3-9 by monitoring fluorescence and static light scattering as a function of temperature in buffers of different pH. The first thermal denaturation transition (Tm1) which typically represents denaturation of the CH2 domain of IgG1 antibodies was determined by fluorescence and is shown in Table 18, and the onset of aggregation (Tagg) which typically represents denaturation of the FAB domain of IgG1 antibodies was measured by static light scattering and is shown in Table 19. At neutral pH (pH 7.0) in Tris/PBS formulation the Tm1 values for the three antibodies were P1-061029 (67.4 °C), P1-068761 (67.0 °C), and P1-068767 (65.3 °C), with Tagg values of P1-061029 (67.8 °C), P1-068761 (67.5 °C), and P1-068767 (65.8 °C). The Tm1 for each antibody in Citrate/PBS formulation at the same neutral pH 7.0 or slightly more acidic pH of 6.0 were all within 0.7° of the Tris/PBS pH 7.0 values. However, Tm1 values were slightly lower (between 0.3° – 1.1° lower) at more basic pH of 8-9, and significantly lower at more acidic pH of 3-5, for each antibody. Compared to neutral pH, the Tagg for P1-061029 was within 0.1° of pH 7.0 value at more basic pH 8.0 – 9.0, was 1.0° lower at pH 5.0, and much lower (6.1° – 19.6° lower) at the most acidic pH conditions pH 3.0 – 4.0. The Tagg for P1-068761 and P1-068767 were also significantly lower at pH 3.0 – 4.0. However at pH 5.0 the Tagg for P1-068761 was only 0.2° lower than Tagg at pH 6.0, whereas Tagg for P1-068767 was 2.2° lower at pH 5.0 than at pH 6.0, demonstrating some differences in Tagg for each antibody, Table 19.

Table 18: Thermal stability (Tm1 values) for P1-061029, P1-068761, P1-068767 across the pH range of pH3 – pH 9 as determined by fluorescence spectroscopy

pH	Buffer	Tm1 (°C) P1-061029	Tm1 (°C) P1-068761	Tm1 (°C) P1-068767
9	20mM Tris / 1 X PBS	66.6	65.9	65.0
8	20mM Tris / 1 X PBS	67.0	66.5	64.8
7	20mM Tris / 1 X PBS	67.4	67.0	65.3
7	20mM citrate / 1 X PBS	67.2	66.9	64.8
6	20mM citrate / 1 X PBS	67.6	67.5	65.0
5	20mM citrate / 1 X PBS	64.4	64.7	62.1
4	20mM citrate / 1 X PBS	51.8	52.0	50.8
3	20mM citrate / 1 X PBS	30.7	28.1	28.7

Table 19: Thermal stability (Tagg values) for P1-061029, P1-068761, P1-068767 across the pH range of pH3 – pH 9 as determined by static light scattering

pH	Buffer	Tagg (°C) P1-061029	Tagg (°C) P1-068761	Tagg (°C) P1-068767
9	20mM Tris / 1 X PBS	67.7	67.1	66.0
8	20mM Tris / 1 X PBS	67.8	67.5	65.8
7	20mM Tris / 1 X PBS	67.8	68.2	65.9
7	20mM citrate / 1 X PBS	67.8	68.1	65.7
6	20mM citrate / 1 X PBS	68.1	68.9	65.6
5	20mM citrate / 1 X PBS	66.8	68.7	63.7
4	20mM citrate / 1 X PBS	61.7	63.6	56.9
3	20mM citrate / 1 X PBS	48.2	48.8	41.0

The apparent viscosity of P1-061029, P1-068761, and P1-068767 was measured using a bead-based DLS method which measures the diffusion rate of polystyrene beads in the presence of formulated antibody solutions. Comparison of all three antibodies at 44 mg/ml shows similar viscosity for both engineered antibodies as the parent antibody under these conditions, Table 20. In a second study additional protein material for P1-068761 and P1-068767 was concentrated to higher concentrations to analyze viscosity at 136 mg/ml, 100 mg/ml, and 50 mg/ml. These data show increased apparent viscosity at higher antibody

concentrations, with maximum apparent viscosity of 5.7 ± 0.7 for P1-068761 and 5.3 ± 0.6 for P1-068767 at 136 mg/ml.

Table 20: Apparent viscosity (in cP) for antibodies in 20mM histidine, 260mM sucrose pH 6.0 at 25°C as determined by bead based DLS method. Values represent the average and standard deviation of data from three UNi lanes

Antibody	Apparent Viscosity (cP) @ 136 mg/ml	Apparent Viscosity (cP) @ 100 mg/ml	Apparent Viscosity (cP) @ 50 mg/ml	Apparent Viscosity (cP) @ 44 mg/ml
P1-061029				1.6 ± 0.1
P1-068761	5.7 ± 0.7	3.1 ± 0.0	1.4 ± 0.2	1.5 ± 0.4
P1-068767	5.3 ± 0.6	3.0 ± 0.3	1.7 ± 0.2	1.6 ± 0.2

The physical stability of 50 mg/ml samples of P1-061029, P1-068761, and P1-068767 in 20 mM histidine, 260 mM sucrose pH 6.0 was studied under accelerated stress conditions of 40°C for 4 weeks. The oligomeric state of the antibodies was monitored by aSEC for samples immediately prior to 40°C incubation (time zero = t0), as well as after 1 week (1w) and 4 weeks (4w) of 40°C stress. These data show that all three antibodies remain more than 96% monomeric after 4 weeks at 40°C, with low levels of HMW species (< 1.6 % HMW) and low levels of LMW species (< 2.0 % LMW), Table 21.

Table 21: aSEC data for anti-VISTA antibody accelerated stability samples, showing the percentage of high molecular weight species (%HMW), percentage of monomeric/main species (%Main) and percentage of low molecular weight species (%LMW), for t0, 1w, and 4w samples

Antibody	Sample	% HMW	% Main	% LMW
P1-061029	t0	0.4	99.7	0.0
	1w	0.5	99.4	0.2
	4w	0.8	97.2	2.0
P1-068761	t0	0.6	99.4	0.0
	1w	0.9	98.8	0.3
	4w	1.6	96.4	2.0
P1-068767	t0	0.5	99.5	0.0
	1w	0.8	98.9	0.3
	4w	1.6	96.4	2.0

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Sequence Table

The following is a table of certain sequences referred to in this application. In SEQ ID NO: 2, amino acid position 187 may be either a D or an E.

In the antibody sequences below, the VH CDR1, CDR2, and CDR3 sequences are located at amino acid positions comprising amino acids 26-35, 50-66, and 99-110, respectively, and the VL CDR1, CDR2, and CDR3 sequences are located at amino acid positions comprising amino acids 24-35, 51-57, and 90-98, respectively. The VH CDR1 is numbered according to AbM (AA 26-35; Abhinandan and Martin (2008) Mol. Immunol. 45:3832-3839; Swindells et al. (2017) J. Mol. Biol. 429:356-364) and all other CDRs (VH CDR2, VH CDR3, VL CDR1-3) are numbered according to Kabat. The CDR sequences of particular antibody species are bold and underlined below on their VH and VL sequences.

SEQ ID NO	Name	Sequence
1	hVISTA (with leader sequence)	MGVPTALEAG SWRWGSLLFA LFLAASLGPV AAFKVATPYS LYVCPEGQNV TLTCRLLGPV DKGHDVTFYK TWYRSSRGEV QTCSERRPIR NLTFQDLHLH HGGHQAANTS HDLAQRHGLE SASDHHGNFS ITMRNLTLLD SGLYCCLVVE IRHHHHSEHRV HGAMELQVQT GKDAPSNCVV YPSSSQDSEN ITAAALATGA CIVGILCLPL ILLLVYKQRQ AASNRRAQEL VRMDSNIQGI ENPGFEASPP AQGIPEAKVR HPLSYVAQRQ PSESGRHLLS EPSTPLSPPG PGDVFFPSLD PVPDSPNFEV I
2	hVISTA (no leader sequence)	FKVATPYSLY VCPEGQNVTL TCRLLGPVDK GHDVTFYKTW YRSSRGEVQT CSERRPIRNL TFQDLHLHHG GHQAANTSHD LAQRHGLESA SDHHGNFSIT MRNLTLLDSG LYCCLVVEIR HHHHSEHRVH G AMELQVQTGK DAPSNCVVYP SSSQ[D/E]SENIT AAALATGACI VGILCLPLIL LLVYKQRQAA SNRRAQELVR MDSNIQGIEN PGFEASPPAQ GIPEAKVRHP LSYVAQRQPS ESGRHLLSEP STPLSPPGPG DVFFPSLDPV PDSPNFEVI
3	Human PSGL-1 isoform 2 precursor, with signal peptide	MPLQLLLLLI LLGPGNSLQL WDTWADEAEK ALGPLLARDR RQATEYEYLD YDFLPETEPP EMLRNSTDTT PLTGPGTPES TTVEPAARRS TGLDAGGAVT ELTTELANMG NLSTDSAAME IQTTQPAATE AQTTQPVPTE AQTTPLAATE AQTTRLTATE AQTTPLAATE AQTTPPAATE AQTTQPTGLE AQTTAPAAME AQTTAPAAME AQTTPPAAME AQTTQTTAME AQTTAPEATE AQTTQPTATE AQTTPLAAME ALSTEPSATE ALSMEPTTKR GLFIPFSVSS VTHKGIPMAA SNLSVNYPVG APDHISVKQC LLAILILALV ATIFFVCTVV LAVRLSRKGH MYPVRNYSPT EMVCISSLLP DGGEGPSATA NGGLSKAKSP GLTPEPREDR EGDDLTLHSF LP
4	Human PSGL-1 isoform 2, without signal peptide	LQL WDTWADEAEK ALGPLLARDR RQATEYEYLD YDFLPETEPP EMLRNSTDTT PLTGPGTPES TTVEPAARRS TGLDAGGAVT ELTTELANMG NLSTDSAAME IQTTQPAATE AQTTQPVPTE AQTTPLAATE AQTTRLTATE

SEQ ID NO	Name	Sequence
		AQTTPLAATE AQTTPPAATE AQTTQPTGLE AQTTAPAAME AQTTAPAAME AQTTPPAAME AQTTQTTAME AQTTAPEATE AQTTQPTATE AQTTPLAAME ALSTEPSATE ALSMEPTTKR GLFIPFSVSS VTHKGIPMAA SNLSVNYPVG APDHISVKQC LLAILILALV ATIFFVCTVV LAVRLSRKGH MYPVRNYSPT EMVCISSLLP DGGEGPSATA NGGLSKAKSP GLTPEPREDR EGDDLTLHSF LP
5	Human PSGL-1 isoform 2 ECD, with signal peptide	MPLQLLLLLL LLGPGNSLQL WDTWADEAEK ALGPLLARDR RQATEYEYLD YDFLPETEPP EMLRNSTDTT PLTGPGTPES TTVEPAARRS TGLDAGGAVT ELTTELANMG NLSTDSAAME IQTTQPAATE AQTTQPVPTE AQTTPLAATE AQTTRLTATE AQTTPLAATE AQTTPPAATE AQTTQPTGLE AQTTAPAAME AQTTAPAAME AQTTPPAAME AQTTQT
6	Human PSGL-1 isoform 2 ECD, without signal peptide	LQL WDTWADEAEK ALGPLLARDR RQATEYEYLD YDFLPETEPP EMLRNSTDTT PLTGPGTPES TTVEPAARRS TGLDAGGAVT ELTTELANMG NLSTDSAAME IQTTQPAATE AQTTQPVPTE AQTTPLAATE AQTTRLTATE AQTTPLAATE AQTTPPAATE AQTTQPTGLE AQTTAPAAME AQTTAPAAME AQTTPPAAME AQTTQT
7	Human PSGL-1 ECD (N-terminal positions 42 to 295 of a full length Human PSGL-1 Accession No. AAC50061)	QATEYEYLD YDFLPETEPP EMLRNSTDTT PLTGPGTPES TTVEPAARRS TGLDAGGAVT ELTTELANMG NLSTDSAAME IQTTQPAATE AQTTPLAATE AQTTRLTATE AQTTPLAATE AQTTPPAATE AQTTQPTGLE AQTTAPAAME AQTTAPAAME AQTTPPAAME AQTTQTTAME AQTTAPEATE AQTTQPTATE AQTTPLAAME ALSTEPSATE ALSMEPTTKR GLFIPFSVSS VTHKGIPMAA SNLSV
8	HumPSGL-1 isoform 1 precursor, with signal peptide NP_001193538	MAVGASGLEG DKMAGAMPLQ LLLLLILLGP GNSLQLWDTW ADEAEKALGP LLARDRRQAT EYEYLDYDFL PETEPPEMLR NSTDTTPLTG PGTPESTTVE PAARRSTGLD AGGAVTELTT ELANMGNLST DSAAMEIQTT QPAATEAQTT QPVPTEAQTT PLAATEAQTT RLTATEAQTT PLAATEAQTT PPAATEAQTT QPTGLEAQTT APAAMEAQTT APAAMEAQTT PPAAMEAQTT QTTAMEAQTT APEATEAQTT QPTATEAQTT PLAAMEALST EPSATEALSM EPTTKRGLFI PFSVSSVTHK GIPMAASNLS VNYPVGAPDH ISVKQCLLAI LILALVATIF FVCTVVLAVR LSRKGHMYPV RNYSPTEMVC ISSLLPDGGE GPSATANGGL SKAKSPGLTP EPREDREGDD LTLHSFLP
9	Human PSGL-1, without signal peptide	LQLWDTW ADEAEKALGP LLARDRRQAT EYEYLDYDFL PETEPPEMLR NSTDTTPLTG PGTPESTTVE PAARRSTGLD AGGAVTELTT ELANMGNLST DSAAMEIQTT QPAATEAQTT QPVPTEAQTT PLAATEAQTT RLTATEAQTT PLAATEAQTT PPAATEAQTT QPTGLEAQTT APAAMEAQTT APAAMEAQTT PPAAMEAQTT QTTAMEAQTT APEATEAQTT QPTATEAQTT PLAAMEALST EPSATEALSM EPTTKRGLFI PFSVSSVTHK GIPMAASNLS VNYPVGAPDH ISVKQCLLAI LILALVATIF FVCTVVLAVR LSRKGHMYPV RNYSPTEMVC ISSLLPDGGE GPSATANGGL SKAKSPGLTP EPREDREGDD LTLHSFLP
10	Human PSGL-1 ECD, with signal peptide	MAVGASGLEG DKMAGAMPLQ LLLLLILLGP GNSLQLWDTW ADEAEKALGP LLARDRRQAT EYEYLDYDFL PETEPPEMLR NSTDTTPLTG PGTPESTTVE PAARRSTGLD AGGAVTELTT ELANMGNLST DSAAMEIQTT QPAATEAQTT QPVPTEAQTT

SEQ ID NO	Name	Sequence
		PLAATEAQTT RLTATEAQTT PLAATEAQTT PPAATEAQTT QPTGLEAQTT APAAMEAQTT APAAMEAQTT PPAAMEAQTT QT
11	P1-069059 VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDYAMH**WVRQAPGKGLEW VS**GINWNSDHIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAEDD**WGQGTMVTVSS
12	P1-069059 VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
13	P1-069059 IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDYAMHWVRQAPGKGLEW VSGINWNSDHIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAEDDWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
14	P1-069059 LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
15	P1-069061 VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDYAMH**WVRQAPGKGLEW VS**GINWNSAEIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAEDD**WGQGTMVTVSS
16	P1-069061 VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
17	P1-069061 IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDYAMHWVRQAPGKGLEW VSGINWNSAEIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAEDDWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
18	P1-069061 LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
19	P1-069063 VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDYAMH**WVRQAPGKGLEW VS**GINWNSAEIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDADDE**WGQGTMVTVSS
20	P1-069063 VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK

SEQ ID NO	Name	Sequence
21	P1-069063 IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDYAMHWVRQAPGKGLEW VSGINWNSAEIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDADDEWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
22	P1-069063 LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
23	P1-069065 VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDEAMH**WVRQAPGKGLEW VS**GINWNSDDIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAFDV**WGQGTMVTVSS
24	P1-069065 VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
25	P1-069065 IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDEAMHWVRQAPGKGLEW VSGINWNSDDIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAFDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
26	P1-069065 LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
27	P1-069067 VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLDDYAMH**WVRQAPGKGLEW VS**GINWNSEEIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDADDE**WGQGTMVTVSS
28	P1-069067 VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
29	P1-069067 IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLDDYAMHWVRQAPGKGLEW VSGINWNSEEIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDADDEWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW

SEQ ID NO	Name	Sequence
		QQGNVFSCSVMHEALHNHYTQKSLSLSPG
30	P1-069067 LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
31	P1-069069 VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLDDYAMH**WVRQAPGKGLEW VS**GINWNSEEIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDADDV**WGQGTMVTVSS
32	P1-069069 VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
33	P1-069069 IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLDDYAMHWVRQAPGKGLEW VSGINWNSEEIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDADDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
34	P1-069069 LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
35	P1-069071 VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDEAMH**WVRQAPGKGLEW VS**GINWNSADIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSEGWIDAFDV**WGQGTMVTVSS
36	P1-069071 VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
37	P1-069071 IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDEAMHWVRQAPGKGLEW VSGINWNSADIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSEGWIDAFDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
38	P1-069071 LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
39	P1-069073 VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDEAMH**WVRQAPGKGLEW VS**GINWNSAEIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAEDV**WGQGTMVTVSS

SEQ ID NO	Name	Sequence
40	P1-069073 VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
41	P1-069073 IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDEAMHWVRQAPGKGLEW VSGINWNSAEIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAEDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
42	P1-069073 LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
43	P1-069075 VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDYAMH**WVRQAPGKGLEW VS**GINWDSAEIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSHGWIDAEDV**WGQGTMVTVSS
44	P1-069075 VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
45	P1-069075 IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDYAMHWVRQAPGKGLEW VSGINWDSAEIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSHGWIDAEDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
46	P1-069075 LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
47	P1-069077 VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDEAMH**WVRQAPGKGLEW VS**GINWNSDEIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAFDV**WGQGTMVTVSS
48	P1-069077 VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
49	P1-069077 IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDEAMHWVRQAPGKGLEW VSGINWNSDEIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAFDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN

SEQ ID NO	Name	Sequence
		WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
50	P1-069077 LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
51	P1-068761 VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDEAMH**WVRQAPGKGLEW VS**GINWNSEEIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSHGWIDAEDV**WGQGTMVTVSS
52	P1-068761 VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
53	P1-068761 IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDEAMHWVRQAPGKGLEW VSGINWNSEEIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSHGWIDAEDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
54	P1-068761 LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
55	P1-068767 VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDYAMH**WVRQAPGKGLEW VS**GIDWNSENIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAEDD**WGQGTMVTVSS
56	P1-068767 VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
57	P1-068767 IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDYAMHWVRQAPGKGLEW VSGIDWNSENIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAEDDWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
58	P1-068767 LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO	Name	Sequence
59	P1-068773 VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDYAMH**WVRQAPGKGLEW VS**GIDWNSDNIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAEDD**WGQGTMVTVSS
60	P1-068773 VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
61	P1-068773 IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDYAMHWVRQAPGKGLEW VSGIDWNSDNIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAEDDWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
62	P1-068773 LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
63	P1-068765 VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTDEDYAMH**WVRQAPGKGLEW VS**GINWNSEEIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAEDD**WGQGTMVTVSS
64	P1-068765 VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
65	P1-068765 IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTDEDYAMHWVRQAPGKGLEW VSGINWNSEEIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAEDDWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
66	P1-068765 LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
67	P1-061029 VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLDDYAMH**WVRQAPGKGLEW VS**GINWNSANIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAFDV**WGQGTMVTVSS
68	P1-061029 VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
69	P1-061029 IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLDDYAMHWVRQAPGKGLEW VSGINWNSANIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAFDVWGQGTMVTVSSASTKGPSVFPLAPSSKST

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		SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
70	P1-061029 LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
71	P1-068757 VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDEAMH**WVRQAPGKGLEW VS**GINWNSEEIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAEDD**WGQGTMVTVSS
72	P1-068757 VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
73	P1-068757 IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDEAMHWVRQAPGKGLEW VSGINWNSEEIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAEDDWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
74	P1-068757 LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
75	P1-068771 VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDEAMH**WVRQAPGKGLEW VS**GINWNSHEIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAEDD**WGQGTMVTVSS
76	P1-068771 VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
77	P1-068771 IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDEAMHWVRQAPGKGLEW VSGINWNSHEIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAEDDWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
78	P1-068771 LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS

SEQ ID NO	Name	Sequence
		SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
79	P1-068775 VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDEAMH**WVRQAPGKGLEW VS**GIDWNSEEIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSHGWIDAEDD**WGQGTMVTVSS
80	P1-068775 VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
81	P1-068775 IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDEAMHWVRQAPGKGLEW VSGIDWNSEEIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSHGWIDAEDDWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
82	P1-068775 LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
83	P1-068769 VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDEAMH**WVRQAPGKGLEW VS**GINWNSDHIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAEDD**WGQGTMVTVSS
84	P1-068769 VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
85	P1-068769 IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDEAMHWVRQAPGKGLEW VSGINWNSDHIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAEDDWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
86	P1-068769 LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
87	P1-068759 VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDEAMH**WVRQAPGKGLEW VS**GIDWNSENIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAEDD**WGQGTMVTVSS
88	P1-068759 VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK

SEQ ID NO	Name	Sequence
89	P1-068759 IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDEAMHWVRQAPGKGLEW VSGIDWNSENIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAEDDWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
90	P1-068759 LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
91	P1-068763 VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDYAMH**WVRQAPGKGLEW VS**GIDWNSENIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSHGWIDAEDV**WGQGTMVTVSS
92	P1-068763 VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
93	P1-068763 IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDYAMHWVRQAPGKGLEW VSGIDWNSENIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSHGWIDAEDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
94	P1-068763 LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
95	P1-061015 VH	QVQLVESGGGVVQPGRSLRLSCAAS**GFTFSSYAMH**WVRQAPGKGLEW VA**IIWYDGSNKYYADSVKG**RFTISRDNSKNTLYLQMNSLRAEDTAVY YCAR**DSGFYSSYYFDY**WGQGTLVTVSS
96	P1-061015 VL	EIVLTQSPATLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**DASNRAT**GIPARFSGSGSGTDFTLTISSLEPEDFATYYC**QQYNS YPYT**FGQGTKLEIK
97	P1-061015 IgG1.3 HC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEW VAIIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY YCARDSGFYSSYYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPA PEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ

SEQ ID NO	Name	Sequence
		GNVFSCSVMHEALHNHYTQKSLSLSPG
98	P1-061015 LC	EIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFATYYCQQYNS YPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
99	P1-068748 VH	QVQLVESGGGVVQPGRSLRLSCAAS**GFTFSHHAMH**WVRQAPGKGLEW VA**IIWYDGSNDDYADSVKG**RFTISRDNSKNTLYLQMNSLRAEDTAVY YCAR**DSGFYDSYYFDY**WGQGTLVTVSS
100	P1-068748 VL	EIVLTQSPATLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**DASNRAT**GIPARFSGSGSGTDFTLTISSLEPEDFATYYC**QQYNS YPYT**FGQGTKLEIK
101	P1-068748 IgG1.3 HC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSHHAMHWVRQAPGKGLEW VAIIWYDGSNDDYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY YCARDSGFYDSYYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPA PEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPG
102	P1-068748 LC	EIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFATYYCQQYNS YPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
103	P1-068744 VH	QVQLVESGGGVVQPGRSLRLSCAAS**GFTFSEYAMH**WVRQAPGKGLEW VA**HIWYDGSNKYEADSVKG**RFTISRDNSKNTLYLQMNSLRAEDTAVY YCAR**DSGFYESYYFDE**WGQGTLVTVSS
104	P1-068744 VL	EIVLTQSPATLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**DASNRAT**GIPARFSGSGSGTDFTLTISSLEPEDFATYYC**QQYNS YPYT**FGQGTKLEIK
105	P1-068744 IgG1.3 HC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSEYAMHWVRQAPGKGLEW VAHIWYDGSNKYEADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY YCARDSGFYESYYFDEWGQGTLVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPA PEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPG
106	P1-068744 LC	EIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFATYYCQQYNS YPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
107	P1-068736 VH	QVQLVESGGGVVQPGRSLRLSCAAS**GFTFSEYAMH**WVRQAPGKGLEW VA**IDWYDGSNKDYADSVKG**RFTISRDNSKNTLYLQMNSLRAEDTAVY YCAR**DSGFYDSYYFDD**WGQGTLVTVSS

SEQ ID NO	Name	Sequence
108	P1-068736 VL	EIVLTQSPATLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**DASNRAT**GIPARFSGSGSGTDFTLTISSLEPEDFATYYC**QQYNS YPYT**FGQGTKLEIK
109	P1-068736 IgG1.3 HC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSEYAMHWVRQAPGKGLEW VAIDWYDGSNKDYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY YCARDSGFYDSYYFDDWGQGTLVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPA PEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPG
110	P1-068736 LC	EIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFATYYCQQYNS YPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
111	P1-068752 VH	QVQLVESGGGVVQPGRSLRLSCAAS**GFTFSSYAMH**WVRQAPGKGLEW VA**EIWYDGSNKDYADSVKG**RFTISRDNSKNTLYLQMNSLRAEDTAVY YCAR**DSGFYDSYYFDE**WGQGTLVTVSS
112	P1-068752 VL	EIVLTQSPATLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**DASNRAT**GIPARFSGSGSGTDFTLTISSLEPEDFATYYC**QQYNS YPYT**FGQGTKLEIK
113	P1-068752 IgG1.3 HC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEW VAEIWYDGSNKDYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY YCARDSGFYDSYYFDEWGQGTLVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPA PEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPG
114	P1-068752 LC	EIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFATYYCQQYNS YPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
115	P1-068740 VH	QVQLVESGGGVVQPGRSLRLSCAAS**GFTFSDYAMH**WVRQAPGKGLEW VA**IIWYDGSDKDYADSVKG**RFTISRDNSKNTLYLQMNSLRAEDTAVY YCAR**DSGFYDSYYFDD**WGQGTLVTVSS
116	P1-068740 VL	EIVLTQSPATLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**DASNRAT**GIPARFSGSGSGTDFTLTISSLEPEDFATYYC**QQYNS YPYT**FGQGTKLEIK
117	P1-068740 IgG1.3 HC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSDYAMHWVRQAPGKGLEW VAIIWYDGSDKDYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY YCARDSGFYDSYYFDDWGQGTLVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPA PEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY

SEQ ID NO	Name	Sequence
		VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPG
118	P1-068740 LC	EIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFATYYCQQYNS YPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
119	P1-068742 VH	QVQLVESGGGVVQPGRSLRLSCAAS**GFTFSDYAMH**WVRQAPGKGLEW VA**IIWYDGSDKDYADSVKG**RFTISRDNSKNTLYLQMNSLRAEDTAVY YCAR**DSGFYEDYYFDY**WGQGTLVTVSS
120	P1-068742 VL	EIVLTQSPATLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**DASNRAT**GIPARFSGSGSGTDFTLTISSLEPEDFATYYC**QQYNS YPYT**FGQGTKLEIK
121	P1-068742 IgG1.3 HC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSDYAMHWVRQAPGKGLEW VAIIWYDGSDKDYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY YCARDSGFYEDYYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPA PEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPG
122	P1-068742 LC	EIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFATYYCQQYNS YPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
123	P1-068746 VH	QVQLVESGGGVVQPGRSLRLSCAAS**GFTFSSYAMH**WVRQAPGKGLEW VA**IIWYDGSNHHYADSVKG**RFTISRDNSKNTLYLQMNSLRAEDTAVY YCAR**DSGFYDSYYFDY**WGQGTLVTVSS
124	P1-068746 VL	EIVLTQSPATLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**DASNRAT**GIPARFSGSGSGTDFTLTISSLEPEDFATYYC**QQYNS YPYT**FGQGTKLEIK
125	P1-068746 IgG1.3 HC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEW VAIIWYDGSNHHYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY YCARDSGFYDSYYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPA PEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPG
126	P1-068746 LC	EIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFATYYCQQYNS YPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO	Name	Sequence
127	P1-068750 VH	QVQLVESGGGVVQPGRSLRLSCAAS**GFTFSDYDMH**WVRQAPGKGLEW VA**EIWDDGSNKYYADSVKG**RFTISRDNSKNTLYLQMNSLRAEDTAVY YCAR**DEEFYSSYYFDY**WGQGTLVTVSS
128	P1-068750 VL	EIVLTQSPATLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**DASNRAT**GIPARFSGSGSGTDFTLTISSLEPEDFATYYC**QQYNS YPYT**FGQGTKLEIK
129	P1-068750 IgG1.3 HC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSDYDMHWVRQAPGKGLEW VAEIWDDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY YCARDEEFYSSYYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPA PEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPG
130	P1-068750 LC	EIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFATYYCQQYNS YPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
131	P1-068738 VH	QVQLVESGGGVVQPGRSLRLSCAAS**GFTFSEYAHH**WVRQAPGKGLEW VA**IIWDDGSNHYYADSVKG**RFTISRDNSKNTLYLQMNSLRAEDTAVY YCAR**DSGFYEDYYFDY**WGQGTLVTVSS
132	P1-068738 VL	EIVLTQSPATLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**DASNRAT**GIPARFSGSGSGTDFTLTISSLEPEDFATYYC**QQYNS YPYT**FGQGTKLEIK
133	P1-068738 IgG1.3 HC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSEYAHHWVRQAPGKGLEW VAIIWDDGSNHYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY YCARDSGFYEDYYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPA PEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPG
134	P1-068738 LC	EIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFATYYCQQYNS YPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
135	P1-068754 VH	QVQLVESGGGVVQPGRSLRLSCAAS**GFTFSDYDMH**WVRQAPGKGLEW VA**EIWDDGSNKYYADSVKG**RFTISRDNSKNTLYLQMNSLRAEDTAVY YCAR**DSGFHSDYYFDY**WGQGTLVTVSS
136	P1-068754 VL	EIVLTQSPATLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**DASNRAT**GIPARFSGSGSGTDFTLTISSLEPEDFATYYC**QQYNS YPYT**FGQGTKLEIK
137	P1-068754 IgG1.3 HC	QVQLVESGGGVVQPGRSLRLSCAASGFTFSDYDMHWVRQAPGKGLEW VAEIWDDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVY YCARDSGFHSDYYFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSG

SEQ ID NO	Name	Sequence
		GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS VVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPA PEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPG
138	P1-068754 LC	EIVLTQSPATLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFATYYCQQYNS YPYTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
139	P1-069293 VH (P1-068761.IgG1f)	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDEAMH**WVRQAPGKGLEW VS**GINWNSEEIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSHGWIDAEDV**WGQGTMVTVSS
140	P1-069293 VL (P1-068761.IgG1f)	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
141	P1-069293 HC (P1-068761.IgG1f)	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDEAMHWVRQAPGKGLEW VSGINWNSEEIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSHGWIDAEDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
142	P1-069293 LC (P1-068761.IgG1f)	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
143	P1-069298 VH (P1-068767.IgG1f)	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDYAMH**WVRQAPGKGLEW VS**GIDWNSENIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAEDD**WGQGTMVTVSS
144	P1-069298 VL (P1-068767.IgG1f)	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
145	P1-069298 HC (P1-068767.IgG1f)	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDYAMHWVRQAPGKGLEW VSGIDWNSENIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAEDDWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
146	P1-069298 LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS

SEQ ID NO	Name	Sequence
	(P1-068767.IgG1f)	SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
147	P1-069302 VH (P1-061029.IgG1f)	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLDDYAMH**WVRQAPGKGLEW VS**GINWNSANIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAFDV**WGQGTMVTVSS
148	P1-069302 VL (P1-061029.IgG1f)	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
149	P1-069302 HC (P1-061029.IgG1f)	EVQLVESGGGLVQPGKSLRLSCAASGFTLDDYAMHWVRQAPGKGLEW VSGINWNSANIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAFDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
150	P1-069302 LC (P1-061029.IgG1f)	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
151	P1-069312 VH (P1-068761.IgG1f afucosylated)	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDEAMH**WVRQAPGKGLEW VS**GINWNSEEIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSHGWIDAEDV**WGQGTMVTVSS
152	P1-069312 VL (P1-068761.IgG1f afucosylated)	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
153	P1-069312 HC (P1-068761.IgG1f afucosylated)	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDEAMHWVRQAPGKGLEW VSGINWNSEEIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSHGWIDAEDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
154	P1-069312 LC (P1-068761.IgG1f afucosylated)	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO	Name	Sequence
155	P1-069309 VH (P1-068767.IgG1f afucosylated)	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDYAMH**WVRQAPGKGLEW VS**GIDWNSENIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAEDD**WGQGTMVTVSS
156	P1-069309 VL (P1-068767.IgG1f afucosylated)	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
157	P1-069309 HC (P1-068767.IgG1f afucosylated)	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDYAMHWVRQAPGKGLEW VSGIDWNSENIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAEDDWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
158	P1-069309 LC (P1-068767.IgG1f afucosylated)	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
159	P1-069307 VH (P1-061029.IgG1f afucosylated)	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLDDYAMH**WVRQAPGKGLEW VS**GINWNSANIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAFDV**WGQGTMVTVSS
160	P1-069307 VL (P1-061029.IgG1f afucosylated)	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
161	P1-069307 HC (P1-061029.IgG1f afucosylated)	EVQLVESGGGLVQPGKSLRLSCAASGFTLDDYAMHWVRQAPGKGLEW VSGINWNSANIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAFDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
162	P1-069307 LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS

SEQ ID NO	Name	Sequence
	(P1-061029.IgG1f afucosylated)	SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
163	IgG1.3 (or IgG1.3f) heavy chain constant region (L234A, L235E, G237A)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV DKRVEPKSCDKTHTCPPCPAPEAEGAPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
164	Exemplary light chain constant region	RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGL SSPVTKSFNRGEC
165	Human VISTA NP_071436.1 (Fig. 1B)	See Fig. 1B
166	Cyno VISTA XP_005565644.1 (Fig. 1B)	See Fig. 1B
167	Mouse VISTA NP_083008.1 (Fig. 1B)	See Fig. 1B
168	P1-061029 HDR3 chip oligo (Fig. 7A)	**X**PGYSGGWIDAFDV
169	P1-061029 HDR3 chip oligo (Fig. 7A)	**XX**GYSGGWIDAFDV
170	P1-061029 HDR3 chip oligo (Fig. 7A)	**X**P**X**YSGGWIDAFDV
171	P1-061029 HDR3 chip oligo (Fig. 7A)	**X**PG**X**SGGWIDAFDV
172	P1-061029 HDR3 chip oligo (Fig. 7A)	**X**PGY**X**GGWIDAFDV
173	P1-061029 HDR3 chip oligo (Fig. 7A)	**X**PGYS**X**GWIDAFDV
174	P1-061029 HDR3 chip oligo (Fig. 7A)	**X**PGYSG**X**WIDAFDV
175	P1-061029 HDR3 chip oligo (Fig. 7A)	**X**PGYSGG**X**IDAFDV
176	P1-061029 HDR3 chip oligo (Fig. 7A)	**X**PGYSGGW**X**DAFDV
177	P1-061029 HDR3	**X**PGYSGGWI**X**AFDV

SEQ ID NO	Name	Sequence
	chip oligo (Fig. 7A)	
178	P1-061029 HDR3 chip oligo (Fig. 7A)	**X**PGYSGGWID**X**FDV
179	P1-061029 HDR3 chip oligo (Fig. 7A)	**X**PGYSGGWIDA**X**DV
180	P1-061029 HDR3 chip oligo (Fig. 7A)	**X**PGYSGGWIDAF**X**V
181	P1-061029 HDR3 chip oligo (Fig. 7A)	**X**PGYSGGWIDAFD**X**
182	IgG1f (human wild-type allotype f) heavy chain constant region	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV DKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
183	IgG1.1f Heavy chain constant region (L234A, L235E, G237A, A330S, P331S)	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV DKRVEPKSCDKTHTCPPCPAPEAEGAPSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPSSIEKTISKAKGQPREPQVYTLP PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
184	IgG1fa.P238K (or IgG1.P238K) heavy chain constant region	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV DKRVEPKSCDKTHTCPPCPAPELLGGKSVFLFPPKPKDTLMISRTPE VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
185	P1-070864 P1-068761_E30D VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLDDEAMH**WVRQAPGKGLEW VS**GINWNSEEIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSHGWIDAEDV**WGQGTMVTVSS
186	P1-070864 P1-068761_E30D VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
187	P1-070864 P1-068761_E30D IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLDDEAMHWVRQAPGKGLEW VSGINWNSEEIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSHGWIDAEDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO	Name	Sequence
188	P1-070864 P1-068761_E30D LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
189	P1-070866 P1-068761_E32Y VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDYAMH**WVRQAPGKGLEW VS**GINWNSEEIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSHGWIDAEDV**WGQGTMVTVSS
190	P1-070866 P1-068761_E32Y VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
191	P1-070866 P1-068761_E32Y IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDYAMHWVRQAPGKGLEW VSGINWNSEEIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSHGWIDAEDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
192	P1-070866 P1-068761_E32Y LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
193	P1-070868 P1-068761_E55A VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDEAMH**WVRQAPGKGLEW VS**GINWNSAEIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSHGWIDAEDV**WGQGTMVTVSS
194	P1-070868 P1-068761_E55A VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
195	P1-070868 P1-068761_E55A IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDEAMHWVRQAPGKGLEW VSGINWNSAEIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSHGWIDAEDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
196	P1-070868 P1-068761_E55A LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
197	P1-070870 P1-068761_E56N VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDEAMH**WVRQAPGKGLEW VS**GINWNSENIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSHGWIDAEDV**WGQGTMVTVSS

SEQ ID NO	Name	Sequence
198	P1-070870 P1-068761_E56N VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
199	P1-070870 P1-068761_E56N IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDEAMHWVRQAPGKGLEW VSGINWNSENIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSHGWIDAEDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
200	P1-070870 P1-068761_E56N LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
201	P1-070872 P1-068761_H100G VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDEAMH**WVRQAPGKGLEW VS**GINWNSEEIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAEDV**WGQGTMVTVSS
202	P1-070872 P1-068761_H100G VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
203	P1-070872 P1-068761_H100G IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDEAMHWVRQAPGKGLEW VSGINWNSEEIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAEDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
204	P1-070872 P1-068761_H100G LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
205	P1-070874 P1-068761_E100fF VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDEAMH**WVRQAPGKGLEW VS**GINWNSEEIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSHGWIDAFDV**WGQGTMVTVSS
206	P1-070874 P1-068761_E100fF VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
207	P1-070874 P1-068761_E100fF IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDEAMHWVRQAPGKGLEW VSGINWNSEEIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSHGWIDAFDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN

SEQ ID NO	Name	Sequence
		WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
208	P1-070874 P1-068761_E100fF LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
209	P1-070876 P1-068761_E30D_E32Y VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLDDYAMH**WVRQAPGKGLEW VS**GINWNSEEIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSHGWIDAEDV**WGQGTMVTVSS
210	P1-070876 P1-068761_E30D_E32Y VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
211	P1-070876 P1-068761_E30D_E32Y IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLDDYAMHWVRQAPGKGLEW VSGINWNSEEIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSHGWIDAEDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
212	P1-070876 P1-068761_E30D_E32Y LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
213	P1-070878 P1-068761_E55A_E56N VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDEAMH**WVRQAPGKGLEW VS**GINWNSANIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSHGWIDAEDV**WGQGTMVTVSS
214	P1-070878 P1-068761_E55A_E56N VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
215	P1-070878 P1-068761_E55A_E56N IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDEAMHWVRQAPGKGLEW VSGINWNSANIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSHGWIDAEDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO	Name	Sequence
216	P1-070878 P1-068761_E55A_E56N LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
217	P1-070880 P1-068761_H100G_E100fF VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDEAMH**WVRQAPGKGLEW VS**GINWNSEEIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAFDV**WGQGTMVTVSS
218	P1-070880 P1-068761_H100G_E100fF VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
219	P1-070880 P1-068761_H100G_E100fF IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDEAMHWVRQAPGKGLEW VSGINWNSEEIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAFDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
220	P1-070880 P1-068761_H100G_E100fF LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
221	P1-070882 P1-068761_E32Y_E55A VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDYAMH**WVRQAPGKGLEW VS**GINWNSAEIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSHGWIDAEDV**WGQGTMVTVSS
222	P1-070882 P1-068761_E32Y_E55A VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
223	P1-070882 P1-068761_E32Y_E55A IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDYAMHWVRQAPGKGLEW VSGINWNSAEIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSHGWIDAEDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
224	P1-070882 P1-068761_E32Y_E55A	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY

SEQ ID NO	Name	Sequence
	LC	PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
225	P1-070884 P1-068761_E32Y_E56N VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDYAMH**WVRQAPGKGLEW VS**GINWNSENIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSHGWIDAEDV**WGQGTMVTVSS
226	P1-070884 P1-068761_E32Y_E56N VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
227	P1-070884 P1-068761_E32Y_E56N IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDYAMHWVRQAPGKGLEW VSGINWNSENIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSHGWIDAEDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
228	P1-070884 P1-068761_E32Y_E56N LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
229	P1-070886 P1-068761_E32Y_H100G VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDYAMH**WVRQAPGKGLEW VS**GINWNSEEIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAEDV**WGQGTMVTVSS
230	P1-070886 P1-068761_E32Y_H100G VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
231	P1-070886 P1-068761_E32Y_H100G IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDYAMHWVRQAPGKGLEW VSGINWNSEEIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAEDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
232	P1-070886 P1-068761_E32Y_H100G LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
233	P1-070888 P1-068761_E32Y_E100f	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDYAMH**WVRQAPGKGLEW VS**GINWNSEEIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSHGWIDAFDV**WGQGTMVTVSS

