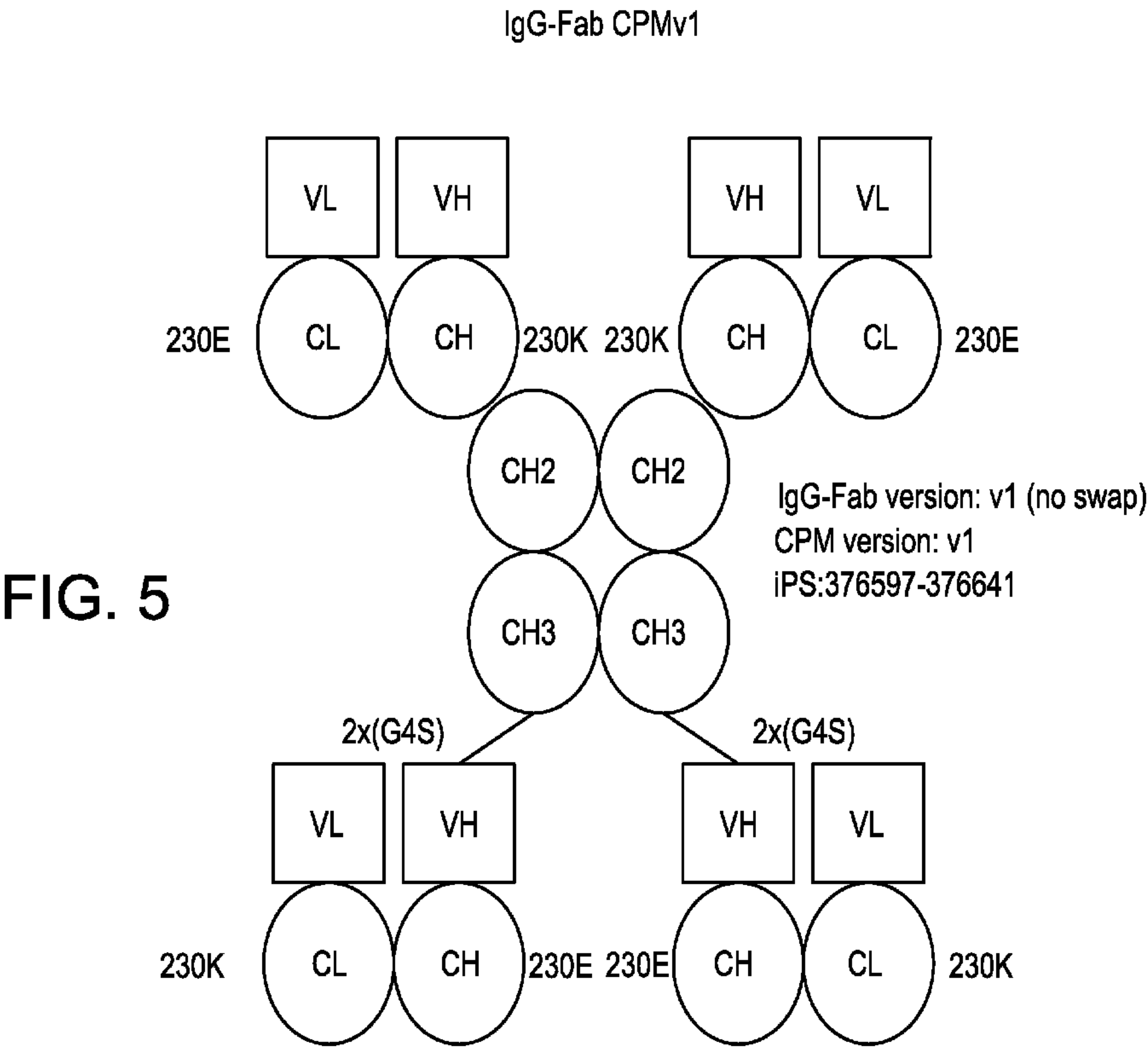




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(54) Title: TETRAVALENT BISPECIFIC AND TETRASPECIFIC ANTIGEN BINDING PROTEINS AND USES THEREOF



(57) **Abrégé/Abstract:**
The present invention relates to tetravalent bispecific and tetraspecific antigen binding proteins that are capable of binding to multiple targets. Pharmaceutical compositions comprising the bispecific and tetraspecific antigen binding proteins as well as methods for producing them are also disclosed.

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(71) Applicant: AMGEN INC. [US/US]; One Amgen Center Drive, Thousand Oaks, California 91320-1799 (US).

(72) Inventors: KANNAN, Gunasekaran; 151 Crestview Circle, Daly City, California 94015 (US). HORTTER, Michelle; 455 Mariposa Drive, Camarillo, California 93012 (US). BELOUSKI, Edward J.; 761 Camino Las Conchas, Thousand Oaks, California 91360 (US).

(74) Agent: DERMOTT, Jonathan M.; Amgen Inc., One Amgen Center Drive, Thousand Oaks, California 91320-1799 (US).

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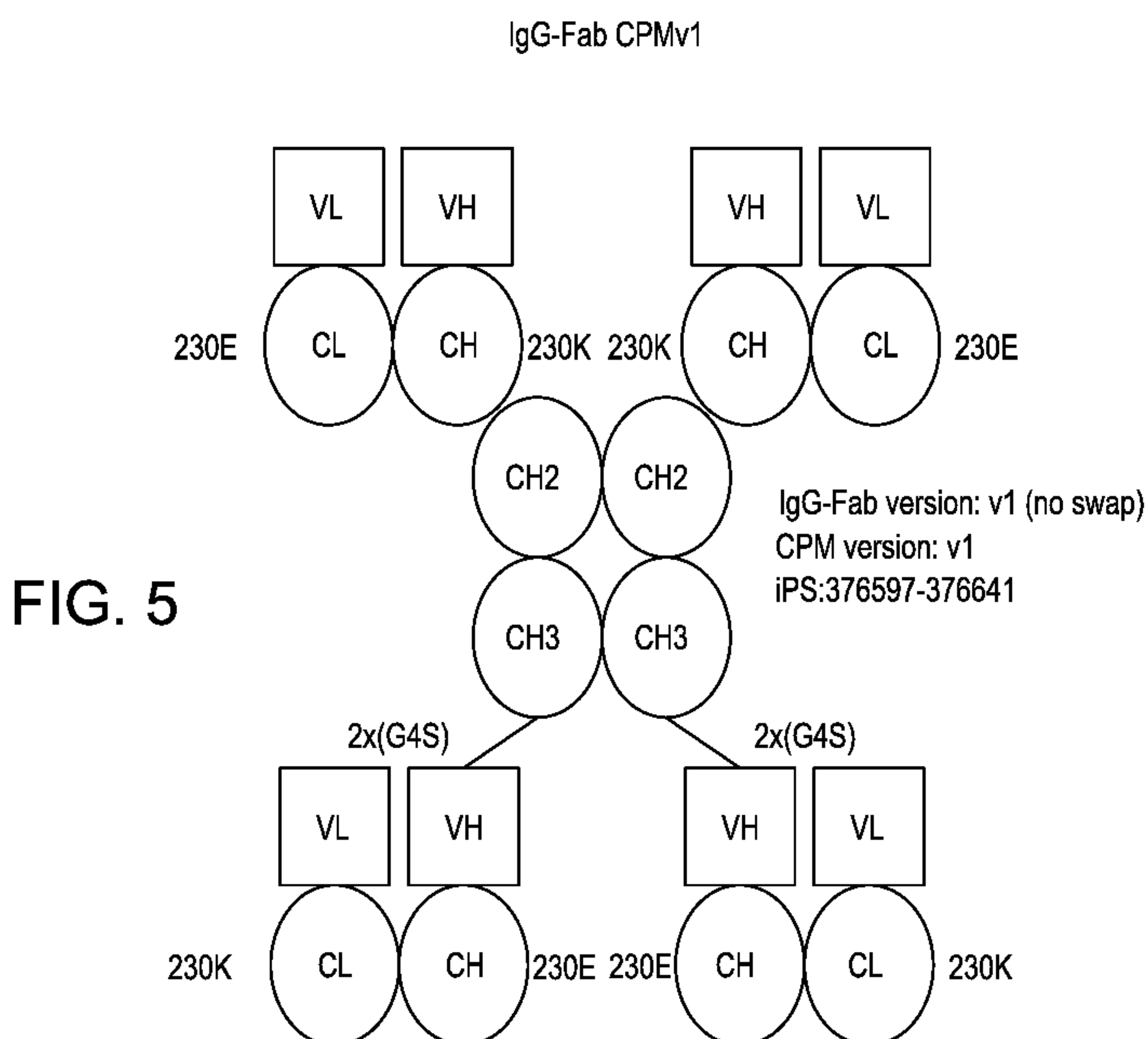
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(54) Title: TETRAVALENT BISPECIFIC AND TETRASPECIFIC ANTIGEN BINDING PROTEINS AND USES THEREOF



(57) Abstract: The present invention relates to tetravalent bispecific and tetraspecific antigen binding proteins that are capable of binding to multiple targets. Pharmaceutical compositions comprising the bispecific and tetraspecific antigen binding proteins as well as methods for producing them are also disclosed.

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TETRAVALENT BISPECIFIC AND TETRASPECIFIC ANTIGEN BINDING PROTEINS AND USES THEREOF

FIELD OF THE INVENTION

[0001] The present invention relates to tetravalent bispecific and tetraspecific antibodies, polynucleotides encoding tetravalent bispecific and tetraspecific antibodies, and methods of making tetravalent bispecific and tetraspecific antibodies.

BACKGROUND OF THE INVENTION

[0002] Current bispecific antibody technologies mostly rely on the scFv (single-chain fragment of the variable regions) format (Coloma and Morrison, *Nature Biotechnol.* 15:159, 1997; Lu et al, *J. Biol. Chem.* 280:19665, 2005) in which each VH (variable region of the heavy chain) is covalently linked to its cognate VL (variable region of the light chain), because in a Fab format there is yet no existing technology that can direct the specific pairing of a free light chain to only its cognate heavy chain and therefore the free light chains of different antigen specificity pair randomly with the heavy chains. However, expression of single-chain antibodies is often technically challenging, due to possible loss of binding affinity, protein aggregation, poor stability, and low production level (Demarest et al, *Curr. Opin. Drug Discov. Devel.* 11:675, 2008; Michaelson et al, *mAbs* 1:2, 128-141, 2009). This is especially true if the starting antibody is from a hybridoma (as opposed to a single-chain antibody from a phage display library) that has to be reformatted into a single-chain antibody. On the other hand, scFv's isolated from phages often are expressed poorly in mammalian cells.

[0003] Several innovative technologies have enabled the almost exclusive assembly of the Fc heterodimer to provide the backbone for designing bispecificity, e.g. knob-in-hole (Ridgway et al, *Protein Eng.* 9:617, 1996), electrostatic steering (Gunasekaran et al, *J. Biol. Chem.* 285:19637, 2010) and strand-exchange engineering domain (SEED) (Davis, *Protein Eng. Des. & Sel.* 23:195, 2010). In the Dual Variable Domains (DVD)-Ig approach, the VL and VH of the second antibody are fused via flexible linkers to the N-termini of the light and heavy chains, respectively, of the first antibody, creating two variable domains (VD) in tandem, called the outer VD and the inner VD (Wu et al, *ibid*). Due to the steric hindrance caused by the proximity of the outer VD to the ligand-binding site of the inner VD, extensive optimization involving VD selection from a number of available monoclonal antibodies,

orientation of VDs, and linker designs, most of which have to be empirically determined, is necessary to retain the binding affinity of the inner VD (DiGiammarino et al, Methods Mol. Biol. 899:145, 2012).

[0004] Another method takes advantage of the species-restricted heavy and light chain pairing in rat/mouse quadromas (Lindhofer et al, J. Immunol. 155:219, 1995). However, the bispecific antibody generated is a rat/mouse antibody, which obviously has immunogenicity issues as a therapeutic.

[0005] The Crossmab approach, based on the knob-into-hole heterodimerized heavy chains, in addition uses immunoglobulin domain crossover as a generic approach for the production of bispecific IgG antibodies (Schaefer et al, Proc. Natl. Acad. Sci. USA, 108:11187, 2011). Nevertheless, the correct pairings of the H chain heterodimer and the cognate Fv's are not exclusive, and the unwanted side products have to be removed during purification.

[0006] An extension of the Crossmab approach was used to generate a tetravalent bispecific antibody by tagging an extra set of Fab and Crossmab Fab fragments to the C-termini of Crossmab (Regula et al, US Patent Application No: 2010/0322934), and the challenges of obtaining exclusively correct pairings of the H chain heterodimer and the cognate Fv's remain.

[0007] A further approach to bispecificity is to use a single binding site to target two different antigens was demonstrated by a "two-in-one" antibody. One such "two-in-one" antibody is a variant of the antibody Herceptin, which interacts with both Her2 and VEGF (Bostrom et al, Science 323:1610, 2009). This approach is attractive for clinical applications because it provides a bispecific antibody that has an identical format as a normal IgG. However, screening for such a variant is very labor intensive and there is no guarantee that a single binding site which can bind both antigens of interest can be obtained.

[0008] A stable multivalent antibody with only monospecificity based on a single set of Fab fragments was described in US published patent application US2011/0076722. Another technology uses Dock-and-Lock domains to link preformed Fab fragments of a different specificity to an antibody to form a hexavalent bispecific antibody (Rossi et al, Cancer Res. 68:8384, 2008). Since the vast majority of antibodies (i.e. those generated from hybridomas, Fab libraries and B-cell cloning, regardless of whether the origin is from normal mice, rats, and rabbits, or transgenic (humanized) mice or rats, or patients) have a free light chain paired with its cognate heavy chain, a Fab-based technology for bispecific antibodies that circumvents the problem of random light chain pairing is urgently needed. Such a technology would facilitate straightforward and efficient production of a bispecific antibody from two

existing antibodies, which can be used first as a versatile tool molecule to probe the potential synergism of dual targeting, and secondly as a therapeutic to exploit the dual targeting in the context of a complete antibody in the disease setting to be treated.

SUMMARY OF THE INVENTION

[0009] The present invention is directed to a bispecific antigen binding protein is comprised of an antibody against a first target and a Fab fragment derived from an antibody against a second target. In this IgG-Fab format, the bispecific, multivalent antigen binding protein comprises (i) a first polypeptide comprising a first heavy chain (VH2-CH1-CH2-CH3) from the first antibody, wherein the first heavy chain is fused at its carboxyl terminus (optionally through a peptide linker) to a polypeptide comprising VH2-CH1 domains of a second antibody to form a modified heavy chain, (ii) a second polypeptide comprising a light chain from a first antibody (VL1-CL) and (iii) a third polypeptide comprising VL2-CL domains of the second antibody. The CL and CH1 domains of the first antibody may be switched in some embodiments between the first and second polypeptide. In such embodiments, the second polypeptide comprises VL1-CH1, while the first polypeptide comprises VH1-CL-CH2-CH3-VH2-CH1. The third polypeptide comprises VL2-CL. Alternatively, the CL and CH1 domains of the second antibody may be switched in some embodiments between the first and third polypeptides. In such embodiments, the third polypeptide comprises VL2-CH1, while the first polypeptide comprises VH1-CH1-CH2-CH3-VH2-CL. The first polypeptide comprises VL1-CL. In yet another embodiment, the CL and CH1 domains of both antibodies are switched between the first, second and third polypeptides. In such embodiments, the first polypeptide comprises VH1-CL-CH2-CH3-VH2-CL, the second polypeptide comprises VL1-CH1, and the third polypeptide comprises VL2-CH1.

[0010] In one aspect, the present invention comprises a bispecific, tetravalent antigen binding protein, comprising a) a first heavy chain of a first antibody (VH1), wherein the first antibody specifically binds to a first antigen, and wherein the first heavy chain is fused through its C-terminus to the N-terminus of a moiety comprising a second heavy chain of a second antibody (VH2), wherein the second antibody specifically binds to a second antigen; b) two light chains of the first antibody of a); and c) two light chains of the second antibody of a).

[0011] In another aspect, the present invention comprises a bispecific antigen binding protein comprising (i) a first binding domain that specifically binds to a first antigen comprising a first light chain immunoglobulin variable region (VL1) and a first heavy chain

immunoglobulin variable region (VH1); (ii) a second binding domain that specifically binds to a second antigen comprising a second light chain immunoglobulin variable region (VL2) and a second heavy chain immunoglobulin variable region (VH2); and (iii) a human immunoglobulin Fc region, wherein one of the binding domains is positioned at the amino terminus of the Fc region and the other binding domain is positioned at the carboxyl terminus of the Fc region, wherein the carboxyl-terminal binding domain is a Fab and is fused through a peptide linker to the carboxyl terminus of the Fc region, and wherein the Fab is fused to the Fc region through the amino terminus of the VH region of the Fab.

[0012] In another aspect, the present invention comprises a tetraspecific, tetravalent antigen binding protein, comprising a) a first heavy chain of a first antibody (VH1), wherein the first antibody specifically binds to a first antigen, wherein the CH1 domain of the first heavy chain is replaced by the CL domain of a light chain, and wherein the first heavy chain is fused through its C-terminus to the N-terminus of a moiety comprising a second heavy chain of a second antibody (VH2), wherein the second antibody specifically binds to a second antigen; b) a first light chain of the first antibody of a), wherein the CL domain of the first light chain is replaced by the CH1 domain of a heavy chain; c) a second light chain of the second antibody of a); d) a second heavy chain of a third antibody (VH3), wherein the third antibody specifically binds to a third antigen, wherein the CH1 domain of the second heavy chain is replaced by the CL domain of a light chain, and wherein the third heavy chain is fused through its C-terminus to the N-terminus of a moiety comprising a fourth heavy chain of a fourth antibody (VH4), wherein the fourth antibody specifically binds to a fourth antigen; e) a third light chain of the third antibody of d), wherein the CL domain of the third light chain is replaced by the CH1 domain of a heavy chain; and f) a fourth light chain of the fourth antibody of d).

[0013] In another aspect, the present invention comprises a bispecific, tetravalent antigen binding protein, comprising:

[0014] a) a first polypeptide comprising a first heavy chain of a first antibody comprising a first heavy chain variable region (VH1) and a first CH1 domain, wherein the first antibody specifically binds to a first antigen, and wherein the first heavy chain is fused through its C-terminus to the N-terminus of a polypeptide comprising a second heavy chain variable region of a second antibody (VH2), wherein the VH2 is fused through its C-terminus to the N-terminus of a second CH1 domain, and wherein the second antibody specifically binds to a second antigen; wherein

[0015] i) the VH1 or first CH1 domain comprises at least one amino acid substitution to introduce a charged amino acid at a residue selected from the group consisting of positions 39, 44, and 183 using EU numbering; and

[0016] ii) the VH2 or second CH1 domain comprises at least one amino acid substitution to introduce a charged amino acid at a residue selected from the group consisting of a residue that corresponds to positions 39, 44, and 183 using EU numbering, wherein the charge is the opposite of the substituted residue of the VH1 or first CH1 of the first heavy chain; and

[0017] b) a second polypeptide comprising a first light chain of the first antibody of a), wherein the first light chain comprises a first light chain variable region (VL1) and a first CL region; and wherein the VL1 or first CL domain comprises at least one amino acid substitution to introduce a charged amino acid at a residue selected from the group consisting of positions 38, 100, and 176 using EU numbering, wherein

[0018] the charge at position 38 is the opposite of the substituted residue of the VH1 or first CH1 of the first heavy chain at position 39; the charge at position 100 is the opposite of the substituted residue of the VH1 or first CH1 of the first heavy chain at position 44; the charge at position 176 is the opposite of the substituted residue of the VH1 or first CH1 of the first heavy chain at position 183; and

[0019] c) a third polypeptide comprising a second light chain of the second antibody of a), wherein the second light chain comprises a second light chain variable region (VL2) and a second CL region; and wherein the VL2 or second CL domain comprises at least one amino acid substitution to introduce a charged amino acid at a residue selected from the group consisting of positions 38, 100, and 176 using EU numbering, wherein the charge at position 38 is the opposite of the substituted residue of the VH2 or second CH1 of the second heavy chain at position 39; the charge at position 100 is the opposite of the substituted residue of the VH2 or second CH1 of the second heavy chain at position 44; the charge at position 176 is the opposite of the substituted residue of the VH2 or second CH1 of the second heavy chain at position 183.