SEQ ID NO	Name	Sequence
	F VH	
234	P1-070888 P1- 068761_E32Y_E100f F VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS** **SPFT**FGPGTKVDIK
235	P1-070888 P1- 068761_E32Y_E100f F IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDYAMHWVRQAPGKGLEW VSGINWNSEEIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSHGWIDAFDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
236	P1-070888 P1- 068761_E32Y_E100f F LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
237	P1-070890 P1- 068761_E30D_E55A VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLDDEAMH**WVRQAPGKGLEW VS**GINWNSAEIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSHGWIDAEDV**WGQGTMVTVSS
238	P1-070890 P1- 068761_E30D_E55A VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS** **SPFT**FGPGTKVDIK
239	P1-070890 P1- 068761_E30D_E55A IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLDDEAMHWVRQAPGKGLEW VSGINWNSAEIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSHGWIDAEDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
240	P1-070890 P1- 068761_E30D_E55A LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
241	P1-070892 P1- 068761_E30D_E56N VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLDDEAMH**WVRQAPGKGLEW VS**GINWNSENIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSHGWIDAEDV**WGQGTMVTVSS
242	P1-070892 P1-	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS**

SEQ ID NO	Name	Sequence
	068761_E30D_E56N VL	**SPFT**FGPGTKVDIK
243	P1-070892 P1-068761_E30D_E56N IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLDDEAMHWVRQAPGKGLEW VSGINWNSENIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSHGWIDAEDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
244	P1-070892 P1-068761_E30D_E56N LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
245	P1-070894 P1-068761_E30D_H100G VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLDDEAMH**WVRQAPGKGLEW VS**GINWNSEEIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAEDV**WGQGTMVTVSS
246	P1-070894 P1-068761_E30D_H100G VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
247	P1-070894 P1-068761_E30D_H100G IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLDDEAMHWVRQAPGKGLEW VSGINWNSEEIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAEDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
248	P1-070894 P1-068761_E30D_H100G LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
249	P1-070896 P1-068761_E30D_E100fF VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLDDEAMH**WVRQAPGKGLEW VS**GINWNSEEIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSHGWIDAFDV**WGQGTMVTVSS
250	P1-070896 P1-068761_E30D_E100fF VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK

SEQ ID NO	Name	Sequence
251	P1-070896 P1-068761_E30D_E100fF IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLDDEAMHWVRQAPGKGLEW VSGINWNSEEIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSHGWIDAFDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
252	P1-070896 P1-068761_E30D_E100fF LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
253	P1-070898 P1-068761_E55A_E100fF VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDEAMH**WVRQAPGKGLEW VS**GINWNSAEIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSHGWIDAFDV**WGQGTMVTVSS
254	P1-070898 P1-068761_E55A_E100fF VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
255	P1-070898 P1-068761_E55A_E100fF IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDEAMHWVRQAPGKGLEW VSGINWNSAEIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSHGWIDAFDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
256	P1-070898 P1-068761_E55A_E100fF LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
257	P1-070900 P1-068761_E56N_H100GVH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDEAMH**WVRQAPGKGLEW VS**GINWNSENIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAEDV**WGQGTMVTVSS
258	P1-070900 P1-068761_E56N_H100GVL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
259	P1-070900 P1-068761_E56N_H100G	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDEAMHWVRQAPGKGLEW VSGINWNSENIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAEDVWGQGTMVTVSSASTKGPSVFPLAPSSKST

SEQ ID NO	Name	Sequence
	IgG1.3 HC	SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
260	P1-070900 P1-068761_E56N_H100G LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
261	P1-070902 P1-068761_E56N_E100fF VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDEAMH**WVRQAPGKGLEW VS**GINWNSENIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSHGWIDAFDV**WGQGTMVTVSS
262	P1-070902 P1-068761_E56N_E100fF VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
263	P1-070902 P1-068761_E56N_E100fF IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDEAMHWVRQAPGKGLEW VSGINWNSENIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSHGWIDAFDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
264	P1-070902 P1-068761_E56N_E100fF LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
265	P1-070904 P1-068767_E30D VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLDDYAMH**WVRQAPGKGLEW VS**GIDWNSENIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAEDD**WGQGTMVTVSS
266	P1-070904 P1-068767_E30D VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
267	P1-070904 P1-068767_E30D IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLDDYAMHWVRQAPGKGLEW VSGIDWNSENIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAEDDWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK

SEQ ID NO	Name	Sequence
		GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
268	P1-070904 P1-068767_E30D LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
269	P1-070906 P1-068767_D52N VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDYAMH**WVRQAPGKGLEW VS**GINWNSENIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAEDD**WGQGTMVTVSS
270	P1-070906 P1-068767_D52N VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
271	P1-070906 P1-068767_D52N IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDYAMHWVRQAPGKGLEW VSGINWNSENIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAEDDWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
272	P1-070906 P1-068767_D52N LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
273	P1-070908 P1-068767_E55A VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDYAMH**WVRQAPGKGLEW VS**GIDWNSANIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAEDD**WGQGTMVTVSS
274	P1-070908 P1-068767_E55A VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
275	P1-070908 P1-068767_E55A IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDYAMHWVRQAPGKGLEW VSGIDWNSANIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAEDDWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
276	P1-070908 P1-068767_E55A LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
277	P1-070910 P1-068767_E100fF	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDYAMH**WVRQAPGKGLEW VS**GIDWNSENIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY

SEQ ID NO	Name	Sequence
	VH	YCAK**VPGYSGGWIDAFDD**WGQGTMVTVSS
278	P1-070910 P1-068767_E100fF VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
279	P1-070910 P1-068767_E100fF IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDYAMHWVRQAPGKGLEW VSGIDWNSENIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAFDDWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
280	P1-070910 P1-068767_E100fF LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
281	P1-070912 P1-068767_D102V VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDYAMH**WVRQAPGKGLEW VS**GIDWNSENIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAEDV**WGQGTMVTVSS
282	P1-070912 P1-068767_D102V VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
283	P1-070912 P1-068767_D102V IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDYAMHWVRQAPGKGLEW VSGIDWNSENIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAEDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
284	P1-070912 P1-068767_D102V LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
285	P1-070914 P1-068767_E30D_D52N VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLDDYAMH**WVRQAPGKGLEW VS**GINWNSENIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAEDD**WGQGTMVTVSS
286	P1-070914 P1-068767_E30D_D52N VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
287	P1-070914 P1-068767_E30D_D52N	EVQLVESGGGLVQPGKSLRLSCAASGFTLDDYAMHWVRQAPGKGLEW VSGINWNSENIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAEDDWGQGTMVTVSSASTKGPSVFPLAPSSKST

SEQ ID NO	Name	Sequence
	IgG1.3 HC	SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
288	P1-070914 P1-068767_E30D_D52N LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
289	P1-070916 P1-068767_D52N_E55A VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDYAMH**WVRQAPGKGLEW VS**GINWNSANIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAEDD**WGQGTMVTVSS
290	P1-070916 P1-068767_D52N_E55A VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
291	P1-070916 P1-068767_D52N_E55A IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDYAMHWVRQAPGKGLEW VSGINWNSANIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAEDDWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
292	P1-070916 P1-068767_D52N_E55A LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
293	P1-070918 P1-068767_E55A_E100fF VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDYAMH**WVRQAPGKGLEW VS**GIDWNSANIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAFDD**WGQGTMVTVSS
294	P1-070918 P1-068767_E55A_E100fF VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
295	P1-070918 P1-068767_E55A_E100fF IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDYAMHWVRQAPGKGLEW VSGIDWNSANIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAFDDWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN

SEQ ID NO	Name	Sequence
		WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
296	P1-070918 P1-068767_E55A_E100fF LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
297	P1-070920 P1-068767_E100fF_D102V VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDYAMHW**VRQAPGKGLEW VS**GIDWNSENIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAFDV**WGQGTMVTVSS
298	P1-070920 P1-068767_E100fF_D102V VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
299	P1-070920 P1-068767_E100fF_D102V IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDYAMHWVRQAPGKGLEW VSGIDWNSENIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAFDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
300	P1-070920 P1-068767_E100fF_D102V LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
301	P1-070922 P1-068767_E30D_E55A VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLDDYAMH**WVRQAPGKGLEW VS**GIDWNSANIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAEDD**WGQGTMVTVSS
302	P1-070922 P1-068767_E30D_E55A VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
303	P1-070922 P1-068767_E30D_E55A IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLDDYAMHWVRQAPGKGLEW VSGIDWNSANIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAEDDWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW

SEQ ID NO	Name	Sequence
		QQGNVFSCSVMHEALHNHYTQKSLSLSPG
304	P1-070922 P1-068767_E30D_E55A LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
305	P1-070924 P1-068767_E30D_E100fF VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLDDYAMH**WVRQAPGKGLEW VS**GIDWNSENIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAFDD**WGQGTMVTVSS
306	P1-070924 P1-068767_E30D_E100fF VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYL**AWYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
307	P1-070924 P1-068767_E30D_E100fF IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLDDYAMHWVRQAPGKGLEW VSGIDWNSENIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAFDDWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
308	P1-070924 P1-068767_E30D_E100fF LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
309	P1-070926 P1-068767_E30D_D102V VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLDDYAMH**WVRQAPGKGLEW VS**GIDWNSENIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAEDV**WGQGTMVTVSS
310	P1-070926 P1-068767_E30D_D102V VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
311	P1-070926 P1-068767_E30D_D102V IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLDDYAMHWVRQAPGKGLEW VSGIDWNSENIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAEDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
312	P1-070926 P1-	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS

SEQ ID NO	Name	Sequence
	068767_E30D_D102V LC	SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
313	P1-070928 P1-068767_D52N_E100fF VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDYAMH**WVRQAPGKGLEW VS**GINWNSENIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAFDD**WGQGTMVTVSS
314	P1-070928 P1-068767_D52N_E100fF VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
315	P1-070928 P1-068767_D52N_E100fF IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDYAMHWVRQAPGKGLEW VSGINWNSENIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAFDDWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
316	P1-070928 P1-068767_D52N_E100fF LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
317	P1-070930 P1-068767_D52N_D102V VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDYAMH**WVRQAPGKGLEW VS**GINWNSENIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAED**VWGQGTMVTVSS
318	P1-070930 P1-068767_D52N_D102V VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
319	P1-070930 P1-068767_D52N_D102V IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDYAMHWVRQAPGKGLEW VSGINWNSENIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAEDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
320	P1-070930 P1-068767_D52N_D102V LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO	Name	Sequence
321	P1-070932 P1-068767_E55A_D102V VH	EVQLVESGGGLVQPGKSLRLSCAAS**GFTLEDYAMH**WVRQAPGKGLEW VS**GIDWNSANIGYADSVKG**RFTISRDNAKNSLYLQMNSLRTEDTALY YCAK**VPGYSGGWIDAED**VWGQGTMVTVSS
322	P1-070932 P1-068767_E55A_D102V VL	EIVLTQSPGTLSLSPGERATLSC**RASQSVSSSYLA**WYQQKPGQAPRL LIY**GASSRAT**GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC**QQYGS SPFT**FGPGTKVDIK
323	P1-070932 P1-068767_E55A_D102V IgG1.3 HC	EVQLVESGGGLVQPGKSLRLSCAASGFTLEDYAMHWVRQAPGKGLEW VSGIDWNSANIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALY YCAKVPGYSGGWIDAEDVWGQGTMVTVSSASTKGPSVFPLAPSSKST SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL SSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC PAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPG
324	P1-070932 P1-068767_E55A_D102V LC	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRL LIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS SPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC
325	hVISTA-ECD 6-His tag	AFKVATPYSL YVCPEGQNVT LTCRLLGPVD KGHDVTFYKT WYRSSRGEVQ TCSERRPIRN LTFQDLHLHH GGHQAANTSH DLAQRHGLES ASDHHGNFSI TMRNLTLLDS GLYCCLVVEI RHHHSEHRVH GAMELQVQTG KDAPSNCVVY PSSSQESENI TAHHHHHHH
326	Cyno VISTA-ECD 6-His tag	AFKVATLYSL YVCPEGQNVT LTCRVFGPVD KGHDVTFYKT WYRSSRGEVQ TCSERRPIRN LTFQDLHLHH GGHQAANTSH DLAQRHGLES ASDHHGNFSI TMRNLTLLDS GLYCCLVVEI RHHHSEHRVH GAMELQVQTG KDAPSSCVAY PSSSQESENI TAHHHHHHH
327	P1-069059 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAAGATT ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGACCATATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTGA AGATGACTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
328	P1-069059 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
329	P1-069061 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAAGATT ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG

SEQ ID NO	Name	Sequence
		GTCTCAGGTATTAATTGGAACAGTGCTGAAATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTGA AGATGACTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
330	P1-069061 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
331	P1-069063 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAAGATT ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGCTGAAATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTGA CGATGAATGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
332	P1-069063 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
333	P1-069065 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAAGATG AAGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGACGACATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTTT TGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
334	P1-069065 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
335	P1-069067 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGATGATT ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGAAGAAATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTGA CGATGAATGGGGCCAAGGGACAATGGTCACCGTCTCTTCA

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336	P1-069067 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
337	P1-069069 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGATGATT ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGAAGAAATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTGA CGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
338	P1-069069 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
339	P1-069071 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAAGATG AAGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGCTGACATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGAAGGCTGGATTGACGCTTT TGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
340	P1-069071 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
341	P1-069073 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAAGATG AAGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGCTGAAATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTGA AGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
342	P1-069073 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC

SEQ ID NO	Name	Sequence
		TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
343	P1-069075 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAAGATT ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGGACAGTGCTGAAATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCCATGGCTGGATTGACGCTGA AGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
344	P1-069075 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
345	P1-069077 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAAGATG AAGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGACGAAATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTTT TGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
346	P1-069077 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
347	P1-068761 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATG AGGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGAAGAGATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCCATGGCTGGATTGACGCTGA AGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
348	P1-068761 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
349	P1-068767 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATT ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTGATTGGAACAGTGAAAACATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC

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		TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTGA AGATGACTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
350	P1-068767 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
351	P1-068773 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATT ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTGATTGGAACAGTGATAACATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTGA AGATGACTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
352	P1-068773 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
353	P1-068765 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCGATGAGGATT ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGAAGAGATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTGA AGATGACTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
354	P1-068765 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
355	P1-061029 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGATGATT ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGCTAACATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTTT TGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
356	P1-061029 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC

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		CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
357	P1-068757 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATG AGGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGAAGAGATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTGA AGATGACTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
358	P1-068757 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
359	P1-068771 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATG AGGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTCATGAGATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTGA AGATGACTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
360	P1-068771 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
361	P1-068775 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATG AGGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTGATTGGAACAGTGAAGAGATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCCATGGCTGGATTGACGCTGA AGATGACTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
362	P1-068775 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
363	P1-068769 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATG

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		AGGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGATCACATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTGA AGATGACTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
364	P1-068769 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
365	P1-068759 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATG AGGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTGATTGGAACAGTGAAAACATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTGA AGATGACTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
366	P1-068759 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
367	P1-068763 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATT ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTGATTGGAACAGTGAAAACATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCCATGGCTGGATTGACGCTGA AGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
368	P1-068763 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
369	P1-061015 VH DNA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAG GTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCT ATGCCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGG GTGGCAATTATATGGTATGATGGAAGTAATAAATACTATGCAGACTC CGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGC TGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTAT TACTGTGCGAGAGATAGTGGTTTTTACTCCTCGTACTACTTTGACTA CTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA

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370	P1-061015 VL DNA	GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTT CAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCC TGGAGCCTGAAGATTTTGCAACTTATTACTGCCAACAGTATAATAGT TACCCGTACACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA
371	P1-068748 VH DNA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAG GTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTCACC ATGCCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGG GTGGCAATTATATGGTATGATGGAAGTAATGACGACTATGCAGACTC CGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGC TGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTAT TACTGTGCGAGAGATAGTGGTTTTTACGACTCGTACTACTTTGACTA CTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
372	P1-068748 VL DNA	GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTT CAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCC TGGAGCCTGAAGATTTTGCAACTTATTACTGCCAACAGTATAATAGT TACCCGTACACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA
373	P1-068744 VH DNA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAG GTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTGAGT ATGCCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGG GTGGCACATATATGGTATGATGGAAGTAATAAATACGAGGCAGACTC CGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGC TGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTAT TACTGTGCGAGAGATAGTGGTTTTTACGAATCGTACTACTTTGACGA GTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
374	P1-068744 VL DNA	GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTT CAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCC TGGAGCCTGAAGATTTTGCAACTTATTACTGCCAACAGTATAATAGT TACCCGTACACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA
375	P1-068736 VH DNA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAG GTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTGAGT ATGCCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGG GTGGCAATTGATTGGTATGATGGAAGTAATAAAGACTATGCAGACTC CGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGC TGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTAT TACTGTGCGAGAGATAGTGGTTTTTTACGACTCGTACTACTTTGACGA CTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
376	P1-068736 VL DNA	GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTT CAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCC TGGAGCCTGAAGATTTTGCAACTTATTACTGCCAACAGTATAATAGT

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		TACCCGTACACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA
377	P1-068752 VH DNA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAG GTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCT ATGCCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGG GTGGCAGAGATATGGTATGATGGAAGTAATAAAGACTATGCAGACTC CGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGC TGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTAT TACTGTGCGAGAGATAGTGGTTTTTACGACTCGTACTACTTTGACGA GTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
378	P1-068752 VL DNA	GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTT CAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCC TGGAGCCTGAAGATTTTGCAACTTATTACTGCCAACAGTATAATAGT TACCCGTACACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA
379	P1-068740 VH DNA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAG GTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTGACT ATGCCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGG GTGGCAATTATATGGTATGATGGAAGTGATAAAGACTATGCAGACTC CGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGC TGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTAT TACTGTGCGAGAGATAGTGGTTTTTACGACTCGTACTACTTTGACGA CTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
380	P1-068740 VL DNA	GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTT CAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCC TGGAGCCTGAAGATTTTGCAACTTATTACTGCCAACAGTATAATAGT TACCCGTACACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA
381	P1-068742 VH DNA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAG GTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTGACT ATGCCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGG GTGGCAATTATATGGTATGATGGAAGTGATAAAGACTATGCAGACTC CGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGC TGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTAT TACTGTGCGAGAGATAGTGGTTTTTACGAAGATTACTACTTTGACTA CTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
382	P1-068742 VL DNA	GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTT CAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCC TGGAGCCTGAAGATTTTGCAACTTATTACTGCCAACAGTATAATAGT TACCCGTACACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA
383	P1-068746 VH DNA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAG GTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCT ATGCCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGG GTGGCAATTATATGGTATGATGGAAGTAATCACCACTATGCAGACTC CGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGC

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		TGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTAT TACTGTGCGAGAGATAGTGGTTTTTACGACTCGTACTACTTTGACTA CTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
384	P1-068746 VL DNA	GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTT CAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCC TGGAGCCTGAAGATTTTGCAACTTATTACTGCCAACAGTATAATAGT TACCCGTACACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA
385	P1-068750 VH DNA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAG GTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTGACT ATGACATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGG GTGGCAGAGATATGGGATGATGGAAGTAATAAATACTATGCAGACTC CGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGC TGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTAT TACTGTGCGAGAGATGAGGAATTTTACTCCTCGTACTACTTTGACTA CTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
386	P1-068750 VL DNA	GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTT CAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCC TGGAGCCTGAAGATTTTGCAACTTATTACTGCCAACAGTATAATAGT TACCCGTACACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA
387	P1-068738 VH DNA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAG GTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTGAGT ATGCCCATCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGG GTGGCAATTATATGGGATGATGGAAGTAATCACTACTATGCAGACTC CGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGC TGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTAT TACTGTGCGAGAGATAGTGGTTTTTACGAAGATTACTACTTTGACTA CTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
388	P1-068738 VL DNA	GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTT CAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCC TGGAGCCTGAAGATTTTGCAACTTATTACTGCCAACAGTATAATAGT TACCCGTACACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA
389	P1-068754 VH DNA	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAG GTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCTTCAGTGACT ATGACATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGG GTGGCAGAGATATGGGATGATGGAAGTAATAAATACTATGCAGACTC CGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGC TGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTAT TACTGTGCGAGAGATAGTGGTTTTCACTCCGATTACTACTTTGACTA CTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
390	P1-068754 VL DNA	GAAATTGTGTTGACACAGTCTCCAGCCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCTC

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		CTCATCTATGATGCATCCAACAGGGCCACTGGCATCCCAGCCAGGTT CAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCC TGGAGCCTGAAGATTTTGCAACTTATTACTGCCAACAGTATAATAGT TACCCGTACACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA
391	P1-070864 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGATGATG AGGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGAAGAGATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCCATGGCTGGATTGACGCTGA AGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
392	P1-070864 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
393	P1-070866 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATT ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGAAGAGATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCCATGGCTGGATTGACGCTGA AGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
394	P1-070866 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
395	P1-070868 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATG AGGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGCTGAGATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCCATGGCTGGATTGACGCTGA AGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
396	P1-070868 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
397	P1-070870 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATG

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		AGGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGAAAACATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCCATGGCTGGATTGACGCTGA AGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
398	P1-070870 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
399	P1-070872 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATG AGGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGAAGAGATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTGA AGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
400	P1-070872 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
401	P1-070874 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATG AGGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGAAGAGATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCCATGGCTGGATTGACGCTTT TGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
402	P1-070874 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
403	P1-070876 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGATGATT ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGAAGAGATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCCATGGCTGGATTGACGCTGA AGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA

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404	P1-070876 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
405	P1-070878 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATG AGGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGCTAACATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCCATGGCTGGATTGACGCTGA AGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
406	P1-070878 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
407	P1-070880 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATG AGGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGAAGAGATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTTT TGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
408	P1-070880 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
409	P1-070882 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATT ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGCTGAGATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCCATGGCTGGATTGACGCTGA AGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
410	P1-070882 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC

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		TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
411	P1-070884 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATT ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGAAAACATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCCATGGCTGGATTGACGCTGA AGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
412	P1-070884 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
413	P1-070886 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATT ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGAAGAGATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTGA AGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
414	P1-070886 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
415	P1-070888 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATT ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGAAGAGATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCCATGGCTGGATTGACGCTTT TGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
416	P1-070888 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
417	P1-070890 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGATGATG AGGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGCTGAGATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC

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		TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCCATGGCTGGATTGACGCTGA AGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
418	P1-070890 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
419	P1-070892 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGATGATG AGGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGAAAACATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCCATGGCTGGATTGACGCTGA AGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
420	P1-070892 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
421	P1-070894 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGATGATG AGGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGAAGAGATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTGA AGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
422	P1-070894 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
423	P1-070896 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGATGATG AGGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGAAGAGATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCCATGGCTGGATTGACGCTTT TGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
424	P1-070896 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC

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		CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
425	P1-070898 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATG AGGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGCTGAGATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCCATGGCTGGATTGACGCTTT TGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
426	P1-070898 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
427	P1-070900 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATG AGGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGAAAACATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTGA AGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
428	P1-070900 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
429	P1-070902 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATG AGGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGAAAACATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCCATGGCTGGATTGACGCTTT TGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
430	P1-070902 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
431	P1-070904 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGATGATT

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		ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTGATTGGAACAGTGAAAACATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTGA AGATGACTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
432	P1-070904 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
433	P1-070906 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATT ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGAAAACATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTGA AGATGACTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
434	P1-070906 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
435	P1-070908 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATT ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTGATTGGAACAGTGCTAACATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTGA AGATGACTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
436	P1-070908 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
437	P1-070910 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATT ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTGATTGGAACAGTGAAAACATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTTT TGATGACTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA

SEQ ID NO	Name	Sequence
438	P1-070910 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
439	P1-070912 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATT ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTGATTGGAACAGTGAAAACATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTGA AGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
440	P1-070912 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
441	P1-070914 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGATGATT ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGAAAACATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTGA AGATGACTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
442	P1-070914 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
443	P1-070916 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATT ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGCTAACATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTGA AGATGACTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
444	P1-070916 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC

SEQ ID NO	Name	Sequence
		TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
445	P1-070918 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATT ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTGATTGGAACAGTGCTAACATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTTT TGATGACTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
446	P1-070918 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
447	P1-070920 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATT ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTGATTGGAACAGTGAAAACATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTTT TGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
448	P1-070920 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
449	P1-070922 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGATGATT ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTGATTGGAACAGTGCTAACATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTGA AGATGACTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
450	P1-070922 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
451	P1-070924 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGATGATT ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTGATTGGAACAGTGAAAACATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC

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		TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTTT TGATGACTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
452	P1-070924 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
453	P1-070926 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGATGATT ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTGATTGGAACAGTGAAAACATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTGA AGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
454	P1-070926 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
455	P1-070928 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATT ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGAAAACATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTTT TGATGACTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
456	P1-070928 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
457	P1-070930 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATT ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTAATTGGAACAGTGAAAACATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTGA AGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
458	P1-070930 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC

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		CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
459	P1-070932 VH DNA	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAA GTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCCTTGAGGATT ATGCCATGCACTGGGTCCGGCAAGCTCCAGGGAAGGGCCTGGAGTGG GTCTCAGGTATTGATTGGAACAGTGCTAACATAGGCTATGCGGACTC TGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCCC TGTATCTGCAAATGAACAGTCTGAGAACTGAGGACACGGCCTTGTAT TACTGTGCAAAAGTTCCTGGGTATAGCGGTGGCTGGATTGACGCTGA AGATGTCTGGGGCCAAGGGACAATGGTCACCGTCTCTTCA
460	P1-070932 VL DNA	GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGG GGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCA GCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTC CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTT CAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGAC TGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGC TCACCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAA
461	IgG1.3 heavy chain constant region DNA	GCGTCGACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAA GAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACT ACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACC AGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTA CTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCC AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG GACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCC ACCGTGCCCAGCACCTGAAGCCGAAGGGGCCCCGTCAGTCTTCCTCT TCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAG GTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAA AGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC CTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTG CAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCT CCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCC CCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCT GGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCA ATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGAC TCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGCGTCGAC CAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCT CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGT GCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCA GCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAG AGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCC CAGCACCTGAAGCCGAAGGGGCCCCGTCAGTCTTCCTCTTCCCCCCA AAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATG CGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACT GGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGG GAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGT CCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCT

SEQ ID NO	Name	Sequence
		CCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCG GGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAG GCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG CCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGG CTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGC AGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC AACCACTACACGCAGAAGAGCCTCTCCCTGTCCCCGGGTTGA
462	Exemplary light chain constant region DNA	CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGA GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACT TCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTC CAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGA CAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACT ACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTG AGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG

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THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. An antibody that binds specifically to human V-domain lg Suppressor of T cell Activation (hVISTA), wherein the antibody comprises

(i) a light chain variable region (VL) comprising VL CDR1, CDR2, and CDR3 comprising positions 24-35, 51-57, and 90-98 of SEQ ID NO: 68 and a heavy chain variable region (VH) comprising VH CDR 1, CDR2 and CDR3 comprising

positions 26-35, 50-66, and 99-112 of SEQ ID NO: 55,
positions 26-35, 50-66, and 99-112 of SEQ ID NO: 51,
positions 26-35, 50-66 and 99-112 of SEQ ID NO: 15,
positions 26-35, 50-66, and 99-112 of SEQ ID NO: 11,
positions 26-35, 50-66, and 99-112 of SEQ ID NO: 59,
positions 26-35, 50-66, and 99-112 of SEQ ID NO: 39,
positions 26-35, 50-66, and 99-112 of SEQ ID NO: 63,
positions 26-35, 50-66, and 99-112 of SEQ ID NO: 71,
positions 26-35, 50-66, and 99-112 of SEQ ID NO: 75,
positions 26-35, 50-66, and 99-112 of SEO ID NO: 83,
positions 26-35, 50-66, and 99-112 of SEO ID NO: 79,
positions 26-35, 50-66, and 99-112 of SEO ID NO: 87,
positions 26-35, 50-66, and 99-112 of SEO ID NO: 193,
positions 26-35, 50-66, and 99-112 of SEO ID NO: 201,
positions 26-35, 50-66, and 99-112 of SEO ID NO: 197,
positions 26-35, 50-66, and 99-112 of SEO ID NO: 213,
positions 26-35, 50-66, and 99-112 of SEO ID NO: 185,
positions 26-35, 50-66, and 99-112 of SEO ID NO: 237,
positions 26-35, 50-66, and 99-112 of SEO ID NO: 257,
positions 26-35, 50-66, and 99-112 of SEO ID NO: 245,
positions 26-35, 50-66, and 99-112 of SEO ID NO: 241,
positions 26-35, 50-66, and 99-112 of SEO ID NO: 269,

positions 26-35, 50-66, and 99-112 of SEO ID NO: 289,
positions 26-35, 50-66, and 99-112 of SEO ID NO: 273,
positions 26-35, 50-66, and 99-112 of SEO ID NO: 285,
positions 26-35, 50-66, and 99-112 of SEO ID NO: 265,
positions 26-35, 50-66, and 99-112 of SEO ID NO: 301,
positions 26-35, 50-66, and 99-112 of SEO ID NO: 293,
positions 26-35, 50-66, and 99-112 of SEO ID NO: 313,
positions 26-35, 50-66, and 99-112 of SEO ID NO: 277, or
positions 26-35, 50-66, and 99-112 of SEO ID NO: 305,
or wherein the antibody comprises

(ii) a VL comprising VL CDR1, CDR2, and CDR3 comprising positions 24-35, 51-57, and 90-98 of SEQ ID NO: 96 and a VH comprising VH CDR 1, CDR2 and CDR3 comprising

positions 26-35, 50-66, and 99-110 of SEO ID NO: 99,
positions 26-35, 50-66, and 99-110 of SEO ID NO: 103,
positions 26-35, 50-66, and 99-110 of SEO ID NO: 107, or
positions 26-35, 50-66, and 99-110 of SEO ID NO: 111.

2. The antibody of claim 1, wherein the antibody comprises a VH comprising an amino acid sequence that is at least 90% identical to that of SEQ ID NO: 55, 51, 15, 11, 59, 39, 63, 71, 75, 83, 79, 87, 193, 201, 197, 213, 185, 237, 257, 245, 241, 269, 289, 273, 285, 265, 301, 293, 313, 277, 305, 99, 103, 107, or 111.

3. The antibody of claim 1 or 2, wherein the antibody comprises a VH comprising the amino acid sequence of SEQ ID NO: 55, 51, 15, 11, 59, 39, 63, 71, 75, 83, 79, 87, 193, 201, 197, 213, 185, 237, 257, 245, 241, 269, 289, 273, 285, 265, 301, 293, 313, 277, 305, 99, 103, 107, or 111.

4. The antibody of claim 1 or 2, wherein the antibody comprises a VH comprising the amino acid sequence that is at least 90% identical to that of SEQ ID NO: 55, 51, 15, 11, 59, 39, 63, 71, 75, 83, 79, 87, 193, 201, 197, 213, 185, 237, 257, 245, 241, 269,

289, 273, 285, 265, 301, 293, 313, 277, or 305; and wherein the antibody comprises a VL comprising a VL CDR1, CDR2, and CDR3 comprising positions 24-35, 51-57, and 90-98 of SEQ ID NO: 68.

5. The antibody of any one of claims 1-3, wherein the antibody comprises a VH comprising the amino acid sequence of SEQ ID NO: 55, 51, 15, 11, 59, 39, 63, 71, 75, 83, 79, 87, 193, 201, 197, 213, 185, 237, 257, 245, 241, 269, 289, 273, 285, 265, 301, 293, 313, 277, or 305; and wherein the antibody comprises a VL comprising a VL CDR1, CDR2, and CDR3 comprising positions 24-35, 51-57, and 90-98 of SEQ ID NO: 68.

6. The antibody of claim 1 or 2, wherein the antibody comprises a VH comprising an amino acid sequence that is at least 90% identical to that of SEQ ID NO 99, 103, 107, or 111; and wherein the antibody comprises a VL comprising a VL CDR1, CDR2, and CDR3 comprising positions 24-35, 51-57, and 90-98 of SEQ ID NO: 96.

7. The antibody of any one of claims 1-3, wherein the antibody comprises a VH comprising the amino acid sequence of SEQ ID NO: 99, 103, 107, or 111; and wherein the antibody comprises a VL comprising a VL CDR1, CDR2, and CDR3 comprising positions 24-35, 51-57, and 90-98 of SEQ ID NO: 96.

8. The antibody of any one of claims 1-7, wherein the antibody comprises a VL comprising an amino acid sequence that is at least 90% identical to that of SEQ ID NO: 68 or 96.

9. The antibody of any one of claims 1-8, wherein the antibody comprises a VL comprising the amino acid sequence of SEQ ID NO: 68 or 96.

10. The antibody of any one of claims 1-9, wherein the antibody binds to hVISTA in neutral or physiological conditions with a KD of 10-5 M or more, wherein neutral conditions are conditions having a pH of 7 .0, and wherein physiological conditions are conditions having a pH of 7.4; and/or wherein the antibody binds to hVISTA in

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acidic conditions with a K_D of 10^{-7} M or less, wherein acidic conditions are conditions having a pH of 6.0 to 6.5.

11. The antibody of any one of claims 1-10, wherein the antibody has one or more of the following properties:

a. binds to hVISTA in acidic conditions with a K_D that is at least 10 fold lower than its K_D in neutral or physiological conditions, wherein acidic conditions are conditions having a pH of 6.0 to 6.5, wherein neutral conditions are conditions having a pH of 7 .0, and wherein physiological conditions are conditions having a pH of 7.4;

b. binds to hVISTA in acidic conditions with a k_{off} that is at least 5 fold lower than its k_{off} in neutral or physiological conditions, wherein acidic conditions are conditions having a pH of 6.0 to 6.5, wherein neutral conditions are conditions having a pH of 7 .0, and wherein physiological conditions are conditions having a pH of 7.4;

c. inhibits the binding of hVISTA to human T cells in conditions having a pH of less than pH 7.0;

d. inhibits the binding of hVISTA to huPSGL-1 in conditions having a pH of less than pH 7.0;

e. inhibits the binding of hVISTA to heparan sulfate proteoglycans;

f. inhibits the binding of hVISTA to heparan sulfate proteoglycans in conditions having a pH of less than pH 7.0;

g. stimulates T cell activation in conditions having a pH of less than pH 7.0;

h. reduces VISTA mediated cell-cell adhesion;

i. has a mean residence time of at least 500 hours in Cynomolgus macaques;

j. does not significantly bind to VISTA positive cells in the peripheral blood of a subject to whom it is administered; and

k. does not significantly deplete VISTA positive cells in peripheral blood of a subject to whom it is administered.

12. The antibody of any one of claims 1-11, wherein the antibody has one or more of the following properties:

a. binds at or near the histidine rich region of hVISTA in conditions having a pH of 6.0-6.5;

b. does not bind significantly to hVISTA, in which one or more of the following amino acid residues have been mutated: T35, Y37, K38, T39, Y41, R54, T61, F62, Q63, L65, H66, L67, H68, H69, F97, L115, V117, I119, H121, H122, S124, E125, R127; and

c. has an isoelectric point (pI) between 6.5 and 6.8, as measured by icIEF.

13. The antibody of any one of claims 1-5, which is an IgG1, IgG2 or IgG4 antibody, optionally wherein the IgG4 antibody has an S228P substitution.

14. The antibody of any one of claims 1-13, wherein:

a. the antibody is an effectorless antibody, optionally wherein the effectorless antibody comprises a heavy chain constant region comprising 1-5 mutations that reduce effector function of the antibody;

b. wherein the heavy chain constant region of the antibody is an IgG1.3, an IgG1.1 or an IgG1 with a P238K substitution; or

c. wherein the antibody has effector function.

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15. The antibody of claim 1-13, wherein the antibody has effector function and is afucosylated; and/or wherein the antibody has effector function and comprises a heavy chain constant region comprising 1-5 mutations that enhance effector function of the antibody.

16. The antibody of any one of claims 1- 15, which is a full length antibody.

17. The antibody of any one of claims 1-12, which is an antigen binding fragment of the antibody.

18. The antibody of any one of claims 1-17, which is one of more of the following:

a. a multimeric antibody;

b. linked to another molecule, optionally wherein said another molecule is a label or a peptide, and

c an antibody drug conjugate (ADC).

19. A nucleic acid encoding an antibody of any one of claims 1-18.

20. A composition comprising the nucleic acid of claim 19.

21. A cell comprising the nucleic acid of claim 19, or the composition of claim 20.

22. A method of preparing an antibody, comprising culturing the cell of claim 21 in conditions under which the antibody is expressed.

23. A composition comprising an antibody of any one of claims 1-18, the nucleic acid of claim 19, composition of claim 19 or cell of claim 21 and a pharmaceutically acceptable carrier.

24. Use of an antibody of any one of claims 1-18 in the preparation of a medicament for treating a subject having cancer.

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25. The use of claim 24, wherein the subject has VISTA positive cells in a tumor of the cancer, such as VISTA positive infiltrating lymphocytic (e.g. T cells) or myelomonocytic cells; and/or wherein the subject is first tested for the presence of VISTA positive cells in a tumor.

26. Use of an antibody of any one of claims 1-18 in the preparation of a medicament for treating an infectious disease (e.g., viral disease) in a subject.

27. A method of treating cancer in a subject in need thereof, comprising administering an antibody of any one of claims 1-18 to the subject.

28. The method of claim 27, wherein the subject has VISTA positive cells in a tumor of the cancer, such as VISTA positive infiltrating lymphocytic (e.g. T cells) or myelomonocytic cells; and/or wherein the subject is first tested for the presence of VISTA positive cells in a tumor.

29. A method of treating an infectious disease (e.g., viral disease) in a subject in need thereof, comprising administering an antibody of any one of claims 1-18 to the subject.