[0020] In certain embodiments, the first heavy chain is fused to the VH2 via a peptide linker. In certain embodiments, the peptide linker comprises a sequence selected from the group consisting of (Gly₃Ser)₂, (Gly₄Ser)₂, (Gly₃Ser)₃, (Gly₄Ser)₃, (Gly₃Ser)₄, (Gly₄Ser)₄, (Gly₃Ser)₅, (Gly₄Ser)₅, (Gly₃Ser)₆, and (Gly₄Ser)₆.

[0021] In certain embodiments, the antigen binding protein according to claim 15, wherein a) the VH1 comprises a Q39E mutation and the first CH1 domain comprises a S183K mutation using EU numbering; b) the VH2 comprises a Q39K mutation and the second CH1 domain

comprises a S183E mutation using EU numbering; c) the VL1 comprises a Q38K mutation and the first CL domain comprises a S176E mutation using EU numbering; and d) the VL2 comprises a Q38E mutation and the second CL domain comprises a S176K mutation using EU numbering.

[0022] In certain embodiments, the antigen binding protein according to claim 16, wherein a) the first CH1 domain comprises G44E and S183K mutations using EU numbering; b) the second CH1 domain comprises G44K and S183E mutations using EU numbering; c) the first CL domain comprises G100K and S176E mutations using EU numbering; and d) the second CL domain comprises G100E and S176K mutations using EU numbering.

[0023] In certain embodiments, the antigen binding protein according to claim 16, wherein a) the VH1 comprises a Q39K mutation and the first CH1 domain comprises a S183E mutation using EU numbering; b) the VH2 comprises a Q39E mutation and the second CH1 domain comprises a S183K mutation using EU numbering; c) the VL1 comprises a Q38E mutation and the first CL domain comprises a S176K mutation using EU numbering; and d) the VL2 comprises a Q38K mutation and the second CL domain comprises a S176E mutation using EU numbering.

[0024] In certain embodiments, the antigen binding protein according to claim 16, wherein a) the first CH1 domain comprises G44K and S183E mutations using EU numbering; b) the second CH1 domain comprises G44E and S183K mutations using EU numbering; c) the first CL domain comprises G100E and S176K mutations using EU numbering; and d) the second CL domain comprises G100K and S176E mutations using EU numbering.

[0025] The present invention includes one or more nucleic acids encoding any of the bispecific antigen binding proteins described herein or components thereof, as well as vectors comprising the nucleic acids. Also encompassed within the invention is a recombinant host cell, such as a CHO cell, that expresses any of the bispecific antigen binding proteins.

[0026] The present invention also provides a pharmaceutical composition comprising a bispecific antigen binding protein and a pharmaceutically acceptable diluent, excipient or carrier.

BRIEF DESCRIPTION OF THE DRAWINGS

[0027] Figure 1 depicts a schematic representation of a bispecific IgG-Fab format of the present invention. In this format, one polypeptide chain of a Fab fragment from a second antibody (e.g. the heavy chain (VH2-CH1) is fused to the carboxyl terminus of the heavy

chain of a first antibody through a peptide linker to produce a modified heavy chain. The complete molecule is a homohexamer comprising two modified heavy chains, two light chains from the first antibody, and two polypeptide chains containing the other half of the Fab fragment from the second antibody (e.g. the light chain (VL2-CL)). Charge pair mutations (represented by the circles) can be introduced into the Fab regions of the first antibody (Fab 1) and/or second antibody (Fab 2) to promote correct heavy chain-light chain pairs.

[0028] Figure 2 depicts a schematic representation of a bispecific IgG-Fab format of the present invention using immunoglobulin domain crossover. In this format, one polypeptide chain of a Fab fragment from a second antibody (e.g. the heavy chain (VH2-CH1)) is fused to the carboxyl terminus of the heavy chain comprising a CL instead of a CH1 domain of a first antibody through a peptide linker to produce a modified heavy chain. The complete molecule is a homohexamer comprising two modified heavy chains, two light chains from the first antibody comprising a CH1 domain instead of a CL domain, and two polypeptide chains containing the other half of the Fab fragment from the second antibody (e.g. the light chain (VL2-CL)). Charge pair mutations (represented by the circles) can be introduced into the Fab regions of the first antibody (Fab 1) and/or second antibody (Fab 2) to promote correct heavy chain-light chain pairs.

[0029] Figure 3 depicts a schematic representation of a tetraspecific IgG-Fab format of the present invention using immunoglobulin domain crossover with heavy chain heterodimers. In this format, one polypeptide chain of a Fab fragment from a second antibody (e.g. the heavy chain (VH2-CH1)) is fused to the carboxyl terminus of the heavy chain comprising a CL instead of a CH1 domain of a first antibody through a peptide linker to produce a first modified heavy chain. Similarly, another polypeptide chain of a Fab fragment from a fourth antibody (e.g. the heavy chain (VH4-CH1)) is fused to the carboxyl terminus of the heavy chain comprising a CL instead of a CH1 domain of a third antibody through a peptide linker to produce a second modified heavy chain. The two heavy chains can be engineered to preferentially form heterodimers as opposed to homodimers. The complete molecule is a hexamer comprising two modified heavy chains that form heterodimers, one light chain from the first antibody comprising a CH1 domain instead of a CL domain, one light chain from the third antibody comprising a CH1 domain instead of a CL domain, one polypeptide chain containing the other half of the Fab fragment from the second antibody (e.g. the light chain (VL2-CL)), and one polypeptide chain containing the other half of the Fab fragment from the fourth antibody (e.g. the light chain (VL4-CL)). Charge pair mutations (represented by the

circles) can be introduced into the Fab regions of the antibodies to promote correct heavy chain-light chain pairs.

[0030] Figure 4 depicts a schematic representation of a tetraspecific IgG-Fab format the same as in Figure 3, except that the charges of the mutated residues of the heavy chain heterodimer are reversed.

[0031] Figure 5 depicts a schematic representation of a tetravalent, bispecific IgG-Fab format (IgG-Fab CPMv1) of the present invention constructed using insertion of charged amino acids at heavy chain position 230 (AHO numbering) and light chain position 230 (AHO numbering).

[0032] Figure 6 depicts a schematic representation of a tetravalent, bispecific IgG-Fab format (IgG-Fab CPMv1 N-term CH/CL swap) of the present invention constructed using insertion of charged amino acids at heavy chain position 230 (AHO numbering) and light chain position 230 (AHO numbering) and swapping of CH1 and CL domains in the N-terminal region of the molecule.

[0033] Figure 7 depicts a schematic representation of a tetravalent, bispecific IgG-Fab format (IgG-Fab CPMv1 C-term CH/CL swap) of the present invention constructed using insertion of charged amino acids at heavy chain position 230 (AHO numbering) and light chain position 230 (AHO numbering) and swapping of CH1 and CL domains in the C-terminal region of the molecule.

[0034] Figure 8 depicts a schematic representation of a tetravalent, bispecific IgG-Fab format (IgG-Fab CPMv1 CH/CL both swap) of the present invention constructed using insertion of charged amino acids at heavy chain position 230 (AHO numbering) and light chain position 230 (AHO numbering) and swapping of CH1 and CL domains in both the N-terminal and C-terminal regions of the molecule.

[0035] Figure 9 depicts a schematic representation of a tetravalent, bispecific IgG-Fab format (IgG-Fab CPMv2) of the present invention constructed using insertion of charged amino acids at heavy chain positions 46 and 230 (AHO numbering) and light chain positions 46 and 230 (AHO numbering).

[0036] Figure 10 depicts a schematic representation of a tetravalent, bispecific IgG-Fab format (IgG-Fab CPMv2 N-term CH/CL swap) of the present invention constructed using insertion of charged amino acids at heavy chain positions 46 and 230 (AHO numbering) and light chain positions 46 and 230 (AHO numbering) and swapping of CH1 and CL domains in the N-terminal region of the molecule.

[0037] Figure 11 depicts a schematic representation of a tetravalent, bispecific IgG-Fab format (IgG-Fab CPMv2 C-term CH/CL swap) of the present invention constructed using insertion of charged amino acids at heavy chain positions 46 and 230 (AHO numbering) and light chain positions 46 and 230 (AHO numbering) and swapping of CH1 and CL domains in the C-terminal region of the molecule.

[0038] Figure 12 depicts a schematic representation of a tetravalent, bispecific IgG-Fab format (IgG-Fab CPMv2 CH/CL both swap) of the present invention constructed using insertion of charged amino acids at heavy chain positions 46 and 230 (AHO numbering) and light chain positions 46 and 230 (AHO numbering) and swapping of CH1 and CL domains in both the N-terminal and C-terminal regions of the molecule.

[0039] Figure 13 depicts a schematic representation of a tetravalent, bispecific IgG-Fab format (IgG-Fab CPMv3) of the present invention constructed using insertion of charged amino acids at heavy chain positions 51 and 230 (AHO numbering) and light chain positions 141 and 230 (AHO numbering).

[0040] Figure 14 depicts a schematic representation of a tetravalent, bispecific IgG-Fab format (IgG-Fab CPMv3 N-term CH/CL swap) of the present invention constructed using insertion of charged amino acids at heavy chain positions 51 and 230 (AHO numbering) and light chain positions 141 and 230 (AHO numbering) and swapping of CH1 and CL domains in the N-terminal region of the molecule.

[0041] Figure 15 depicts a schematic representation of a tetravalent, bispecific IgG-Fab format (IgG-Fab CPMv3 C-term CH/CL swap) of the present invention constructed using insertion of charged amino acids at heavy chain positions 51 and 230 (AHO numbering) and light chain positions 141 and 230 (AHO numbering) and swapping of CH1 and CL domains in the C-terminal region of the molecule.

[0042] Figure 16 depicts a schematic representation of a tetravalent, bispecific IgG-Fab format (IgG-Fab CPMv3 CH/CL both swap) of the present invention constructed using insertion of charged amino acids at heavy chain positions 51 and 230 (AHO numbering) and light chain positions 141 and 230 (AHO numbering) and swapping of CH1 and CL domains in both the N-terminal and C-terminal regions of the molecule.

[0043] Figure 17 compares the expression titer of IgG-Fabs based on domain swapping format.

[0044] Figure 18 compares the expression titer of IgG-Fabs based on type of charge pair mutation(s).

[0045] Figure 19 compares the purity of IgG-Fabs based on domain swapping format.

[0046] Figure 20 compares the anti-TL1A potency of IgG-Fabs based on domain swapping format.

[0047] Figure 21 compares the anti-TNF α potency of IgG-Fabs based on domain swapping format.