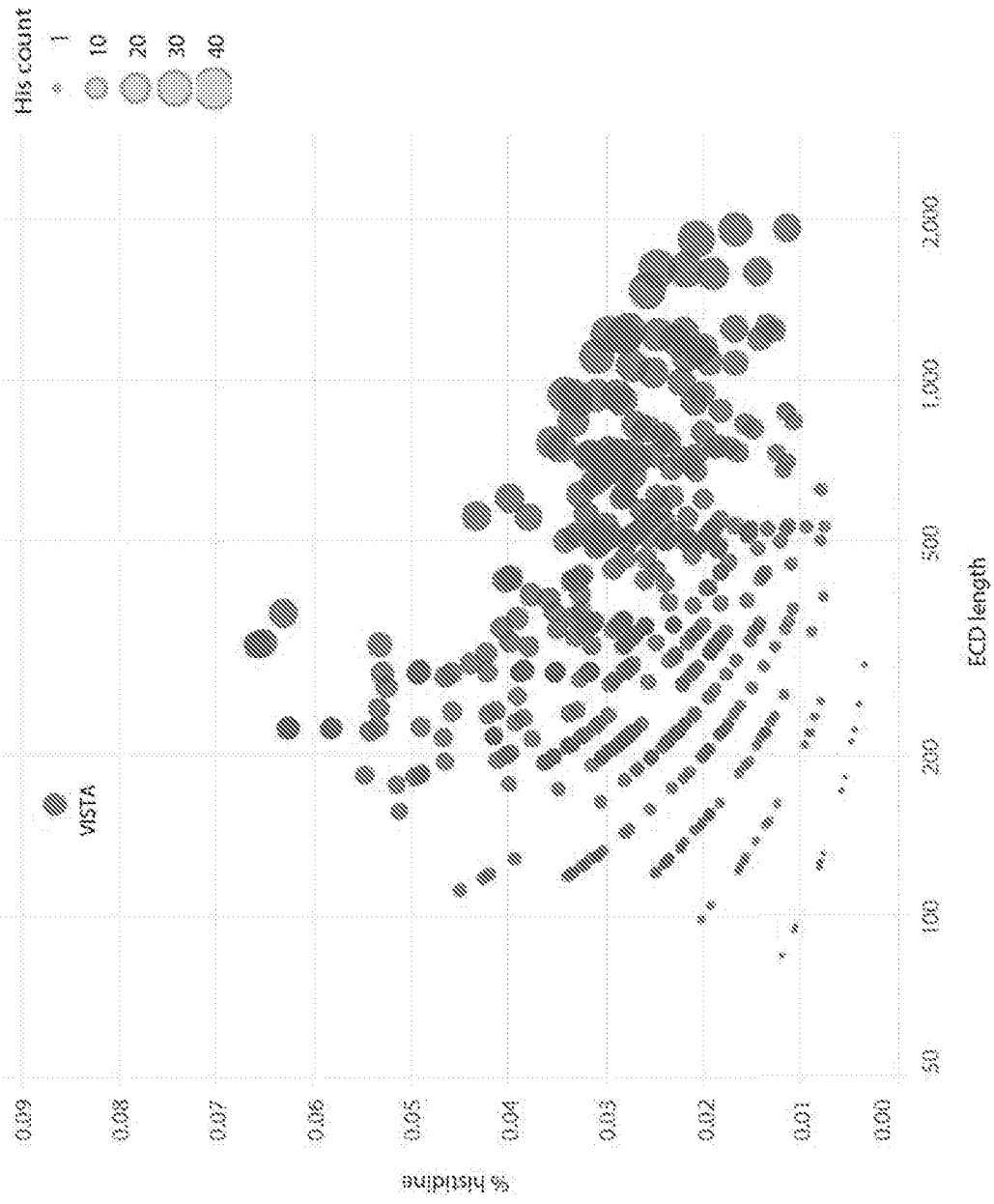

His count
1
10
20
30
40
VISTA
% histidine
0.09
0.08
0.07
0.06
0.05
0.04
0.03
0.02
0.01
0.00
50
100
200
500
1,000
2,000
ECD length

FIG. 1A

Hu/Cy/Ms conserved histidines (bold, underlined)
Hu/Cy-conserved histidines (bold)

Human NP_071436.1 Sig- FKVATPYSLYVCPEGQNVTLTCRLLGPVDKG**H**DVTFYKTWYR
Cyno XP_005565644.1 Sig- FKVATLYSLYVCPEGQNVTLTCRVFGPVDKG**H**DVTFYKTWYR
Mouse NP_083008.1 Sig- FKVTTPYSLYVCPEGQNATLTCRILGPVSKG**H**DVTIYKTWYL

Human NP_071436.1 SSRGEVQTCSERRPIRNLTFQDL**H**L**HH**GG**H**QAANTS**H**DLAQR**H**GLES
Cyno XP_005565644.1 SSRGEVQTCSERRPIRNLTFQDL**H**L**HH**GG**H**QAANTS**H**DLAQR**H**GLES
Mouse NP_083008.1 SSRGEVQMCKEHRPIRNFTLQHLQ-**HH**GS**H**LKANAS**H**DQPQK**H**GLEL

Human NP_071436.1 ASD**HH**GNFSITMRNLTLLDSGLYCCLVVEIR**HHH**SE**H**RV**H**GAMELQV
Cyno XP_005565644.1 ASD**HH**GNFSITMRNLTLLDSGLYCCLVVEIR**HHH**SE**H**RV**H**GAMELQV
Mouse NP_083008.1 ASD**HH**GNFSITLRNVTPRDSGLYCCLVIELKN**HH**PEQRFYGSMELQV

Human NP_071436.1 QTGKDAPSNCVVYPSSSQDSENITAA -TMD
Cyno XP_005565644.1 QTGKDAPSSCVAYPSSSQESENITAA -TMD
Mouse NP_083008.1 QAGKGSGSTCMA--SNEQDSDSITAA -TMD

FIG. 1B

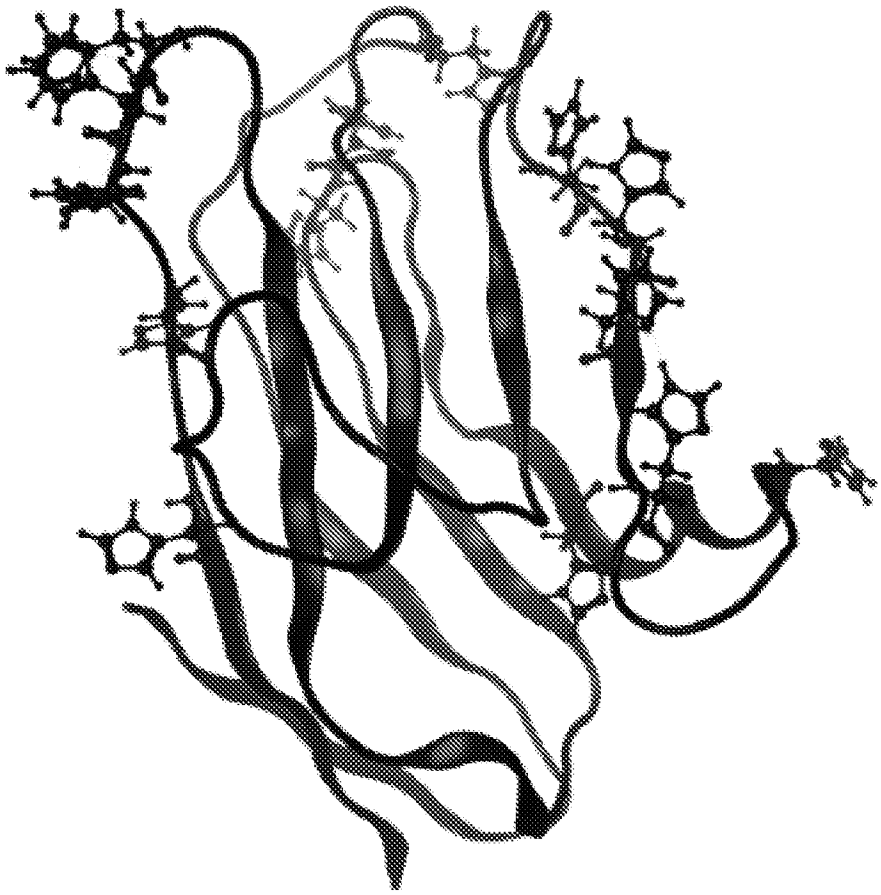


FIG. 1C

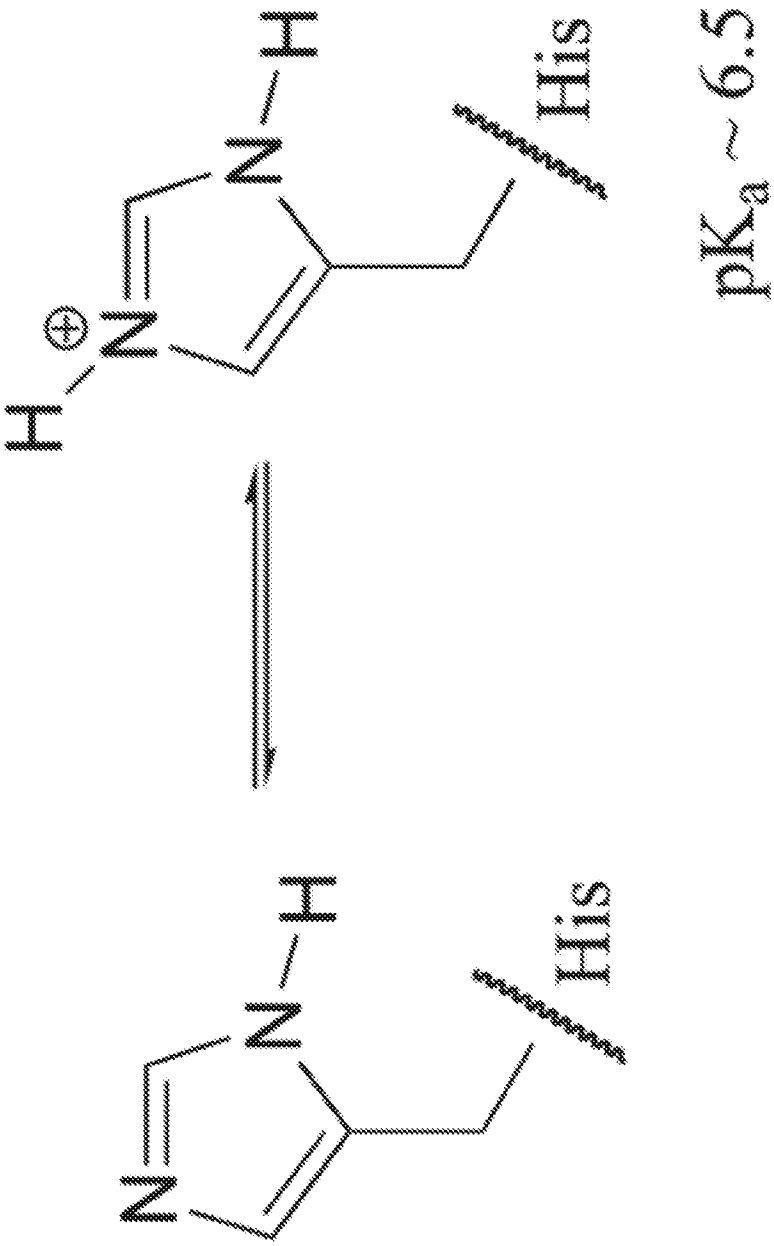


FIG. 2A

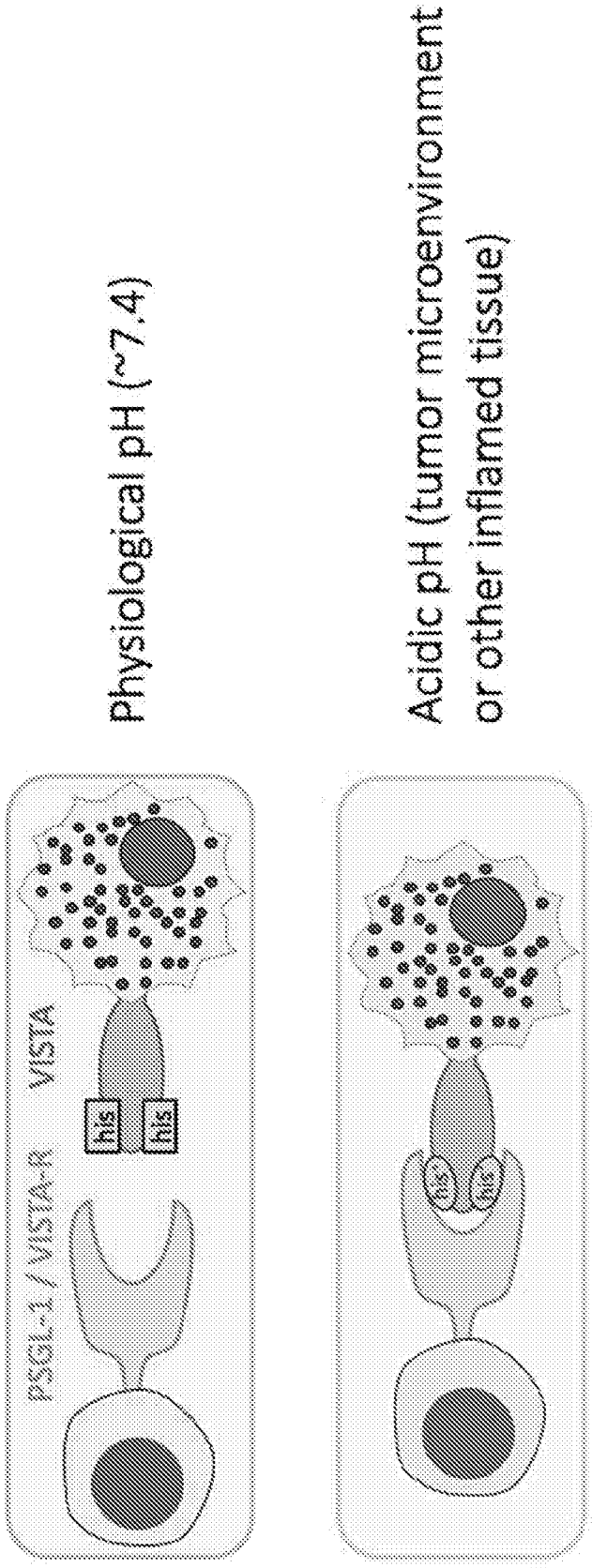

Physiological pH (~7.4)
Acidic pH (tumor microenvironment or other inflamed tissue)
PSGL-1 / VISTA-R
VISTA
his
his
his
his

FIG. 2B

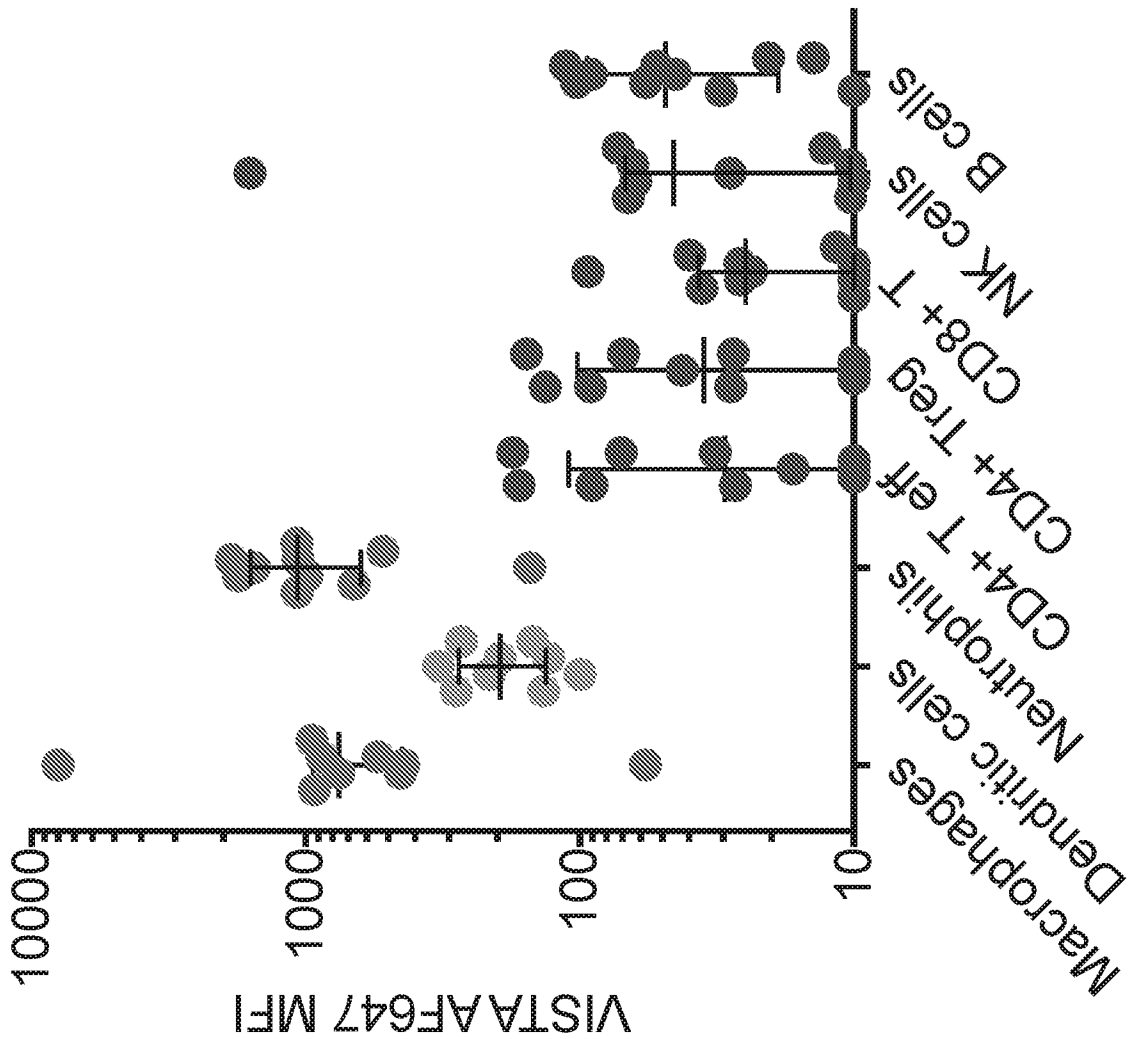

VISTA AF647 MFI
10000
1000
100
10
Macrophages
Dendritic cells
Neutrophils
CD4+ T eff
CD4+ Treg
CD8+ T
NK cells
B cells

FIG. 3

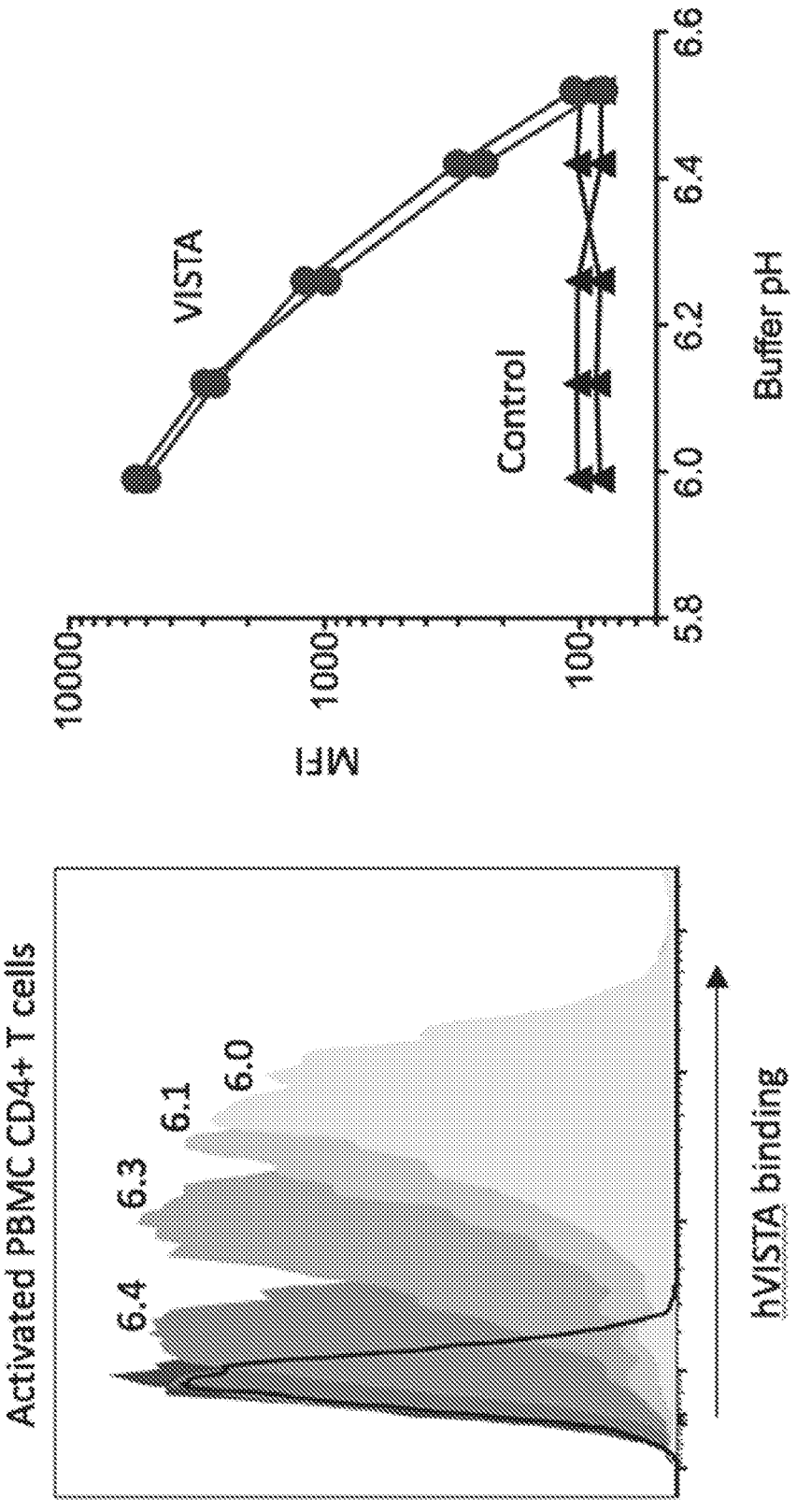

Activated PBMC CD4+ T cells
6.4
6.3
6.1
6.0
hVISTA binding
MFI
10000
1000
100
VISTA
Control
5.8
6.0
6.2
6.4
6.6
Buffer pH

FIG. 4A

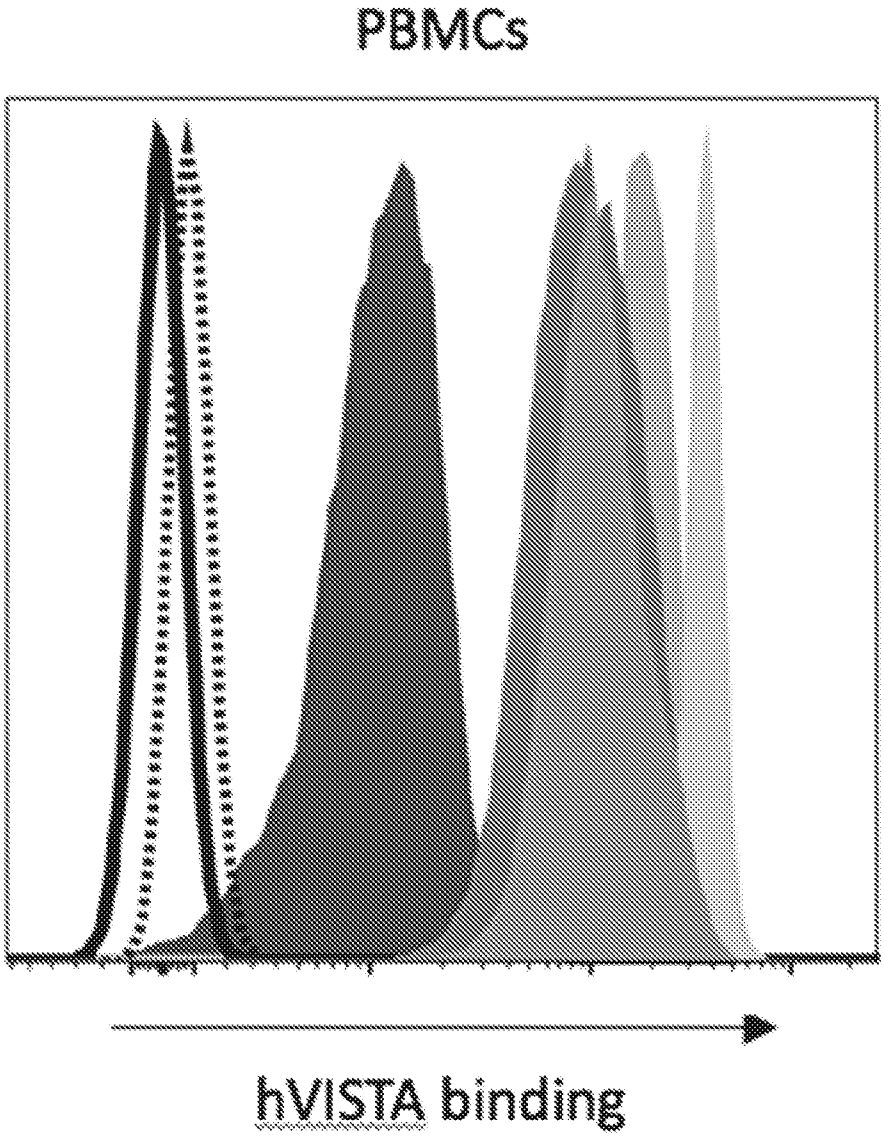


FIG. 4B

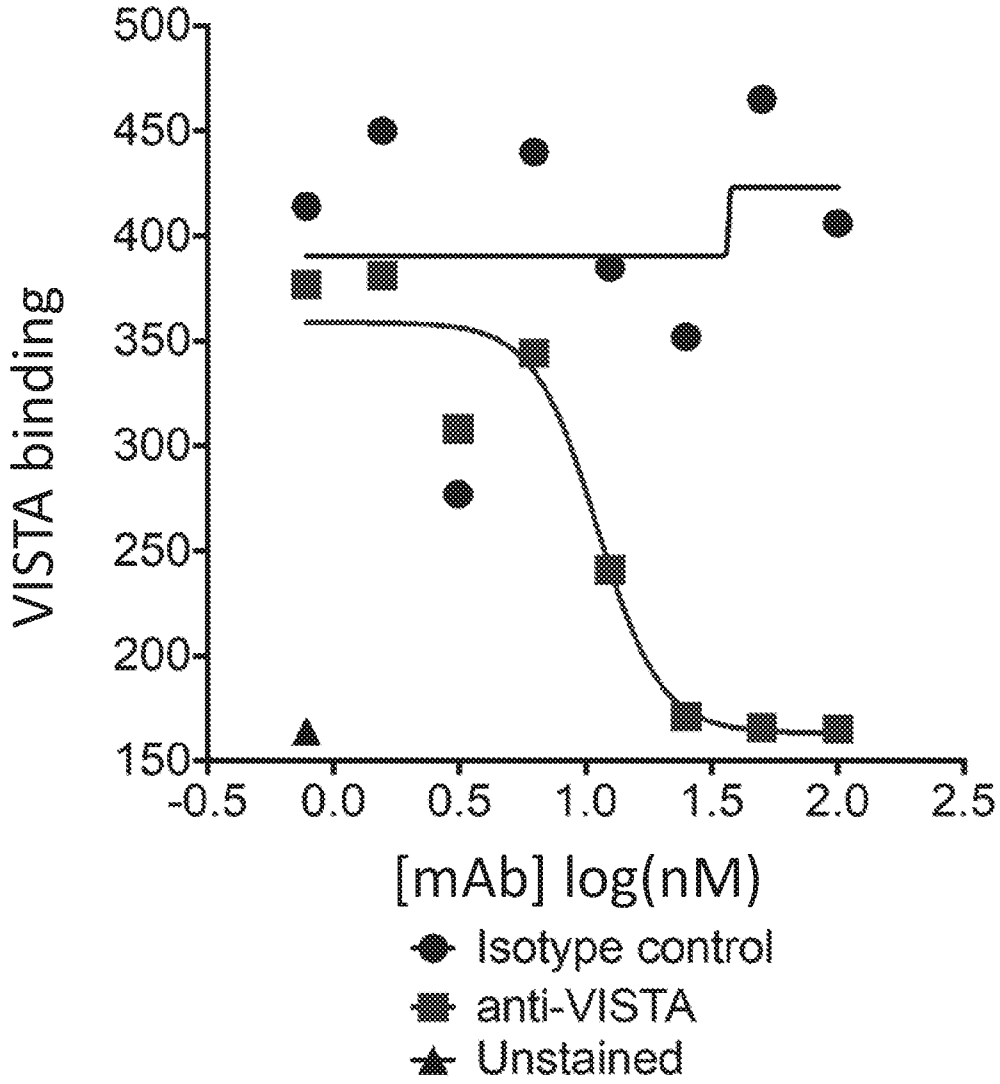

VISTA binding
500
450
400
350
300
250
200
150
-0.5
0.0
0.5
1.0
1.5
2.0
2.5
[mAb] log(nM)
Isotype control
anti-VISTA
Unstained

FIG. 4C

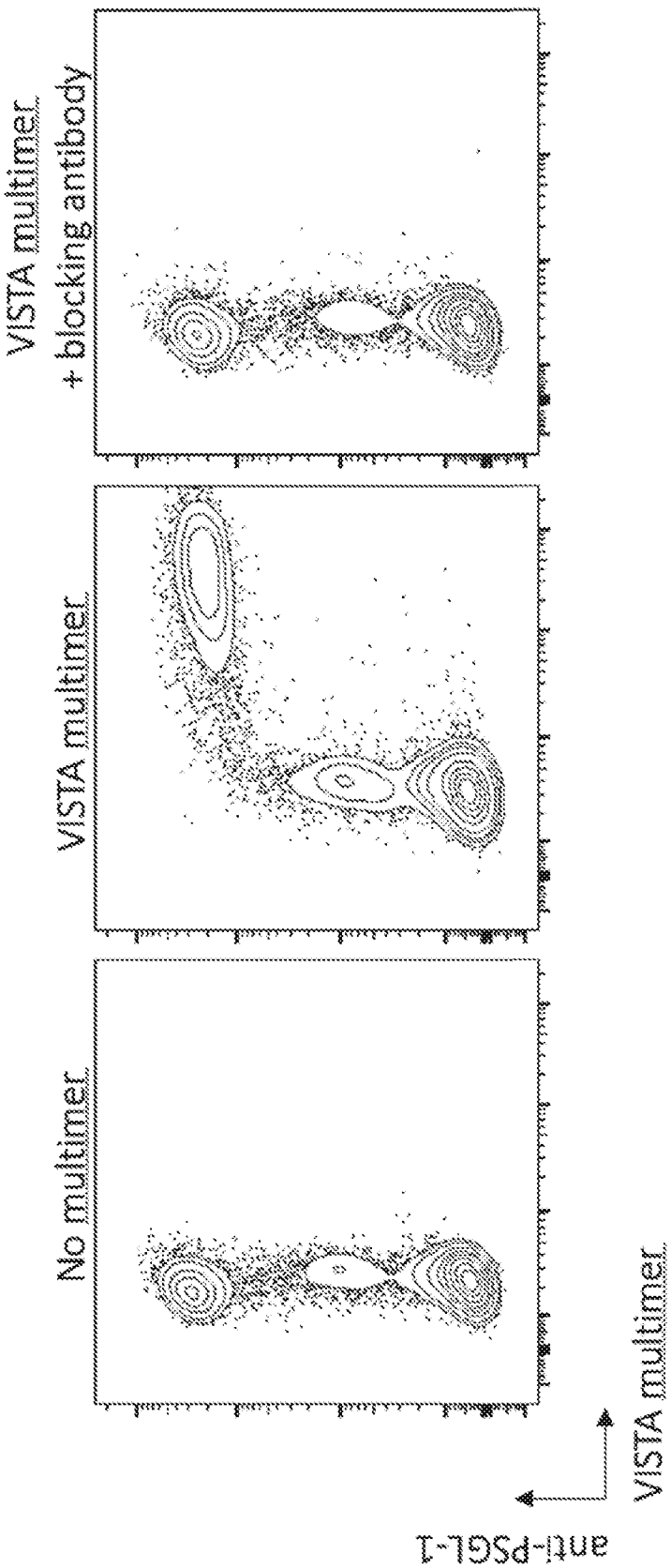

No multimer
VISTA multimer
VISTA multimer
+ blocking antibody
anti-PSGL-1
VISTA multimer

FIG. 4D

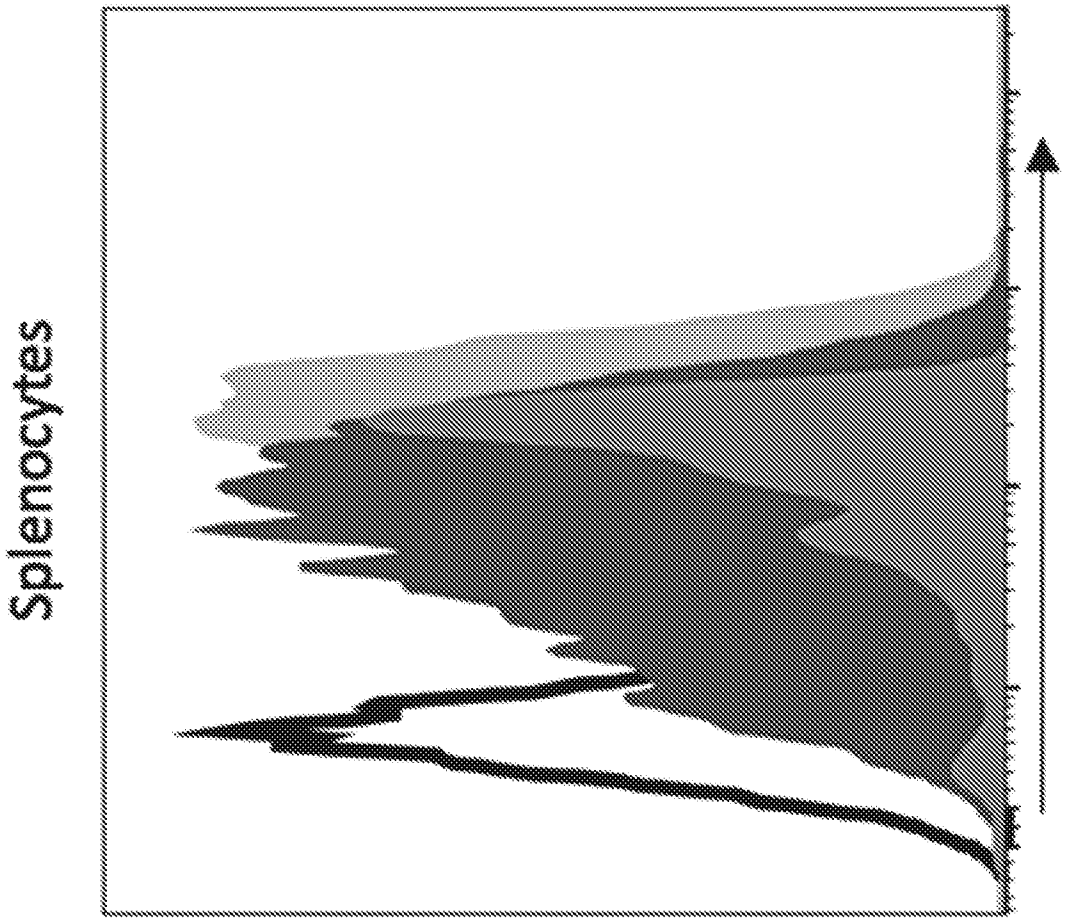


FIG. 4E

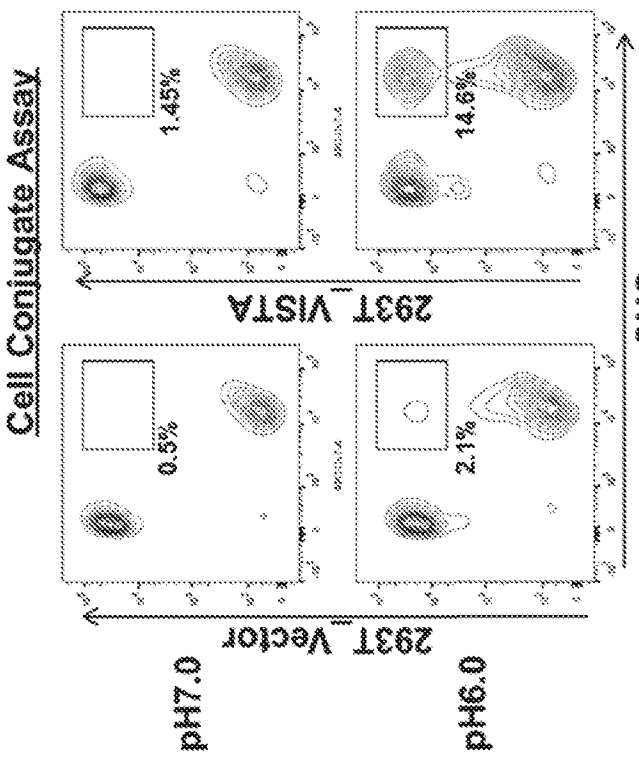

Cell Conjugate Assay
pH7.0
pH6.0
293T_Vector
293T_VISTA
CHO
0.5%
1.45%
2.1%
14.6%

FIG. 5A

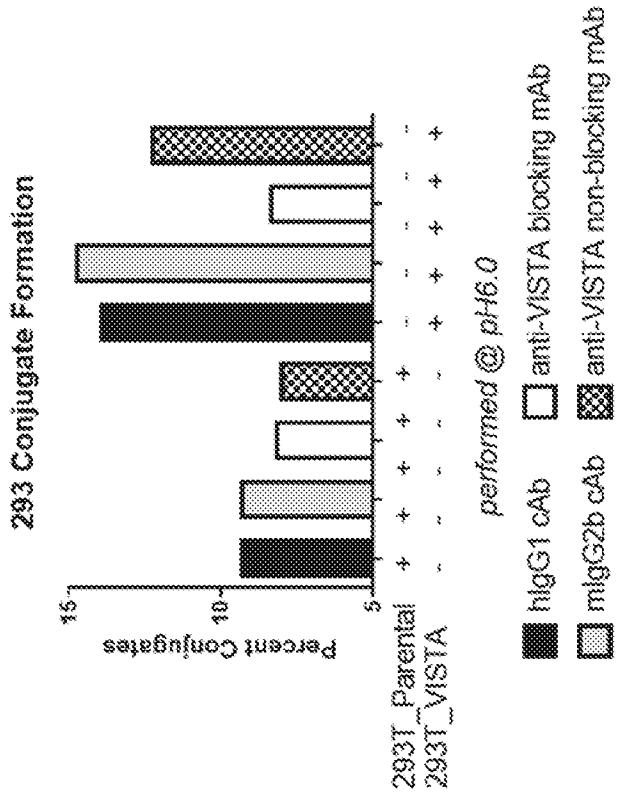

293 Conjugate Formation
Percent Conjugates
15
10
5
293T_Parental
293T_VISTA
performed @ pH6.0
hIgG1 cAb
mIgG2b cAb
anti-VISTA blocking mAb
anti-VISTA non-blocking mAb

FIG. 5B

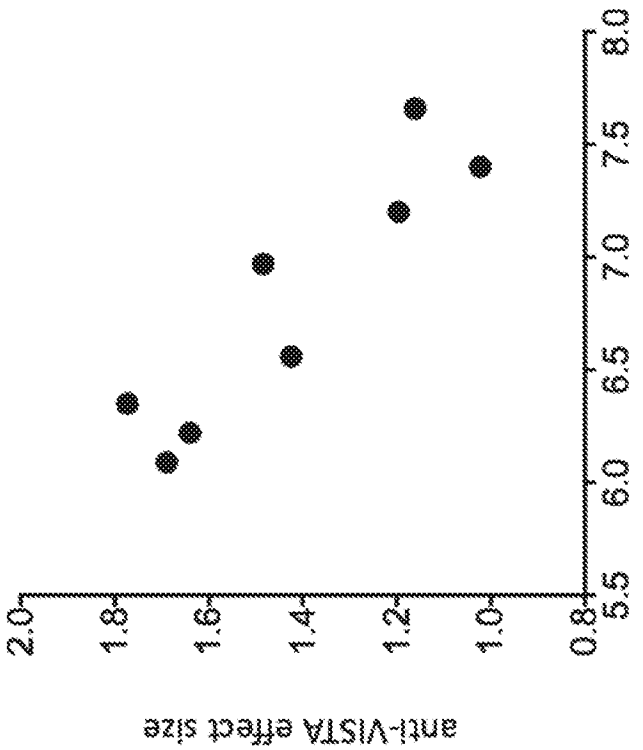

anti-VISTA effect size
2.0
1.8
1.6
1.4
1.2
1.0
0.8
5.5
6.0
6.5
7.0
7.5
8.0
Buffer pH

FIG. 5D

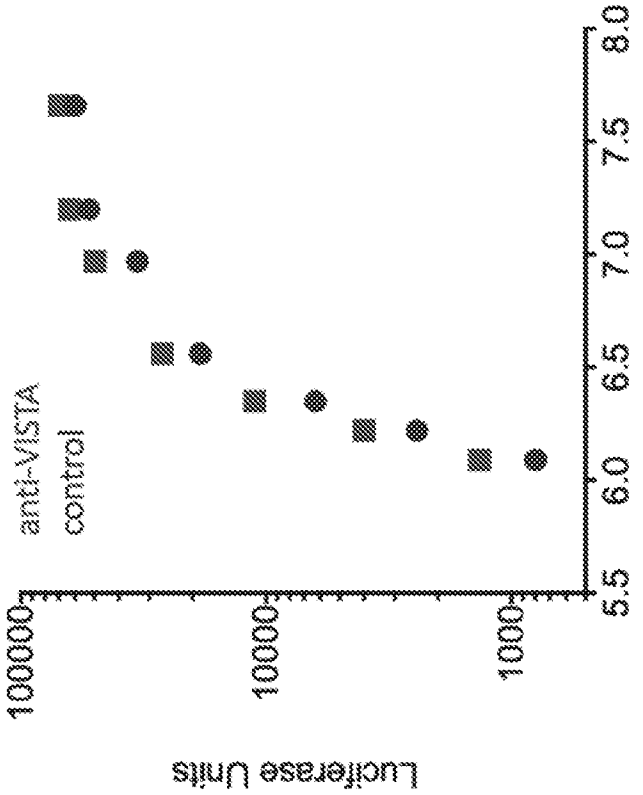

Luciferase Units
100000
10000
1000
anti-VISTA
control
5.5
6.0
6.5
7.0
7.5
8.0
Buffer pH

FIG. 5C

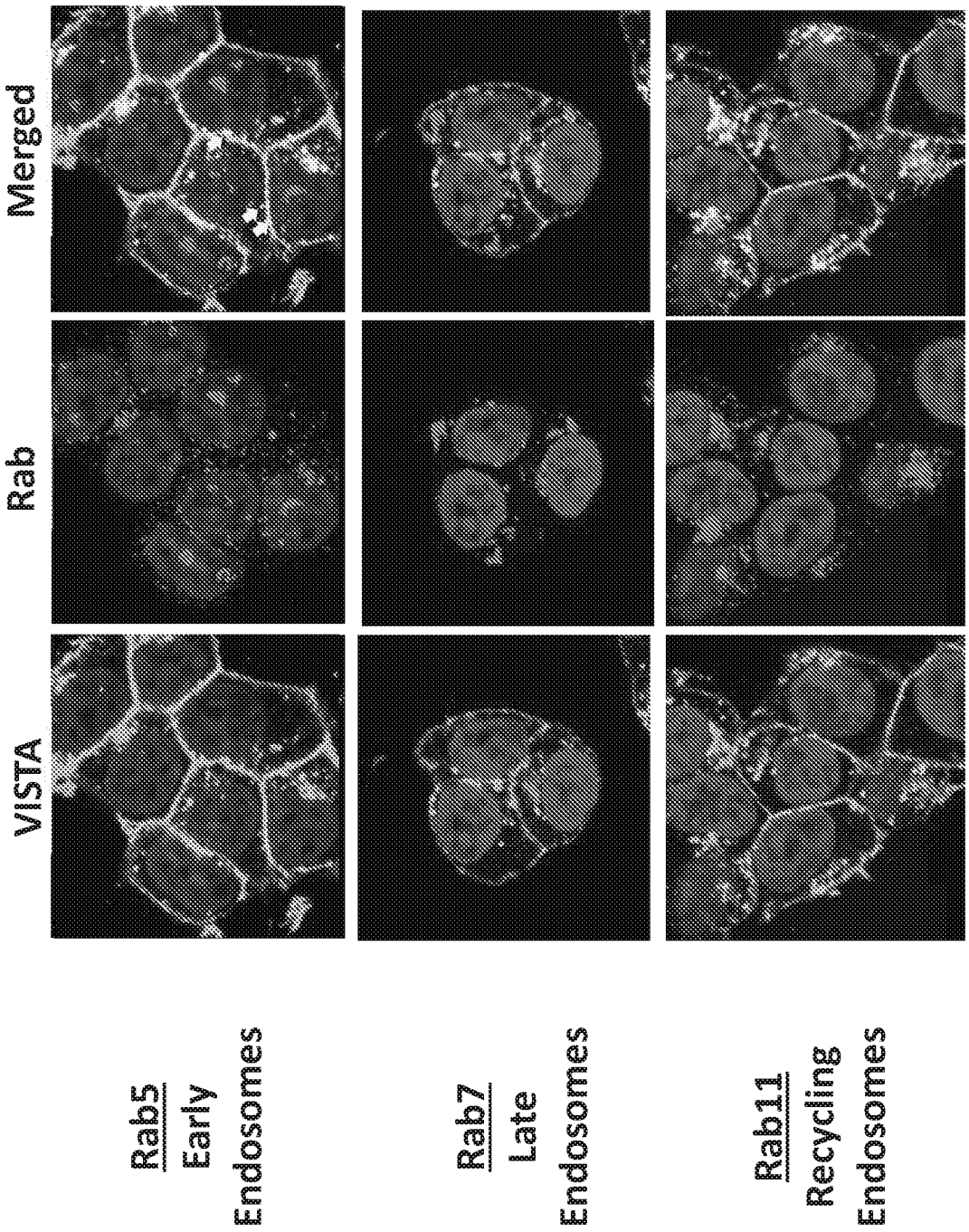

VISTA
Rab
Merged
Rab5
Early
Endosomes
Rab7
Late
Endosomes
Rab11
Recycling
Endosomes