[0048] Figure 22 compares the anti-TL1A potency of IgG-Fabs based on type of charge pair mutation(s).

[0049] Figure 23 compares the anti-TNF α potency of IgG-Fabs based on type of charge pair mutation(s).

DETAILED DESCRIPTION

[0050] As used herein, the term “antigen binding protein” refers to a protein that specifically binds to one or more target antigens. An antigen binding protein can include an antibody and functional fragments thereof. A “functional antibody fragment” is a portion of an antibody that lacks at least some of the amino acids present in a full-length heavy chain and/or light chain, but which is still capable of specifically binding to an antigen. A functional antibody fragment includes, but is not limited to, a Fab fragment, a Fab' fragment, a F(ab')₂ fragment, a Fv fragment, a Fd fragment, and a complementarity determining region (CDR) fragment, and can be derived from any mammalian source, such as human, mouse, rat, rabbit, or camelid. Functional antibody fragments may compete for binding of a target antigen with an intact antibody and the fragments may be produced by the modification of intact antibodies (e.g. enzymatic or chemical cleavage) or synthesized *de novo* using recombinant DNA technologies or peptide synthesis.

[0051] “Heavy” and “light” chains refer to the two polypeptides which comprise an IgG. A heavy chain can be broken down into the following domains from N-terminus to C-terminus: VH, CH1, CH2, and CH3. A light chain can be broken down into the following domains from N-terminus to C-terminus: VL and CL. The CH1 and CL domains will interact such that the VH and VL domains form a functional conformation.

[0052] An antigen binding protein can also include a protein comprising one or more functional antibody fragments incorporated into a single polypeptide chain or into multiple polypeptide chains. For instance, antigen binding proteins can include, but are not limited to, a diabody (*see, e.g.*, EP 404,097; WO 93/11161; and Hollinger *et al.*, Proc. Natl. Acad. Sci. USA, Vol. 90:6444-6448, 1993); an intrabody; a domain antibody (single VL or VH domain or two or more VH domains joined by a peptide linker; *see Ward et al.*, Nature, Vol.

341:544-546, 1989); a maxibody (2 scFvs fused to Fc region, *see* Fredericks *et al.*, Protein Engineering, Design & Selection, Vol. 17:95-106, 2004 and Powers *et al.*, Journal of Immunological Methods, Vol. 251:123-135, 2001); a triabody; a tetrabody; a minibody (scFv fused to CH3 domain; *see* Olafsen *et al.*, Protein Eng Des Sel. , Vol.17:315-23, 2004); a peptibody (one or more peptides attached to an Fc region, *see* WO 00/24782); a linear antibody (a pair of tandem Fd segments (VH-CH1-VH-CH1) which, together with complementary light chain polypeptides, form a pair of antigen binding regions, *see* Zapata *et al.*, Protein Eng., Vol. 8:1057-1062, 1995); a small modular immunopharmaceutical (*see* U.S. Patent Publication No. 20030133939); and immunoglobulin fusion proteins (e.g. IgG-scFv, IgG-Fab, 2scFv-IgG, 4scFv-IgG, VH-IgG, IgG-VH, and Fab-scFv-Fc).

[0053] In certain aspects, the antigen binding proteins of the present invention are “bispecific” meaning that they are capable of specifically binding to two different antigens. In another aspect, the antigen binding proteins of the present invention are “tetraspecific” meaning that they are capable of specifically binding to four different antigens. As used herein, an antigen binding protein “specifically binds” to a target antigen when it has a significantly higher binding affinity for, and consequently is capable of distinguishing, that antigen, compared to its affinity for other unrelated proteins, under similar binding assay conditions. Antigen binding proteins that specifically bind an antigen may have an equilibrium dissociation constant (K_D) $\leq 1 \times 10^{-6}$ M. The antigen binding protein specifically binds antigen with “high affinity” when the K_D is $\leq 1 \times 10^{-8}$ M. In one embodiment, the antigen binding proteins of the invention bind to target antigen(s) with a K_D of $\leq 5 \times 10^{-7}$ M. In another embodiment, the antigen binding proteins of the invention bind to target antigen(s) with a K_D of $\leq 1 \times 10^{-7}$ M.

[0054] Affinity is determined using a variety of techniques, an example of which is an affinity ELISA assay. In various embodiments, affinity is determined by a surface plasmon resonance assay (e.g., BIAcore®-based assay). Using this methodology, the association rate constant (k_a in $M^{-1}s^{-1}$) and the dissociation rate constant (k_d in s^{-1}) can be measured. The equilibrium dissociation constant (K_D in M) can then be calculated from the ratio of the kinetic rate constants (k_d/k_a). In some embodiments, affinity is determined by a kinetic method, such as a Kinetic Exclusion Assay (KinExA) as described in Rathanaswami *et al.* Analytical Biochemistry, Vol. 373:52-60, 2008. Using a KinExA assay, the equilibrium dissociation constant (K_D in M) and the association rate constant (k_a in $M^{-1}s^{-1}$) can be measured. The dissociation rate constant (k_d in s^{-1}) can be calculated from these values ($K_D \times k_a$). In other embodiments, affinity is determined by an equilibrium/solution method. In

certain embodiments, affinity is determined by a FACS binding assay. In certain embodiments of the invention, the antigen binding protein specifically binds to target antigen(s) expressed by a mammalian cell (e.g., CHO, HEK 293, Jurkat), with a K_D of 20 nM (2.0×10^{-8} M) or less, K_D of 10 nM (1.0×10^{-8} M) or less, K_D of 1 nM (1.0×10^{-9} M) or less, K_D of 500 pM (5.0×10^{-10} M) or less, K_D of 200 pM (2.0×10^{-10} M) or less, K_D of 150 pM (1.50×10^{-10} M) or less, K_D of 125 pM (1.25×10^{-10} M) or less, K_D of 105 pM (1.05×10^{-10} M) or less, K_D of 50 pM (5.0×10^{-11} M) or less, or K_D of 20 pM (2.0×10^{-11} M) or less, as determined by a Kinetic Exclusion Assay, conducted by the method described in Rathanaswami *et al.* Analytical Biochemistry, Vol. 373:52-60, 2008. In some embodiments, the bispecific antigen binding proteins described herein exhibit desirable characteristics such as binding avidity as measured by k_d (dissociation rate constant) for target antigen(s) of about 10^{-2} , 10^{-3} , 10^{-4} , 10^{-5} , 10^{-6} , 10^{-7} , 10^{-8} , 10^{-9} , 10^{-10} s $^{-1}$ or lower (lower values indicating higher binding avidity), and/or binding affinity as measured by K_D (equilibrium dissociation constant) for target antigen(s) of about 10^{-9} , 10^{-10} , 10^{-11} , 10^{-12} , 10^{-13} , 10^{-14} , 10^{-15} , 10^{-16} M or lower (lower values indicating higher binding affinity).

[0055] In certain embodiments of the invention, the antigen binding proteins are multivalent. The valency of the binding protein denotes the number of individual antigen binding domains within the binding protein. For example, the terms “monovalent,” “bivalent,” and “tetravalent” with reference to the antigen binding proteins of the invention refer to binding proteins with one, two, and four antigen binding domains, respectively. Thus, a tetravalent antigen binding protein comprises four or more antigen binding domains. In other embodiments, the bispecific antigen binding proteins are multivalent. For instance, in certain embodiments, the bispecific antigen binding proteins are tetravalent comprising four antigen-binding domains: two antigen-binding domains binding to a first target antigen and two antigen-binding domains binding to a second target antigen. A tetraspecific antigen binding protein is tetravalent and comprises four antigen-binding domains: one to antigen-binding domain binding to a first target antigen, one antigen-binding domain binding to a second target antigen, one to antigen-binding domain binding to a third target antigen, and one antigen-binding domain binding to a fourth target antigen.

[0056] In one embodiment the tetravalent bispecific antibody binds two distinct targets on two different cell types. An exemplary embodiment includes a tetravalent bispecific antibody bridging between target tumor cell and a natural killer cell to direct the natural killer cell to the tumor. In yet another embodiment of the invention, the tetravalent bispecific antibody binds two different epitopes on the same molecular target (i.e. biparatopic). It is also apparent

to the one skilled in the art that one or both of the targets of the tetravalent bispecific antibody can be soluble or expressed on a cell surface.

[0057] As used herein, the term “antigen binding domain,” which is used interchangeably with “binding domain,” refers to the region of the antigen binding protein that contains the amino acid residues that interact with the antigen and confer on the antigen binding protein its specificity and affinity for the antigen. In some embodiments, the binding domain may be derived from the natural ligands of the target antigen(s). As used herein, the term “target antigen(s)” refers to a first target antigen and/or a second target antigen of a bispecific molecule and also refers to a first target antigen, a second target antigen, a third target antigen, and/or a fourth target antigen of a tetraspecific molecule.

[0058] In certain embodiments of the bispecific and tetraspecific antigen binding proteins of the invention, the binding domain may be derived from an antibody or functional fragment thereof. For instance, the binding domains of the bispecific and tetraspecific antigen binding proteins of the invention may comprise one or more complementarity determining regions (CDR) from the light and heavy chain variable regions of antibodies that specifically bind to target antigen(s). As used herein, the term “CDR” refers to the complementarity determining region (also termed “minimal recognition units” or “hypervariable region”) within antibody variable sequences. There are three heavy chain variable region CDRs (CDRH1, CDRH2 and CDRH3) and three light chain variable region CDRs (CDRL1, CDRL2 and CDRL3). The term “CDR region” as used herein refers to a group of three CDRs that occur in a single variable region (i.e. the three light chain CDRs or the three heavy chain CDRs). The CDRs in each of the two chains typically are aligned by the framework regions to form a structure that binds specifically with a specific epitope or domain on the target protein. From N-terminus to C-terminus, naturally-occurring light and heavy chain variable regions both typically conform with the following order of these elements: FR1, CDR1, FR2, CDR2, FR3, CDR3 and FR4.

[0059] Both the EU index as in Kabat *et al.*, Sequences of Proteins of Immunological Interest, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD (1991) and AHo numbering schemes (Honegger A. and Plückthun A. *J Mol Biol.* 2001 Jun 8;309(3):657-70) can be used in the present invention. Amino acid positions and complementarity determining regions (CDRs) and framework regions (FR) of a given antibody may be identified using either system. For example, EU heavy chain positions of 39, 44, 183, 356, 357, 370, 392, 399, and 409 are equivalent to AHo heavy chain positions 46, 51, 230, 484, 485, 501, 528, 535, and 551, respectively. Similarly, EU light chain positions

38, 100, and 176 are equivalent to AHO light chain positions 46 141, and 230, respectively.