FIG. 6A

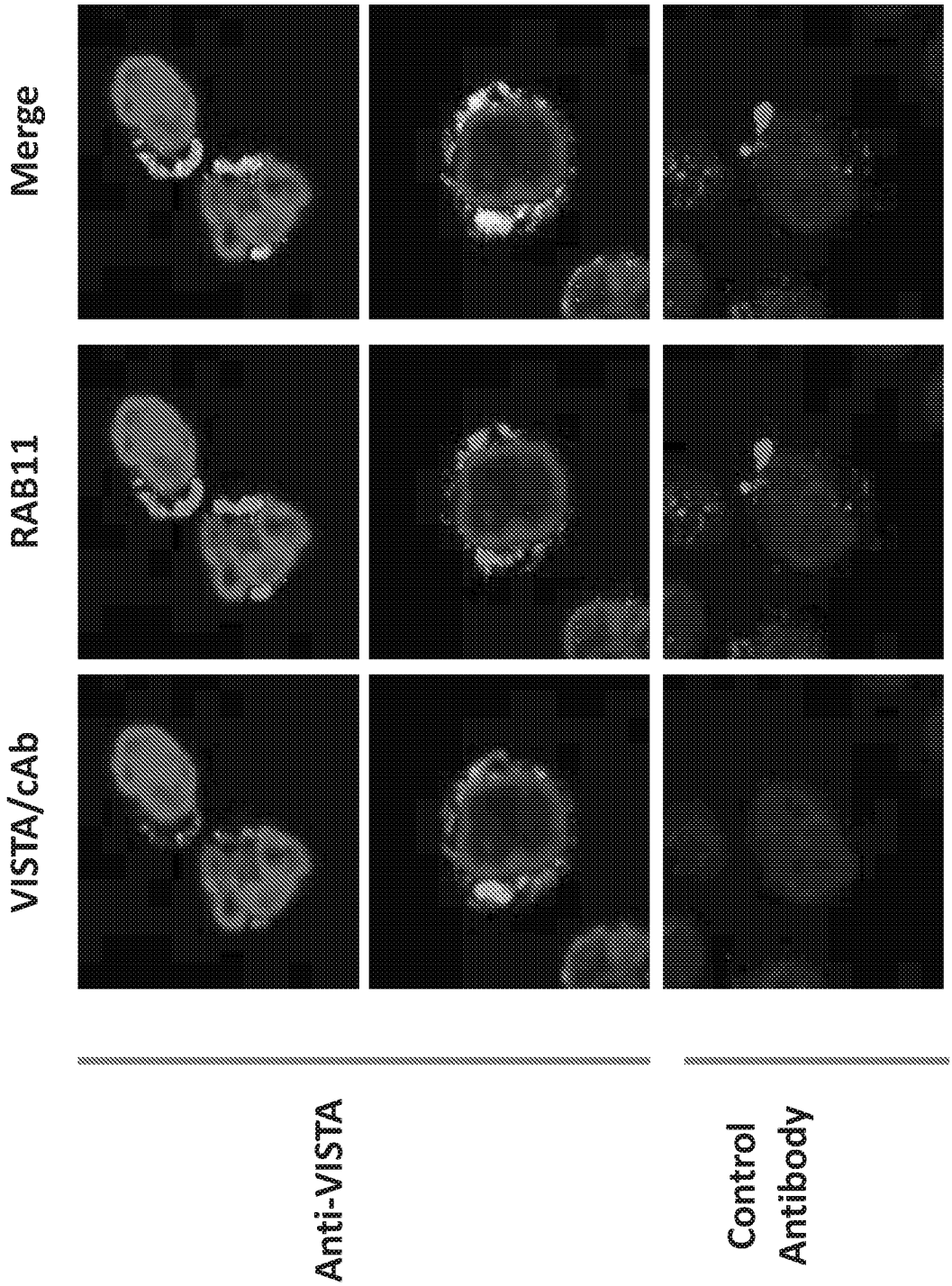


FIG. 6B

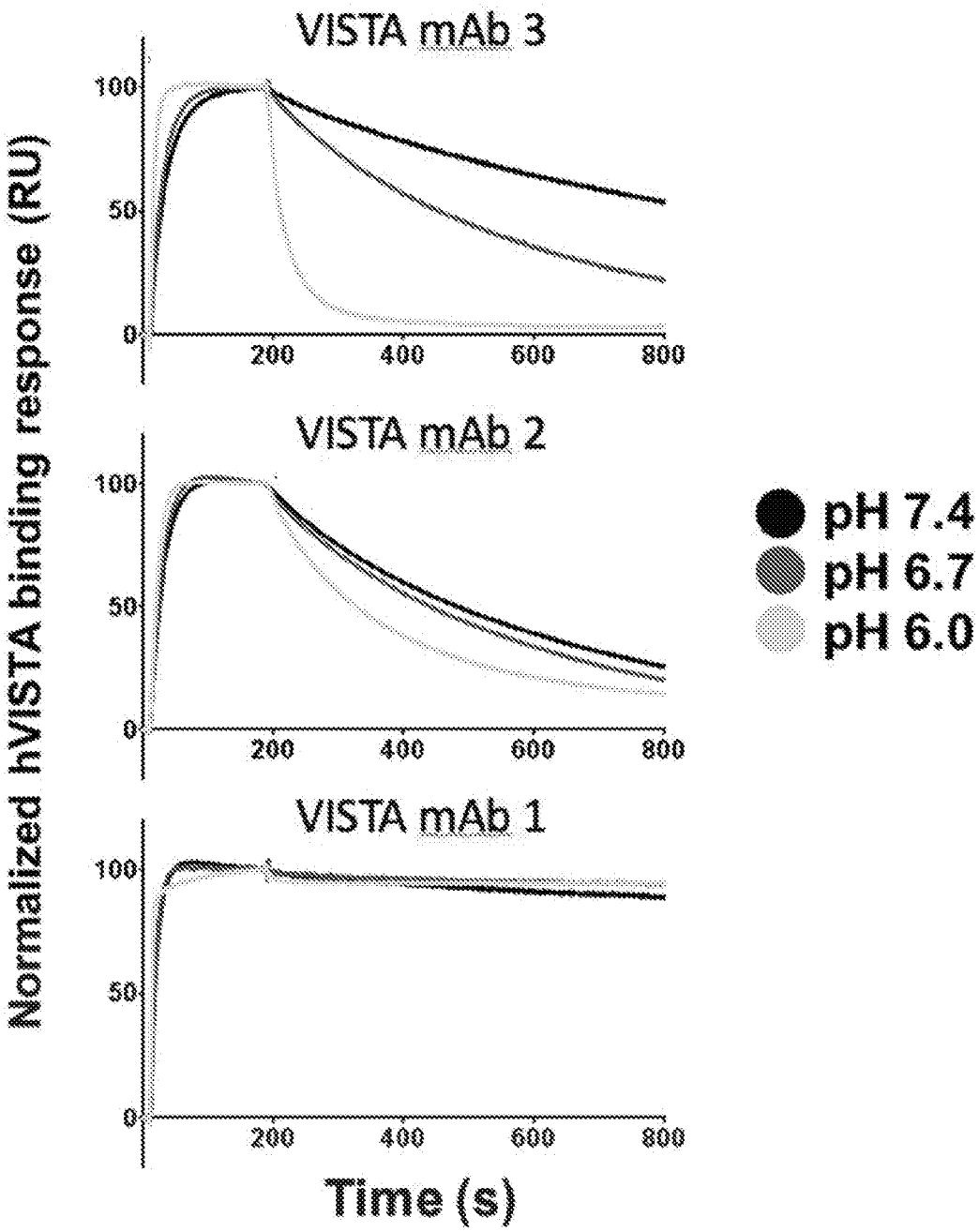

VISTA mAb 3
VISTA mAb 2
VISTA mAb 1
Normalized hVISTA binding response (RU)
100
50
0
200
400
600
800
Time (s)
pH 7.4
pH 6.7
pH 6.0

FIG. 6C

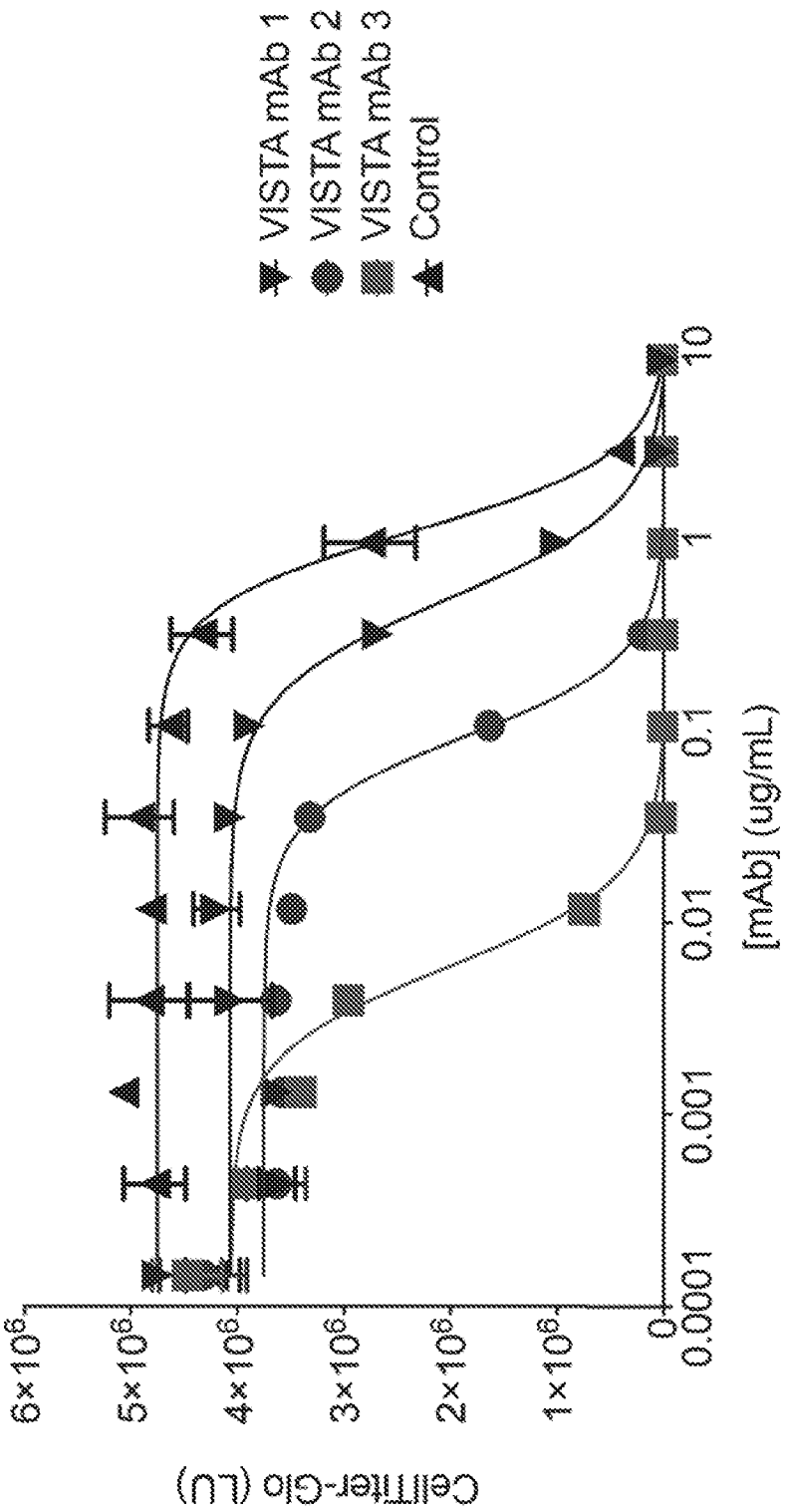

VISTA mAb 1
VISTA mAb 2
VISTA mAb 3
Control
CellTiter-Glo (LU)
6×10^6
5×10^6
4×10^6
3×10^6
2×10^6
1×10^6
0
0.0001
0.001
0.01
0.1
1
10
[mAb] (ug/mL)

FIG. 6D

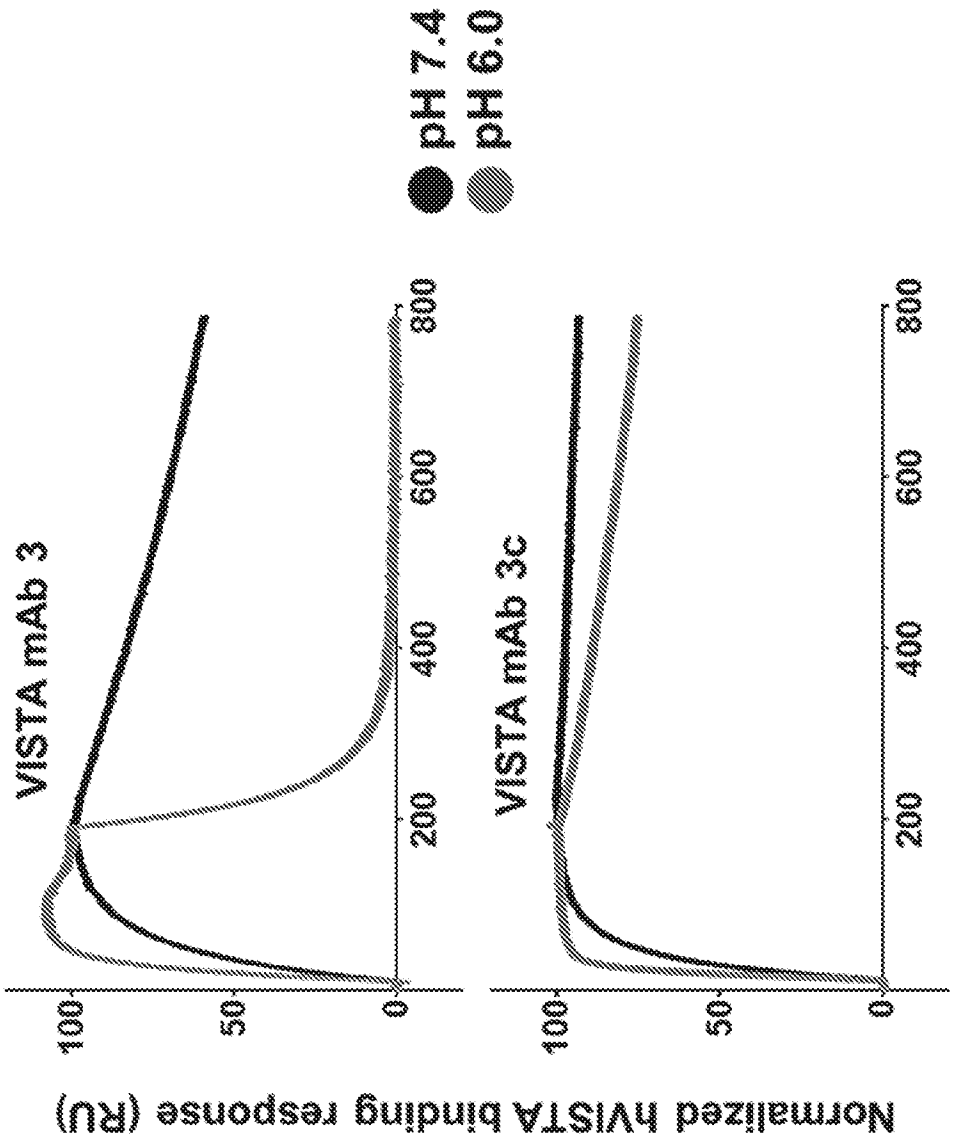

pH 7.4
pH 6.0
VISTA mAb 3
VISTA mAb 3c
Normalized hVISTA binding response (RU)
Time (s)
100
50
0
200
400
600
800

FIG. 6E

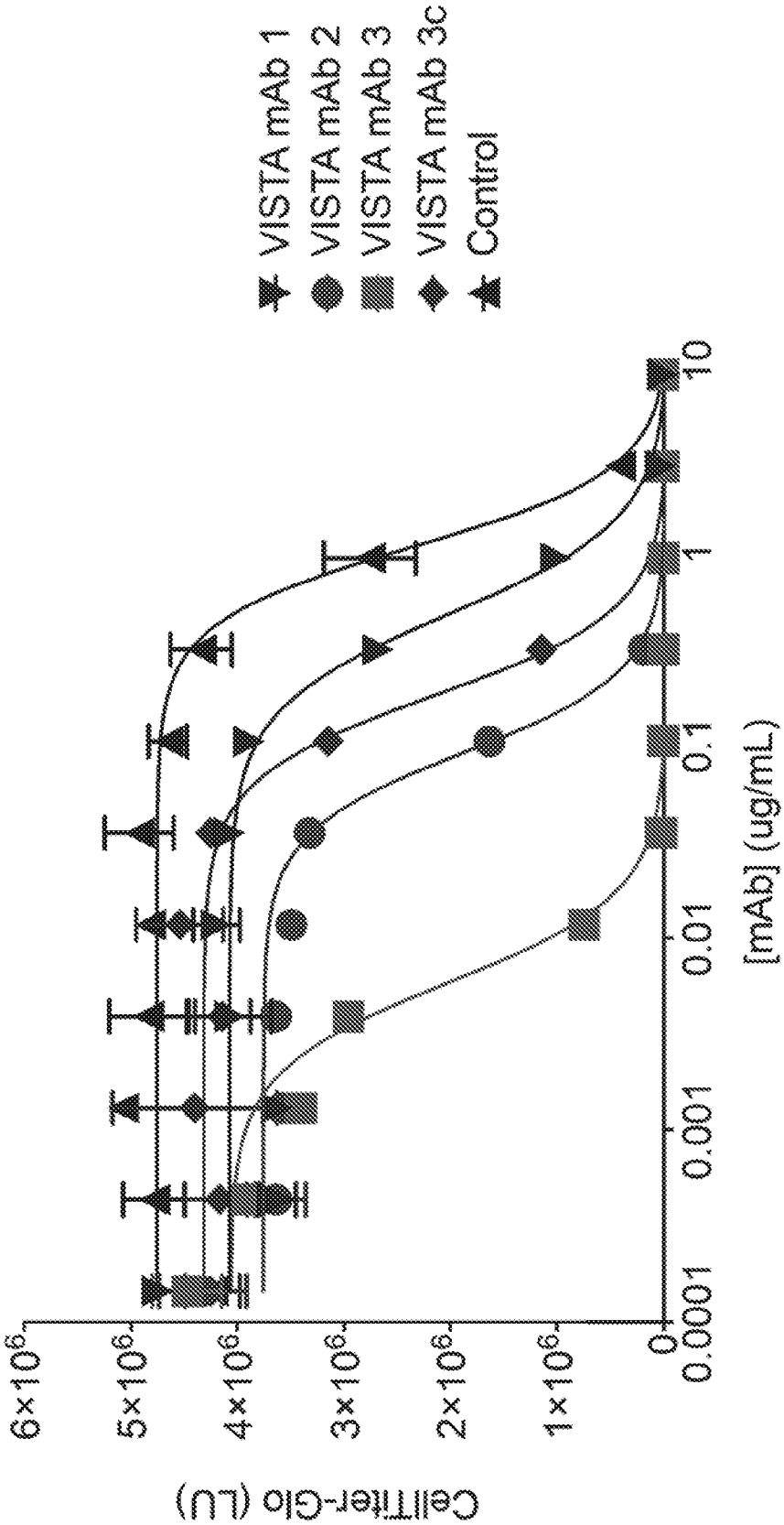

VISTA mAb 1
VISTA mAb 2
VISTA mAb 3
VISTA mAb 3c
Control
CellTiter-Glo (LU)
6×10^6
5×10^6
4×10^6
3×10^6
2×10^6
1×10^6
0
0.0001
0.001
0.01
0.1
1
10
[mAb] (ug/mL)

FIG. 6F

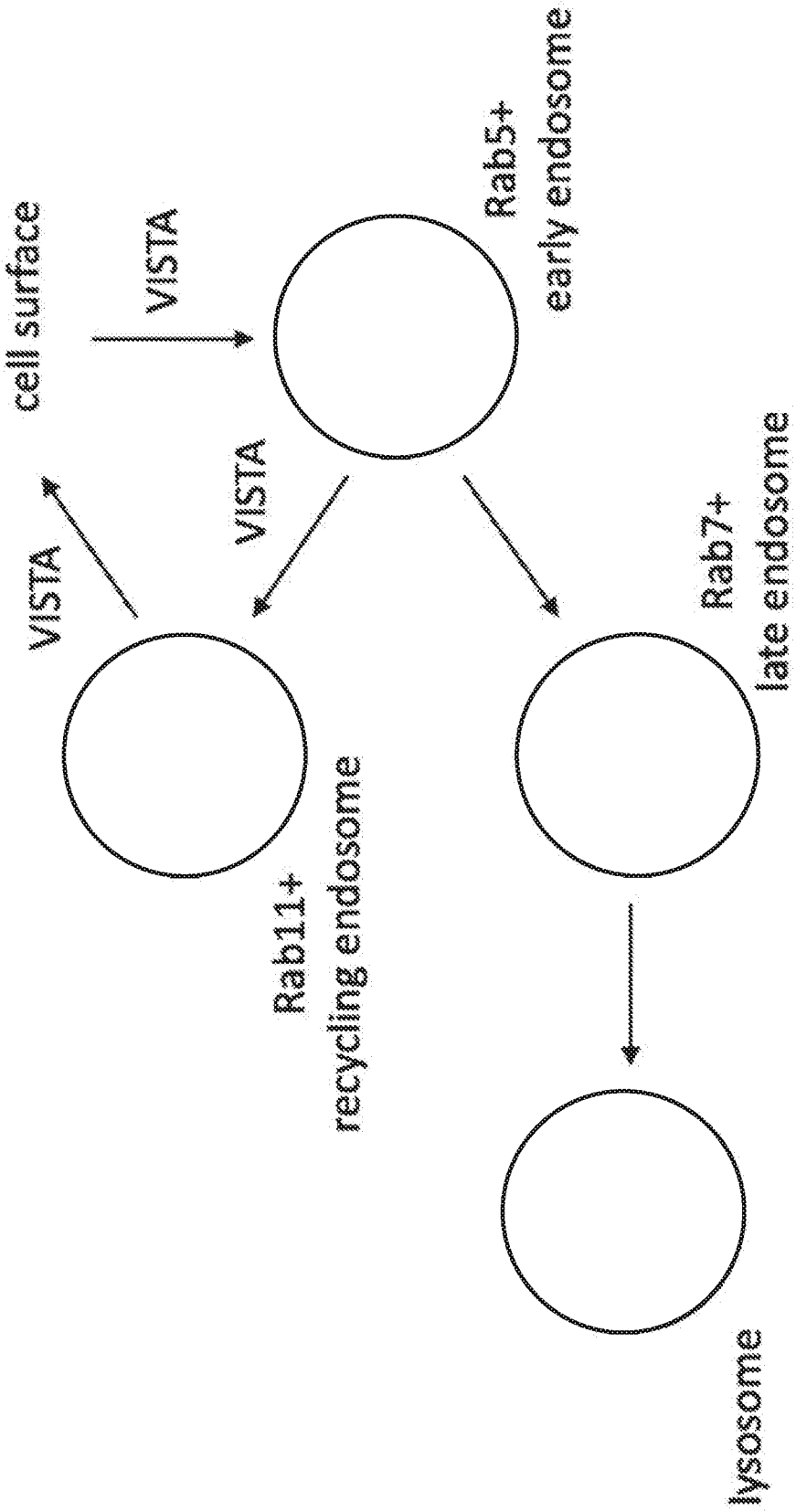
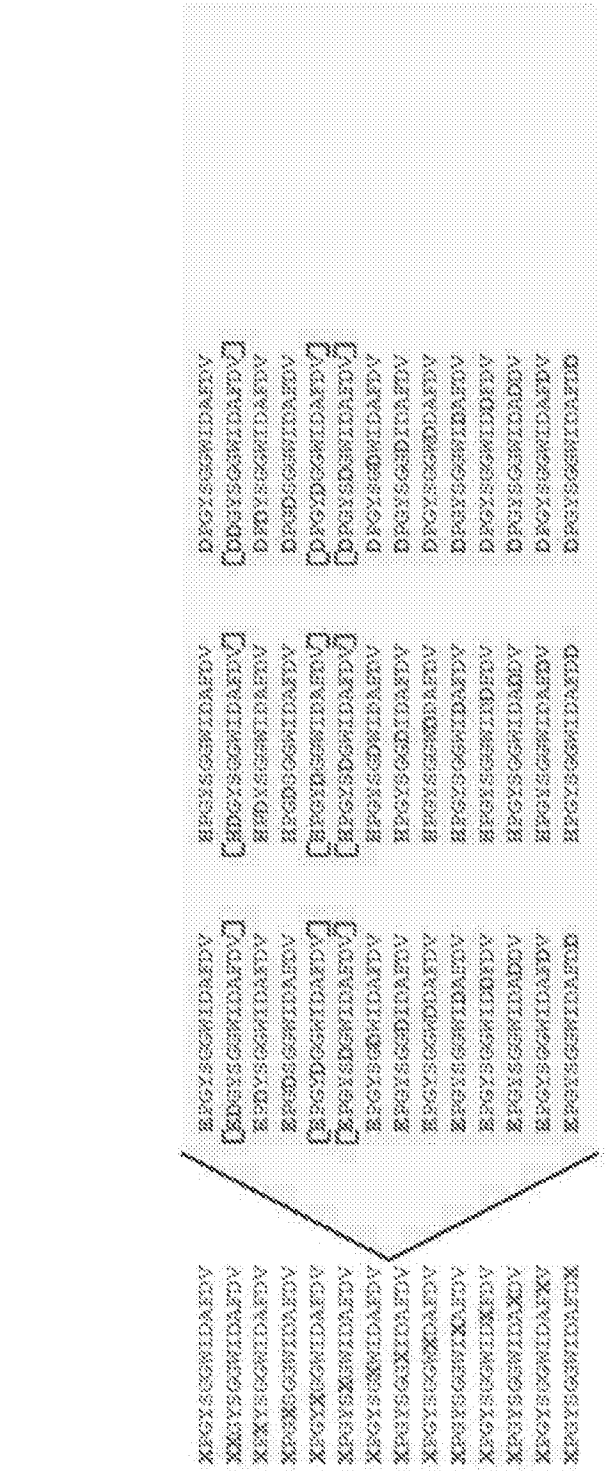

cell surface
VISTA
Rab5+
early endosome
VISTA
VISTA
Rab7+
late endosome
Rab11+
recycling endosome
lysosome

FIG. 6G



1. X = H, D, or E
2. Bracketed sequences were removed from synthesis to avoid introducing liabilities
3. A total of 647 unique sequences of P1-061029 HCDR3 with 1-2 mutations were synthesized

FIG. 7A

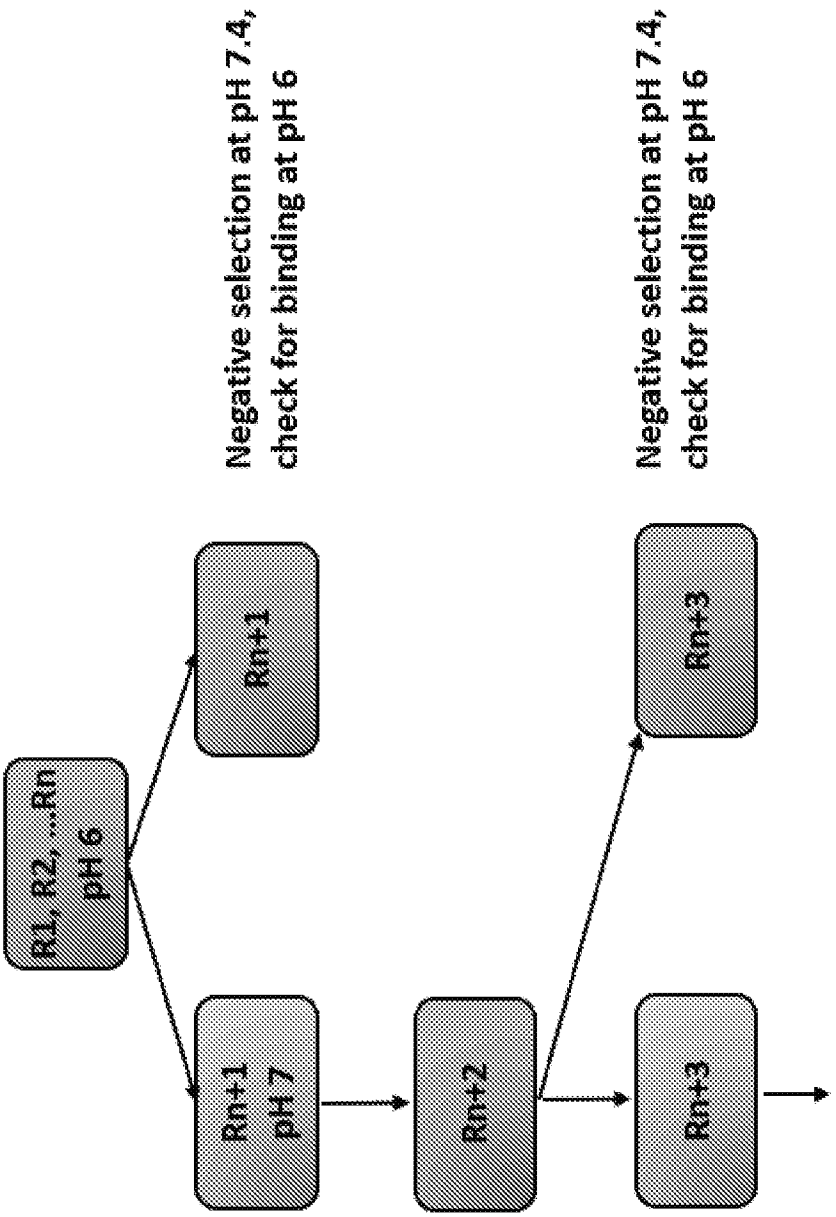

R1, R2, ...Rn
pH 6
Rn+1
Negative selection at pH 7.4,
check for binding at pH 6
Rn+1
pH 7
Rn+2
Rn+3
Negative selection at pH 7.4,
check for binding at pH 6
Rn+3

FIG. 7B

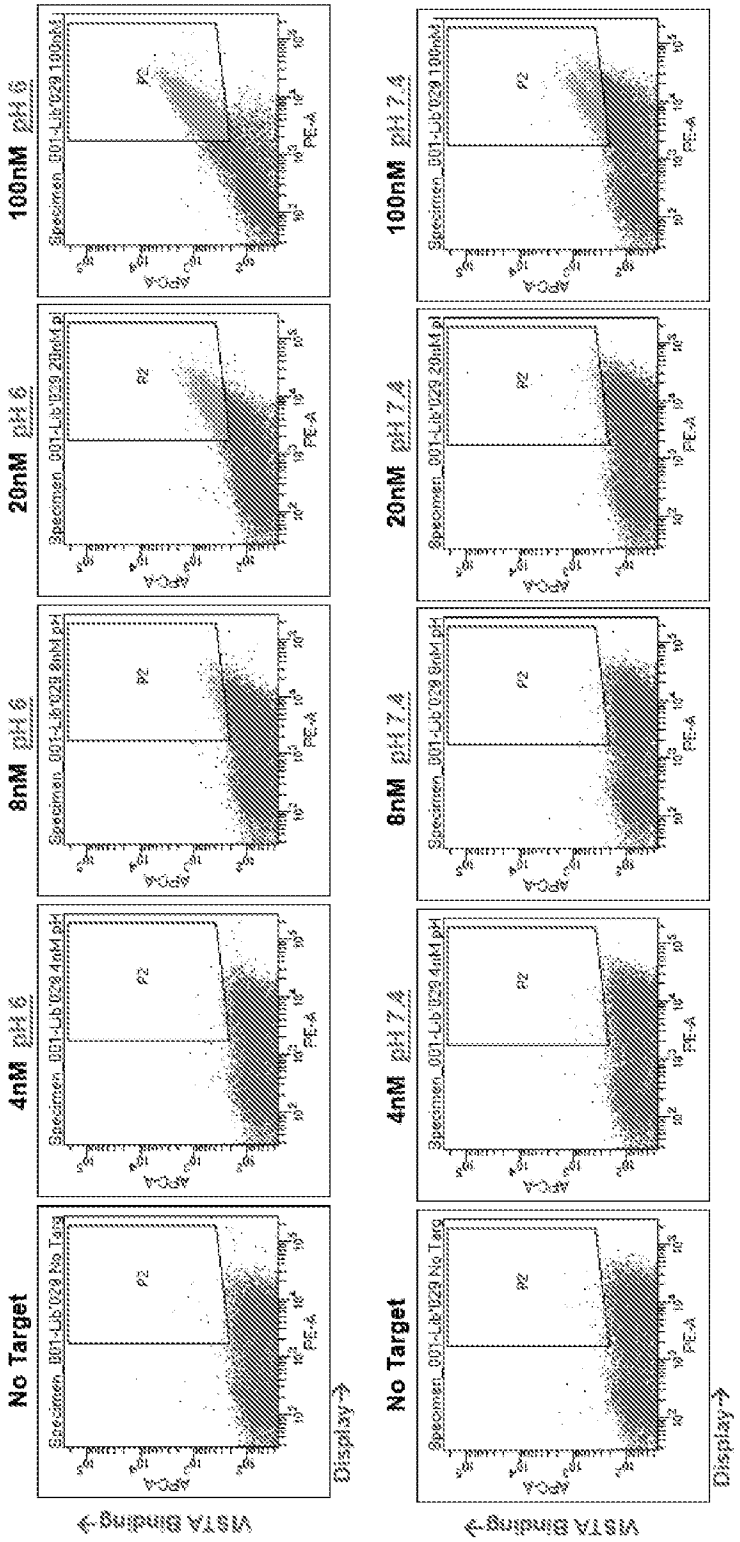

No Target
4nM pH 6
8nM pH 6
20nM pH 6
100nM pH 6
4nM pH 7.4
8nM pH 7.4
20nM pH 7.4
100nM pH 7.4
VISTA Binding
Display
APC-A
PE-A
P2

FIG. 7C

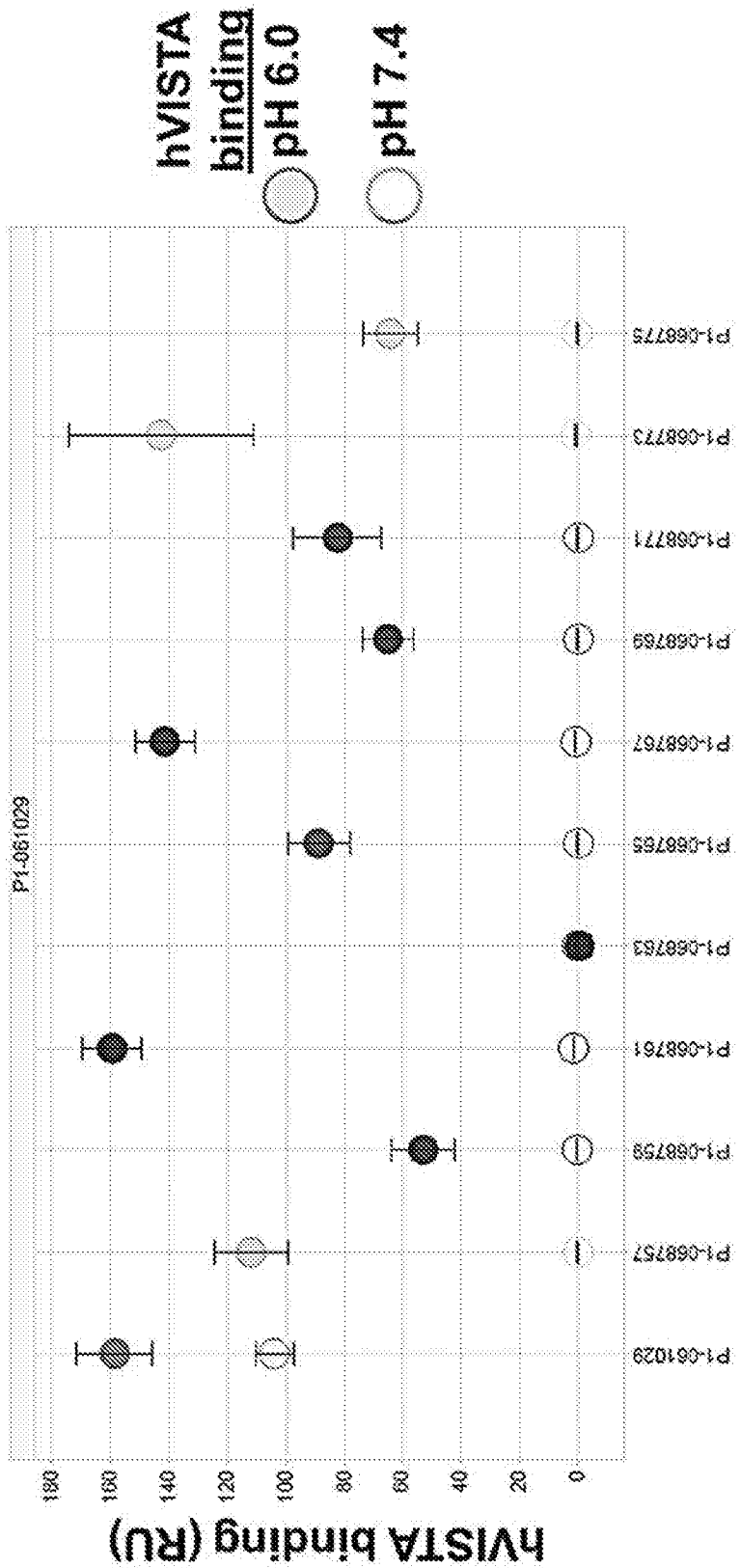

hVISTA binding (RU)
hVISTA binding
pH 6.0
pH 7.4
P1-061029
P1-068775
P1-068773
P1-068771
P1-068769
P1-068767
P1-068765
P1-068763
P1-068761
P1-068759
P1-068757
P1-061029
180
160
140
120
100
80
60
40
20
0

FIG. 7D

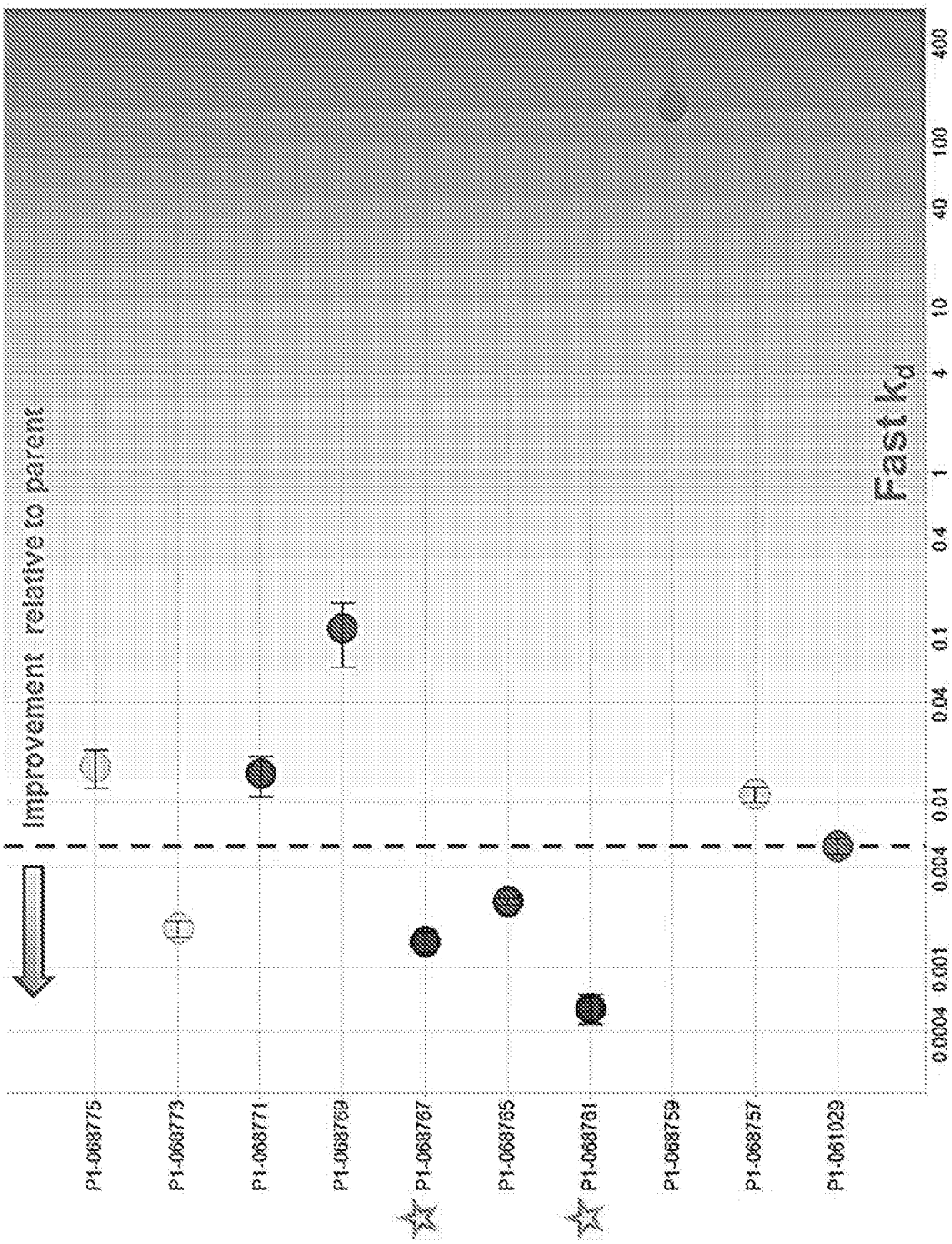

Improvement relative to parent
Fast k_d
P1-068775
P1-068773
P1-068771
P1-068769
P1-068767
P1-068765
P1-068761
P1-068759
P1-068757
P1-061029
0.0004
0.001
0.004
0.01
0.04
0.1
0.4
1
4
10
40
100
400
pH 6.0 k_d (1/s)

FIG. 7E

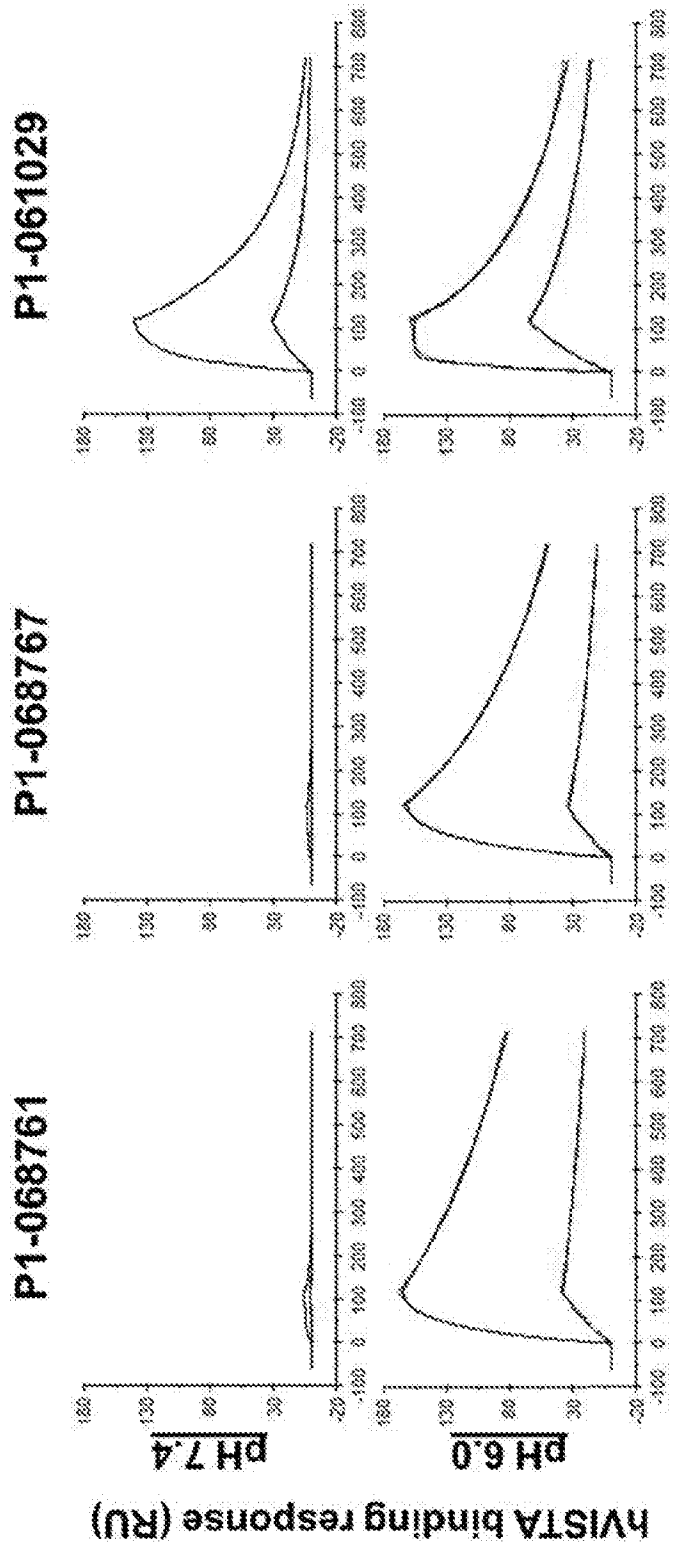

P1-061029
P1-068767
P1-068761
pH 7.4
pH 6.0
hVISTA binding response (RU)
Time (s)

FIG. 7F

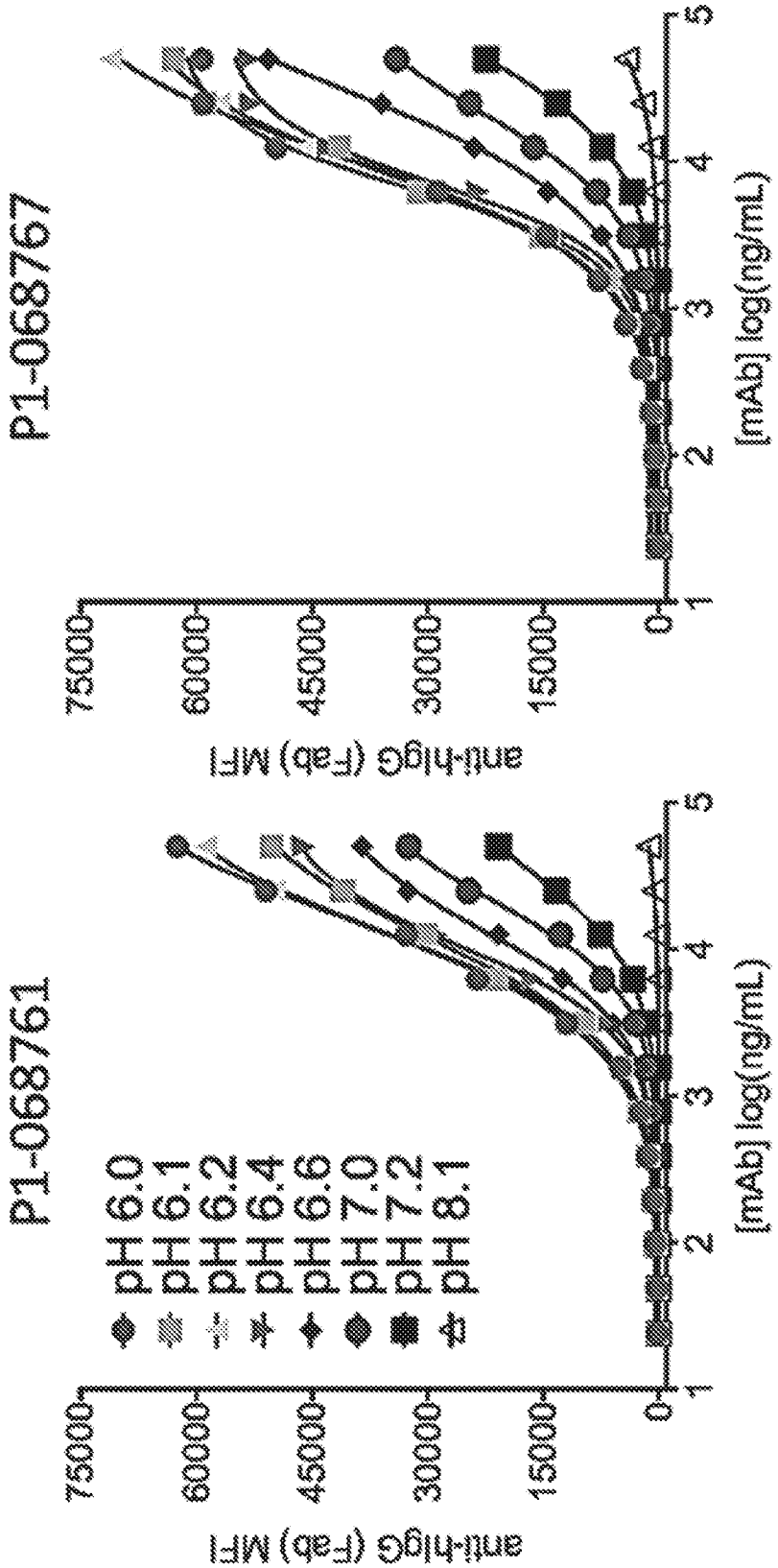

P1-068761
P1-068767
anti-hIgG (Fab) MFI
75000
60000
45000
30000
15000
0
1
2
3
4
5
[mAb] log(ng/mL)
pH 6.0
pH 6.1
pH 6.2
pH 6.4
pH 6.6
pH 7.0
pH 7.2
pH 8.1

FIG. 8A

FIG. 8B

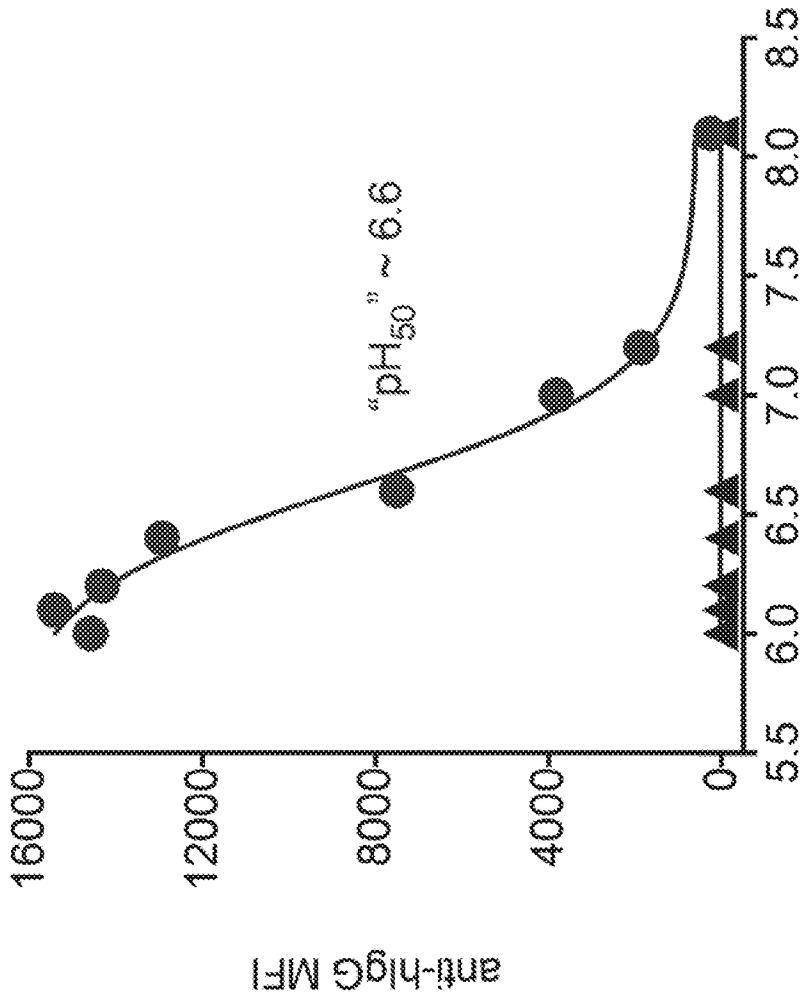

anti-hIgG MFI
16000
12000
8000
4000
0
5.5
6.0
6.5
7.0
7.5
8.0
8.5
Buffer pH
"pH50" ~ 6.6
P1-068767
Control

FIG. 8C

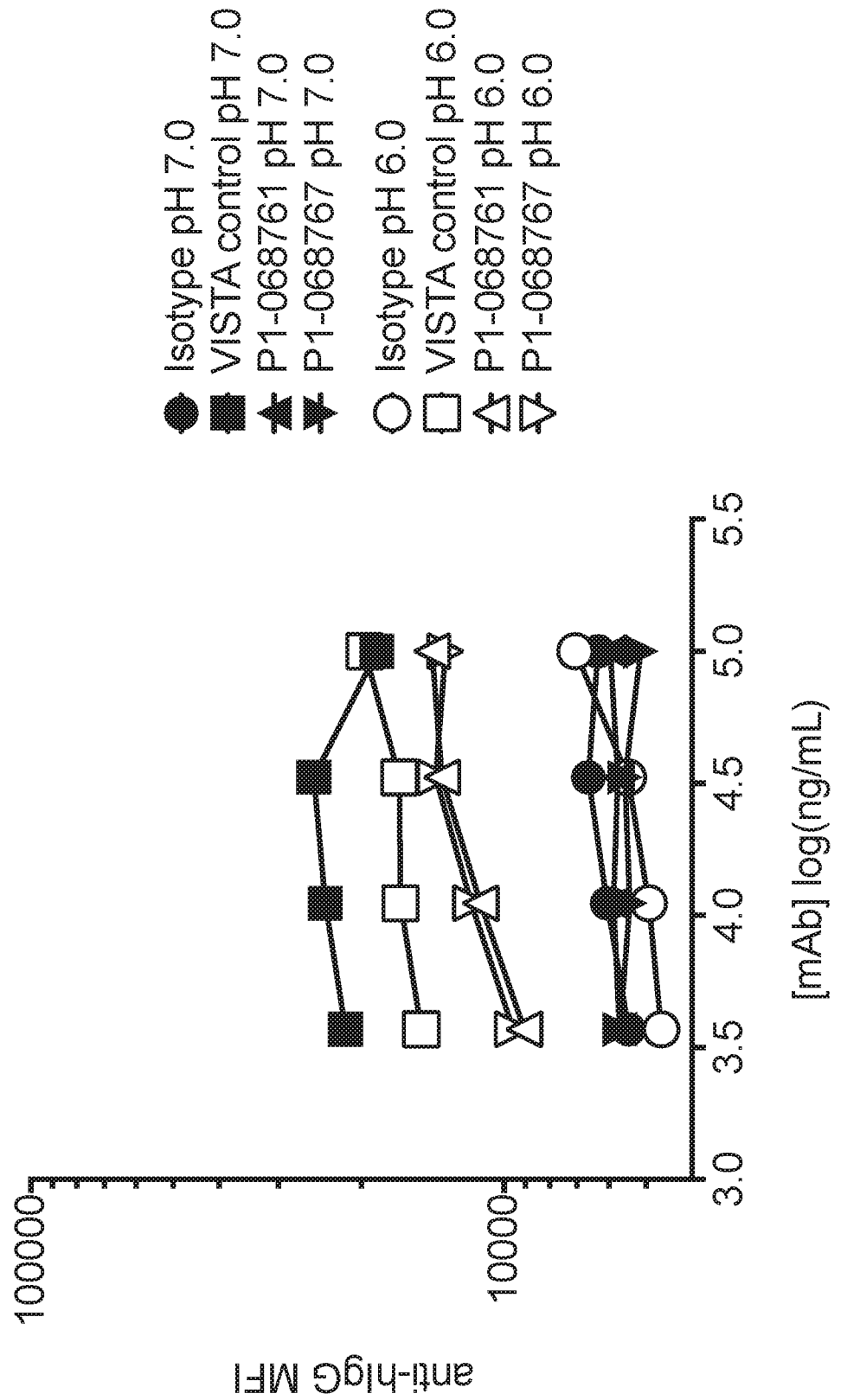

Isotype pH 7.0
VISTA control pH 7.0
P1-068761 pH 7.0
P1-068767 pH 7.0
Isotype pH 6.0
VISTA control pH 6.0
P1-068761 pH 6.0
P1-068767 pH 6.0
anti-hIgG MFI
100000
10000
3.0
3.5
4.0
4.5
5.0
5.5
[mAb] log(ng/mL)

FIG. 8D

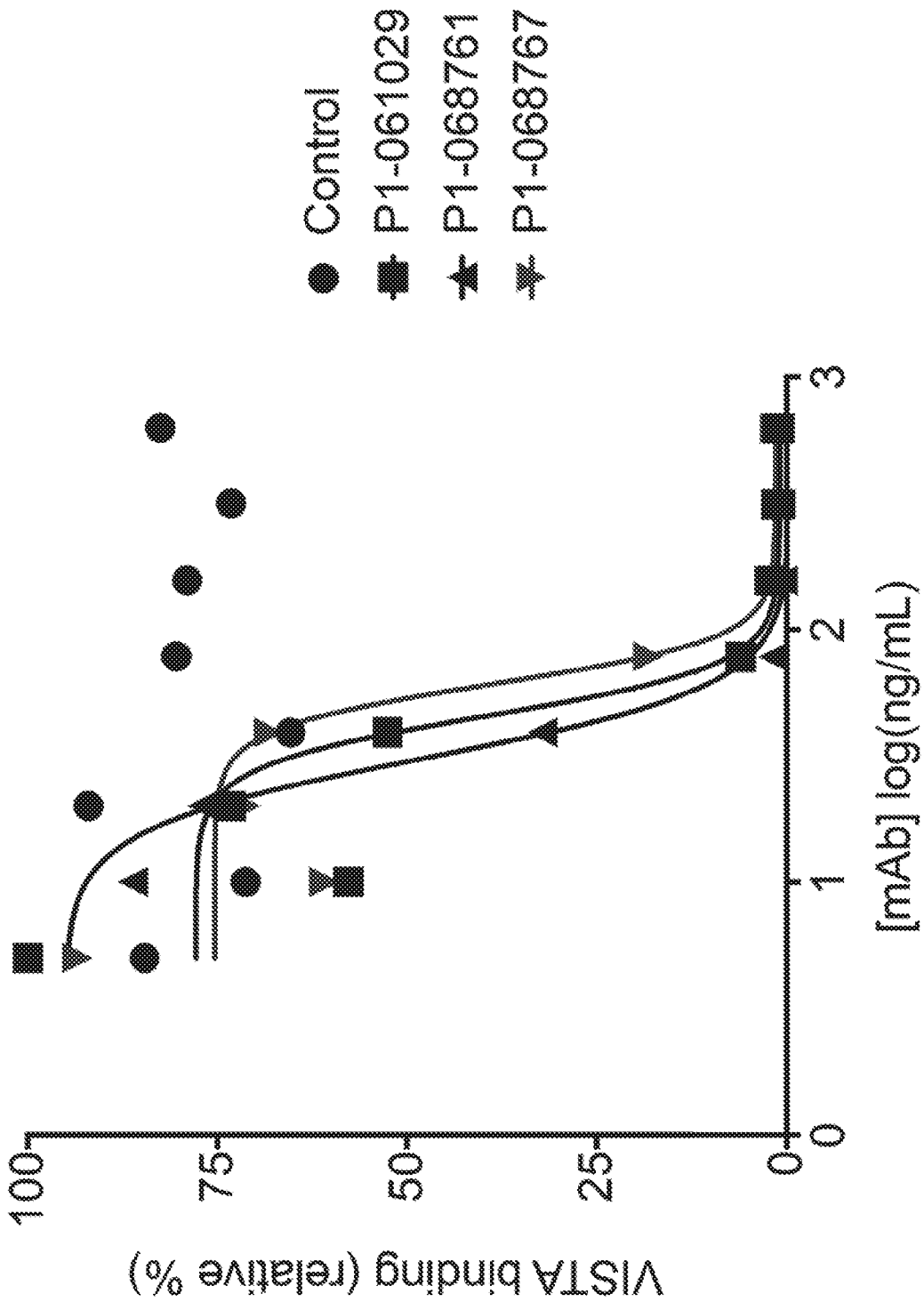

Control
P1-061029
P1-068761
P1-068767
VISTA binding (relative %)
100
75
50
25
0
0
1
2
3
[mAb] log(ng/mL)

FIG. 8E

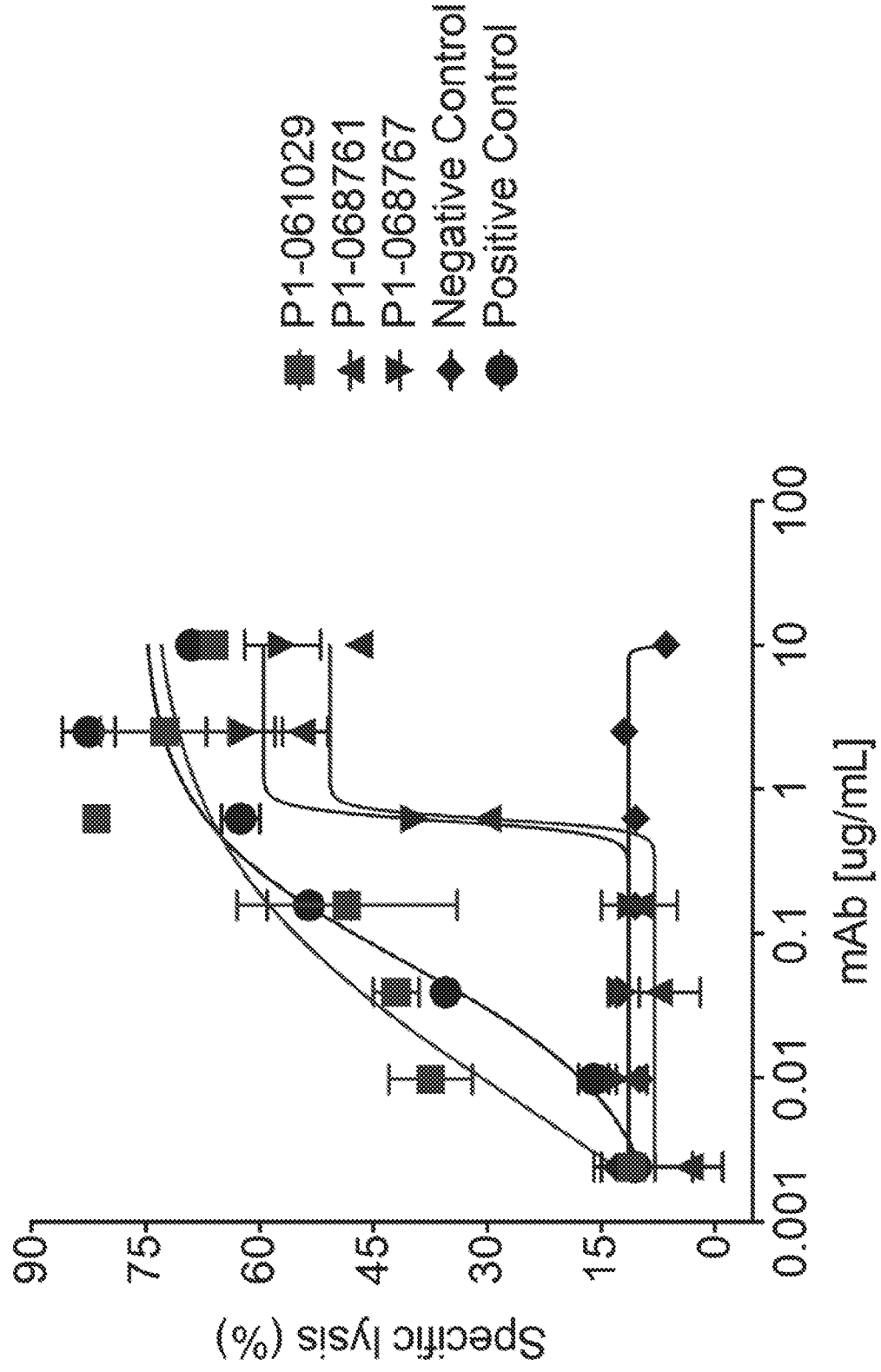

P1-061029
P1-068761
P1-068767
Negative Control
Positive Control
Specific lysis (%)
90
75
60
45
30
15
0
0.001
0.01
0.1
1
10
100
mAb [ug/mL]

FIG. 8F

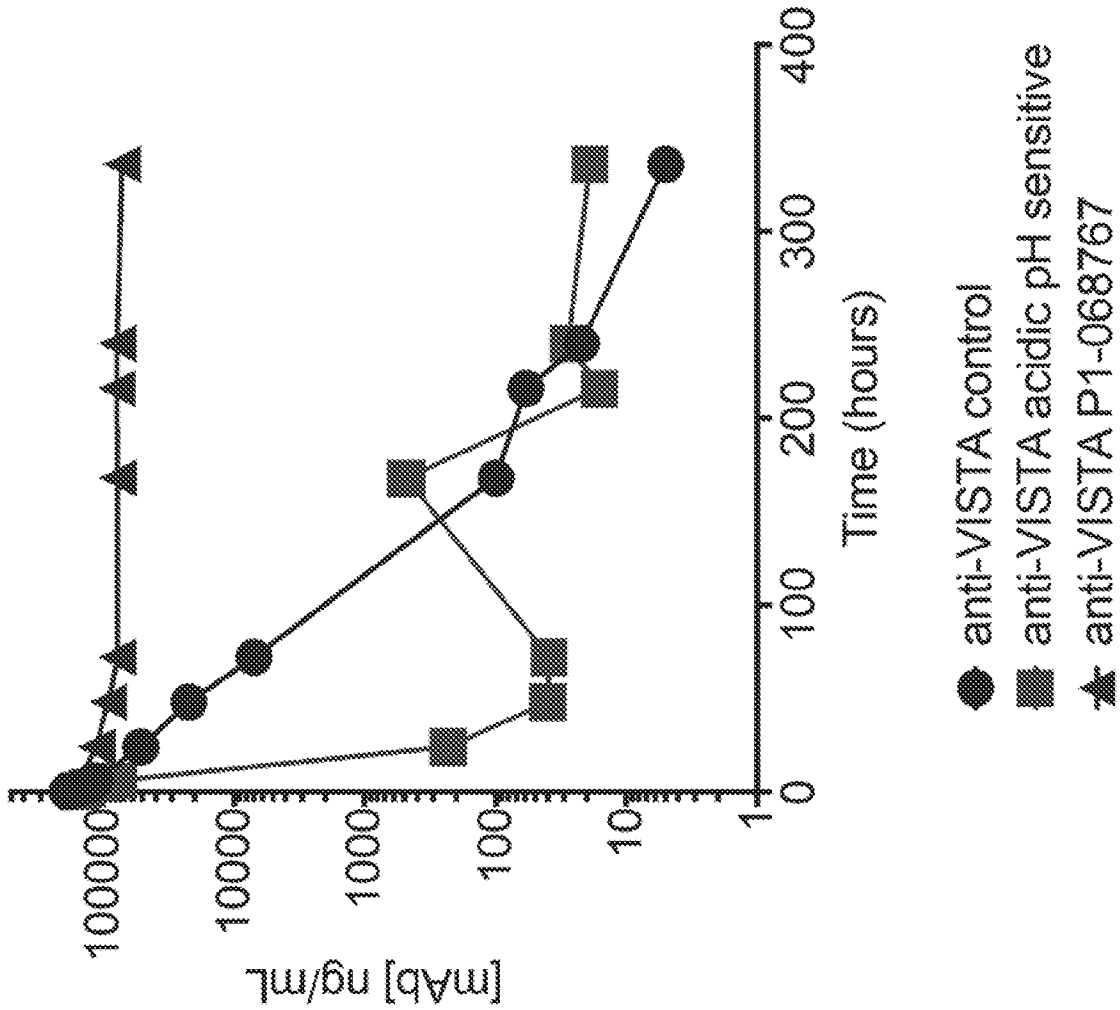

[mAb] ng/mL
100000
10000
1000
100
10
1
0
100
200
300
400
Time (hours)
anti-VISTA control
anti-VISTA acidic pH sensitive
anti-VISTA P1-068767

FIG. 9

Antibody	P1 ID	pH 7.4			pH 6.7			pH 6.0			HCDR1	HCDR2	HCDR3
		kd (1/s)	KD (M)	hVISTA %Rmax	kd (1/s)	KD (M)	hVISTA %Rmax	kd (1/s)	KD (M)	hVISTA %Rmax			
P1-068761_E100fF	P1-070874	1.3E-03	2.0E-08	73.3	2.2E-04	1.3E-09	117.0	1.3E-04	1.9E-10	130.1	....E.E...	.....EE.....	.....H.....
P1-068761_E55A_E100fF	P1-070898	1.7E-03	1.4E-08	82.3	2.8E-04	1.5E-09	119.8	1.8E-04	2.6E-10	133.7	....E.E...	.....E.....	.....H.....
P1-068761_H100G_E100fF	P1-070880	2.3E-03	4.1E-08	61.8	4.0E-04	2.3E-09	116.7	2.1E-04	2.3E-10	126.7	....E.E...	.....EE.....	.....
P1-068761_E30D_E100fF	P1-070896	3.5E-03	4.8E-08	65.2	5.7E-04	3.7E-09	112.6	3.3E-04	4.3E-10	130.4	.....E....	.....EE.....	.....H.....
P1-068761_E56N_E100fF	P1-070902	3.0E-03	6.5E-08	47.4	6.1E-04	6.5E-09	85.9	3.8E-04	1.4E-09	116.5	....E.E...	.....E.....	.....H.....
P1-068761_E32Y	P1-070866	2.5E-03	1.8E-08	102.5	6.4E-04	1.6E-09	120.9	4.1E-04	2.1E-10	123.1	....E.....	.....EE.....	.....H.....E..
P1-068761_E32Y_E55A	P1-070882	2.7E-03	2.3E-08	89.3	6.0E-04	2.0E-09	116.3	5.7E-04	3.1E-10	117.6	....E.....	.....E.....	.....H.....E..
P1-068761_E32Y_E56N	P1-070884	3.2E-03	4.2E-08	73.7	8.3E-04	5.1E-09	104.4	7.0E-04	1.2E-09	115.8	....E.....	.....E.....	.....H.....E..
P1-068761_E30D_E32Y	P1-070876	3.5E-03	2.1E-08	110.8	9.9E-04	2.0E-09	124.0	7.1E-04	2.4E-10	124.9	.....	.....EE.....	.....H.....E..
P1-068761_E32Y_H100G	P1-070886	5.5E-03	7.2E-08	68.0	1.3E-03	5.0E-09	113.4	9.2E-04	4.8E-10	120.4	....E.....	.....EE.....	.....H.....
P1-068761_E32Y_E100fF	P1-070888	1.9E-03	3.7E-09	132.1	9.5E-04	1.1E-09	125.0	1.1E-03	2.5E-10	120.8	....E.....	.....EE.....	.....H.....
P1-068761	P1-068761	%%	%%	0.7	6.6E-03	7.1E-08	49.7	1.4E-03	2.6E-09	122.5	....E.E...	.....EE.....	.....H.....E..
P1-068761_E55A	P1-070868	%%	%%	2.8	6.4E-03	1.2E-07	42.2	1.7E-03	3.4E-09	113.1	....E.E...	.....E.....	.....H.....E..
P1-068761_H100G	P1-070872	%%	%%	2.9	1.4E-02	2.3E-07	36.1	5.2E-03	4.4E-09	121.0	....E.E...	.....EE.....	.....E.....
P1-068761_E56N	P1-070870	%%	%%	1.7	>1E-02	~8.2E-06	17.6	5.5E-03	1.9E-08	86.3	....E.E...	.....E.....	.....H.....E..
P1-068761_E55A_E56N	P1-070878	%%	%%	0.9	2.9E-02	2.1E-07	16.4	5.6E-03	2.1E-08	79.3	....E.E...	.....	.....H.....E..
P1-068761_E30D	P1-070864	%%	%%	0.4	1.8E-02	3.7E-07	25.6	6.2E-03	8.3E-09	109.9	.....	.....EE.....	.....H.....E..
P1-068761_E30D_E55A	P1-070890	%%	%%	1.8	>1E-02	~1.1E-07	22.1	7.4E-03	1.2E-08	99.1	.....E....	.....E.....	.....H.....E..
P1-061029	P1-061029	7.5E-03	3.2E-08	93.4	4.4E-03	1.1E-08	96.9	8.2E-03	4.5E-09	98.5	GFTIDDYAMH	GINWNSANIGYADSVKG	VPGYSGGWIDAFDV
P1-068761_E56N_H100G	P1-070900	%%	%%	4.4	%%	%%	19.4	8.1E-03	1.0E-08	110.9	....E.E...	.....E.....	.....E.....E..
P1-068761_E30D_H100G	P1-070894	%%	%%	3.1	>1E-02	~8.1E-08	14.6	2.1E-02	1.5E-08	91.9	.....E....	.....EE.....	.....E.....E..
P1-068761_E30D_E56N	P1-070892	%%	%%	0.4	>1E-02	~3.2E-08	8.3	3.4E-02	5.0E-08	56.3	.....E....	.....E.....	.....H.....E..

FIG. 10A

Antibody	P1 ID	pH 7.4			pH 6.7			pH 6.0			HCDR1	HCDR2	HCDR3
		kd (1/s)	KD (M)	hVISTA %Rmax	kd (1/s)	KD (M)	hVISTA %Rmax	kd (1/s)	KD (M)	hVISTA %Rmax			
P1-068767_D52N_D102V	P1-070930	6.7E-03	8.7E-08	60.0	1.8E-03	7.5E-09	101.0	1.2E-03	8.8E-10	114.6	....E.....	......E.....	..........E..
P1-068767_D52N	P1-070906	%%	%%	3.9	6.7E-03	2.1E-07	38.9	1.5E-03	3.2E-09	116.6	....E.....	......E.....	..........E.D
P1-068767_D52N_E55A	P1-070916	%%	%%	2.3	5.5E-03	1.2E-07	33.7	1.5E-03	4.0E-09	112.0	....E.....	..D.................	..........E.D
P1-068767_E55A_D102V	P1-070932	1.0E-02	2.8E-07	35.4	3.1E-03	1.5E-08	85.7	2.0E-03	1.9E-09	111.3	....E.....	..D.................	..........E..
P1-068767_D102V	P1-070912	9.2E-03	1.7E-07	44.7	2.8E-03	1.4E-08	98.5	2.0E-03	1.3E-09	111.9	....E.....	..D...E..........	..........E..
P1-068767_E55A	P1-070908	%%	%%	2.8	8.5E-03	3.8E-07	26.8	2.3E-03	5.7E-09	108.0	....E.....	..D.................	..........E.D
P1-068767_E30D_D52N	P1-070914	%%	%%	4.5	1.1E-02	1.2E-07	35.8	2.3E-03	5.8E-09	105.7	....	......E..........	..........E.D
P1-068767	P1-068767	%%	%%	1.9	7.2E-03	1.8E-07	31.1	2.4E-03	5.2E-09	111.7	....E.....	..D...E..........	..........E.D
P1-068767_E30D_D102V	P1-070926	1.1E-02	2.2E-07	40.8	3.5E-03	1.7E-08	95.7	3.0E-03	2.1E-09	114.8	....	..D...E..........	..........E..
P1-068767_E30D	P1-070904	%%	%%	5.8	%%	%%	21.0	3.2E-03	9.6E-09	99.8	....	..D...E..........	..........E.D
P1-068767_E30D_E55A	P1-070922	%%	%%	3.5	%%	%%	22.6	3.5E-03	8.3E-09	108.8	....	..D.................	..........E.D
P1-061029	P1-061029	7.5E-03	3.2E-08	93.4	4.4E-03	1.1E-08	96.9	8.2E-03	4.5E-09	98.5	GFTLDDYAMH	GIWWNSANIGYADSVKG	VPGYSGGWIDAFDV
P1-068767_E100fF_D102V	P1-070920	8.3E-03	4.1E-08	86.8	4.7E-03	1.1E-08	103.4	8.2E-03	2.7E-09	103.4	....E.....	..D...E..........	....
P1-068767_E55A_E100fF	P1-070918	%%	%%	1.8	%%	%%	8.6	1.3E-02	6.2E-08	42.5	....E.....	..D.................	..........D
P1-068767_D52N_E100fF	P1-070928	%%	%%	9.4	>1E-02	~3.9E-08	22.7	6.6E-02	2.0E-08	64.0	....E.....	......E..........	..........D
P1-068767_E100fF	P1-070910	%%	%%	1.8	2.6E-02	5.2E-06	9.6	>1E-02	~4.2E-08	49.4	....E.....	..D...E..........	..........D
P1-068767_E30D_E100fF	P1-070924	%%	%%	1.0	2.7E-02	1.0E-05	7.0	>1E-02	~8.2E-08	32.9	....	..D...E..........	..........D

FIG. 10B

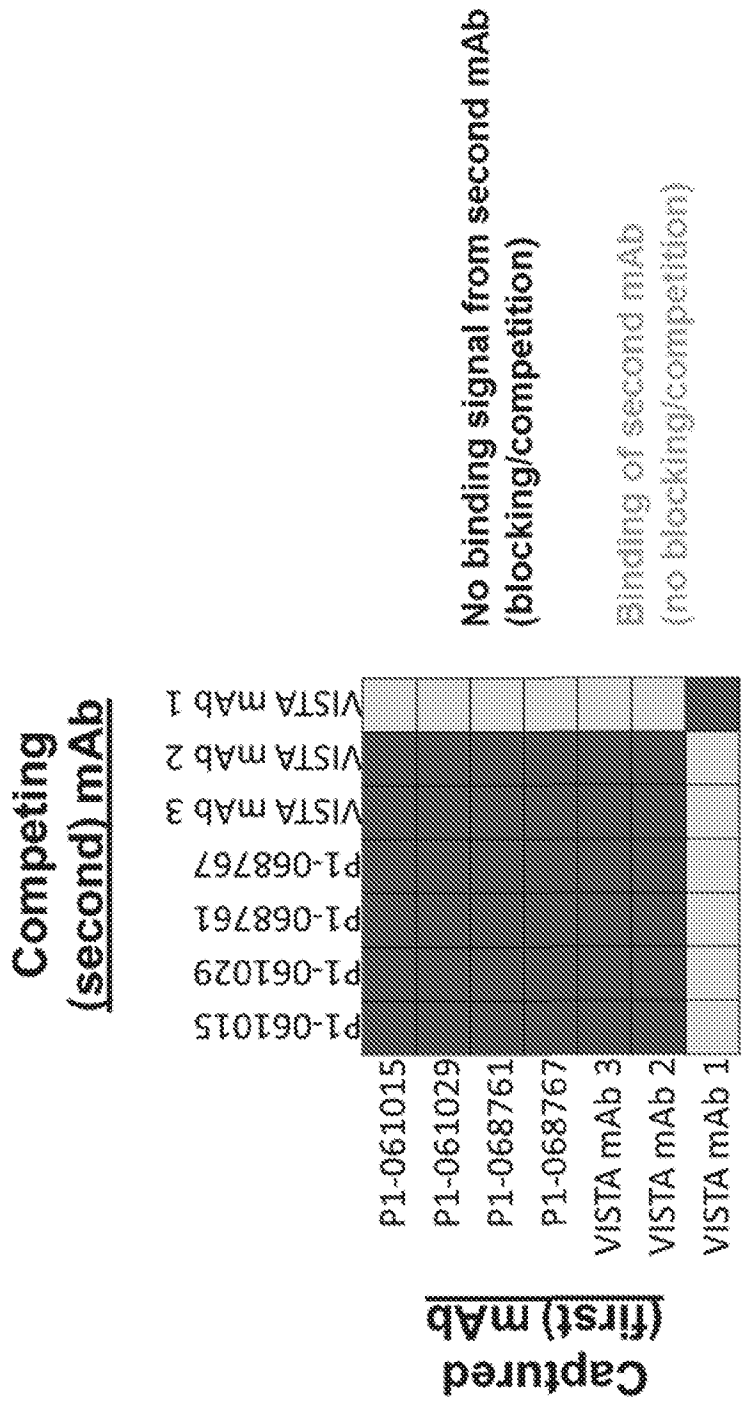

Competing (second) mAb
P1-061015
P1-061029
P1-068761
P1-068767
VISTA mAb 3
VISTA mAb 2
VISTA mAb 1
Captured (first) mAb
P1-061015
P1-061029
P1-068761
P1-068767
VISTA mAb 3
VISTA mAb 2
VISTA mAb 1
No binding signal from second mAb (blocking/competition)
Binding of second mAb (no blocking/competition)

FIG. 11A

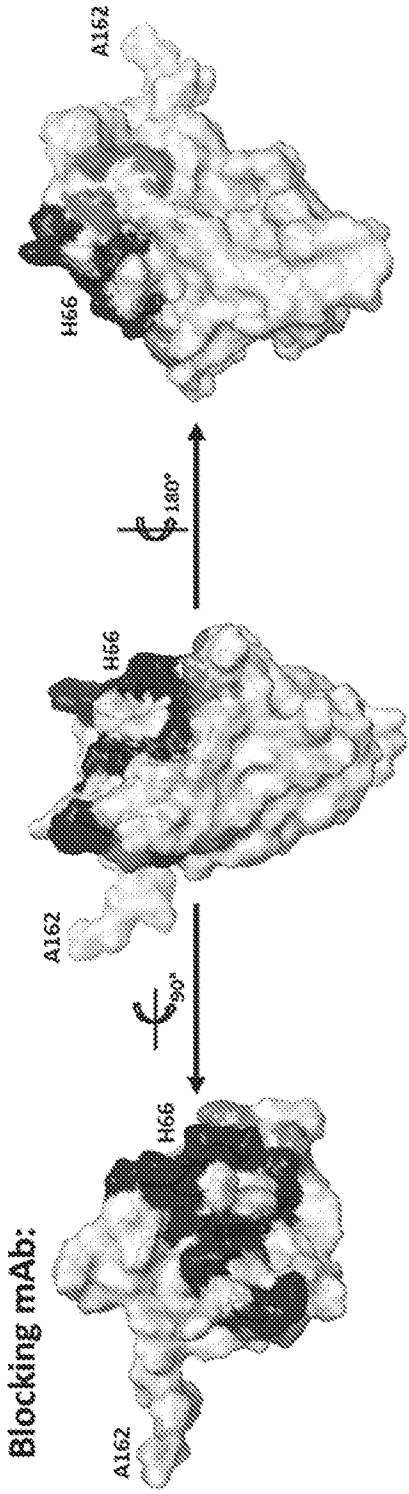


FIG. 11B

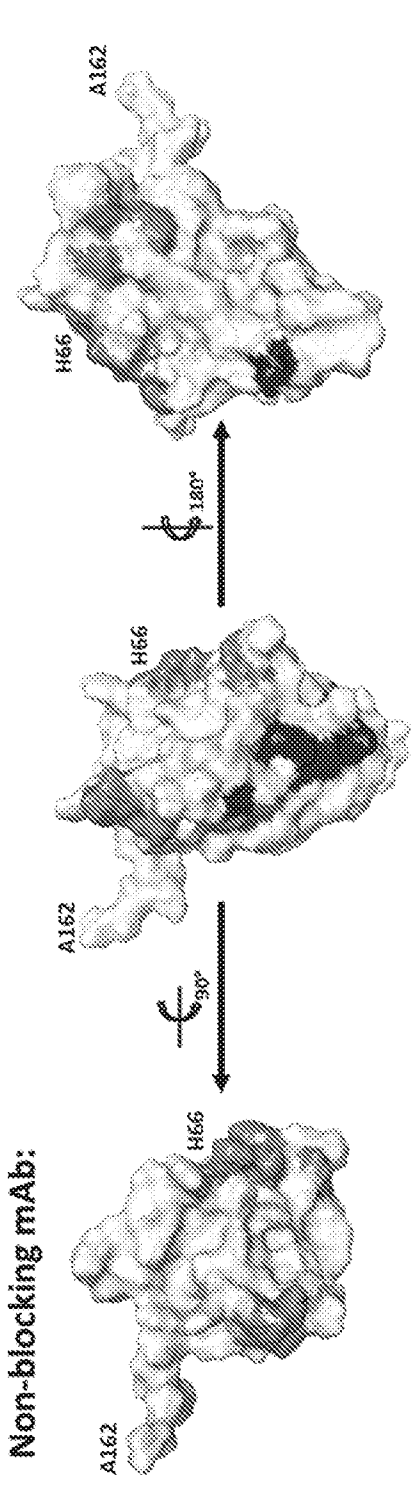


FIG. 11C

FIG. 12A

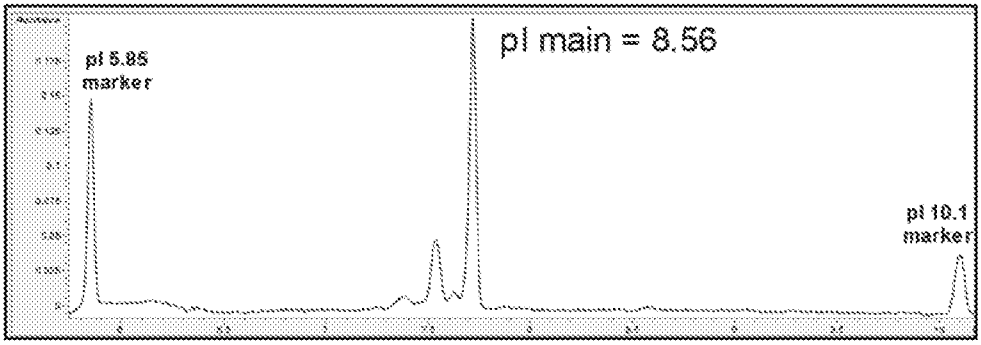


FIG. 12B

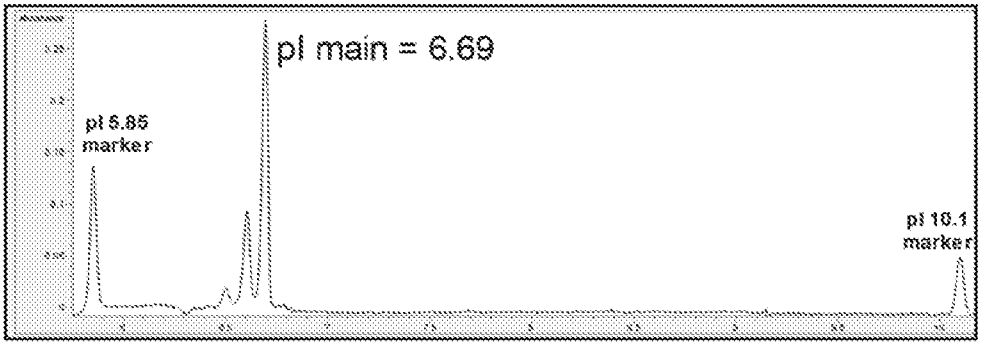
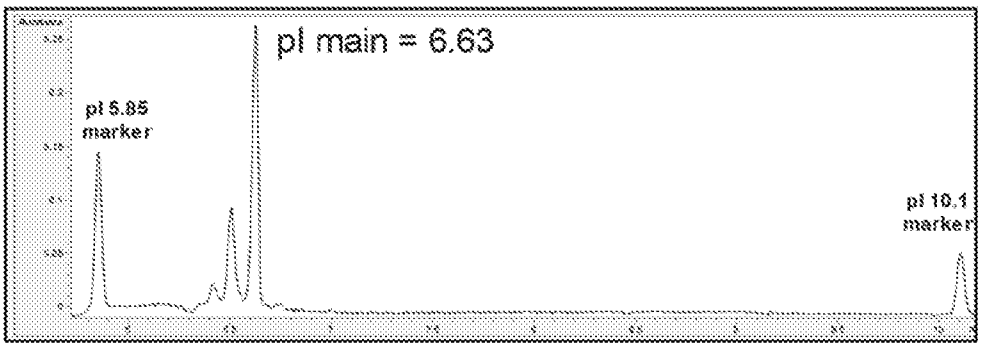