Tables 1, 2, and 3 below demonstrate the equivalence between numbering positions.

Table 1 - v1

Chain	Domain	Mutation	AHo #	EU #	Kabat #
LC-E	Constant	E	230	176	176
LC-K	Constant	K	230	176	176
HC-E	CH1	E	230	183	188
HC-K	CH1	K	230	183	188

Table 2 - v2

Chain	Domain	Mutation	AHo #	EU #	Kabat #
LC-E	Variable	E	46	38	38
	Constant	E	230	176	176
LC-K	Variable	K	46	38	38
	Constant	K	230	176	176
HC-E	Variable	E	46	39	39
	CH1	E	230	183	188
HC-K	Variable	K	46	39	39
	CH1	K	230	183	188

Table 3 - v3

Chain	Domain	Mutation	AHo #	EU #	Kabat #
LC-E	Variable	E	141	100	100
	Constant	E	230	176	176
LC-K	Variable	K	141	100	100
	Constant	K	230	176	176
HC-E	Variable	E	51	44	44
	CH1	E	230	183	188
HC-K	Variable	K	51	44	44
	CH1	K	230	183	188

[0060] Papain digestion of antibodies produces two identical antigen-binding fragments, called “Fab” fragments, each with a single antigen-binding site, and a residual “Fc” fragment which contains the immunoglobulin constant region. The Fab fragment contains all of the variable domain, as well as the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Thus, a “Fab fragment” is comprised of one immunoglobulin light chain (light chain variable region (VL) and constant region (CL)) and the CH1 region and variable region (VH) of one immunoglobulin heavy chain. The heavy chain of a Fab molecule cannot form a disulfide bond with another heavy chain molecule.

The Fc fragment displays carbohydrates and is responsible for many antibody effector functions (such as binding complement and cell receptors), that distinguish one class of antibody from another. The “Fd fragment” comprises the VH and CH1 domains from an immunoglobulin heavy chain. The Fd fragment represents the heavy chain component of the Fab fragment.

[0061] A “Fab' fragment” is a Fab fragment having at the C-terminus of the CH1 domain one or more cysteine residues from the antibody hinge region.

[0062] A “F(ab')₂ fragment” is a bivalent fragment including two Fab' fragments linked by a disulfide bridge between the heavy chains at the hinge region.

[0063] The “Fv” fragment is the minimum fragment that contains a complete antigen recognition and binding site from an antibody. This fragment consists of a dimer of one immunoglobulin heavy chain variable region (VH) and one immunoglobulin light chain variable region (VL) in tight, non-covalent association. It is in this configuration that the three CDRs of each variable region interact to define an antigen binding site on the surface of the VH-VL dimer. A single light chain or heavy chain variable region (or half of an Fv fragment comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site comprising both VH and VL.

[0064] The “variable region,” used interchangeably herein with “variable domain” (variable region of a light chain (VL), variable region of a heavy chain (VH)) refers to the region in each of the light and heavy immunoglobulin chains which is involved directly in binding the antibody to the antigen. As discussed above, the regions of variable light and heavy chains have the same general structure and each region comprises four framework (FR) regions whose sequences are widely conserved, connected by three CDRs. The framework regions adopt a beta-sheet conformation and the CDRs may form loops connecting the beta-sheet structure. The CDRs in each chain are held in their three-dimensional structure by the framework regions and form, together with the CDRs from the other chain, the antigen binding site.

[0065] The “immunoglobulin domain” represents a peptide comprising an amino acid sequence similar to that of immunoglobulin and comprising approximately 100 amino acid residues including at least two cysteine residues. Examples of the immunoglobulin domain include VH, CH1, CH2, and CH3 of an immunoglobulin heavy chain, and VL and CL of an immunoglobulin light chain. In addition, the immunoglobulin domain is found in proteins other than immunoglobulin. Examples of the immunoglobulin domain in proteins other than

immunoglobulin include an immunoglobulin domain included in a protein belonging to an immunoglobulin super family, such as a major histocompatibility complex (MHC), CD1, B7, T-cell receptor (TCR), and the like. Any of the immunoglobulin domains can be used as an immunoglobulin domain for the multivalent antibody of the present invention.

[0066] In a human antibody, CH1 means a region having the amino acid sequence at positions 118 to 215 of the EU index. A highly flexible amino acid region called a “hinge region” exists between CH1 and CH2. CH2 represents a region having the amino acid sequence at positions 231 to 340 of the EU index, and CH3 represents a region having the amino acid sequence at positions 341 to 446 of the EU index.

[0067] “CL” represents a constant region of a light chain. In the case of a κ chain of a human antibody, CL represents a region having the amino acid sequence at positions 108 to 214 of the EU index. In a λ chain, CL represents a region having the amino acid sequence at positions 108 to 215.

[0068] The binding domains that specifically bind to target antigen(s) can be derived a) from known antibodies to these antigens or b) from new antibodies or antibody fragments obtained by *de novo* immunization methods using the antigen proteins or fragments thereof, by phage display, or other routine methods. The antibodies from which the binding domains for the bispecific and tetraspecific antigen binding proteins are derived can be monoclonal antibodies, polyclonal antibodies, recombinant antibodies, human antibodies, or humanized antibodies. In certain embodiments, the antibodies from which the binding domains are derived are monoclonal antibodies. In these and other embodiments, the antibodies are human antibodies or humanized antibodies and can be of the IgG1-, IgG2-, IgG3-, or IgG4-type.

[0069] The term “monoclonal antibody” (or “mAb”) as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally occurring mutations that may be present in minor amounts. Monoclonal antibodies are highly specific, being directed against an individual antigenic site or epitope, in contrast to polyclonal antibody preparations that typically include different antibodies directed against different epitopes. Monoclonal antibodies may be produced using any technique known in the art, e.g., by immortalizing spleen cells harvested from the transgenic animal after completion of the immunization schedule. The spleen cells can be immortalized using any technique known in the art, e.g., by fusing them with myeloma cells to produce hybridomas. Myeloma cells for use in hybridoma-producing fusion procedures are non-antibody-producing, have high fusion efficiency, and enzyme deficiencies that render them incapable of growing in certain

selective media which support the growth of only the desired fused cells (hybridomas). Examples of suitable cell lines for use in mouse fusions include Sp-20, P3-X63/Ag8, P3-X63-Ag8.653, NS1/1.Ag 4 1, Sp210-Ag14, FO, NSO/U, MPC-11, MPC11-X45-GTG 1.7 and S194/5XXO Bul; examples of cell lines used in rat fusions include R210.RCY3, Y3-Ag 1.2.3, IR983F and 4B210. Other cell lines useful for cell fusions are U-266, GM1500-GRG2, LICR-LON-HMy2 and UC729-6.

[0070] In some instances, a hybridoma cell line is produced by immunizing an animal (e.g., a transgenic animal having human immunoglobulin sequences) with a target antigen(s) immunogen; harvesting spleen cells from the immunized animal; fusing the harvested spleen cells to a myeloma cell line, thereby generating hybridoma cells; establishing hybridoma cell lines from the hybridoma cells, and identifying a hybridoma cell line that produces an antibody that binds target antigen(s).

[0071] Monoclonal antibodies secreted by a hybridoma cell line can be purified using any technique known in the art, such as protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography. Hybridomas or mAbs may be further screened to identify mAbs with particular properties, such as the ability to bind cells expressing target antigen(s), ability to block or interfere with the binding of target antigen(s) to their respective receptors or ligands, or the ability to functionally block either of target antigen(s).

[0072] In some embodiments, the binding domains of the bispecific and tetraspecific antigen binding proteins of the invention may be derived from humanized antibodies against target antigen(s). A “humanized antibody” refers to an antibody in which regions (e.g. framework regions) have been modified to comprise corresponding regions from a human immunoglobulin. Generally, a humanized antibody can be produced from a monoclonal antibody raised initially in a non-human animal. Certain amino acid residues in this monoclonal antibody, typically from non-antigen recognizing portions of the antibody, are modified to be homologous to corresponding residues in a human antibody of corresponding isotype. Humanization can be performed, for example, using various methods by substituting at least a portion of a rodent variable region for the corresponding regions of a human antibody (see, e.g., United States Patent Nos. 5,585,089 and 5,693,762; Jones *et al.*, Nature, Vol. 321:522-525, 1986; Riechmann *et al.*, Nature, Vol. 332:323-27, 1988; Verhoeyen *et al.*, Science, Vol. 239:1534-1536, 1988). The CDRs of light and heavy chain variable regions of antibodies generated in another species can be grafted to consensus human FRs. To create

consensus human FRs, FRs from several human heavy chain or light chain amino acid sequences may be aligned to identify a consensus amino acid sequence.

[0073] New antibodies generated against the target antigen(s) from which binding domains for the bispecific and tetraspecific antigen binding proteins of the invention can be derived can be fully human antibodies. A “fully human antibody” is an antibody that comprises variable and constant regions derived from human germ line immunoglobulin sequences. One specific means provided for implementing the production of fully human antibodies is the “humanization” of the mouse humoral immune system. Introduction of human immunoglobulin (Ig) loci into mice in which the endogenous Ig genes have been inactivated is one means of producing fully human monoclonal antibodies (mAbs) in mouse, an animal that can be immunized with any desirable antigen. Using fully human antibodies can minimize the immunogenic and allergic responses that can sometimes be caused by administering mouse or mouse-derived mAbs to humans as therapeutic agents.