FIG. 12C



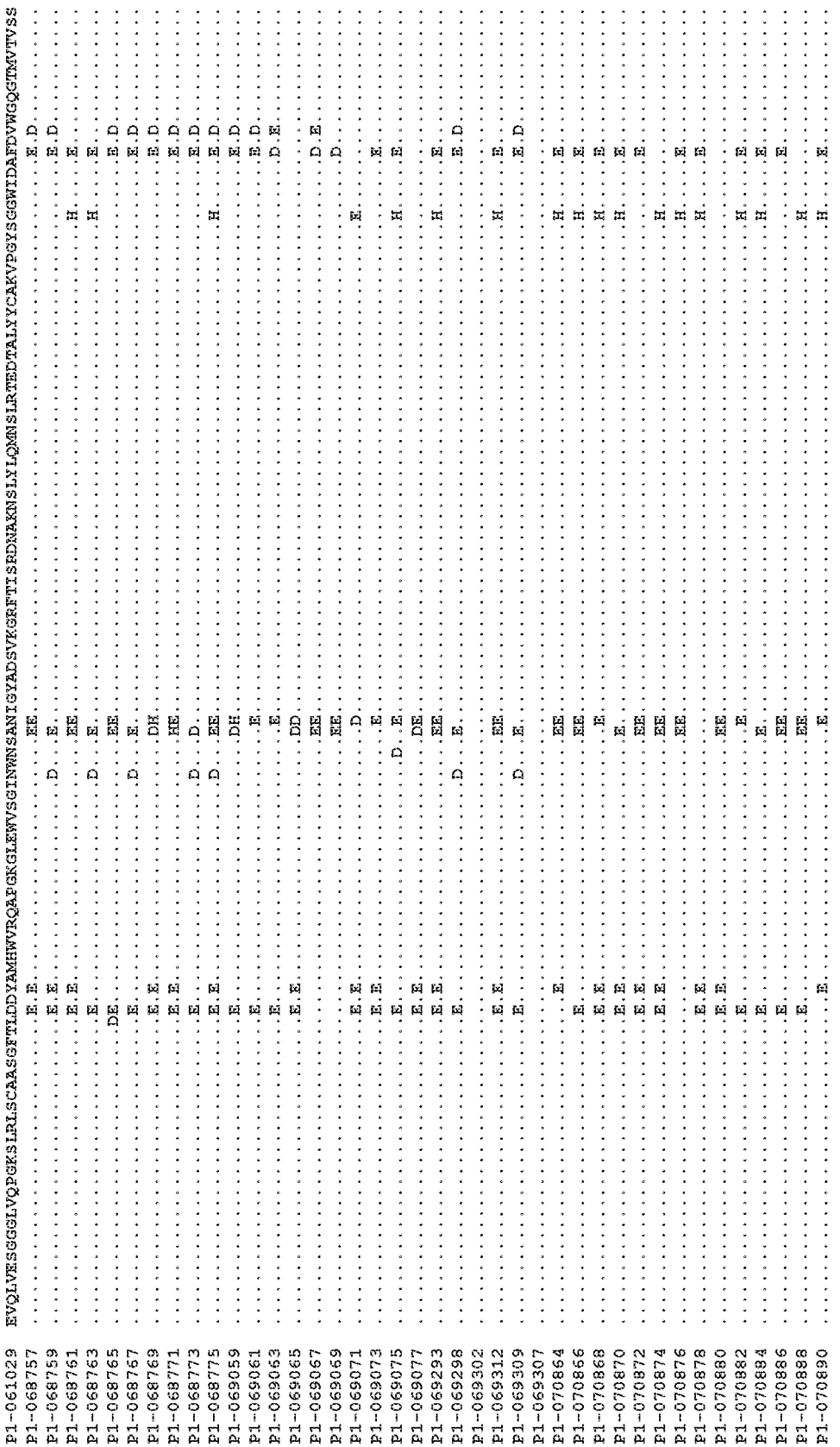

10 20 30 40 50 60 70 80 90 100 110 120
P1-061029 EVQLVESGGGLVQPGKSLRLSCAASGFTLDDYAMHWVRQAPGKGLEWVSGINWNSANIGYADSVKGRFTISRDNAKNSLYLQMNSLRTEDTALYYCAKVPGYSGGWTDAFDVWGQGTMVTVSS
P1-068757
P1-068759
P1-068761
P1-068763
P1-068765
P1-068767
P1-068769
P1-068771
P1-068773
P1-068775
P1-069059
P1-069061
P1-069063
P1-069065
P1-069067
P1-069069
P1-069071
P1-069073
P1-069075
P1-069077
P1-069293
P1-069298
P1-069302
P1-069312
P1-069309
P1-069307
P1-070864
P1-070866
P1-070868
P1-070870
P1-070872
P1-070874
P1-070876
P1-070878
P1-070880
P1-070882
P1-070884
P1-070886
P1-070888
P1-070890

FIG. 13A

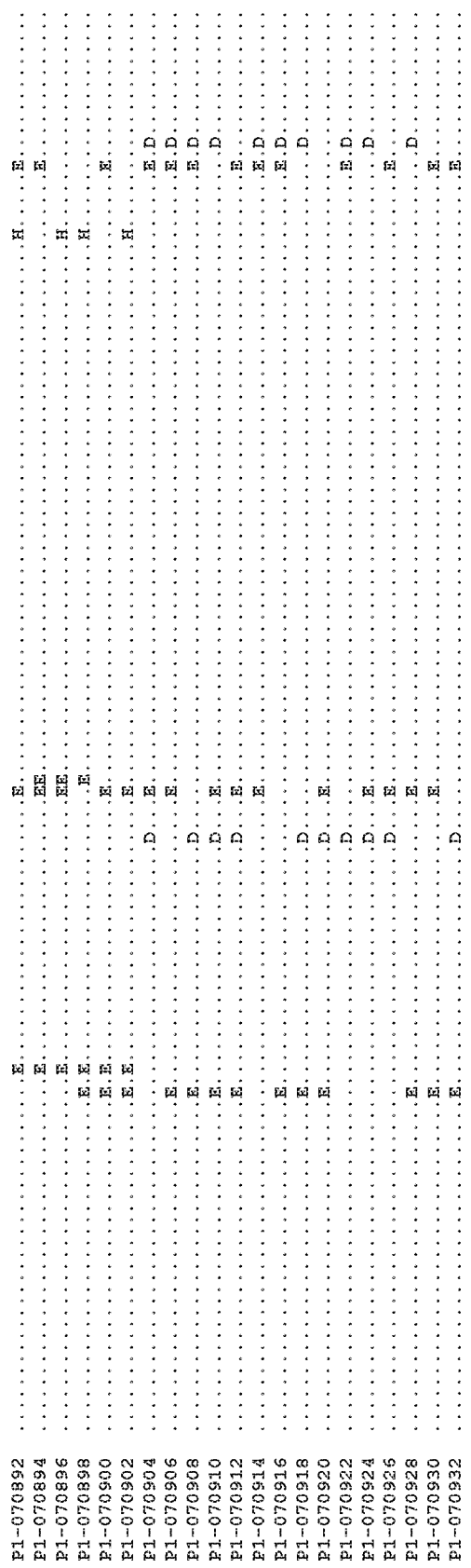

P1-070892
P1-070894
P1-070896
P1-070898
P1-070900
P1-070902
P1-070904
P1-070906
P1-070908
P1-070910
P1-070912
P1-070914
P1-070916
P1-070918
P1-070920
P1-070922
P1-070924
P1-070926
P1-070928
P1-070930
P1-070932

FIG. 13A (cont.)

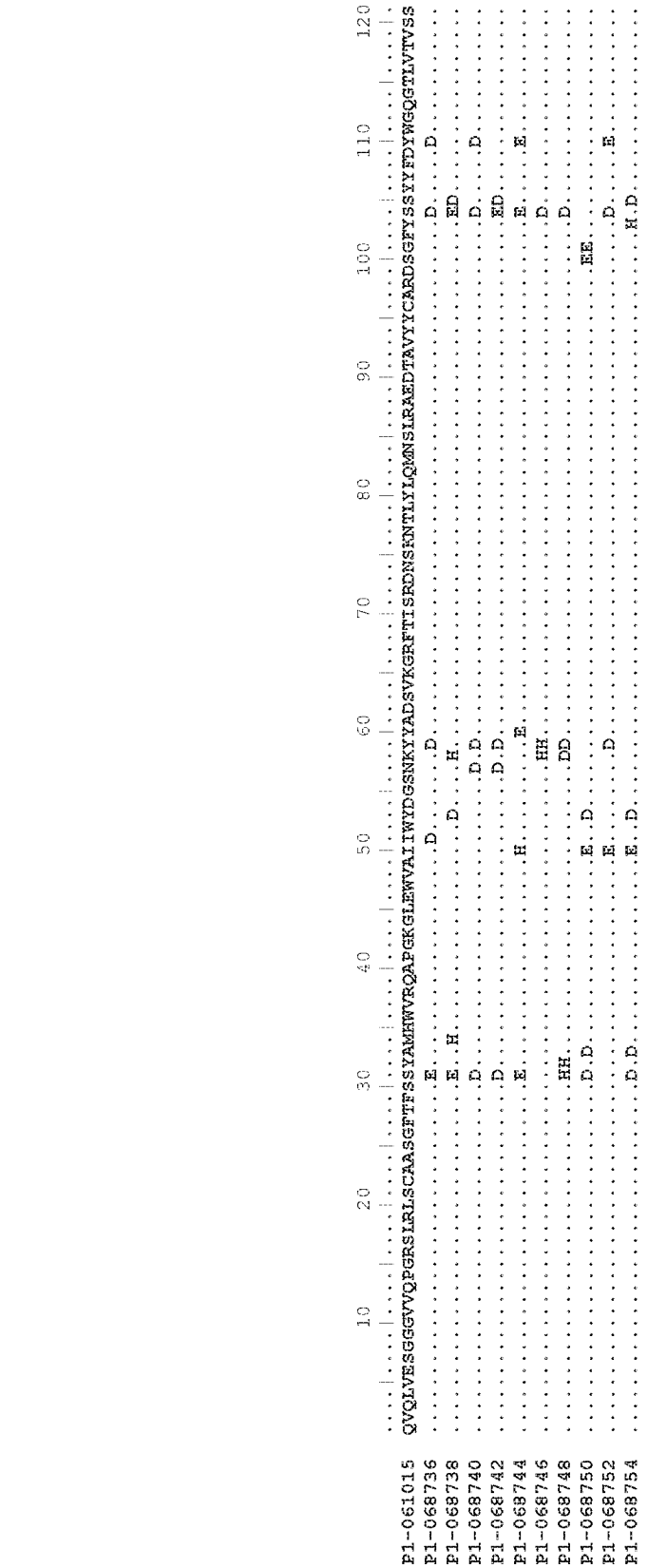

10 20 30 40 50 60 70 80 90 100 110 120
P1-061015 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMMWVRQAPGKGLEWVAIIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDSGFYSSYYFDYWGQGTLVTVSS
P1-068736 .....E.....D.....D.....D.....
P1-068738 .....E..H.....D....H.....ED.....
P1-068740 .....D.....D.D.....D.....D.....
P1-068742 .....D.....D.D.....ED.....
P1-068744 .....E.....H.....E.....E.....E.....
P1-068746 .....HH.....D.....
P1-068748 .....HH.....DD.....D.....
P1-068750 .....D.D.....E..D.....EE.....
P1-068752 .....E.....D.....D.....E.....
P1-068754 .....D.D.....E..D.....M.D.....

FIG. 13B

SEQUENCE LISTING

<110> Five Prime Therapeutics, Inc.
Bristol-Myers Squibb Company

<120> ANTIBODIES BINDING TO VISTA AT ACIDIC pH

<130> 01134-0048-00PCT

<150> US62/471,196
<151> 2017-03-14

<150> US62/636,746
<151> 2018-02-28

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<170> PatentIn version 3.5

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Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Pro Val Ala Ala
20 25 30

Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro Glu Gly Gln
35 40 45

Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val Asp Lys Gly His
50 55 60

Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser Ser Arg Gly Glu Val
65 70 75 80

Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg Asn Leu Thr Phe Gln Asp
85 90 95

Leu His Leu His His Gly Gly His Gln Ala Ala Asn Thr Ser His Asp
100 105 110

```
Leu Ala Gln Arg His Gly Leu Glu Ser Ala Ser Asp His His Gly Asn
        115                 120                 125

Phe Ser Ile Thr Met Arg Asn Leu Thr Leu Leu Asp Ser Gly Leu Tyr
    130                 135                 140

Cys Cys Leu Val Val Glu Ile Arg His His His Ser Glu His Arg Val
145                 150                 155                 160

His Gly Ala Met Glu Leu Gln Val Gln Thr Gly Lys Asp Ala Pro Ser
                165                 170                 175

Asn Cys Val Val Tyr Pro Ser Ser Ser Gln Asp Ser Glu Asn Ile Thr
            180                 185                 190

Ala Ala Ala Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu
        195                 200                 205

Pro Leu Ile Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn
    210                 215                 220

Arg Arg Ala Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile
225                 230                 235                 240

Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro Glu
                245                 250                 255

Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln Pro Ser
            260                 265                 270

Glu Ser Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro Leu Ser Pro
        275                 280                 285

Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp Pro Val Pro Asp
    290                 295                 300

Ser Pro Asn Phe Glu Val Ile
305                 310
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Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val Asp Lys Gly His
            20                  25                  30

Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser Ser Arg Gly Glu Val
        35                  40                  45

Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg Asn Leu Thr Phe Gln Asp
    50                  55                  60

Leu His Leu His His Gly Gly His Gln Ala Ala Asn Thr Ser His Asp
65                  70                  75                  80

Leu Ala Gln Arg His Gly Leu Glu Ser Ala Ser Asp His His Gly Asn
                85                  90                  95

Phe Ser Ile Thr Met Arg Asn Leu Thr Leu Leu Asp Ser Gly Leu Tyr
            100                 105                 110

Cys Cys Leu Val Val Glu Ile Arg His His His Ser Glu His Arg Val
        115                 120                 125

His Gly Ala Met Glu Leu Gln Val Gln Thr Gly Lys Asp Ala Pro Ser
    130                 135                 140

Asn Cys Val Val Tyr Pro Ser Ser Ser Gln Xaa Ser Glu Asn Ile Thr
```

145 150 155 160

Ala Ala Ala Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu
165 170 175

Pro Leu Ile Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn
180 185 190

Arg Arg Ala Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile
195 200 205

Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro Glu
210 215 220

Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln Pro Ser
225 230 235 240

Glu Ser Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro Leu Ser Pro
245 250 255

Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp Pro Val Pro Asp
260 265 270

Ser Pro Asn Phe Glu Val Ile
275

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Ser Leu Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu
20 25 30

Gly Pro Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr
35 40 45

```
Leu Asp Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro Glu Met Leu Arg
    50                  55                  60

Asn Ser Thr Asp Thr Thr Pro Leu Thr Gly Pro Gly Thr Pro Glu Ser
65                  70                  75                  80

Thr Thr Val Glu Pro Ala Ala Arg Arg Ser Thr Gly Leu Asp Ala Gly
                85                  90                  95

Gly Ala Val Thr Glu Leu Thr Thr Glu Leu Ala Asn Met Gly Asn Leu
            100                 105                 110

Ser Thr Asp Ser Ala Ala Met Glu Ile Gln Thr Thr Gln Pro Ala Ala
        115                 120                 125

Thr Glu Ala Gln Thr Thr Gln Pro Val Pro Thr Glu Ala Gln Thr Thr
    130                 135                 140

Pro Leu Ala Ala Thr Glu Ala Gln Thr Thr Arg Leu Thr Ala Thr Glu
145                 150                 155                 160

Ala Gln Thr Thr Pro Leu Ala Ala Thr Glu Ala Gln Thr Thr Pro Pro
                165                 170                 175

Ala Ala Thr Glu Ala Gln Thr Thr Gln Pro Thr Gly Leu Glu Ala Gln
            180                 185                 190

Thr Thr Ala Pro Ala Ala Met Glu Ala Gln Thr Thr Ala Pro Ala Ala
        195                 200                 205

Met Glu Ala Gln Thr Thr Pro Pro Ala Ala Met Glu Ala Gln Thr Thr
    210                 215                 220

Gln Thr Thr Ala Met Glu Ala Gln Thr Thr Ala Pro Glu Ala Thr Glu
225                 230                 235                 240

Ala Gln Thr Thr Gln Pro Thr Ala Thr Glu Ala Gln Thr Thr Pro Leu
                245                 250                 255
```

```
Ala Ala Met Glu Ala Leu Ser Thr Glu Pro Ser Ala Thr Glu Ala Leu
            260                 265                 270

Ser Met Glu Pro Thr Thr Lys Arg Gly Leu Phe Ile Pro Phe Ser Val
        275                 280                 285

Ser Ser Val Thr His Lys Gly Ile Pro Met Ala Ala Ser Asn Leu Ser
    290                 295                 300

Val Asn Tyr Pro Val Gly Ala Pro Asp His Ile Ser Val Lys Gln Cys
305                 310                 315                 320

Leu Leu Ala Ile Leu Ile Leu Ala Leu Val Ala Thr Ile Phe Phe Val
                325                 330                 335

Cys Thr Val Val Leu Ala Val Arg Leu Ser Arg Lys Gly His Met Tyr
            340                 345                 350

Pro Val Arg Asn Tyr Ser Pro Thr Glu Met Val Cys Ile Ser Ser Leu
        355                 360                 365

Leu Pro Asp Gly Gly Glu Gly Pro Ser Ala Thr Ala Asn Gly Gly Leu
    370                 375                 380

Ser Lys Ala Lys Ser Pro Gly Leu Thr Pro Glu Pro Arg Glu Asp Arg
385                 390                 395                 400

Glu Gly Asp Asp Leu Thr Leu His Ser Phe Leu Pro
                405                 410
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1               5                   10                  15
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Pro Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr Leu
            20                  25                  30

Asp Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro Glu Met Leu Arg Asn
        35                  40                  45

Ser Thr Asp Thr Thr Pro Leu Thr Gly Pro Gly Thr Pro Glu Ser Thr
    50                  55                  60

Thr Val Glu Pro Ala Ala Arg Arg Ser Thr Gly Leu Asp Ala Gly Gly
65                  70                  75                  80

Ala Val Thr Glu Leu Thr Thr Glu Leu Ala Asn Met Gly Asn Leu Ser
                85                  90                  95

Thr Asp Ser Ala Ala Met Glu Ile Gln Thr Thr Gln Pro Ala Ala Thr
            100                 105                 110

Glu Ala Gln Thr Thr Gln Pro Val Pro Thr Glu Ala Gln Thr Thr Pro
        115                 120                 125

Leu Ala Ala Thr Glu Ala Gln Thr Thr Arg Leu Thr Ala Thr Glu Ala
    130                 135                 140

Gln Thr Thr Pro Leu Ala Ala Thr Glu Ala Gln Thr Thr Pro Pro Ala
145                 150                 155                 160

Ala Thr Glu Ala Gln Thr Thr Gln Pro Thr Gly Leu Glu Ala Gln Thr
                165                 170                 175

Thr Ala Pro Ala Ala Met Glu Ala Gln Thr Thr Ala Pro Ala Ala Met
            180                 185                 190

Glu Ala Gln Thr Thr Pro Pro Ala Ala Met Glu Ala Gln Thr Thr Gln
        195                 200                 205

Thr Thr Ala Met Glu Ala Gln Thr Thr Ala Pro Glu Ala Thr Glu Ala
    210                 215                 220
```

```
Gln Thr Thr Gln Pro Thr Ala Thr Glu Ala Gln Thr Thr Pro Leu Ala
225                 230                 235                 240


Ala Met Glu Ala Leu Ser Thr Glu Pro Ser Ala Thr Glu Ala Leu Ser
                245                 250                 255


Met Glu Pro Thr Thr Lys Arg Gly Leu Phe Ile Pro Phe Ser Val Ser
            260                 265                 270


Ser Val Thr His Lys Gly Ile Pro Met Ala Ala Ser Asn Leu Ser Val
        275                 280                 285


Asn Tyr Pro Val Gly Ala Pro Asp His Ile Ser Val Lys Gln Cys Leu
    290                 295                 300


Leu Ala Ile Leu Ile Leu Ala Leu Val Ala Thr Ile Phe Phe Val Cys
305                 310                 315                 320


Thr Val Val Leu Ala Val Arg Leu Ser Arg Lys Gly His Met Tyr Pro
                325                 330                 335


Val Arg Asn Tyr Ser Pro Thr Glu Met Val Cys Ile Ser Ser Leu Leu
            340                 345                 350


Pro Asp Gly Gly Glu Gly Pro Ser Ala Thr Ala Asn Gly Gly Leu Ser
        355                 360                 365


Lys Ala Lys Ser Pro Gly Leu Thr Pro Glu Pro Arg Glu Asp Arg Glu
    370                 375                 380


Gly Asp Asp Leu Thr Leu His Ser Phe Leu Pro
385                 390                 395


<210>  5
<211>  226
<212>  PRT
<213>  Homo sapiens

<400>  5
```

```
Met Pro Leu Gln Leu Leu Leu Leu Leu Ile Leu Leu Gly Pro Gly Asn
1               5                  10                  15


Ser Leu Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu
            20                  25                  30


Gly Pro Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr
        35                  40                  45


Leu Asp Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro Glu Met Leu Arg
    50                  55                  60


Asn Ser Thr Asp Thr Thr Pro Leu Thr Gly Pro Gly Thr Pro Glu Ser
65                  70                  75                  80


Thr Thr Val Glu Pro Ala Ala Arg Arg Ser Thr Gly Leu Asp Ala Gly
                85                  90                  95


Gly Ala Val Thr Glu Leu Thr Thr Glu Leu Ala Asn Met Gly Asn Leu
            100                 105                 110


Ser Thr Asp Ser Ala Ala Met Glu Ile Gln Thr Thr Gln Pro Ala Ala
        115                 120                 125


Thr Glu Ala Gln Thr Thr Gln Pro Val Pro Thr Glu Ala Gln Thr Thr
    130                 135                 140


Pro Leu Ala Ala Thr Glu Ala Gln Thr Thr Arg Leu Thr Ala Thr Glu
145                 150                 155                 160


Ala Gln Thr Thr Pro Leu Ala Ala Thr Glu Ala Gln Thr Thr Pro Pro
                165                 170                 175


Ala Ala Thr Glu Ala Gln Thr Thr Gln Pro Thr Gly Leu Glu Ala Gln
            180                 185                 190


Thr Thr Ala Pro Ala Ala Met Glu Ala Gln Thr Thr Ala Pro Ala Ala
        195                 200                 205
```

Met Glu Ala Gln Thr Thr Pro Pro Ala Ala Met Glu Ala Gln Thr Thr
    210   215   220

Gln Thr
225

<210> 6
<211> 209
<212> PRT
<213> Homo sapiens

<400> 6

Leu Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu Gly
1   5   10   15

Pro Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr Leu
            20   25   30

Asp Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro Glu Met Leu Arg Asn
        35   40   45

Ser Thr Asp Thr Thr Pro Leu Thr Gly Pro Gly Thr Pro Glu Ser Thr
    50   55   60

Thr Val Glu Pro Ala Ala Arg Arg Ser Thr Gly Leu Asp Ala Gly Gly
65   70   75   80

Ala Val Thr Glu Leu Thr Thr Glu Leu Ala Asn Met Gly Asn Leu Ser
                85   90   95

Thr Asp Ser Ala Ala Met Glu Ile Gln Thr Thr Gln Pro Ala Ala Thr
            100   105   110

Glu Ala Gln Thr Thr Gln Pro Val Pro Thr Glu Ala Gln Thr Thr Pro
        115   120   125

Leu Ala Ala Thr Glu Ala Gln Thr Thr Arg Leu Thr Ala Thr Glu Ala
    130   135   140

Gln Thr Thr Pro Leu Ala Ala Thr Glu Ala Gln Thr Thr Pro Pro Ala

145 150 155 160

Ala Thr Glu Ala Gln Thr Thr Gln Pro Thr Gly Leu Glu Ala Gln Thr
165 170 175

Thr Ala Pro Ala Ala Met Glu Ala Gln Thr Thr Ala Pro Ala Ala Met
180 185 190

Glu Ala Gln Thr Thr Pro Pro Ala Ala Met Glu Ala Gln Thr Thr Gln
195 200 205

Thr

<210> 7
<211> 254
<212> PRT
<213> Homo sapiens

<400> 7

Gln Ala Thr Glu Tyr Glu Tyr Leu Asp Tyr Asp Phe Leu Pro Glu Thr
1 5 10 15

Glu Pro Pro Glu Met Leu Arg Asn Ser Thr Asp Thr Thr Pro Leu Thr
20 25 30

Gly Pro Gly Thr Pro Glu Ser Thr Thr Val Glu Pro Ala Ala Arg Arg
35 40 45

Ser Thr Gly Leu Asp Ala Gly Gly Ala Val Thr Glu Leu Thr Thr Glu
50 55 60

Leu Ala Asn Met Gly Asn Leu Ser Thr Asp Ser Ala Ala Met Glu Ile
65 70 75 80

Gln Thr Thr Gln Pro Ala Ala Thr Glu Ala Gln Thr Thr Pro Leu Ala
85 90 95

Ala Thr Glu Ala Gln Thr Thr Arg Leu Thr Ala Thr Glu Ala Gln Thr
100 105 110

```
Thr Pro Leu Ala Ala Thr Glu Ala Gln Thr Thr Pro Pro Ala Ala Thr
        115                 120                 125


Glu Ala Gln Thr Thr Gln Pro Thr Gly Leu Glu Ala Gln Thr Thr Ala
    130                 135                 140


Pro Ala Ala Met Glu Ala Gln Thr Thr Ala Pro Ala Ala Met Glu Ala
145                 150                 155                 160


Gln Thr Thr Pro Pro Ala Ala Met Glu Ala Gln Thr Thr Gln Thr Thr
                165                 170                 175


Ala Met Glu Ala Gln Thr Thr Ala Pro Glu Ala Thr Glu Ala Gln Thr
            180                 185                 190


Thr Gln Pro Thr Ala Thr Glu Ala Gln Thr Thr Pro Leu Ala Ala Met
        195                 200                 205


Glu Ala Leu Ser Thr Glu Pro Ser Ala Thr Glu Ala Leu Ser Met Glu
    210                 215                 220


Pro Thr Thr Lys Arg Gly Leu Phe Ile Pro Phe Ser Val Ser Ser Val
225                 230                 235                 240


Thr His Lys Gly Ile Pro Met Ala Ala Ser Asn Leu Ser Val
                245                 250


<210>  8
<211>  428
<212>  PRT
<213>  Homo sapiens

<400>  8

Met Ala Val Gly Ala Ser Gly Leu Glu Gly Asp Lys Met Ala Gly Ala
1               5                   10                  15


Met Pro Leu Gln Leu Leu Leu Leu Leu Ile Leu Leu Gly Pro Gly Asn
            20                  25                  30
```

```
Ser Leu Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu
        35                  40                  45

Gly Pro Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr
    50                  55                  60

Leu Asp Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro Glu Met Leu Arg
65                  70                  75                  80

Asn Ser Thr Asp Thr Thr Pro Leu Thr Gly Pro Gly Thr Pro Glu Ser
                85                  90                  95

Thr Thr Val Glu Pro Ala Ala Arg Arg Ser Thr Gly Leu Asp Ala Gly
            100                 105                 110

Gly Ala Val Thr Glu Leu Thr Thr Glu Leu Ala Asn Met Gly Asn Leu
        115                 120                 125

Ser Thr Asp Ser Ala Ala Met Glu Ile Gln Thr Thr Gln Pro Ala Ala
    130                 135                 140

Thr Glu Ala Gln Thr Thr Gln Pro Val Pro Thr Glu Ala Gln Thr Thr
145                 150                 155                 160

Pro Leu Ala Ala Thr Glu Ala Gln Thr Thr Arg Leu Thr Ala Thr Glu
                165                 170                 175

Ala Gln Thr Thr Pro Leu Ala Ala Thr Glu Ala Gln Thr Thr Pro Pro
            180                 185                 190

Ala Ala Thr Glu Ala Gln Thr Thr Gln Pro Thr Gly Leu Glu Ala Gln
        195                 200                 205

Thr Thr Ala Pro Ala Ala Met Glu Ala Gln Thr Thr Ala Pro Ala Ala
    210                 215                 220

Met Glu Ala Gln Thr Thr Pro Pro Ala Ala Met Glu Ala Gln Thr Thr
225                 230                 235                 240
```

```
Gln Thr Thr Ala Met Glu Ala Gln Thr Thr Ala Pro Glu Ala Thr Glu
                245                 250                 255


Ala Gln Thr Thr Gln Pro Thr Ala Thr Glu Ala Gln Thr Thr Pro Leu
            260                 265                 270


Ala Ala Met Glu Ala Leu Ser Thr Glu Pro Ser Ala Thr Glu Ala Leu
        275                 280                 285


Ser Met Glu Pro Thr Thr Lys Arg Gly Leu Phe Ile Pro Phe Ser Val
    290                 295                 300


Ser Ser Val Thr His Lys Gly Ile Pro Met Ala Ala Ser Asn Leu Ser
305                 310                 315                 320


Val Asn Tyr Pro Val Gly Ala Pro Asp His Ile Ser Val Lys Gln Cys
                325                 330                 335


Leu Leu Ala Ile Leu Ile Leu Ala Leu Val Ala Thr Ile Phe Phe Val
            340                 345                 350


Cys Thr Val Val Leu Ala Val Arg Leu Ser Arg Lys Gly His Met Tyr
        355                 360                 365


Pro Val Arg Asn Tyr Ser Pro Thr Glu Met Val Cys Ile Ser Ser Leu
    370                 375                 380


Leu Pro Asp Gly Gly Glu Gly Pro Ser Ala Thr Ala Asn Gly Gly Leu
385                 390                 395                 400


Ser Lys Ala Lys Ser Pro Gly Leu Thr Pro Glu Pro Arg Glu Asp Arg
                405                 410                 415


Glu Gly Asp Asp Leu Thr Leu His Ser Phe Leu Pro
            420                 425


<210>  9
<211>  395
<212>  PRT
```

<213> Homo sapiens

<400> 9

```
Leu Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu Gly
1               5                  10                  15


Pro Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr Leu
            20                  25                  30


Asp Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro Glu Met Leu Arg Asn
        35                  40                  45


Ser Thr Asp Thr Thr Pro Leu Thr Gly Pro Gly Thr Pro Glu Ser Thr
    50                  55                  60


Thr Val Glu Pro Ala Ala Arg Arg Ser Thr Gly Leu Asp Ala Gly Gly
65                  70                  75                  80


Ala Val Thr Glu Leu Thr Thr Glu Leu Ala Asn Met Gly Asn Leu Ser
                85                  90                  95


Thr Asp Ser Ala Ala Met Glu Ile Gln Thr Thr Gln Pro Ala Ala Thr
            100                 105                 110


Glu Ala Gln Thr Thr Gln Pro Val Pro Thr Glu Ala Gln Thr Thr Pro
        115                 120                 125


Leu Ala Ala Thr Glu Ala Gln Thr Thr Arg Leu Thr Ala Thr Glu Ala
    130                 135                 140


Gln Thr Thr Pro Leu Ala Ala Thr Glu Ala Gln Thr Thr Pro Pro Ala
145                 150                 155                 160


Ala Thr Glu Ala Gln Thr Thr Gln Pro Thr Gly Leu Glu Ala Gln Thr
                165                 170                 175


Thr Ala Pro Ala Ala Met Glu Ala Gln Thr Thr Ala Pro Ala Ala Met
            180                 185                 190
```

```
Glu Ala Gln Thr Thr Pro Pro Ala Ala Met Glu Ala Gln Thr Thr Gln
        195                 200                 205


Thr Thr Ala Met Glu Ala Gln Thr Thr Ala Pro Glu Ala Thr Glu Ala
    210                 215                 220


Gln Thr Thr Gln Pro Thr Ala Thr Glu Ala Gln Thr Thr Pro Leu Ala
225                 230                 235                 240


Ala Met Glu Ala Leu Ser Thr Glu Pro Ser Ala Thr Glu Ala Leu Ser
                245                 250                 255


Met Glu Pro Thr Thr Lys Arg Gly Leu Phe Ile Pro Phe Ser Val Ser
            260                 265                 270


Ser Val Thr His Lys Gly Ile Pro Met Ala Ala Ser Asn Leu Ser Val
        275                 280                 285


Asn Tyr Pro Val Gly Ala Pro Asp His Ile Ser Val Lys Gln Cys Leu
    290                 295                 300


Leu Ala Ile Leu Ile Leu Ala Leu Val Ala Thr Ile Phe Phe Val Cys
305                 310                 315                 320


Thr Val Val Leu Ala Val Arg Leu Ser Arg Lys Gly His Met Tyr Pro
                325                 330                 335


Val Arg Asn Tyr Ser Pro Thr Glu Met Val Cys Ile Ser Ser Leu Leu
            340                 345                 350


Pro Asp Gly Gly Glu Gly Pro Ser Ala Thr Ala Asn Gly Gly Leu Ser
        355                 360                 365


Lys Ala Lys Ser Pro Gly Leu Thr Pro Glu Pro Arg Glu Asp Arg Glu
    370                 375                 380


Gly Asp Asp Leu Thr Leu His Ser Phe Leu Pro
385                 390                 395
```

<210> 10
<211> 242
<212> PRT
<213> Homo sapiens

<400> 10

```
Met Ala Val Gly Ala Ser Gly Leu Glu Gly Asp Lys Met Ala Gly Ala
1               5                  10                  15


Met Pro Leu Gln Leu Leu Leu Leu Leu Ile Leu Leu Gly Pro Gly Asn
            20                  25                  30


Ser Leu Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu
        35                  40                  45


Gly Pro Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr
    50                  55                  60


Leu Asp Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro Glu Met Leu Arg
65                  70                  75                  80


Asn Ser Thr Asp Thr Thr Pro Leu Thr Gly Pro Gly Thr Pro Glu Ser
                85                  90                  95


Thr Thr Val Glu Pro Ala Ala Arg Arg Ser Thr Gly Leu Asp Ala Gly
            100                 105                 110


Gly Ala Val Thr Glu Leu Thr Thr Glu Leu Ala Asn Met Gly Asn Leu
        115                 120                 125


Ser Thr Asp Ser Ala Ala Met Glu Ile Gln Thr Thr Gln Pro Ala Ala
    130                 135                 140


Thr Glu Ala Gln Thr Thr Gln Pro Val Pro Thr Glu Ala Gln Thr Thr
145                 150                 155                 160


Pro Leu Ala Ala Thr Glu Ala Gln Thr Thr Arg Leu Thr Ala Thr Glu
                165                 170                 175


Ala Gln Thr Thr Pro Leu Ala Ala Thr Glu Ala Gln Thr Thr Pro Pro
```

180 185 190

Ala Ala Thr Glu Ala Gln Thr Thr Gln Pro Thr Gly Leu Glu Ala Gln
195 200 205

Thr Thr Ala Pro Ala Ala Met Glu Ala Gln Thr Thr Ala Pro Ala Ala
210 215 220

Met Glu Ala Gln Thr Thr Pro Pro Ala Ala Met Glu Ala Gln Thr Thr
225 230 235 240

Gln Thr

<210> 11
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069059 VH

<400> 11

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

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

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

Ser Gly Ile Asn Trp Asn Ser Asp His Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 12
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069059 VL

<400> 12

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 Ser Ser Ser
20 25 30

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

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

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

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 13
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069059 IgG1.3 HC

<400> 13

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1               5                  10                  15


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


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


Ser Gly Ile Asn Trp Asn Ser Asp His Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60


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


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


Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
            100                 105                 110


Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125


Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140


Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160


Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175


Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190
```

```
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205


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


Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240


Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255


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


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


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


Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320


Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335


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


Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365


Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380


Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400
```

```
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  14
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-069059 LC

<400>  14

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 Ser Ser Ser
            20                  25                  30


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


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


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


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


Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
```

```
            100                 105                 110

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

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

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

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

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

Tyr 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>  15
<211>  123
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-069061 VH

<400>  15

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

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

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

```
Ser Gly Ile Asn Trp Asn Ser Ala Glu Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60


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


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


Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
            100                 105                 110


Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210>  16
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-069061 VL

<400>  16

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 Ser Ser Ser
            20                  25                  30


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


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


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


Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
```

85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 17
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069061 IgG1.3 HC

<400> 17

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

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

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

Ser Gly Ile Asn Trp Asn Ser Ala Glu Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
130 135 140

```
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

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

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

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

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

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

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350
```

```
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365


Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380


Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400


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


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  18
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-069061 LC

<400>  18

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 Ser Ser Ser
            20                  25                  30


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


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
```

```
    50                  55                  60

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

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110

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

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

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

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

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

Tyr 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>  19
<211>  123
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-069063 VH

<400>  19
```

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1               5                   10                  15


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


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


Ser Gly Ile Asn Trp Asn Ser Ala Glu Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60


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


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


Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Asp Asp Glu
            100                 105                 110


Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210>  20
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-069063 VL

<400>  20

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
```

35 40 45

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

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

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 21
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069063 IgG1.3 HC

<400> 21

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

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

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

Ser Gly Ile Asn Trp Asn Ser Ala Glu Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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

```
Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Asp Asp Glu
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

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

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

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

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

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

```
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320


Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335


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


Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365


Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380


Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400


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


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  22
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-069063 LC

<400>  22

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 Ser Ser Ser
            20                  25                  30

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

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

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

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110

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

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

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

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

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

Tyr 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> 23
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069065 VH

<400> 23

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
20 25 30

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

Ser Gly Ile Asn Trp Asn Ser Asp Asp Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Phe Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 24
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069065 VL

<400> 24

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 Ser Ser Ser
20 25 30

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

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

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

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 25
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069065 IgG1.3 HC

<400> 25

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
20 25 30

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

```
Ser Gly Ile Asn Trp Asn Ser Asp Asp Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60

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

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

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Phe Asp Val
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

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

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255
```

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

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

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

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

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

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

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

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly
    450
```

<210> 26
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069065 LC

<400> 26

```
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 Ser Ser Ser
            20                  25                  30


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


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


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


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


Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110


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


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


Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160


Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
```

165 170 175

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

Tyr 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> 27
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069067 VH

<400> 27

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

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

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

Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Asp Asp Glu
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 28
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069067 VL

<400> 28

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 Ser Ser Ser
20 25 30

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

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

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

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 29
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069067 IgG1.3 HC

<400> 29

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1               5                  10                  15

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

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

Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60

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

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

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Asp Asp Glu
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205
```

```
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

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

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

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

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

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

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415
```

```
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  30
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-069067 LC

<400>  30

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 Ser Ser Ser
            20                  25                  30