[0074] Fully human antibodies can be produced by immunizing transgenic animals (usually mice) that are capable of producing a repertoire of human antibodies in the absence of endogenous immunoglobulin production. Antigens for this purpose typically have six or more contiguous amino acids, and optionally are conjugated to a carrier, such as a hapten. *See, e.g.,* Jakobovits *et al.*, 1993, *Proc. Natl. Acad. Sci. USA* 90:2551-2555; Jakobovits *et al.*, 1993, *Nature* 362:255-258; and Bruggermann *et al.*, 1993, *Year in Immunol.* 7:33. In one example of such a method, transgenic animals are produced by incapacitating the endogenous mouse immunoglobulin loci encoding the mouse heavy and light immunoglobulin chains therein, and inserting into the mouse genome large fragments of human genome DNA containing loci that encode human heavy and light chain proteins. Partially modified animals, which have less than the full complement of human immunoglobulin loci, are then cross-bred to obtain an animal having all of the desired immune system modifications. When administered an immunogen, these transgenic animals produce antibodies that are immunospecific for the immunogen but have human rather than murine amino acid sequences, including the variable regions. For further details of such methods, *see, for example,* WO96/33735 and WO94/02602. Additional methods relating to transgenic mice for making human antibodies are described in United States Patent No. 5,545,807; No. 6,713,610; No. 6,673,986; No. 6,162,963; No. 5,939,598; No. 5,545,807; No. 6,300,129; No. 6,255,458; No. 5,877,397; No. 5,874,299 and No. 5,545,806; in PCT publications WO91/10741, WO90/04036, WO 94/02602, WO 96/30498, WO 98/24893 and in EP 546073B1 and EP 546073A1.

[0075] The transgenic mice described above, referred to herein as “HuMab” mice, contain a human immunoglobulin gene minilocus that encodes unrearranged human heavy (mu and gamma) and kappa light chain immunoglobulin sequences, together with targeted mutations that inactivate the endogenous mu and kappa chain loci (Lonberg *et al.*, 1994, Nature 368:856-859). Accordingly, the mice exhibit reduced expression of mouse IgM or kappa and in response to immunization, and the introduced human heavy and light chain transgenes undergo class switching and somatic mutation to generate high affinity human IgG kappa monoclonal antibodies (Lonberg *et al.*, *supra.*; Lonberg and Huszar, 1995, Intern. Rev. Immunol. 13: 65-93; Harding and Lonberg, 1995, Ann. N.Y Acad. Sci. 764:536-546). The preparation of HuMab mice is described in detail in Taylor *et al.*, 1992, Nucleic Acids Research 20:6287-6295; Chen *et al.*, 1993, International Immunology 5:647-656; Tuailon *et al.*, 1994, J. Immunol. 152:2912-2920; Lonberg *et al.*, 1994, Nature 368:856-859; Lonberg, 1994, Handbook of Exp. Pharmacology 113:49-101; Taylor *et al.*, 1994, International Immunology 6:579-591; Lonberg and Huszar, 1995, Intern. Rev. Immunol. 13:65-93; Harding and Lonberg, 1995, Ann. N.Y Acad. Sci. 764:536-546; Fishwild *et al.*, 1996, Nature Biotechnology 14:845-851; the foregoing references are hereby incorporated by reference in their entirety for all purposes. *See*, further United States Patent No. 5,545,806; No. 5,569,825; No. 5,625,126; No. 5,633,425; No. 5,789,650; No. 5,877,397; No. 5,661,016; No. 5,814,318; No. 5,874,299; and No. 5,770,429; as well as United States Patent No. 5,545,807; International Publication Nos. WO 93/1227; WO 92/22646; and WO 92/03918, the disclosures of all of which are hereby incorporated by reference in their entirety for all purposes. Technologies utilized for producing human antibodies in these transgenic mice are disclosed also in WO 98/24893, and Mendez *et al.*, 1997, Nature Genetics 15:146-156, which are hereby incorporated by reference.

[0076] Human-derived antibodies can also be generated using phage display techniques. Phage display is described in e.g., Dower *et al.*, WO 91/17271, McCafferty *et al.*, WO 92/01047, and Caton and Koprowski, Proc. Natl. Acad. Sci. USA, 87:6450-6454 (1990), each of which is incorporated herein by reference in its entirety. The antibodies produced by phage technology are usually produced as antigen binding fragments, e.g. Fv or Fab fragments, in bacteria and thus lack effector functions. Effector functions can be introduced by one of two strategies: The fragments can be engineered either into complete antibodies for expression in mammalian cells, or into bispecific and tetraspecific antibody fragments with a second binding site capable of triggering an effector function, if desired. Typically, the Fd fragment (VH-CH1) and light chain (VL-CL) of antibodies are separately cloned by PCR and

recombined randomly in combinatorial phage display libraries, which can then be selected for binding to a particular antigen. The antibody fragments are expressed on the phage surface, and selection of Fv or Fab (and therefore the phage containing the DNA encoding the antibody fragment) by antigen binding is accomplished through several rounds of antigen binding and re-amplification, a procedure termed panning. Antibody fragments specific for the antigen are enriched and finally isolated. Phage display techniques can also be used in an approach for the humanization of rodent monoclonal antibodies, called "guided selection" (see Jespers, L. S., et al., *Bio/Technology* 12, 899-903 (1994)). For this, the Fd fragment of the mouse monoclonal antibody can be displayed in combination with a human light chain library, and the resulting hybrid Fab library may then be selected with antigen. The mouse Fd fragment thereby provides a template to guide the selection. Subsequently, the selected human light chains are combined with a human Fd fragment library. Selection of the resulting library yields entirely human Fab.

[0077] The term "identity," as used herein, refers to a relationship between the sequences of two or more polypeptide molecules or two or more nucleic acid molecules, as determined by aligning and comparing the sequences. "Percent identity," as used herein, means the percent of identical residues between the amino acids or nucleotides in the compared molecules and is calculated based on the size of the smallest of the molecules being compared. For these calculations, gaps in alignments (if any) must be addressed by a particular mathematical model or computer program (i.e., an "algorithm"). Methods that can be used to calculate the identity of the aligned nucleic acids or polypeptides include those described in *Computational Molecular Biology*, (Lesk, A. M., ed.), 1988, New York: Oxford University Press; *Biocomputing Informatics and Genome Projects*, (Smith, D. W., ed.), 1993, New York: Academic Press; *Computer Analysis of Sequence Data, Part I*, (Griffin, A. M., and Griffin, H. G., eds.), 1994, New Jersey: Humana Press; von Heinje, G., 1987, *Sequence Analysis in Molecular Biology*, New York: Academic Press; *Sequence Analysis Primer*, (Gribskov, M. and Devereux, J., eds.), 1991, New York: M. Stockton Press; and Carillo et al., 1988, *SIAM J. Applied Math.* 48:1073. For example, sequence identity can be determined by standard methods that are commonly used to compare the similarity in position of the amino acids of two polypeptides. Using a computer program such as BLAST or FASTA, two polypeptide or two polynucleotide sequences are aligned for optimal matching of their respective residues (either along the full length of one or both sequences, or along a pre-determined portion of one or both sequences). The programs provide a default opening penalty and a default gap penalty, and a scoring matrix such as PAM 250 (a standard scoring matrix; see Dayhoff et al.,

in Atlas of Protein Sequence and Structure, vol. 5, supp. 3 (1978)) can be used in conjunction with the computer program. For example, the percent identity can then be calculated as: the total number of identical matches multiplied by 100 and then divided by the sum of the length of the longer sequence within the matched span and the number of gaps introduced into the longer sequences in order to align the two sequences. In calculating percent identity, the sequences being compared are aligned in a way that gives the largest match between the sequences.

[0078] The GCG program package is a computer program that can be used to determine percent identity, which package includes GAP (Devereux et al., 1984, Nucl. Acid Res. 12:387; Genetics Computer Group, University of Wisconsin, Madison, WI). The computer algorithm GAP is used to align the two polypeptides or two polynucleotides for which the percent sequence identity is to be determined. The sequences are aligned for optimal matching of their respective amino acid or nucleotide (the “matched span”, as determined by the algorithm). A gap opening penalty (which is calculated as 3x the average diagonal, wherein the “average diagonal” is the average of the diagonal of the comparison matrix being used; the “diagonal” is the score or number assigned to each perfect amino acid match by the particular comparison matrix) and a gap extension penalty (which is usually 1/10 times the gap opening penalty), as well as a comparison matrix such as PAM 250 or BLOSUM 62 are used in conjunction with the algorithm. In certain embodiments, a standard comparison matrix (see, Dayhoff et al., 1978, Atlas of Protein Sequence and Structure 5:345-352 for the PAM 250 comparison matrix; Henikoff et al., 1992, Proc. Natl. Acad. Sci. U.S.A. 89:10915-10919 for the BLOSUM 62 comparison matrix) is also used by the algorithm.

[0079] Recommended parameters for determining percent identity for polypeptides or nucleotide sequences using the GAP program include the following:

Algorithm: Needleman et al., 1970, J. Mol. Biol. 48:443-453;

Comparison matrix: BLOSUM 62 from Henikoff et al., 1992, *supra*;

Gap Penalty: 12 (but with no penalty for end gaps)

Gap Length Penalty: 4

Threshold of Similarity: 0

[0080] Certain alignment schemes for aligning two amino acid sequences may result in matching of only a short region of the two sequences, and this small aligned region may have very high sequence identity even though there is no significant relationship between the two full-length sequences. Accordingly, the selected alignment method (GAP program) can be

adjusted if so desired to result in an alignment that spans at least 50 contiguous amino acids of the target polypeptide.

[0081] In certain embodiments, the bispecific and tetraspecific antigen binding proteins of the invention comprise antibodies. As used herein, the term “antibody” refers to a tetrameric immunoglobulin protein comprising two light chain polypeptides (about 25 kDa each) and two heavy chain polypeptides (about 50-70 kDa each). The term “light chain” or “immunoglobulin light chain” refers to a polypeptide comprising, from amino terminus to carboxyl terminus, a single immunoglobulin light chain variable region (VL) and a single immunoglobulin light chain constant domain (CL). The immunoglobulin light chain constant domain (CL) can be kappa (κ) or lambda (λ). The term “heavy chain” or “immunoglobulin heavy chain” refers to a polypeptide comprising, from amino terminus to carboxyl terminus, a single immunoglobulin heavy chain variable region (VH), an immunoglobulin heavy chain constant domain 1 (CH1), an immunoglobulin hinge region, an immunoglobulin heavy chain constant domain 2 (CH2), an immunoglobulin heavy chain constant domain 3 (CH3), and optionally an immunoglobulin heavy chain constant domain 4 (CH4). Heavy chains are classified as mu (μ), delta (Δ), gamma (γ), alpha (α), and epsilon (ϵ), and define the antibody's isotype as IgM, IgD, IgG, IgA, and IgE, respectively. The IgG-class and IgA-class antibodies are further divided into subclasses, namely, IgG1, IgG2, IgG3, and IgG4, and IgA1 and IgA2, respectively. The heavy chains in IgG, IgA, and IgD antibodies have three domains (CH1, CH2, and CH3), whereas the heavy chains in IgM and IgE antibodies have four domains (CH1, CH2, CH3, and CH4). The immunoglobulin heavy chain constant domains can be from any immunoglobulin isotype, including subtypes. The antibody chains are linked together via inter-polypeptide disulfide bonds between the CL domain and the CH1 domain (i.e. between the light and heavy chain) and between the hinge regions of the antibody heavy chains.