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


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


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


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


Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110


Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
```

115 120 125

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

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

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

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

Tyr 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> 31
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069069 VH

<400> 31

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

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

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

Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
50 55 60

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


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


Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Asp Asp Val
            100                 105                 110


Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210>  32
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-069069 VL

<400>  32

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 Ser Ser Ser
            20                  25                  30


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


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


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


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


Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
```

100 105

<210> 33
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069069 IgG1.3 HC

<400> 33

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

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

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

Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Asp Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145 150 155 160

```
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

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

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

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

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

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

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

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

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365
```

```
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380


Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400


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


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  34
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-069069 LC

<400>  34

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 Ser Ser Ser
            20                  25                  30


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


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


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
```

65 70 75 80

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
100 105 110

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

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

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

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

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

Tyr 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> 35
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069071 VH

<400> 35

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
20 25 30

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

Ser Gly Ile Asn Trp Asn Ser Ala Asp Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Val Pro Gly Tyr Ser Glu Gly Trp Ile Asp Ala Phe Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 36
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069071 VL

<400> 36

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 Ser Ser Ser
20 25 30

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

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

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

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 37
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069071 IgG1.3 HC

<400> 37

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
20 25 30

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

Ser Gly Ile Asn Trp Asn Ser Ala Asp Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Val Pro Gly Tyr Ser Glu Gly Trp Ile Asp Ala Phe Asp Val
100 105 110

```
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125


Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140


Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160


Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175


Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190


Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205


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


Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240


Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255


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


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


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


Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320
```

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Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335


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


Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365


Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380


Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400


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


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  38
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-069071 LC

<400>  38

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 Ser Ser Ser
```

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            20                  25                  30

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

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

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

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110

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

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

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

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

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

Tyr 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> 39

<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069073 VH

<400> 39

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
20 25 30

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

Ser Gly Ile Asn Trp Asn Ser Ala Glu Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 40
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069073 VL

<400> 40

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 Ser Ser Ser
20 25 30

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

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

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

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 41
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069073 IgG1.3 HC

<400> 41

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
20 25 30

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

Ser Gly Ile Asn Trp Asn Ser Ala Glu Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Val
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

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

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

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

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


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


Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320


Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335


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


Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365


Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380


Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400


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


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  42
<211>  215
<212>  PRT
```

<213> Artificial Sequence

<220>
<223> P1-069073 LC

<400> 42

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 Ser Ser Ser
20 25 30

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

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

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

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
100 105 110

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

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

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

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

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val

180 185 190

Tyr 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> 43
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069075 VH

<400> 43

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

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

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

Ser Gly Ile Asn Trp Asp Ser Ala Glu Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 44
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069075 VL

<400> 44

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 Ser Ser Ser
20 25 30

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

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

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

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 45
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069075 IgG1.3 HC

<400> 45

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

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

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

Ser Gly Ile Asn Trp Asp Ser Ala Glu Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60

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

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

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Val
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220
```

```
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

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

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

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

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

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

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

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

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430
```

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
435 440 445

Leu Ser Pro Gly
450

<210> 46
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069075 LC

<400> 46

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 Ser Ser Ser
20 25 30

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

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

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

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
100 105 110

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

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu

130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

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

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

Tyr 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> 47
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069077 VH

<400> 47

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
20 25 30

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

Ser Gly Ile Asn Trp Asn Ser Asp Glu Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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


Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Phe Asp Val
            100                 105                 110


Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210>  48
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-069077 VL

<400>  48

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 Ser Ser Ser
            20                  25                  30


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


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


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


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


Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100                 105


<210>  49
```

<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069077 IgG1.3 HC

<400> 49

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
20 25 30

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

Ser Gly Ile Asn Trp Asn Ser Asp Glu Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Phe Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
165 170 175

```
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

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

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

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

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

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

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

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

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380
```

```
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400


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


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  50
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-069077 LC

<400>  50

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 Ser Ser Ser
            20                  25                  30


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


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


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


Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
```

85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
100 105 110

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

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

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

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

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

Tyr 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> 51
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068761 VH

<400> 51

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
20 25 30

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


Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60


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


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


Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Val
            100                 105                 110


Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210>  52
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-068761 VL

<400>  52

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 Ser Ser Ser
            20                  25                  30


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


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


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
```

65 70 75 80

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 53
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068761 IgG1.3 HC

<400> 53

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
20 25 30

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

Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

```
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

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

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

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

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

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

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335
```

```
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350


Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365


Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380


Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400


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


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  54
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-068761 LC

<400>  54

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
```

35 40 45

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

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

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
100 105 110

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

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

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

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

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

Tyr 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> 55
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068767 VH

<400> 55

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

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

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

Ser Gly Ile Asp Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
    50   55   60

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

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

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
            100   105   110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115   120

<210> 56
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068767 VL

<400> 56

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 Ser Ser Ser

20 25 30

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

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

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

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 57
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068767 IgG1.3 HC

<400> 57

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

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

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

Ser Gly Ile Asp Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

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

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

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

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

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

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

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

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

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

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly
    450
```

<210> 58
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068767 LC

<400> 58

```
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 Ser Ser Ser
            20                  25                  30


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


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


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


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


Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110


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


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


Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160


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


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


Tyr 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> 59
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068773 VH

<400> 59

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

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

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

Ser Gly Ile Asp Trp Asn Ser Asp Asn Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 60
<211> 108
<212> PRT

<213> Artificial Sequence

<220>
<223> P1-068773 VL

<400> 60

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 Ser Ser Ser
20 25 30

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

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

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

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 61
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068773 IgG1.3 HC

<400> 61

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

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

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

Ser Gly Ile Asp Trp Asn Ser Asp Asn Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60

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

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

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

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

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240
```

```
Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

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

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

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

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

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

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

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

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445
```

Leu Ser Pro Gly
450

<210> 62
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068773 LC

<400> 62

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 Ser Ser Ser
20 25 30

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

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

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

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
100 105 110

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

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

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser

145 150 155 160

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

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

Tyr 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> 63
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068765 VH

<400> 63

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

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

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

Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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

```
Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
            100                 105                 110


Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210>  64
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-068765 VL

<400>  64

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 Ser Ser Ser
            20                  25                  30


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


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


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


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


Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100                 105


<210>  65
<211>  452
<212>  PRT
<213>  Artificial Sequence
```

<220>
<223> P1-068765 IgG1.3 HC

<400> 65

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

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

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

Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
    50   55   60

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

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

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
            100   105   110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115   120   125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130   135   140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145   150   155   160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165   170   175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180   185   190

```
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

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

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

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

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

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

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

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

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400
```

```
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  66
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-068765 LC

<400>  66

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 Ser Ser Ser
            20                  25                  30


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


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


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


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


Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
```

100 105 110

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

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

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

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

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

Tyr 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> 67
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-061029 VH

<400> 67

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

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

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

Ser Gly Ile Asn Trp Asn Ser Ala Asn Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Phe Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 68
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-061029 VL

<400> 68

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 Ser Ser Ser
20 25 30

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

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

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

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro

85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 69
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-061029 IgG1.3 HC

<400> 69

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

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

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

Ser Gly Ile Asn Trp Asn Ser Ala Asn Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Phe Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
130 135 140

```
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160


Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175


Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190


Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205


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


Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240


Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255


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


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


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


Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320


Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335


Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350
```

```
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365


Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380


Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400


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


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  70
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-061029 LC

<400>  70

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 Ser Ser Ser
            20                  25                  30


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


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
```

```
    50                  55                  60

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

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110

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

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

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

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

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

Tyr 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>  71
<211>  123
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-068757 VH

<400>  71
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```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
            20                  25                  30


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


Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60


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


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


Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
            100                 105                 110


Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210>  72
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-068757 VL

<400>  72

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
```

35 40 45

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

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

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 73
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068757 IgG1.3 HC

<400> 73

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
20 25 30

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

Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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

```
Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

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

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

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

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

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

```
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320


Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335


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


Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365


Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380


Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400


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


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  74
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-068757 LC

<400>  74

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 Ser Ser Ser
            20                  25                  30

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

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

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

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110

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

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

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

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

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

Tyr 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> 75
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068771 VH

<400> 75

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
20 25 30

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

Ser Gly Ile Asn Trp Asn Ser His Glu Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 76
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068771 VL

<400> 76

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 Ser Ser Ser
20 25 30

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

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

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

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 77
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068771 IgG1.3 HC

<400> 77

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
20 25 30

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

```
Ser Gly Ile Asn Trp Asn Ser His Glu Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60

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

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

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

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

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255
```

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

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

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

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

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

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

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

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly
    450
```

<210> 78
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068771 LC

<400> 78

```
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 Ser Ser Ser
            20                  25                  30


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


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


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


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


Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110


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


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


Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160


Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
```

165 170 175

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

Tyr 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> 79
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068775 VH

<400> 79

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
20 25 30

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

Ser Gly Ile Asp Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Asp
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 80
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068775 VL

<400> 80

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 Ser Ser Ser
20 25 30

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

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

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

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 81
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068775 IgG1.3 HC

<400> 81

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
            20                  25                  30

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

Ser Gly Ile Asp Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60

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

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

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Asp
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205
```

```
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

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

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

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

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

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

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415
```

```
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  82
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-068775 LC

<400>  82

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 Ser Ser Ser
            20                  25                  30


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


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


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


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


Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110


Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
```

115 120 125

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

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

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

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

Tyr 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> 83
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068769 VH

<400> 83

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
20 25 30

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

Ser Gly Ile Asn Trp Asn Ser Asp His Ile Gly Tyr Ala Asp Ser Val
50 55 60

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


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


Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
            100                 105                 110


Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210>  84
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-068769 VL

<400>  84

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 Ser Ser Ser
            20                  25                  30


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


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


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


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


Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
```

100 105

<210> 85
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068769 IgG1.3 HC

<400> 85

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
20 25 30

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

Ser Gly Ile Asn Trp Asn Ser Asp His Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145 150 155 160

```
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

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

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

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

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

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

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

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

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365
```

```
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380


Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400


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


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  86
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-068769 LC

<400>  86

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 Ser Ser Ser
            20                  25                  30


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


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


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
```

65 70 75 80

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
100 105 110

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

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

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

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

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

Tyr 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> 87
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068759 VH

<400> 87

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

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
            20                  25                  30


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


Ser Gly Ile Asp Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60


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


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


Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
            100                 105                 110


Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210>  88
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-068759 VL

<400>  88

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 Ser Ser Ser
            20                  25                  30


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


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
```

50 55 60

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

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 89
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068759 IgG1.3 HC

<400> 89

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
20 25 30

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

Ser Gly Ile Asp Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
100 105 110

```
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125


Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140


Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160


Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175


Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190


Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205


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


Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240


Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255


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


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


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


Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320
```

```
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335


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


Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365


Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380


Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400


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


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  90
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-068759 LC

<400>  90

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 Ser Ser Ser
```

20 25 30

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

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

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

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
100 105 110

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

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

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

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

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

Tyr 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> 91

<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068763 VH

<400> 91

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

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

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

Ser Gly Ile Asp Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 92
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068763 VL

<400> 92

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 Ser Ser Ser
20 25 30

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

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

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

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 93
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068763 IgG1.3 HC

<400> 93

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

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

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

Ser Gly Ile Asp Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Val
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

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

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

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

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


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


Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320


Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335


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


Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365


Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380


Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400


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


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  94
<211>  215
<212>  PRT
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<213> Artificial Sequence

<220>
<223> P1-068763 LC

<400> 94

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 Ser Ser Ser
20 25 30

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

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

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

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
100 105 110

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

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

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

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

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val

180 185 190

Tyr 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> 95
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-061015 VH

<400> 95

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

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

Ala Ile Ile Trp Tyr Asp Gly Ser 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 Val Tyr Tyr Cys
85 90 95

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

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 96
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-061015 VL

<400> 96

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

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

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

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

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

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

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 97
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-061015 IgG1.3 HC

<400> 97

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

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

Ala Ile Ile Trp Tyr Asp Gly Ser 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 Val Tyr Tyr Cys
                85                  90                  95

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

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

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

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

```
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly
225                 230                 235                 240


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


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


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


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


Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320


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


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


Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365


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


Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400


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


Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430
```

```
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445


Pro Gly
    450


<210>  98
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-061015 LC

<400>  98

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


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


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


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


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


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


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


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


Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
```

130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

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

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

Tyr 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> 99
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068748 VH

<400> 99

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 His His
20 25 30

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

Ala Ile Ile Trp Tyr Asp Gly Ser Asn Asp Asp 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 Val Tyr Tyr Cys
                85                  90                  95


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


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  100
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-068748 VL

<400>  100

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


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


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


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


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


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


Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210>  101
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<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068748 IgG1.3 HC

<400> 101

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 His His
20 25 30

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

Ala Ile Ile Trp Tyr Asp Gly Ser Asn Asp Asp 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 Val Tyr Tyr Cys
85 90 95

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

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

```
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190


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


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


Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly
225                 230                 235                 240


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


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


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


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


Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320


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


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


Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365


Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380
```

```
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400


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


Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430


His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445


Pro Gly
    450


<210>  102
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-068748 LC

<400>  102

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


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


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


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


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


Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro
```

85 90 95

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

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

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

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

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

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

Tyr 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> 103
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068744 VH

<400> 103

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 Glu Tyr
20 25 30

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


Ala His Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Glu 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 Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Ser Gly Phe Tyr Glu Ser Tyr Tyr Phe Asp Glu Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  104
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-068744 VL

<400>  104

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


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


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


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


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
```

65 70 75 80

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

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 105
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068744 IgG1.3 HC

<400> 105

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 Glu Tyr
20 25 30

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

Ala His Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Glu 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 Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ser Gly Phe Tyr Glu Ser Tyr Tyr Phe Asp Glu Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

```
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

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

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly
225                 230                 235                 240

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

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

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

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

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

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

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


Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365


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


Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400


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


Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430


His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445


Pro Gly
    450


<210>  106
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-068744 LC

<400>  106

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


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


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
```

```
        35                  40                  45

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

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

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

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

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

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

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

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

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

Tyr 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>  107
<211>  121
<212>  PRT
<213>  Artificial Sequence
```

<220>
<223> P1-068736 VH

<400> 107

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 Glu Tyr
            20   25   30

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

Ala Ile Asp Trp Tyr Asp Gly Ser Asn Lys Asp 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 Val Tyr Tyr Cys
                85   90   95

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

Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

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

<220>
<223> P1-068736 VL

<400> 108

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser

20 25 30

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

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

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

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

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 109
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068736 IgG1.3 HC

<400> 109

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 Glu Tyr
20 25 30

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

Ala Ile Asp Trp Tyr Asp Gly Ser Asn Lys Asp 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 Val Tyr Tyr Cys
                85                  90                  95

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

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

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

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly
225                 230                 235                 240

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

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

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

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


Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320


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


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


Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365


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


Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400


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


Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430


His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445


Pro Gly
    450
```

<210> 110
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068736 LC

<400> 110

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

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

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

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

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

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

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

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

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

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

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

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

Tyr 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> 111
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068752 VH

<400> 111

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

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

Ala Glu Ile Trp Tyr Asp Gly Ser Asn Lys Asp 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 Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ser Gly Phe Tyr Asp Ser Tyr Tyr Phe Asp Glu Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 112
<211> 108
<212> PRT

<213> Artificial Sequence

<220>
<223> P1-068752 VL

<400> 112

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

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

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

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

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

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

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 113
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068752 IgG1.3 HC

<400> 113

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

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

Ala Glu Ile Trp Tyr Asp Gly Ser Asn Lys Asp 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 Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Ser Gly Phe Tyr Asp Ser Tyr Tyr Phe Asp Glu Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

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

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly
225                 230                 235                 240
```

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

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

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

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

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

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

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

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

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

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445
```

Pro Gly
450

<210> 114
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068752 LC

<400> 114

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

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

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

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

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

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

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

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

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

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser

145 150 155 160

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

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

Tyr 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> 115
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068740 VH

<400> 115

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 Asp Tyr
20 25 30

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

Ala Ile Ile Trp Tyr Asp Gly Ser Asp Lys Asp 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 Val Tyr Tyr Cys
85 90 95

```
Ala Arg Asp Ser Gly Phe Tyr Asp Ser Tyr Tyr Phe Asp Asp Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  116
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-068740 VL

<400>  116

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


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


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


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


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


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


Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210>  117
<211>  450
<212>  PRT
<213>  Artificial Sequence
```

<220>
<223> P1-068740 IgG1.3 HC

<400> 117

```
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 Asp Tyr
            20                  25                  30


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


Ala Ile Ile Trp Tyr Asp Gly Ser Asp Lys Asp 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 Val Tyr Tyr Cys
                85                  90                  95


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


Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125


Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140


Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160


Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175


Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190
```

```
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly
225                 230                 235                 240

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

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

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

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

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

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

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

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400
```

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

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly
450

<210> 118
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068740 LC

<400> 118

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

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

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

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

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

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

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala

```
            100                 105                 110

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

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

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

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

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

Tyr 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>  119
<211>  121
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-068742 VH

<400>  119

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 Asp Tyr
            20                  25                  30

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

```
Ala Ile Ile Trp Tyr Asp Gly Ser Asp Lys Asp 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 Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Ser Gly Phe Tyr Glu Asp Tyr Tyr Phe Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  120
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-068742 VL

<400>  120

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


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


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


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


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


Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro
```

85 90 95

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 121
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068742 IgG1.3 HC

<400> 121

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 Asp Tyr
20 25 30

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

Ala Ile Ile Trp Tyr Asp Gly Ser Asp Lys Asp 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 Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ser Gly Phe Tyr Glu Asp Tyr Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

```
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160


Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175


Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190


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


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


Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly
225                 230                 235                 240


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


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


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


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


Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320


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


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

```
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365


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


Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400


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


Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430


His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445


Pro Gly
    450


<210>  122
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-068742 LC

<400>  122

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


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


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


Ile Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser
```

50 55 60

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

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

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

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

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

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

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

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

Tyr 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> 123
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068746 VH

<400> 123

```
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


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


Ala Ile Ile Trp Tyr Asp Gly Ser Asn His His 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 Val Tyr Tyr Cys
                85                  90                  95


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


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  124
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-068746 VL

<400>  124

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


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


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
```

35 40 45

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

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

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

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 125
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068746 IgG1.3 HC

<400> 125

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

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

Ala Ile Ile Trp Tyr Asp Gly Ser Asn His His 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 Val Tyr Tyr Cys
85 90 95

```
Ala Arg Asp Ser Gly Phe Tyr Asp Ser Tyr Tyr Phe Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

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

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly
225                 230                 235                 240

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

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

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

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

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Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320


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


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


Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365


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


Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400


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


Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430


His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445


Pro Gly
    450


<210>  126
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-068746 LC

<400>  126

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

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

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

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

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

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

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

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

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

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

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

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

Tyr 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> 127
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068750 VH

<400> 127

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 Asp Tyr
20 25 30

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

Ala Glu Ile Trp Asp Asp Gly Ser 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 Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Glu Glu Phe Tyr Ser Ser Tyr Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 128
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068750 VL

<400> 128

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

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

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

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

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

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

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 129
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068750 IgG1.3 HC

<400> 129

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 Asp Tyr
20 25 30

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

```
Ala Glu Ile Trp Asp Asp Gly Ser 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 Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Glu Glu Phe Tyr Ser Ser Tyr Tyr Phe Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

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

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly
225                 230                 235                 240

Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255
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Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270


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


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


Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320


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


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


Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365


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


Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400


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


Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430


His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445


Pro Gly
    450
```

<210> 130
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068750 LC

<400> 130

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

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

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

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

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

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

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

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

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

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu

165 170 175

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

Tyr 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> 131
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068738 VH

<400> 131

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 Glu Tyr
20 25 30

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

Ala Ile Ile Trp Asp Asp Gly Ser Asn His 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 Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ser Gly Phe Tyr Glu Asp Tyr Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 132
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068738 VL

<400> 132

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

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

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

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

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

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

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 133
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068738 IgG1.3 HC

<400> 133

```
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 Glu Tyr
            20                  25                  30

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

Ala Ile Ile Trp Asp Asp Gly Ser Asn His 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 Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Ser Gly Phe Tyr Glu Asp Tyr Tyr Phe Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
        115                 120                 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145                 150                 155                 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205
```

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


Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly
225                 230                 235                 240


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


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


Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285


His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300


Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320


Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335


Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350


Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365


Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380


Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400


Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415
```

```
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430


His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445


Pro Gly
    450


<210>  134
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-068738 LC

<400>  134

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15


Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser
    50                  55                  60


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65                  70                  75                  80


Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro
                85                  90                  95


Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala
            100                 105                 110


Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
```

115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr 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> 135
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068754 VH

<400> 135

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 Asp Tyr
20 25 30

Asp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Glu Ile Trp Asp Asp Gly Ser 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 Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Ser Gly Phe His Ser Asp Tyr Tyr Phe Asp Tyr Trp Gly
            100                 105                 110


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  136
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-068754 VL

<400>  136

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15


Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser
    50                  55                  60


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65                  70                  75                  80


Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro
                85                  90                  95


Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
```

100 105

<210> 137
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-068754 IgG1.3 HC

<400> 137

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 Asp Tyr
20 25 30

Asp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Glu Ile Trp Asp Asp Gly Ser 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 Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ser Gly Phe His Ser Asp Tyr Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

```
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175


Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
            180                 185                 190


Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205


Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
    210                 215                 220


Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly
225                 230                 235                 240


Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255


Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270


Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285


His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300


Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320


Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335


Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350


Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365
```

```
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380


Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400


Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415


Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430


His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445


Pro Gly
    450


<210>  138
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-068754 LC

<400>  138

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15


Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser
    50                  55                  60


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
```

65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro
85 90 95

Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr 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> 139
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069293 VH (P1-068761.IgG1f)

<400> 139

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 140
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069293 VL (P1-068761.IgG1f)

<400> 140

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 Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 141
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069293 HC (P1-068761.IgG1f)

<400> 141

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Val
100 105 110

```
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125


Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140


Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160


Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175


Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190


Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205


Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220


Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
225                 230                 235                 240


Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255


Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270


Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285


Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300


Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320
```

```
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335


Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350


Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365


Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380


Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400


Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  142
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-069293 LC (P1-068761.IgG1f)

<400>  142

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 Ser Ser Ser
```

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr 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> 143

<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069298 VH (P1-068767.IgG1f)

<400> 143

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asp Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 144
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069298 VL (P1-068767.IgG1f)

<400> 144

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 Ser Ser Ser
            20                  25                  30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100                 105


<210>  145
<211>  452
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-069298 HC (P1-068767.IgG1f)

<400>  145

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
            20                  25                  30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Gly Ile Asp Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60
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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
225                 230                 235                 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270
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Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285


Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300


Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320


Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335


Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350


Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365


Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380


Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400


Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  146
<211>  215
<212>  PRT
```

<213> Artificial Sequence

<220>
<223> P1-069298 LC (P1-068767.IgG1f)

<400> 146

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 Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val

180 185 190

Tyr 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> 147
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069302 VH (P1-061029.IgG1f)

<400> 147

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asn Trp Asn Ser Ala Asn Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Phe Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 148
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069302 VL (P1-061029.IgG1f)

<400> 148

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 Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 149
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069302 HC (P1-061029.IgG1f)

<400> 149

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Asp Tyr
            20                  25                  30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Gly Ile Asn Trp Asn Ser Ala Asn Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Phe Asp Val
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220
```

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Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
225                 230                 235                 240


Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255


Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270


Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285


Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300


Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320


Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335


Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350


Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365


Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380


Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400


Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430
```

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
435 440 445

Leu Ser Pro Gly
450

<210> 150
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069302 LC (P1-061029.IgG1f)

<400> 150

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 Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu

130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr 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> 151
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069312 VH (P1-068761.IgG1f afucosylated)

<400> 151

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

```
Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Val
            100                 105                 110


Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210>  152
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-069312 VL (P1-068761.IgG1f afucosylated)

<400>  152

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80


Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95


Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100                 105


<210>  153
```

<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069312 HC (P1-068761.IgG1f afucosylated)

<400> 153

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
165 170 175

```
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
225                 230                 235                 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380
```

```
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400


Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  154
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-069312 LC (P1-068761.IgG1f afucosylated)

<400>  154

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80


Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
```

85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr 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> 155
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069309 VH (P1-068767.IgG1f afucosylated)

<400> 155

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
20 25 30

```
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Asp Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
            100                 105                 110


Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210>  156
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-069309 VL (P1-068767.IgG1f afucosylated)

<400>  156

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
```

65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 157
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069309 HC (P1-068767.IgG1f afucosylated)

<400> 157

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asp Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

```
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
225                 230                 235                 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335
```

```
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350


Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365


Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380


Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400


Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  158
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-069309 LC (P1-068767.IgG1f afucosylated)

<400>  158

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
```

```
        35                  40                  45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180                 185                 190

Tyr 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>  159
<211>  123
<212>  PRT
<213>  Artificial Sequence
```

<220>
<223> P1-069307 VH (P1-061029.IgG1f afucosylated)

<400> 159

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Asp Tyr
            20   25   30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Asn Trp Asn Ser Ala Asn Ile Gly Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85   90   95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Phe Asp Val
            100   105   110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115   120

<210> 160
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069307 VL (P1-061029.IgG1f afucosylated)

<400> 160

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 Ser Ser Ser

20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 161
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-069307 HC (P1-061029.IgG1f afucosylated)

<400> 161

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asn Trp Asn Ser Ala Asn Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

```
Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Phe Asp Val
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
225                 230                 235                 240

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285
```

```
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300


Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320


Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335


Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350


Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365


Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380


Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400


Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  162
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-069307 LC (P1-061029.IgG1f afucosylated)
```

<400> 162

```
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 Ser Ser Ser
            20                  25                  30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180                 185                 190

Tyr 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> 163
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG1.3 (or IgG1.3f) heavy chain constant region (L234A, L235E, G237A)

<400> 163

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

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg 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

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205

Lys 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 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 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
                325

<210>  164
<211>  107
```

<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary light chain constant region

<400> 164

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1 5 10 15

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
20 25 30

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 165
<211> 162
<212> PRT
<213> Homo sapiens

<400> 165

Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro Glu Gly Gln
1 5 10 15

Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val Asp Lys Gly His
20 25 30

Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser Ser Arg Gly Glu Val

35 40 45

Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg Asn Leu Thr Phe Gln Asp
50 55 60

Leu His Leu His His Gly Gly His Gln Ala Ala Asn Thr Ser His Asp
65 70 75 80

Leu Ala Gln Arg His Gly Leu Glu Ser Ala Ser Asp His His Gly Asn
85 90 95

Phe Ser Ile Thr Met Arg Asn Leu Thr Leu Leu Asp Ser Gly Leu Tyr
100 105 110

Cys Cys Leu Val Val Glu Ile Arg His His His Ser Glu His Arg Val
115 120 125

His Gly Ala Met Glu Leu Gln Val Gln Thr Gly Lys Asp Ala Pro Ser
130 135 140

Asn Cys Val Val Tyr Pro Ser Ser Ser Gln Asp Ser Glu Asn Ile Thr
145 150 155 160

Ala Ala

<210> 166
<211> 162
<212> PRT
<213> Macaca fascicularis

<400> 166

Phe Lys Val Ala Thr Leu Tyr Ser Leu Tyr Val Cys Pro Glu Gly Gln
1 5 10 15

Asn Val Thr Leu Thr Cys Arg Val Phe Gly Pro Val Asp Lys Gly His
20 25 30

Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser Ser Arg Gly Glu Val
35 40 45

```
Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg Asn Leu Thr Phe Gln Asp
    50                  55                  60

Leu His Leu His His Gly Gly His Gln Ala Ala Asn Thr Ser His Asp
65                  70                  75                  80

Leu Ala Gln Arg His Gly Leu Glu Ser Ala Ser Asp His His Gly Asn
                85                  90                  95

Phe Ser Ile Thr Met Arg Asn Leu Thr Leu Leu Asp Ser Gly Leu Tyr
            100                 105                 110

Cys Cys Leu Val Val Glu Ile Arg His His His Ser Glu His Arg Val
        115                 120                 125

His Gly Ala Met Glu Leu Gln Val Gln Thr Gly Lys Asp Ala Pro Ser
    130                 135                 140

Ser Cys Val Ala Tyr Pro Ser Ser Ser Gln Glu Ser Glu Asn Ile Thr
145                 150                 155                 160

Ala Ala
```

<210> 167
<211> 159
<212> PRT
<213> Mus musculus

<400> 167

```
Phe Lys Val Thr Thr Pro Tyr Ser Leu Tyr Val Cys Pro Glu Gly Gln
1               5                   10                  15

Asn Ala Thr Leu Thr Cys Arg Ile Leu Gly Pro Val Ser Lys Gly His
            20                  25                  30

Asp Val Thr Ile Tyr Lys Thr Trp Tyr Leu Ser Ser Arg Gly Glu Val
        35                  40                  45
```

```
Gln Met Cys Lys Glu His Arg Pro Ile Arg Asn Phe Thr Leu Gln His
    50                  55                  60


Leu Gln His His Gly Ser His Leu Lys Ala Asn Ala Ser His Asp Gln
65                  70                  75                  80


Pro Gln Lys His Gly Leu Glu Leu Ala Ser Asp His His Gly Asn Phe
                85                  90                  95


Ser Ile Thr Leu Arg Asn Val Thr Pro Arg Asp Ser Gly Leu Tyr Cys
            100                 105                 110


Cys Leu Val Ile Glu Leu Lys Asn His His Pro Glu Gln Arg Phe Tyr
        115                 120                 125


Gly Ser Met Glu Leu Gln Val Gln Ala Gly Lys Gly Ser Gly Ser Thr
    130                 135                 140


Cys Met Ala Ser Asn Glu Gln Asp Ser Asp Ser Ile Thr Ala Ala
145                 150                 155


<210>  168
<211>  14
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-061029 HDR3 chip oligo (Fig. 7A)


<220>
<221>  MISC_FEATURE
<222>  (1)..(14)
<223>  X = H, D, or E

<400>  168

Xaa Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Phe Asp Val
1               5                   10


<210>  169
<211>  14
<212>  PRT
```

<213> Artificial Sequence

<220>
<223> P1-061029 HDR3 chip oligo (Fig. 7A)

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> X = H, D, or E

<400> 169

Xaa Xaa Gly Tyr Ser Gly Gly Trp Ile Asp Ala Phe Asp Val
1 5 10

<210> 170
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-061029 HDR3 chip oligo (Fig. 7A)

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> X = H, D, or E

<400> 170

Xaa Pro Xaa Tyr Ser Gly Gly Trp Ile Asp Ala Phe Asp Val
1 5 10

<210> 171
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-061029 HDR3 chip oligo (Fig. 7A)

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> X = H, D, or E

<400> 171

Xaa Pro Gly Xaa Ser Gly Gly Trp Ile Asp Ala Phe Asp Val
1 5 10

<210> 172
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-061029 HDR3 chip oligo (Fig. 7A)

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> X = H, D, or E

<400> 172

Xaa Pro Gly Tyr Xaa Gly Gly Trp Ile Asp Ala Phe Asp Val
1 5 10

<210> 173
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-061029 HDR3 chip oligo (Fig. 7A)

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> X = H, D, or E

<400> 173

Xaa Pro Gly Tyr Ser Xaa Gly Trp Ile Asp Ala Phe Asp Val
1 5 10

<210> 174
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-061029 HDR3 chip oligo (Fig. 7A)

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> X = H, D, or E

<400> 174

Xaa Pro Gly Tyr Ser Gly Xaa Trp Ile Asp Ala Phe Asp Val
1 5 10

<210> 175
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-061029 HDR3 chip oligo (Fig. 7A)

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> X = H, D, or E

<400> 175

Xaa Pro Gly Tyr Ser Gly Gly Xaa Ile Asp Ala Phe Asp Val
1 5 10

<210> 176
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-061029 HDR3 chip oligo (Fig. 7A)

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> X = H, D, or E

<400> 176

Xaa Pro Gly Tyr Ser Gly Gly Trp Xaa Asp Ala Phe Asp Val
1 5 10

<210> 177
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-061029 HDR3 chip oligo (Fig. 7A)

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> X = H, D, or E

<400> 177

Xaa Pro Gly Tyr Ser Gly Gly Trp Ile Xaa Ala Phe Asp Val
1 5 10

<210> 178
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-061029 HDR3 chip oligo (Fig. 7A)

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> X = H, D, or E

<400> 178

Xaa Pro Gly Tyr Ser Gly Gly Trp Ile Asp Xaa Phe Asp Val
1 5 10

<210> 179
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-061029 HDR3 chip oligo (Fig. 7A)

<220>
<221> MISC_FEATURE

<222> (1)..(14)
<223> X = H, D, or E

<400> 179

Xaa Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Xaa Asp Val
1 5 10

<210> 180
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-061029 HDR3 chip oligo (Fig. 7A)

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> X = H, D, or E

<400> 180

Xaa Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Phe Xaa Val
1 5 10

<210> 181
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-061029 HDR3 chip oligo (Fig. 7A)

<220>
<221> MISC_FEATURE
<222> (1)..(14)
<223> X = H, D, or E

<400> 181

Xaa Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Phe Asp Xaa
1 5 10

<210> 182
<211> 329
<212> PRT

<213> Artificial Sequence

<220>
<223> IgG1f (human wild-type allotype f) heavy chain constant region

<400> 182

```
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


Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95


Arg 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

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205

Lys 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 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 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
325

<210> 183
<211> 329
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG1.1f Heavy chain constant region (L234A, L235E, G237A, A330S, P331S)

<400> 183

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

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
            100                 105                 110

Pro Ala Pro Glu Ala Glu Gly Ala 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

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205

Lys Ala Leu Pro Ser Ser 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 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 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
                325


<210>  184
<211>  329
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  IgG1fa.P238K (or IgG1.P238K) heavy chain constant region

<400>  184

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

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Arg 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 Lys 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

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205

Lys 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
325

<210> 185
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070864 P1-068761_E30D VH

<400> 185

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Asp Glu
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 186
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070864 P1-068761_E30D VL

<400> 186

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 Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 187
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070864 P1-068761_E30D IgG1.3 HC

<400> 187

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Asp Glu
            20                  25                  30


Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Val
            100                 105                 110


Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125


Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140


Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160


Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175


Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190
```

```
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400
```

```
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  188
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070864 P1-068761_E30D LC

<400>  188

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80


Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95
```

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr 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> 189
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070866 P1-068761_E32Y VH

<400> 189

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

```
Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Val
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210>  190
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070866 P1-068761_E32Y VL

<400>  190

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 Ser Ser Ser
            20                  25                  30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80
```

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 191
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070866 P1-068761_E32Y IgG1.3 HC

<400> 191

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
130 135 140

```
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350
```

```
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365


Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380


Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400


Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  192
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070866 P1-068761_E32Y LC

<400>  192

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45
```

```
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180                 185                 190

Tyr 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>  193
<211>  123
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070868 P1-068761_E55A VH
```

<400> 193

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asn Trp Asn Ser Ala Glu Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 194
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070868 P1-068761_E55A VL

<400> 194

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 Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35   40   45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65   70   75   80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85   90   95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100   105

<210> 195
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070868 P1-068761_E55A IgG1.3 HC

<400> 195

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
            20   25   30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Asn Trp Asn Ser Ala Glu Ile Gly Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85   90   95

```
Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Val
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300
```

```
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly
    450


<210>  196
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070868 P1-068761_E55A LC

<400>  196
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```
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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80


Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95


Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110


Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125


Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140


Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160


Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175


Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180                 185                 190


Tyr 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> 197
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070870 P1-068761_E56N VH

<400> 197

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
            20   25   30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Asn Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85   90   95

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Val
            100   105   110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115   120

<210> 198
<211> 108
<212> PRT
<213> Artificial Sequence

<220>

<223> P1-070870 P1-068761_E56N VL

<400> 198

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 Ser Ser Ser
            20   25   30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35   40   45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65   70   75   80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85   90   95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100   105

<210> 199
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070870 P1-068761_E56N IgG1.3 HC

<400> 199

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
            20   25   30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

```
Ser Gly Ile Asn Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Val
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255
```

```
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly
    450
```

<210> 200
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070870 P1-068761_E56N LC

<400> 200

```
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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80


Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95


Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110


Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125


Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140


Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160
```

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr 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> 201
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070872 P1-068761_H100G VH

<400> 201

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115   120

<210> 202
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070872 P1-068761_H100G VL

<400> 202

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 Ser Ser Ser
            20   25   30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35   40   45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65   70   75   80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85   90   95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100   105

<210> 203
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070872 P1-068761_H100G IgG1.3 HC

<400> 203

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
            20                  25                  30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Val
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205
```

```
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415
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Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  204
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070872 P1-068761_H100G LC

<400>  204

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80


Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95


Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110
```

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115   120   125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130   135   140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145   150   155   160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165   170   175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180   185   190

Tyr 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> 205
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070874 P1-068761_E100fF VH

<400> 205

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
            20   25   30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
    50   55   60

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Phe Asp Val
            100                 105                 110


Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210>  206
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070874 P1-068761_E100fF VL

<400>  206

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80


Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95
```

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 207
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070874 P1-068761_E100fF IgG1.3 HC

<400> 207

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Phe Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145 150 155 160

```
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365
```

```
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly
    450
```

<210> 208
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070874 P1-068761_E100fF LC

<400> 208

```
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 Ser Ser Ser
            20                  25                  30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60
```

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr 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> 209
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070876 P1-068761_E30D_E32Y VH

<400> 209

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Asp Tyr
            20   25   30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85   90   95

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Val
            100   105   110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115   120

<210> 210
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070876 P1-068761_E30D_E32Y VL

<400> 210

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 Ser Ser Ser
            20   25   30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35   40   45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65   70   75   80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85   90   95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100   105

<210> 211
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070876 P1-068761_E30D_E32Y IgG1.3 HC

<400> 211

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Asp Tyr
            20   25   30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85   90   95

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Val
            100   105   110

```
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320
```

```
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly
    450


<210>  212
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070876 P1-068761_E30D_E32Y LC

<400>  212

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15
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```
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
            20                  25                  30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180                 185                 190

Tyr 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> 213
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070878 P1-068761_E55A_E56N VH

<400> 213

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asn Trp Asn Ser Ala Asn Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 214
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070878 P1-068761_E55A_E56N VL

<400> 214

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 Ser Ser Ser
            20   25   30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35   40   45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65   70   75   80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85   90   95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100   105

<210> 215
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070878 P1-068761_E55A_E56N IgG1.3 HC

<400> 215

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
            20   25   30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Asn Trp Asn Ser Ala Asn Ile Gly Tyr Ala Asp Ser Val
    50   55   60

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Val
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270
```

```
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly
    450


<210>  216
<211>  215
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<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070878 P1-068761_E55A_E56N LC

<400> 216

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 Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180   185   190

Tyr 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> 217
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070880 P1-068761_H100G_E100fF VH

<400> 217

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
            20   25   30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85   90   95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Phe Asp Val
            100   105   110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115   120

<210> 218
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070880 P1-068761_H100G_E100fF VL

<400> 218

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 Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 219
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070880 P1-068761_H100G_E100fF IgG1.3 HC

<400> 219

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
            20                  25                  30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Phe Asp Val
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220
```

```
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430
```

```
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  220
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070880 P1-068761_H100G_E100fF LC

<400>  220

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80


Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95


Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110


Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125
```

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130   135   140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145   150   155   160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165   170   175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180   185   190

Tyr 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> 221
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070882 P1-068761_E32Y_E55A VH

<400> 221

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
            20   25   30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Asn Trp Asn Ser Ala Glu Ile Gly Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80

```
Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Val
            100                 105                 110


Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210>  222
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070882 P1-068761_E32Y_E55A VL

<400>  222

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80


Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95


Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100                 105
```

<210> 223
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070882 P1-068761_E32Y_E55A IgG1.3 HC

<400> 223

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asn Trp Asn Ser Ala Glu Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
165 170 175

```
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380
```

```
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400


Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  224
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070882 P1-068761_E32Y_E55A LC

<400>  224

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80
```

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr 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> 225
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070884 P1-068761_E32Y_E56N VH

<400> 225

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
20 25 30

```
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Asn Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Val
            100                 105                 110


Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210>  226
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070884 P1-068761_E32Y_E56N VL

<400>  226

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60
```

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 227
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070884 P1-068761_E32Y_E56N IgG1.3 HC

<400> 227

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asn Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

```
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335
```

```
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350


Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365


Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380


Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400


Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  228
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070884 P1-068761_E32Y_E56N LC

<400>  228

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 Ser Ser Ser
            20                  25                  30
```

```
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180                 185                 190

Tyr 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> 229
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070886 P1-068761_E32Y_H100G VH

<400> 229

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
            20   25   30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85   90   95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Val
            100   105   110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115   120

<210> 230
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070886 P1-068761_E32Y_H100G VL

<400> 230

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 Ser Ser Ser
            20   25   30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35   40   45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65   70   75   80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85   90   95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100   105

<210> 231
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070886 P1-068761_E32Y_H100G IgG1.3 HC

<400> 231

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
            20   25   30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80

```
Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Val
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285
```

```
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly
    450
```

<210> 232
<211> 215
<212> PRT
<213> Artificial Sequence

<220>

<223> P1-070886 P1-068761_E32Y_H100G LC

<400> 232

```
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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80


Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95


Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110


Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125


Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140


Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160


Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175


Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180                 185                 190
```

Tyr 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> 233
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070888 P1-068761_E32Y_E100fF VH

<400> 233

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Phe Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 234
<211> 108

<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070888 P1-068761_E32Y_E100fF VL

<400> 234

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 Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 235
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070888 P1-068761_E32Y_E100fF IgG1.3 HC

<400> 235

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
20 25 30

```
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Phe Asp Val
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240
```

```
Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445
```

Leu Ser Pro Gly
    450

<210> 236
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070888 P1-068761_E32Y_E100fF LC

<400> 236

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 Ser Ser Ser
            20   25   30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35   40   45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65   70   75   80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85   90   95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100   105   110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115   120   125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130   135   140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr 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> 237
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070890 P1-068761_E30D_E55A VH

<400> 237

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Asp Glu
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asn Trp Asn Ser Ala Glu Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 238
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070890 P1-068761_E30D_E55A VL

<400> 238

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 Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 239
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070890 P1-068761_E30D_E55A IgG1.3 HC

<400> 239

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Asp Glu
            20                  25                  30


Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Asn Trp Asn Ser Ala Glu Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Val
            100                 105                 110


Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125


Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140


Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160


Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175


Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190
```

```
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400
```

```
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  240
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070890 P1-068761_E30D_E55A LC

<400>  240

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80


Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95
```

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr 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> 241
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070892 P1-068761_E30D_E56N VH

<400> 241

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Asp Glu
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asn Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 242
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070892 P1-068761_E30D_E56N VL

<400> 242

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 Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 243
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070892 P1-068761_E30D_E56N IgG1.3 HC

<400> 243

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Asp Glu
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asn Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Glu Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
130 135 140

```
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350
```

```
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365


Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380


Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400


Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  244
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070892 P1-068761_E30D_E56N LC

<400>  244

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45
```

```
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180                 185                 190