[0082] In particular embodiments, the bispecific and tetraspecific antigen binding proteins of the invention are heterodimeric antibodies (used interchangeably herein with “hetero immunoglobulins” or “hetero Igs”), which refer to antibodies comprising two different light chains and two different heavy chains.

[0083] The heterodimeric antibodies can comprise any immunoglobulin constant region. The term “constant region” as used herein refers to all domains of an antibody other than the variable region. The constant region is not involved directly in binding of an antigen, but exhibits various effector functions. As described above, antibodies are divided into particular

isotypes (IgA, IgD, IgE, IgG, and IgM) and subtypes (IgG1, IgG2, IgG3, IgG4, IgA1 IgA2) depending on the amino acid sequence of the constant region of their heavy chains. The light chain constant region can be, for example, a kappa- or lambda-type light chain constant region, e.g., a human kappa- or lambda-type light chain constant region, which are found in all five antibody isotypes. Examples of human immunoglobulin light chain constant region sequences are shown in the following table.

Table 4. Exemplary Human Immunoglobulin Light Chain Constant Regions

Designation	SEQ ID NO:	CL Domain Amino Acid Sequence
CL-1	924	GQPKANPTVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKA DGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSC QVTHEGSTVEKTVAPTECS
CL-2	925	GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKA DSSPVKAGVETTTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQ VTHEGSTVEKTVAPTECS
CL-3	926	GQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKA DSSPVKAGVETTTTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQ VTHEGSTVEKTVAPTECS
CL-7	927	GQPKAAPSVTLFPPSSEELQANKATLVCLVSDFYPGAVTVAWK ADGSPVKVGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYS CRVTHEGSTVEKTVAPAECS

[0084] The heavy chain constant region of the heterodimeric antibodies can be, for example, an alpha-, delta-, epsilon-, gamma-, or mu-type heavy chain constant region, e.g., a human alpha-, delta-, epsilon-, gamma-, or mu-type heavy chain constant region. In some embodiments, the heterodimeric antibodies comprise a heavy chain constant region from an IgG1, IgG2, IgG3, or IgG4 immunoglobulin. In one embodiment, the heterodimeric antibody comprises a heavy chain constant region from a human IgG1 immunoglobulin. In another embodiment, the heterodimeric antibody comprises a heavy chain constant region from a human IgG2 immunoglobulin. Examples of human IgG1 and IgG2 heavy chain constant region sequences are shown below in Table 5.

Table 5. Exemplary Human Immunoglobulin Heavy Chain Constant Regions

Ig isotype	SEQ ID NO:	Heavy Chain Constant Region Amino Acid Sequence
Human IgG1z	928	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP APPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDS DGSFFLYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGK
Human IgG1za	929	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCP APPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDS DGSFFLYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGK
Human IgG1f	930	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP APPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDS DGSFFLYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGK
Human IgG1fa	931	ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP APPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP VLDS DGSFFLYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGK
Human IgG2	932	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV LQSSGLYSLSSVVTVPSSNFGTQTYTCNV DHKPSNTKVDKTVERKCCVECP PCPAP PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAK TKPREEQFNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPR EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPMLDS DGSFFLYSKLTVDKSRWQQGNV FSCSV MHEALHNHYTQKSLSLSPGK

[0085] A variable region may be attached to the above light and heavy chain constant regions to form complete antibody light and heavy chains, respectively. Further, each of the so generated heavy and light chain polypeptides may be combined to form a complete bispecific and tetraspecific antibody structure, e.g. a heterodimeric antibody. It should be understood that the heavy chain and light chain variable regions provided herein can also be attached to other constant domains having different sequences than the exemplary sequences listed above.

[0086] In certain embodiments of the invention two different heavy chains are used to form the a heterodimeric molecule of the present invention. To facilitate assembly of the light and heavy chains from into a bispecific and tetraspecific, heterodimeric antibody, the light chains and/or heavy chains from each antibody can be engineered to reduce the formation of mispaired molecules. For example, one approach to promote heterodimer formation over homodimer formation is the so-called “knobs-into-holes” method, which involves introducing

mutations into the CH3 domains of two different antibody heavy chains at the contact interface. Specifically, one or more bulky amino acids in one heavy chain are replaced with amino acids having short side chains (e.g. alanine or threonine) to create a “hole,” whereas one or more amino acids with large side chains (e.g. tyrosine or tryptophan) are introduced into the other heavy chain to create a “knob.” When the modified heavy chains are co-expressed, a greater percentage of heterodimers (knob-hole) are formed as compared to homodimers (hole-hole or knob-knob). The “knobs-into-holes” methodology is described in detail in WO 96/027011; Ridgway *et al.*, Protein Eng., Vol. 9: 617-621, 1996; and Merchant *et al.*, Nat, Biotechnol., Vol. 16: 677-681, 1998, all of which are hereby incorporated by reference in their entireties.

[0087] Another approach for promoting heterodimer formation to the exclusion of homodimer formation entails utilizing an electrostatic steering mechanism (*see* Gunasekaran *et al.*, J. Biol. Chem., Vol. 285: 19637-19646, 2010, which is hereby incorporated by reference in its entirety). This approach involves introducing or exploiting charged residues in the CH3 domain in each heavy chain so that the two different heavy chains associate through opposite charges that cause electrostatic attraction. Homodimerization of the identical heavy chains are disfavored because the identical heavy chains have the same charge and therefore are repelled. This same electrostatic steering technique can be used to prevent mispairing of light chains with the non-cognate heavy chains by introducing residues having opposite charges in the correct light chain – heavy chain pair at the binding interface. The electrostatic steering technique and suitable charge pair mutations for promoting heterodimers and correct light chain/heavy chain pairing is described in WO2009089004 and WO2014081955, both of which are hereby incorporated by reference in their entireties.

[0088] In embodiments in which the bispecific antigen binding proteins of the invention are heterodimeric antibodies comprising a first light chain (LC1) and first heavy chain (HC1) from a first antibody that specifically binds to a first target antigen and a second light chain (LC2) and second heavy chain (HC2) from a second antibody that specifically binds to target 2, HC1 or HC2 may comprise one or more amino acid substitutions to replace a positively-charged amino acid with a negatively-charged amino acid. For instance, in one embodiment, the CH3 domain of HC1 or the CH3 domain of HC2 comprises an amino acid sequence differing from a wild-type IgG amino acid sequence such that one or more positively-charged amino acids (e.g., lysine, histidine and arginine) in the wild-type human IgG amino acid sequence are replaced with one or more negatively-charged amino acids (e.g., aspartic acid and glutamic acid) at the corresponding position(s) in the CH3 domain. In these and other

embodiments, amino acids (e.g. lysine) at one or more positions selected from 370, 392 and 409 (EU numbering system) are replaced with a negatively-charged amino acid (e.g., aspartic acid and glutamic acid). An amino acid substitution in an amino acid sequence is typically designated herein with a one-letter abbreviation for the amino acid residue in a particular position, followed by the numerical amino acid position relative to an original sequence of interest, which is then followed by the one-letter symbol for the amino acid residue substituted in. For example, “T30D” symbolizes a substitution of a threonine residue by an aspartate residue at amino acid position 30, relative to the original sequence of interest. Another example, “S218G” symbolizes a substitution of a serine residue by a glycine residue at amino acid position 218, relative to the original amino acid sequence of interest.

[0089] In certain embodiments, HC1 or HC2 of the heterodimeric antibodies may comprise one or more amino acid substitutions to replace a negatively-charged amino acid with a positively-charged amino acid. For instance, in one embodiment, the CH3 domain of HC1 or the CH3 domain of HC2 comprises an amino acid sequence differing from wild-type IgG amino acid sequence such that one or more negatively-charged amino acids in the wild-type human IgG amino acid sequence are replaced with one or more positively-charged amino acids at the corresponding position(s) in the CH3 domain. In these and other embodiments, amino acids (e.g., aspartic acid or glutamic acid) at one or more positions selected from 356, 357, and 399 (EU numbering system) of the CH3 domain are replaced with a positively-charged amino acid (e.g., lysine, histidine and arginine).

[0090] In particular embodiments, the heterodimeric antibody comprises a first heavy chain comprising negatively-charged amino acids at positions 392 and 409 (e.g., K392D and K409D substitutions), and a second heavy chain comprising positively-charged amino acids at positions 356 and 399 (e.g., E356K and D399K substitutions). In other particular embodiments, the heterodimeric antibody comprises a first heavy chain comprising negatively-charged amino acids at positions 392, 409, and 370 (e.g., K392D, K409D, and K370D substitutions), and a second heavy chain comprising positively-charged amino acids at positions 356, 399, and 357 (e.g., E356K, D399K, and E357K substitutions). In related embodiments, the first heavy chain is from an anti-first target antigen antibody and the second heavy chain is from an anti-second target antigen antibody.

[0091] To facilitate the association of a particular heavy chain with its cognate light chain, both the heavy and light chains may contain complimentary amino acid substitutions. As used herein, “complimentary amino acid substitutions” refer to a substitution to a positively-charged amino acid in one chain paired with a negatively-charged amino acid substitution in

the other chain. For example, in some embodiments, the heavy chain comprises at least one amino acid substitution to introduce a charged amino acid and the corresponding light chain comprises at least one amino acid substitution to introduce a charged amino acid, wherein the charged amino acid introduced into the heavy chain has the opposite charge of the amino acid introduced into the light chain. In certain embodiments, one or more positively-charged residues (e.g., lysine, histidine or arginine) can be introduced into a first light chain (LC1) and one or more negatively-charged residues (e.g., aspartic acid or glutamic acid) can be introduced into the companion heavy chain (HC1) at the binding interface of LC1/HC1, whereas one or more negatively-charged residues (e.g., aspartic acid or glutamic acid) can be introduced into a second light chain (LC2) and one or more positively-charged residues (e.g., lysine, histidine or arginine) can be introduced into the companion heavy chain (HC2) at the binding interface of LC2/HC2. The electrostatic interactions will direct the LC1 to pair with HC1 and LC2 to pair with HC2, as the opposite charged residues (polarity) at the interface attract. The heavy/light chain pairs having the same charged residues (polarity) at an interface (e.g. LC1/HC2 and LC2/HC1) will repel, resulting in suppression of the unwanted HC/LC pairings.