Tyr 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>  245
<211>  123
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070894 P1-068761_E30D_H100G VH
```

<400> 245

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Asp Glu
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 246
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070894 P1-068761_E30D_H100G VL

<400> 246

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 Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35   40   45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65   70   75   80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85   90   95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100   105

<210> 247
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070894 P1-068761_E30D_H100G IgG1.3 HC

<400> 247

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Asp Glu
            20   25   30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85   90   95

```
Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Val
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300
```

```
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly
    450


<210>  248
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070894 P1-068761_E30D_H100G LC

<400>  248
```

```
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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80


Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95


Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110


Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125


Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140


Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160


Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175


Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180                 185                 190


Tyr 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> 249
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070896 P1-068761_E30D_E100fF VH

<400> 249

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Asp Glu
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Phe Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 250
<211> 108
<212> PRT
<213> Artificial Sequence

<220>

<223> P1-070896 P1-068761_E30D_E100fF VL

<400> 250

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 Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 251
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070896 P1-068761_E30D_E100fF IgG1.3 HC

<400> 251

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Asp Glu
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

```
Ser Gly Ile Asn Trp Asn Ser Glu Glu Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Phe Asp Val
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255
```

```
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly
    450
```

<210> 252
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070896 P1-068761_E30D_E100fF LC

<400> 252

```
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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80


Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95


Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110


Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125


Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140


Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160
```

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr 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> 253
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070898 P1-068761_E55A_E100fF VH

<400> 253

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asn Trp Asn Ser Ala Glu Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Phe Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115   120

<210> 254
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070898 P1-068761_E55A_E100fF VL

<400> 254

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 Ser Ser Ser
            20   25   30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35   40   45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65   70   75   80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85   90   95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100   105

<210> 255
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070898 P1-068761_E55A_E100fF IgG1.3 HC

<400> 255

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asn Trp Asn Ser Ala Glu Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Phe Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
165 170 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
180 185 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
195 200 205

```
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415
```

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
435 440 445

Leu Ser Pro Gly
450

<210> 256
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070898 P1-068761_E55A_E100fF LC

<400> 256

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 Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115   120   125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130   135   140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145   150   155   160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165   170   175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180   185   190

Tyr 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> 257
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070900 P1-068761_E56N_H100G VH

<400> 257

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
            20   25   30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Asn Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
    50   55   60

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Val
            100                 105                 110


Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210>  258
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070900 P1-068761_E56N_H100G VL

<400>  258

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80


Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95
```

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 259
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070900 P1-068761_E56N_H100G IgG1.3 HC

<400> 259

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asn Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145 150 155 160

```
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365
```

```
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380


Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400


Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  260
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070900 P1-068761_E56N_H100G LC

<400>  260

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60
```

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr 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> 261
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070902 P1-068761_E56N_E100fF VH

<400> 261

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
            20                  25                  30


Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Asn Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Phe Asp Val
            100                 105                 110


Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210>  262
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070902 P1-068761_E56N_E100fF VL

<400>  262

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45
```

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65   70   75   80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85   90   95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100   105

<210> 263
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070902 P1-068761_E56N_E100fF IgG1.3 HC

<400> 263

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Glu
            20   25   30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Asn Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85   90   95

Ala Lys Val Pro Gly Tyr Ser His Gly Trp Ile Asp Ala Phe Asp Val
            100   105   110

```
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320
```

```
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly
    450


<210>  264
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070902 P1-068761_E56N_E100fF IgG1.3 HC

<400>  264

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 Ser Ser Ser
            20                  25                  30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180                 185                 190

Tyr 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> 265
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070904 P1-068767_E30D VH

<400> 265

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asp Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 266
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070904 P1-068767_E30D VL

<400> 266

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 Ser Ser Ser
            20   25   30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35   40   45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65   70   75   80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85   90   95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100   105

<210> 267
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070904 P1-068767_E30D VL

<400> 267

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Asp Tyr
            20   25   30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Asp Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
    50   55   60

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270
```

```
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly
    450

<210>  268
<211>  215
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<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070904 P1-068767_E30D LC

<400> 268

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 Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180   185   190

Tyr 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> 269
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070906 P1-068767_D52N VH

<400> 269

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
            20   25   30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Asn Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85   90   95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
            100   105   110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115   120

<210> 270
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070906 P1-068767_D52N VL

<400> 270

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 Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 271
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070906 P1-068767_D52N IgG1.3 HC

<400> 271

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
            20                  25                  30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Gly Ile Asn Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220
```

```
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430
```

```
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  272
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070906 P1-068767_D52N LC

<400>  272

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80


Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95


Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110


Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125
```

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130   135   140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145   150   155   160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165   170   175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180   185   190

Tyr 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> 273
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070908 P1-068767_E55A VH

<400> 273

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
            20   25   30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Asp Trp Asn Ser Ala Asn Ile Gly Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80

```
Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
            100                 105                 110


Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210>  274
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070908 P1-068767_E55A VL

<400>  274

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80


Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95


Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100                 105
```

<210> 275
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070908 P1-068767_E55A IgG1.3 HC

<400> 275

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asp Trp Asn Ser Ala Asn Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
165 170 175

```
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380
```

```
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400


Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  276
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070908 P1-068767_E55A LC

<400>  276

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80
```

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr 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> 277
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070910 P1-068767_E100fF VH

<400> 277

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
20 25 30

```
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Asp Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Phe Asp Asp
            100                 105                 110


Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210>  278
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070910 P1-068767_E100fF VL

<400>  278

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60
```

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 279
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070910 P1-068767_E100fF IgG1.3 HC

<400> 279

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asp Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Phe Asp Asp
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

```
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335
```

```
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350


Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365


Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380


Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400


Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  280
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070910 P1-068767_E100fF LC

<400>  280

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 Ser Ser Ser
            20                  25                  30
```

```
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180                 185                 190

Tyr 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> 281
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070912 P1-068767_D102V VH

<400> 281

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
            20   25   30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Asp Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85   90   95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Val
            100   105   110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115   120

<210> 282
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070912 P1-068767_D102V VL

<400> 282

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 Ser Ser Ser
            20   25   30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35   40   45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65   70   75   80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85   90   95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100   105

<210> 283
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070912 P1-068767_D102V IgG1.3 HC

<400> 283

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
            20   25   30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Asp Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80

```
Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Val
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285
```

```
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly
    450
```

<210> 284
<211> 215
<212> PRT
<213> Artificial Sequence

<220>

<223> P1-070912 P1-068767_D102V IgG1.3 HC

<400> 284

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 Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr 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> 285
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070914 P1-068767_E30D_D52N VH

<400> 285

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asn Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 286
<211> 108

<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070914 P1-068767_E30D_D52N VL

<400> 286

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 Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 287
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070914 P1-068767_E30D_D52N IgG1.3 HC

<400> 287

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Asp Tyr
20 25 30

```
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Gly Ile Asn Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240
```

```
Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445
```

```
Leu Ser Pro Gly
    450


<210>  288
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070914 P1-068767_E30D_D52N LC

<400>  288

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80


Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95


Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110


Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125


Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140
```

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr 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> 289
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070916 P1-068767_D52N_E55A VH

<400> 289

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asn Trp Asn Ser Ala Asn Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

```
Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
            100                 105                 110


Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210>  290
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070916 P1-068767_D52N_E55A VL

<400>  290

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80


Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95


Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100                 105


<210>  291
<211>  452
<212>  PRT
<213>  Artificial Sequence
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<220>
<223> P1-070916 P1-068767_D52N_E55A IgG1.3 HC

<400> 291

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
            20                  25                  30


Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Asn Trp Asn Ser Ala Asn Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
            100                 105                 110


Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125


Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140


Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160


Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175


Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190
```

```
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400
```

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
435 440 445

Leu Ser Pro Gly
450

<210> 292
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070916 P1-068767_D52N_E55A LC

<400> 292

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 Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr 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> 293
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070918 P1-068767_E55A_E100fF VH

<400> 293

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asp Trp Asn Ser Ala Asn Ile Gly Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85   90   95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Phe Asp Asp
            100   105   110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115   120

<210> 294
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070918 P1-068767_E55A_E100fF VL

<400> 294

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 Ser Ser Ser
            20   25   30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35   40   45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65   70   75   80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 295
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070918 P1-068767_E55A_E100fF IgG1.3 HC

<400> 295

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asp Trp Asn Ser Ala Asn Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Phe Asp Asp
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
130 135 140

```
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350
```

```
Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365


Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380


Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400


Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  296
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070918 P1-068767_E55A_E100fF LC

<400>  296

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45
```

```
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180                 185                 190

Tyr 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>  297
<211>  123
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070920 P1-068767_E100fF_D102V VH
```

<400> 297

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asp Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Phe Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 298
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070920 P1-068767_E100fF_D102V VL

<400> 298

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 Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35   40   45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65   70   75   80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85   90   95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100   105

<210> 299
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070920 P1-068767_E100fF_D102V IgG1.3 HC

<400> 299

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
            20   25   30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Asp Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85   90   95

```
Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Phe Asp Val
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300
```

```
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly
    450


<210>  300
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070920 P1-068767_E100fF_D102V LC

<400>  300
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```
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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80


Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95


Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110


Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125


Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140


Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160


Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175


Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180                 185                 190


Tyr 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> 301
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070922 P1-068767_E30D_E55A VH

<400> 301

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Asp Tyr
            20   25   30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Asp Trp Asn Ser Ala Asn Ile Gly Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85   90   95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
            100   105   110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115   120

<210> 302
<211> 108
<212> PRT
<213> Artificial Sequence

<220>

<223> P1-070922 P1-068767_E30D_E55A VL

<400> 302

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 Ser Ser Ser
            20   25   30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35   40   45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65   70   75   80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85   90   95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100   105

<210> 303
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070922 P1-068767_E30D_E55A IgG1.3 HC

<400> 303

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Asp Tyr
            20   25   30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

```
Ser Gly Ile Asp Trp Asn Ser Ala Asn Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Asp
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255
```

```
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly
    450
```

<210> 304
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070922 P1-068767_E30D_E55A LC

<400> 304

```
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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80


Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95


Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110


Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125


Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140


Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160
```

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr 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> 305
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070924 P1-068767_E30D_E100fF VH

<400> 305

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asp Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Phe Asp Asp
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115   120

<210> 306
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070924 P1-068767_E30D_E100fF VL

<400> 306

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 Ser Ser Ser
            20   25   30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35   40   45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65   70   75   80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85   90   95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100   105

<210> 307
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070924 P1-068767_E30D_E100fF IgG1.3 HC

<400> 307

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Asp Tyr
            20                  25                  30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Gly Ile Asp Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Phe Asp Asp
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205
```

```
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415
```

```
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  308
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070924 P1-068767_E30D_E100fF LC

<400>  308

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80


Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95


Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110
```

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115   120   125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130   135   140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145   150   155   160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165   170   175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180   185   190

Tyr 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> 309
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070926 P1-068767_E30D_D102V VH

<400> 309

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Asp Tyr
            20   25   30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Asp Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
    50   55   60

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Val
            100                 105                 110


Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210>  310
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070926 P1-068767_E30D_D102V VL

<400>  310

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80


Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95
```

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 311
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070926 P1-068767_E30D_D102V IgG1.3 HC

<400> 311

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asp Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145 150 155 160

```
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365
```

```
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380


Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400


Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  312
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070926 P1-068767_E30D_D102V LC

<400>  312

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60
```

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr 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> 313
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070928 P1-068767_D52N_E100fF VH

<400> 313

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
            20                  25                  30


Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Gly Ile Asn Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95


Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Phe Asp Asp
            100                 105                 110


Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120


<210>  314
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070928 P1-068767_D52N_E100fF VL

<400>  314

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45
```

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65   70   75   80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85   90   95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100   105

<210> 315
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070928 P1-068767_D52N_E100fF IgG1.3 HC

<400> 315

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
            20   25   30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Asn Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
    50   55   60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65   70   75   80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85   90   95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Phe Asp Asp
            100   105   110

```
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320
```

```
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335


Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350


Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365


Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380


Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400


Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430


Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  316
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070928 P1-068767_D52N_E100fF LC

<400>  316

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 Ser Ser Ser
            20                  25                  30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180                 185                 190

Tyr 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> 317
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070930 P1-068767_D52N_D102V VH

<400> 317

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asn Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 318
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070930 P1-068767_D52N_D102V VL

<400> 318

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 Ser Ser Ser
            20   25   30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35   40   45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50   55   60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65   70   75   80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85   90   95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100   105

<210> 319
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070930 P1-068767_D52N_D102V IgG1.3 HC

<400> 319

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
            20   25   30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

Ser Gly Ile Asn Trp Asn Ser Glu Asn Ile Gly Tyr Ala Asp Ser Val
    50   55   60

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Val
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270
```

```
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly
    450


<210>  320
<211>  215
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<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070930 P1-068767_D52N_D102V LC

<400> 320

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 Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr 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> 321
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070932 P1-068767_E55A_D102V VH

<400> 321

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Asp Trp Asn Ser Ala Asn Ile Gly Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Val
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 322
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070932 P1-068767_E55A_D102V VL

<400> 322

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 Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 323
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> P1-070932 P1-068767_E55A_D102V IgG1.3 HC

<400> 323

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Lys
1 5 10 15

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asp Tyr
            20                  25                  30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Gly Ile Asp Trp Asn Ser Ala Asn Ile Gly Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95

Ala Lys Val Pro Gly Tyr Ser Gly Gly Trp Ile Asp Ala Glu Asp Val
            100                 105                 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys
    210                 215                 220
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```
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240


Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255


Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270


Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285


Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300


Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320


Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335


Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350


Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365


Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380


Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400


Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415


Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430
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```
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445


Leu Ser Pro Gly
    450


<210>  324
<211>  215
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  P1-070932 P1-068767_E55A_D102V LC

<400>  324

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 Ser Ser Ser
            20                  25                  30


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45


Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60


Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80


Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95


Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala
            100                 105                 110


Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125
```

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130   135   140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145   150   155   160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165   170   175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180   185   190

Tyr 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> 325
<211> 169
<212> PRT
<213> Artificial Sequence

<220>
<223> hVISTA-ECD 6-His tag

<400> 325

Ala Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro Glu Gly
1   5   10   15

Gln Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val Asp Lys Gly
            20   25   30

His Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser Ser Arg Gly Glu
        35   40   45

Val Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg Asn Leu Thr Phe Gln
    50   55   60

Asp Leu His Leu His His Gly Gly His Gln Ala Ala Asn Thr Ser His
65   70   75   80

```
Asp Leu Ala Gln Arg His Gly Leu Glu Ser Ala Ser Asp His His Gly
                85                  90                  95

Asn Phe Ser Ile Thr Met Arg Asn Leu Thr Leu Leu Asp Ser Gly Leu
            100                 105                 110

Tyr Cys Cys Leu Val Val Glu Ile Arg His His His Ser Glu His Arg
        115                 120                 125

Val His Gly Ala Met Glu Leu Gln Val Gln Thr Gly Lys Asp Ala Pro
    130                 135                 140

Ser Asn Cys Val Val Tyr Pro Ser Ser Ser Gln Glu Ser Glu Asn Ile
145                 150                 155                 160

Thr Ala His His His His His His His
                165


<210>  326
<211>  169
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Cyno VISTA-ECD 6-His tag

<400>  326

Ala Phe Lys Val Ala Thr Leu Tyr Ser Leu Tyr Val Cys Pro Glu Gly
1               5                   10                  15

Gln Asn Val Thr Leu Thr Cys Arg Val Phe Gly Pro Val Asp Lys Gly
            20                  25                  30

His Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser Ser Arg Gly Glu
        35                  40                  45

Val Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg Asn Leu Thr Phe Gln
    50                  55                  60
```

```
Asp Leu His Leu His His Gly Gly His Gln Ala Ala Asn Thr Ser His
65                  70                  75                  80


Asp Leu Ala Gln Arg His Gly Leu Glu Ser Ala Ser Asp His His Gly
                85                  90                  95


Asn Phe Ser Ile Thr Met Arg Asn Leu Thr Leu Leu Asp Ser Gly Leu
            100                 105                 110


Tyr Cys Cys Leu Val Val Glu Ile Arg His His His Ser Glu His Arg
        115                 120                 125


Val His Gly Ala Met Glu Leu Gln Val Gln Thr Gly Lys Asp Ala Pro
    130                 135                 140


Ser Ser Cys Val Ala Tyr Pro Ser Ser Ser Gln Glu Ser Glu Asn Ile
145                 150                 155                 160


Thr Ala His His His His His His His
                165


<210>  327
<211>  369
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  P1-069059 VH DNA

<400>  327
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaagtc cctgagactc       60

tcctgtgcag cctctggatt cacccttgaa gattatgcca tgcactgggt ccggcaagct      120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgacca tataggctat      180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat      240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct      300

gggtatagcg gtggctggat tgacgctgaa gatgactggg gccaagggac aatggtcacc      360

gtctcttca                                                              369
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<210> 328
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-069059 VL DNA

<400> 328
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 329
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-069061 VH DNA

<400> 329
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaagtc cctgagactc 60

tcctgtgcag cctctggatt cacccttgaa gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgctga aataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctgaa gatgactggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 330
<211> 324
<212> DNA
<213> Artificial Sequence

<220>

<223> P1-069061 VL DNA

<400> 330
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 331
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-069063 VH DNA

<400> 331
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaagtc cctgagactc 60

tcctgtgcag cctctggatt cacccttgaa gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgctga aataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctgac gatgaatggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 332
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-069063 VL DNA

<400> 332
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 333
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-069065 VH DNA

<400> 333
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaagtc cctgagactc 60

tcctgtgcag cctctggatt cacccttgaa gatgaagcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgacga cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctttt gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 334
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-069065 VL DNA

<400> 334
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 335
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-069067 VH DNA

<400> 335
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaagtc cctgagactc 60

tcctgtgcag cctctggatt cacccttgat gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgaaga aataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctgac gatgaatggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 336
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-069067 VL DNA

<400> 336
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 337
<211> 369

<212> DNA
<213> Artificial Sequence

<220>
<223> P1-069069 VH DNA

<400> 337
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaagtc cctgagactc 60

tcctgtgcag cctctggatt cacccttgat gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgaaga aataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctgac gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 338
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-069069 VL DNA

<400> 338
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 339
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-069071 VH DNA

<400> 339
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaagtc cctgagactc 60

tcctgtgcag cctctggatt cacccttgaa gatgaagcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgctga cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg aaggctggat tgacgctttt gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 340
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-069071 VL DNA

<400> 340
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 341
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-069073 VH DNA

<400> 341
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaagtc cctgagactc 60

tcctgtgcag cctctggatt cacccttgaa gatgaagcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgctga aataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctgaa gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 342
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-069073 VL DNA

<400> 342
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 343
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-069075 VH DNA

<400> 343
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaagtc cctgagactc 60

tcctgtgcag cctctggatt cacccttgaa gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattggg acagtgctga aataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcc atggctggat tgacgctgaa gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 344
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-069075 VL DNA

<400> 344
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 345
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-069077 VH DNA

<400> 345
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaagtc cctgagactc 60

tcctgtgcag cctctggatt cacccttgaa gatgaagcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgacga aataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctttt gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 346
<211> 324

<212> DNA
<213> Artificial Sequence

<220>
<223> P1-069077 VL DNA

<400> 346
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 347
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-068761 VH DNA

<400> 347
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaagtc cctgagactc 60

tcctgtgcag cctctggatt cacccttgag gatgaggcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgaaga gataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcc atggctggat tgacgctgaa gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 348
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-068761 VL DNA

<400> 348
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

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<213> Artificial Sequence

<220>
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<400> 349
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tcctgtgcag cctctggatt cacccttgag gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attgattgga acagtgaaaa cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctgaa gatgactggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 350
<211> 324
<212> DNA
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<220>
<223> P1-068767 VL DNA

<400> 350
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cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 351
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-068773 VH DNA

<400> 351
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tcctgtgcag cctctggatt cacccttgag gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attgattgga acagtgataa cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctgaa gatgactggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 352
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-068773 VL DNA

<400> 352
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ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 353
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-068765 VH DNA

<400> 353
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tcctgtgcag cctctggatt caccgatgag gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgaaga gataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctgaa gatgactggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 354
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-068765 VL DNA

<400> 354
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cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 355
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-061029 VH DNA

<400> 355
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tcctgtgcag cctctggatt cacccttgat gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgctaa cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctttt gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 356
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-061029 VL DNA

<400> 356
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ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 357
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-068757 VH DNA

<400> 357
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tcctgtgcag cctctggatt cacccttgag gatgaggcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgaaga gataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctgaa gatgactggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 358
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-068757 VL DNA

<400> 358
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ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 359
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-068771 VH DNA

<400> 359
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tcctgtgcag cctctggatt cacccttgag gatgaggcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtcatga gataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctgaa gatgactggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 360
<211> 324
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<220>
<223> P1-068771 VL DNA

<400> 360
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ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 361
<211> 369
<212> DNA
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<220>
<223> P1-068775 VH DNA

<400> 361
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tcctgtgcag cctctggatt cacccttgag gatgaggcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attgattgga acagtgaaga gataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcc atggctggat tgacgctgaa gatgactggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 362
<211> 324
<212> DNA
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<223> P1-068775 VL DNA

<400> 362
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ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 363
<211> 369
<212> DNA
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<220>
<223> P1-068769 VH DNA

<400> 363
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tcctgtgcag cctctggatt cacccttgag gatgaggcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgatca cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctgaa gatgactggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 364
<211> 324
<212> DNA
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<223> P1-068769 VL DNA

<400> 364
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ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 365
<211> 369
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<220>
<223> P1-068759 VH DNA

<400> 365
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tcctgtgcag cctctggatt cacccttgag gatgaggcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attgattgga acagtgaaaa cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctgaa gatgactggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 366
<211> 324
<212> DNA
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<220>
<223> P1-068759 VL DNA

<400> 366
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ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 367
<211> 369
<212> DNA
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<220>
<223> P1-068763 VH DNA

<400> 367
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tcctgtgcag cctctggatt cacccttgag gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attgattgga acagtgaaaa cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcc atggctggat tgacgctgaa gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 368
<211> 324
<212> DNA
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<223> P1-068763 VL DNA

<400> 368
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ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 369
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<220>
<223> P1-061015 VH DNA

<400> 369
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tcctgtgcag cgtctggatt caccttcagt agctatgcca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcaatt atatggtatg atggaagtaa taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagatagt 300

ggtttttact cctcgtacta ctttgactac tggggccagg gaaccctggt caccgtctcc 360

tca 363

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ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccaacagaaa 120

cctggccagg ctcccaggct cctcatctat gatgcatcca acagggccac tggcatccca 180

gccaggttca gcggcagtgg atctgggaca gatttcactc tcaccatcag cagcctggag 240

cctgaagatt ttgcaactta ttactgccaa cagtataata gttacccgta cactttggc 300

caggggacca agctggagat caaa 324

<210> 371
<211> 363
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<220>
<223> P1-068748 VH DNA

<400> 371
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tcctgtgcag cgtctggatt caccttcagt caccatgcca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcaatt atatggtatg atggaagtaa tgacgactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagatagt 300

ggtttttacg actcgtacta ctttgactac tggggccagg gaaccctggt caccgtctcc 360

tca 363

<210> 372
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<400> 372
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ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccaacagaaa 120

cctggccagg ctcccaggct cctcatctat gatgcatcca acagggccac tggcatccca 180

gccaggttca gcggcagtgg atctgggaca gatttcactc tcaccatcag cagcctggag 240

cctgaagatt ttgcaactta ttactgccaa cagtataata gttacccgta cacttttggc 300

caggggacca agctggagat caaa 324

<210> 373
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<223> P1-068744 VH DNA

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tcctgtgcag cgtctggatt caccttcagt gagtatgcca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcacat atatggtatg atggaagtaa taaatacgag 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagatagt 300

ggtttttacg aatcgtacta ctttgacgag tggggccagg gaaccctggt caccgtctcc 360

tca 363

<210> 374
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<400> 374
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cctggccagg ctcccaggct cctcatctat gatgcatcca acagggccac tggcatccca 180

gccaggttca gcggcagtgg atctgggaca gatttcactc tcaccatcag cagcctggag 240

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caggggacca agctggagat caaa 324

<210> 375
<211> 363
<212> DNA
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<220>
<223> P1-068736 VH DNA

<400> 375
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tcctgtgcag cgtctggatt caccttcagt gagtatgcca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcaatt gattggtatg atggaagtaa taaagactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagatagt 300

ggtttttacg actcgtacta ctttgacgac tggggccagg gaaccctggt caccgtctcc 360

tca 363

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<223> P1-068736 VL DNA

<400> 376
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cctggccagg ctcccaggct cctcatctat gatgcatcca acagggccac tggcatccca 180

gccaggttca gcggcagtgg atctgggaca gatttcactc tcaccatcag cagcctggag 240

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caggggacca agctggagat caaa 324

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<220>
<223> P1-068752 VH DNA

<400> 377
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tcctgtgcag cgtctggatt caccttcagt agctatgcca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagag atatggtatg atggaagtaa taaagactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagatagt 300

ggtttttacg actcgtacta ctttgacgag tggggccagg gaaccctggt caccgtctcc 360

tca 363

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<223> P1-068752 VL DNA

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cctggccagg ctcccaggct cctcatctat gatgcatcca acagggccac tggcatccca 180

gccaggttca gcggcagtgg atctgggaca gatttcactc tcaccatcag cagcctggag 240

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caggggacca agctggagat caaa 324

<210> 379
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<212> DNA
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<220>
<223> P1-068740 VH DNA

<400> 379
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tcctgtgcag cgtctggatt caccttcagt gactatgcca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcaatt atatggtatg atggaagtga taaagactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagatagt 300

ggtttttacg actcgtacta ctttgacgac tggggccagg gaaccctggt caccgtctcc 360

tca 363

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<223> P1-068740 VL DNA

<400> 380
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cctggccagg ctcccaggct cctcatctat gatgcatcca acagggccac tggcatccca 180

gccaggttca gcggcagtgg atctgggaca gatttcactc tcaccatcag cagcctggag 240

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caggggacca agctggagat caaa 324

<210> 381
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-068742 VH DNA

<400> 381
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctggatt caccttcagt gactatgcca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcaatt atatggtatg atggaagtga taaagactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagatagt 300

ggtttttacg aagattacta ctttgactac tggggccagg gaaccctggt caccgtctcc 360

tca 363

<210> 382
<211> 324
<212> DNA
<213> Artificial Sequence

<220>

<223> P1-068742 VL DNA

<400> 382
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccaacagaaa 120

cctggccagg ctcccaggct cctcatctat gatgcatcca acagggccac tggcatccca 180

gccaggttca gcggcagtgg atctgggaca gatttcactc tcaccatcag cagcctggag 240

cctgaagatt ttgcaactta ttactgccaa cagtataata gttacccgta cacttttggc 300

caggggacca agctggagat caaa 324

<210> 383
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-068746 VH DNA

<400> 383
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctggatt caccttcagt agctatgcca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcaatt atatggtatg atggaagtaa tcaccactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagatagt 300

ggtttttacg actcgtacta ctttgactac tggggccagg gaaccctggt caccgtctcc 360

tca 363

<210> 384
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-068746 VL DNA

<400> 384
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccaacagaaa 120

cctggccagg ctcccaggct cctcatctat gatgcatcca acagggccac tggcatccca 180

gccaggttca gcggcagtgg atctgggaca gatttcactc tcaccatcag cagcctggag 240

cctgaagatt ttgcaactta ttactgccaa cagtataata gttacccgta cacttttggc 300

caggggacca agctggagat caaa 324

<210> 385
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-068750 VH DNA

<400> 385
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctggatt caccttcagt gactatgaca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagag atatgggatg atggaagtaa taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagatgag 300

gaattttact cctcgtacta ctttgactac tggggccagg gaaccctggt caccgtctcc 360

tca 363

<210> 386
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-068750 VL DNA

<400> 386
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccaacagaaa 120

cctggccagg ctcccaggct cctcatctat gatgcatcca acagggccac tggcatccca 180

gccaggttca gcggcagtgg atctgggaca gatttcactc tcaccatcag cagcctggag 240

cctgaagatt ttgcaactta ttactgccaa cagtataata gttacccgta cacttttggc 300

caggggacca agctggagat caaa 324

<210> 387
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-068738 VH DNA

<400> 387
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctggatt caccttcagt gagtatgccc atcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcaatt atatgggatg atggaagtaa tcactactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagatagt 300

ggtttttacg aagattacta ctttgactac tggggccagg gaaccctggt caccgtctcc 360

tca 363

<210> 388
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-068738 VL DNA

<400> 388
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccaacagaaa 120

cctggccagg ctcccaggct cctcatctat gatgcatcca acagggccac tggcatccca 180

gccaggttca gcggcagtgg atctgggaca gatttcactc tcaccatcag cagcctggag 240

cctgaagatt ttgcaactta ttactgccaa cagtataata gttacccgta cacttttggc 300

caggggacca agctggagat caaa 324

<210> 389
<211> 363

<212> DNA
<213> Artificial Sequence

<220>
<223> P1-068754 VH DNA

<400> 389
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctggatt caccttcagt gactatgaca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagag atatgggatg atggaagtaa taaatactat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagatagt 300

ggttttcact ccgattacta ctttgactac tggggccagg gaaccctggt caccgtctcc 360

tca 363

<210> 390
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-068754 VL DNA

<400> 390
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccaacagaaa 120

cctggccagg ctcccaggct cctcatctat gatgcatcca acagggccac tggcatccca 180

gccaggttca gcggcagtgg atctgggaca gatttcactc tcaccatcag cagcctggag 240

cctgaagatt ttgcaactta ttactgccaa cagtataata gttacccgta cacttttggc 300

caggggacca agctggagat caaa 324

<210> 391
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070864 VH DNA

<400> 391
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaagtc cctgagactc 60

tcctgtgcag cctctggatt cacccttgat gatgaggcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgaaga gataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcc atggctggat tgacgctgaa gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 392
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070864 VL DNA

<400> 392
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 393
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070866 VH DNA

<400> 393
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaagtc cctgagactc 60

tcctgtgcag cctctggatt cacccttgag gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgaaga gataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcc atggctggat tgacgctgaa gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 394
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070866 VL DNA

<400> 394
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 395
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070868 VH DNA

<400> 395
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaagtc cctgagactc 60

tcctgtgcag cctctggatt cacccttgag gatgaggcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgctga gataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcc atggctggat tgacgctgaa gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 396
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070868 VL DNA

<400> 396
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 397
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070870 VH DNA

<400> 397
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tcctgtgcag cctctggatt cacccttgag gatgaggcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgaaaa cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcc atggctggat tgacgctgaa gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 398
<211> 324

<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070870 VL DNA

<400> 398
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 399
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070872 VH DNA

<400> 399
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tcctgtgcag cctctggatt cacccttgag gatgaggcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgaaga gataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctgaa gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 400
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070872 VL DNA

<400> 400
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 401
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070874 VH DNA

<400> 401
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaagtc cctgagactc 60

tcctgtgcag cctctggatt cacccttgag gatgaggcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgaaga gataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcc atggctggat tgacgctttt gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 402
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070874 VL DNA

<400> 402
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 403
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070876 VH DNA

<400> 403
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tcctgtgcag cctctggatt cacccttgat gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgaaga gataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcc atggctggat tgacgctgaa gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 404
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070876 VL DNA

<400> 404
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ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 405
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070878 VH DNA

<400> 405
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tcctgtgcag cctctggatt cacccttgag gatgaggcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgctaa cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcc atggctggat tgacgctgaa gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 406
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070878 VL DNA

<400> 406
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ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 407
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070880 VH DNA

<400> 407
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tcctgtgcag cctctggatt cacccttgag gatgaggcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgaaga gataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctttt gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 408
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070880 VL DNA

<400> 408
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 409
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070882 VH DNA

<400> 409
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tcctgtgcag cctctggatt cacccttgag gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgctga gataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcc atggctggat tgacgctgaa gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 410
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070882 VL DNA

<400> 410
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 411
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070884 VH DNA

<400> 411
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tcctgtgcag cctctggatt cacccttgag gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgaaaa cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcc atggctggat tgacgctgaa gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 412
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070884 VL DNA

<400> 412
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 413
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070886 VH DNA

<400> 413
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaagtc cctgagactc 60

tcctgtgcag cctctggatt cacccttgag gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgaaga gataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctgaa gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 414
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070886 VL DNA

<400> 414
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ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 415
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070888 VH DNA

<400> 415
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaagtc cctgagactc 60

tcctgtgcag cctctggatt cacccttgag gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgaaga gataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcc atggctggat tgacgctttt gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 416
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070888 VL DNA

<400> 416
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 417
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070890 VH DNA

<400> 417
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaagtc cctgagactc 60

tcctgtgcag cctctggatt cacccttgat gatgaggcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgctga gataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcc atggctggat tgacgctgaa gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 418
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070890 VL DNA

<400> 418
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 419
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070892 VH DNA

<400> 419
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tcctgtgcag cctctggatt cacccttgat gatgaggcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgaaaa cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcc atggctggat tgacgctgaa gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 420
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070892 VL DNA

<400> 420
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 421
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070894 VH DNA

<400> 421
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tcctgtgcag cctctggatt cacccttgat gatgaggcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgaaga gataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctgaa gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 422
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070894 VL DNA

<400> 422
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 423
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070896 VH DNA

<400> 423
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tcctgtgcag cctctggatt cacccttgat gatgaggcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgaaga gataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcc atggctggat tgacgctttt gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 424
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070896 VL DNA

<400> 424
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 425
<211> 369
<212> DNA
<213> Artificial Sequence

<220>

<223> P1-070898 VH DNA

<400> 425
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaagtc cctgagactc 60

tcctgtgcag cctctggatt cacccttgag gatgaggcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgctga gataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcc atggctggat tgacgctttt gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 426
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070898 VL DNA

<400> 426
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 427
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070900 VH DNA

<400> 427
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaagtc cctgagactc 60

tcctgtgcag cctctggatt cacccttgag gatgaggcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgaaaa cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctgaa gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 428
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070900 VL DNA

<400> 428
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 429
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070902 VH DNA

<400> 429
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaagtc cctgagactc 60

tcctgtgcag cctctggatt cacccttgag gatgaggcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgaaaa cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcc atggctggat tgacgctttt gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 430
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070902 VL DNA

<400> 430
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ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 431
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070904 VH DNA

<400> 431
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tcctgtgcag cctctggatt cacccttgat gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attgattgga acagtgaaaa cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctgaa gatgactggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 432
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070904 VL DNA

<400> 432
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ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 433
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070906 VH DNA

<400> 433
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaagtc cctgagactc 60

tcctgtgcag cctctggatt cacccttgag gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgaaaa cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctgaa gatgactggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 434
<211> 324
<212> DNA
<213> Artificial Sequence

<220>

<223> P1-070906 VL DNA

<400> 434
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ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 435
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070908 VH DNA

<400> 435
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tcctgtgcag cctctggatt cacccttgag gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attgattgga acagtgctaa cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctgaa gatgactggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 436
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070908 VL DNA

<400> 436
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ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 437
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070910 VH DNA

<400> 437
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tcctgtgcag cctctggatt cacccttgag gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attgattgga acagtgaaaa cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctttt gatgactggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 438
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070910 VL DNA

<400> 438
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ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 439
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070912 VH DNA

<400> 439
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tcctgtgcag cctctggatt cacccttgag gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attgattgga acagtgaaaa cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctgaa gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 440
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070912 VL DNA

<400> 440
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ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 441
<211> 369

<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070914 VH DNA

<400> 441
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tcctgtgcag cctctggatt cacccttgat gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgaaaa cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctgaa gatgactggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 442
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070914 VL DNA

<400> 442
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ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 443
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070916 VH DNA

<400> 443
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaagtc cctgagactc 60

tcctgtgcag cctctggatt cacccttgag gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgctaa cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctgaa gatgactggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 444
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070916 VL DNA

<400> 444
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ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 445
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070918 VH DNA

<400> 445
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaagtc cctgagactc 60

tcctgtgcag cctctggatt cacccttgag gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attgattgga acagtgctaa cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctttt gatgactggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 446
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070918 VL DNA

<400> 446
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 447
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070920 VH DNA

<400> 447
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaagtc cctgagactc 60

tcctgtgcag cctctggatt cacccttgag gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attgattgga acagtgaaaa cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctttt gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 448
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070920 VL DNA

<400> 448
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 449
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070922 VH DNA

<400> 449
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaagtc cctgagactc 60

tcctgtgcag cctctggatt cacccttgat gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attgattgga acagtgctaa cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctgaa gatgactggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 450
<211> 324

<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070922 VL DNA

<400> 450
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 451
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070924 VH DNA

<400> 451
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaagtc cctgagactc 60

tcctgtgcag cctctggatt cacccttgat gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attgattgga acagtgaaaa cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctttt gatgactggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 452
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070924 VL DNA

<400> 452
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 453
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070926 VH DNA

<400> 453
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaagtc cctgagactc 60

tcctgtgcag cctctggatt cacccttgat gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attgattgga acagtgaaaa cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctgaa gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 454
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070926 VL DNA

<400> 454
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 455
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070928 VH DNA

<400> 455
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaagtc cctgagactc 60

tcctgtgcag cctctggatt cacccttgag gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgaaaa cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctttt gatgactggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 456
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070928 VL DNA

<400> 456
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 457
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070930 VH DNA

<400> 457
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaagtc cctgagactc 60

tcctgtgcag cctctggatt cacccttgag gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attaattgga acagtgaaaa cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctgaa gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 458
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070930 VL DNA

<400> 458
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 459
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070932 VH DNA

<400> 459
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggcaagtc cctgagactc 60

tcctgtgcag cctctggatt cacccttgag gattatgcca tgcactgggt ccggcaagct 120

ccagggaagg gcctggagtg ggtctcaggt attgattgga acagtgctaa cataggctat 180

gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240

ctgcaaatga acagtctgag aactgaggac acggccttgt attactgtgc aaaagttcct 300

gggtatagcg gtggctggat tgacgctgaa gatgtctggg gccaagggac aatggtcacc 360

gtctcttca 369

<210> 460
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> P1-070932 VL DNA

<400> 460
gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60

ctctcctgca gggccagtca gagtgttagc agcagctact tagcctggta ccagcagaaa 120

cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180

gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240

cctgaagatt ttgcagtgta ttactgtcag cagtatggta gctcaccatt cactttcggc 300

cctgggacca aagtggatat caaa 324

<210> 461
<211> 1875
<212> DNA
<213> Artificial Sequence

<220>
<223> IgG1.3 heavy chain constant region DNA

<400> 461
gcgtcgacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 60

ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 120

tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 180

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg cacccagacc 240

tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagag agttgagccc 300

aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaagc cgaaggggcc 360

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggacccct 420

gaggtcacat gcgtggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 480

tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 540

agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 600

gagtacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 660

aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 720

atgaccaaga accaggtcag cctgacctgc ctggtcaaag gcttctatcc cagcgacatc 780

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 840

ctggactccg acggctcctt cttcctctat agcaagctca ccgtggcgtc gaccaagggc 900

ccatcggtct tccccctggc accctcctcc aagagcacct ctgggggcac agcggccctg 960

ggctgcctgg tcaaggacta cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc 1020

ctgaccagcg gcgtgcacac cttcccggct gtcctacagt cctcaggact ctactccctc 1080

agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg 1140

aatcacaagc ccagcaacac caaggtggac aagagagttg agcccaaatc ttgtgacaaa 1200

actcacacat gcccaccgtg cccagcacct gaagccgaag gggccccgtc agtcttcctc 1260

ttcccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg 1320

gtggtggacg tgagccacga agaccctgag gtcaagttca actggtacgt ggacggcgtg 1380

gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg 1440

gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgcaag 1500

gtctccaaca aagccctccc agcccccatc gagaaaacca tctccaaagc caaagggcag 1560

ccccgagaac cacaggtgta caccctgccc ccatcccggg aggagatgac caagaaccag 1620

gtcagcctga cctgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag 1680

agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1740

tccttcttcc tctatagcaa gctcaccgtg gacaagagca ggtggcagca ggggaacgtc 1800

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc 1860

ctgtccccgg gttga 1875

<210> 462
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Exemplary light chain constant region DNA

<400> 462
cgtacggtgg ctgcaccatc tgtcttcatc ttcccgccat ctgatgagca gttgaaatct 60

ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag 120

tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac 180

agcaaggaca gcacctacag cctcagcagc accctgacgc tgagcaaagc agactacgag 240

aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag 300

agcttcaaca ggggagagtg ttag 324

<210> 463
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary CDR1

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> X is D or L

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> X is E or D

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> X is E or Y

<400> 463

Gly Phe Thr Xaa Xaa Asp Xaa Ala Met His
1   5   10

<210> 464
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary CDR2

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> X is D or N

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> X is D or N

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> X is D, E, H or A

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> X is D, E, H or N

<400> 464

Gly Ile Xaa Trp Xaa Ser Xaa Xaa Ile Gly Tyr Ala Asp Ser Val Lys
1   5   10   15

Gly

<210> 465

<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary CDR3

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> X is E, H or G

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> X is E, D or F

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> X is D, E or V

<400> 465

Val Pro Gly Tyr Ser Xaa Gly Trp Ile Asp Ala Xaa Asp Xaa
1 5 10

<210> 466
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary CDR1

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> X is E, D, H or S

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> X is H or Y

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> X is D or A

<400> 466

Gly Phe Thr Phe Xaa Xaa Xaa Met His
1 5

<210> 467
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary CDR2

<220>
<221> misc_feature
<222> (1)..(1)
<223> X is E, H or I

<220>
<221> misc_feature
<222> (2)..(2)
<223> X is D or I

<220>
<221> misc_feature
<222> (4)..(4)
<223> X is D or Y

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> X is D or N

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> X is D, H or K

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> X is D, H or Y

<220>
<221> misc_feature
<222> (11)..(11)
<223> X is E or Y

<400> 467

Xaa Xaa Trp Xaa Asp Gly Ser Xaa Xaa Xaa Xaa Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 468
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Exemplary CDR3

<220>
<221> misc_feature
<222> (2)..(2)
<223> X is E or S

<220>
<221> misc_feature
<222> (3)..(3)
<223> X is E or G

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> X is D, E or S

<220>
<221> misc_feature
<222> (7)..(7)
<223> X is D or S

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> X is D, E or Y

<400> 468

Asp Xaa Xaa Phe Tyr Xaa Xaa Tyr Tyr Asp Phe Xaa
1 5 10