[0092] In these and other embodiments, the CH1 domain of the heavy chain or the CL domain of the light chain comprises an amino acid sequence differing from wild-type IgG amino acid sequence such that one or more positively-charged amino acids in wild-type IgG amino acid sequence is replaced with one or more negatively-charged amino acids.

Alternatively, the CH1 domain of the heavy chain or the CL domain of the light chain comprises an amino acid sequence differing from wild-type IgG amino acid sequence such that one or more negatively-charged amino acids in wild-type IgG amino acid sequence is replaced with one or more positively-charged amino acids. In some embodiments, one or more amino acids in the CH1 domain of the first and/or second heavy chain in the heterodimeric antibody at an EU position selected from F126, P127, L128, A141, L145, K147, D148, H168, F170, P171, V173, Q175, S176, S183, V185 and K213 is replaced with a charged amino acid. In certain embodiments, a heavy chain residue for substitution with a negatively- or positively- charged amino acid is S183 (EU numbering system). In some embodiments, S183 is substituted with a positively-charged amino acid. In alternative embodiments, S183 is substituted with a negatively-charged amino acid. For instance, in one embodiment, S183 is substituted with a negatively-charged amino acid (e.g. S183E) in the first heavy chain, and S183 is substituted with a positively-charged amino acid (e.g. S183K) in the second heavy chain.

[0093] In embodiments in which the light chain is a kappa light chain, one or more amino acids in the CL domain of the first and/or second light chain in the heterodimeric antibody at a position (EU numbering in a kappa light chain) selected from F116, F118, S121, D122, E123, Q124, S131, V133, L135, N137, N138, Q160, S162, T164, S174 and S176 is replaced with a charged amino acid. In embodiments in which the light chain is a lambda light chain, one or more amino acids in the CL domain of the first and/or second light chain in the heterodimeric antibody at a position (EU numbering in a lambda chain) selected from T116, F118, S121, E123, E124, K129, T131, V133, L135, S137, E160, T162, S165, Q167, A174, S176 and Y178 is replaced with a charged amino acid. In some embodiments, a residue for substitution with a negatively- or positively- charged amino acid is S176 (EU numbering system) of the CL domain of either a kappa or lambda light chain. In certain embodiments, S176 of the CL domain is replaced with a positively-charged amino acid. In alternative embodiments, S176 of the CL domain is replaced with a negatively-charged amino acid. In one embodiment, S176 is substituted with a positively-charged amino acid (e.g. S176K) in the first light chain, and S176 is substituted with a negatively-charged amino acid (e.g. S176E) in the second light chain.

[0094] In addition to or as an alternative to the complimentary amino acid substitutions in the CH1 and CL domains, the variable regions of the light and heavy chains in the heterodimeric antibody may contain one or more complimentary amino acid substitutions to introduce charged amino acids. For instance, in some embodiments, the VH region of the heavy chain or the VL region of the light chain of a heterodimeric antibody comprises an amino acid sequence differing from wild-type IgG amino acid sequence such that one or more positively-charged amino acids in wild-type IgG amino acid sequence is replaced with one or more negatively-charged amino acids. Alternatively, the VH region of the heavy chain or the VL region of the light chain comprises an amino acid sequence differing from wild-type IgG amino acid sequence such that one or more negatively-charged amino acids in wild-type IgG amino acid sequence is replaced with one or more positively-charged amino acids.

[0095] V region interface residues (i.e., amino acid residues that mediate assembly of the VH and VL regions) within the VH region include EU positions 1, 3, 35, 37, 39, 43, 44, 45, 46, 47, 50, 59, 89, 91, and 93. One or more of these interface residues in the VH region can be substituted with a charged (positively- or negatively-charged) amino acid. In certain embodiments, the amino acid at EU position 39 in the VH region of the first and/or second heavy chain is substituted for a positively-charged amino acid, e.g., lysine. In alternative embodiments, the amino acid at EU position 39 in the VH region of the first and/or second

heavy chain is substituted for a negatively-charged amino acid, e.g., glutamic acid. In some embodiments, the amino acid at EU position 39 in the VH region of the first heavy chain is substituted for a negatively-charged amino acid (e.g. G39E), and the amino acid at EU position 39 in the VH region of the second heavy chain is substituted for a positively-charged amino acid (e.g. G39K). In some embodiments, the amino acid at EU position 44 in the VH region of the first and/or second heavy chain is substituted for a positively-charged amino acid, e.g., lysine. In alternative embodiments, the amino acid at EU position 44 in the VH region of the first and/or second heavy chain is substituted for a negatively-charged amino acid, e.g., glutamic acid. In certain embodiments, the amino acid at EU position 44 in the VH region of the first heavy chain is substituted for a negatively-charged amino acid (e.g. G44E), and the amino acid at EU position 44 in the VH region of the second heavy chain is substituted for a positively-charged amino acid (e.g. G44K).

[0096] V region interface residues (i.e., amino acid residues that mediate assembly of the VH and VL regions) within the VL region include EU positions 32, 34, 35, 36, 38, 41, 42, 43, 44, 45, 46, 48, 49, 50, 51, 53, 54, 55, 56, 57, 58, 85, 87, 89, 90, 91, and 100. One or more interface residues in the VL region can be substituted with a charged amino acid, preferably an amino acid that has an opposite charge to those introduced into the VH region of the cognate heavy chain. In some embodiments, the amino acid at EU position 100 in the VL region of the first and/or second light chain is substituted for a positively-charged amino acid, e.g., lysine. In alternative embodiments, the amino acid at EU position 100 in the VL region of the first and/or second light chain is substituted for a negative-charged amino acid, e.g., glutamic acid. In certain embodiments, the amino acid at EU position 100 in the VL region of the first light chain is substituted for a positively-charged amino acid (e.g. G100K), and the amino acid at EU position 100 in the VL region of the second light chain is substituted for a negatively-charged amino acid (e.g. G100E).

[0097] In certain embodiments, a heterodimeric antibody of the invention comprises a first heavy chain and a second heavy chain and a first light chain and a second light chain, wherein the first heavy chain comprises amino acid substitutions at positions 44 (EU), 183 (EU), 392 (EU) and 409 (EU), wherein the second heavy chain comprises amino acid substitutions at positions 44 (EU), 183 (EU), 356 (EU) and 399 (EU), wherein the first and second light chains comprise an amino acid substitution at positions 100 (EU) and 176 (EU), and wherein the amino acid substitutions introduce a charged amino acid at the positions. In related embodiments, the glycine at position 44 (EU) of the first heavy chain is replaced with glutamic acid, the glycine at position 44 (EU) of the second heavy chain is replaced with

lysine, the glycine at position 100 (EU) of the first light chain is replaced with lysine, the glycine at position 100 (EU) of the second light chain is replaced with glutamic acid, the serine at position 176 (EU) of the first light chain is replaced with lysine, the serine at position 176 (EU) of the second light chain is replaced with glutamic acid, the serine at position 183 (EU) of the first heavy chain is replaced with glutamic acid, the lysine at position 392 (EU) of the first heavy chain is replaced with aspartic acid, the lysine at position 409 (EU) of the first heavy chain is replaced with aspartic acid, the serine at position 183 (EU) of the second heavy chain is replaced with lysine, the glutamic acid at position 356 (EU) of the second heavy chain is replaced with lysine, and/or the aspartic acid at position 399 (EU) of the second heavy chain is replaced with lysine.

[0098] In other embodiments, a heterodimeric antibody of the invention comprises a first heavy chain and a second heavy chain and a first light chain and a second light chain, wherein the first heavy chain comprises amino acid substitutions at positions 183 (EU), 392 (EU) and 409 (EU), wherein the second heavy chain comprises amino acid substitutions at positions 183 (EU), 356 (EU) and 399 (EU), wherein the first and second light chains comprise an amino acid substitution at position 176 (EU), and wherein the amino acid substitutions introduce a charged amino acid at the positions. In related embodiments, the serine at position 176 (EU) of the first light chain is replaced with lysine, the serine at position 176 (EU) of the second light chain is replaced with glutamic acid, the serine at position 183 (EU) of the first heavy chain is replaced with glutamic acid, the lysine at position 392 (EU) of the first heavy chain is replaced with aspartic acid, the lysine at position 409 (EU) of the first heavy chain is replaced with aspartic acid, the serine at position 183 (EU) of the second heavy chain is replaced with lysine, the glutamic acid at position 356 (EU) of the second heavy chain is replaced with lysine, and/or the aspartic acid at position 399 (EU) of the second heavy chain is replaced with lysine.

[0099] In still other embodiments, a heterodimeric antibody of the invention comprises a first heavy chain and a second heavy chain and a first light chain and a second light chain, wherein the first heavy chain comprises amino acid substitutions at positions 183 (EU), 392 (EU), 409 (EU), and 370 (EU), wherein the second heavy chain comprises amino acid substitutions at positions 183 (EU), 356 (EU), 399 (EU), and 357 (EU), wherein the first and second light chains comprise an amino acid substitution at position 176 (EU), and wherein the amino acid substitutions introduce a charged amino acid at the positions. In related embodiments, the serine at position 176 (EU) of the first light chain is replaced with lysine, the serine at position 176 (EU) of the second light chain is replaced with glutamic acid, the

serine at position 183 (EU) of the first heavy chain is replaced with glutamic acid, the lysine at position 392 (EU) of the first heavy chain is replaced with aspartic acid, the lysine at position 409 (EU) of the first heavy chain is replaced with aspartic acid, the lysine at position 370 (EU) of the first heavy chain is replaced with aspartic acid, the serine at position 183 (EU) of the second heavy chain is replaced with lysine, the glutamic acid at position 356 (EU) of the second heavy chain is replaced with lysine, the aspartic acid at position 399 (EU) of the second heavy chain is replaced with lysine, and/or the glutamic acid at position 357 (EU) of the second heavy chain is replaced with lysine.

[0100] Any of the constant domains can be modified to contain one or more of the charge pair mutations described above to facilitate correct assembly of a heterodimeric antibody.

[0101] The inventive heterodimeric antibodies also encompass antibodies comprising the heavy chain(s) and/or light chain(s), where one, two, three, four or five amino acid residues are lacking from the N-terminus or C-terminus, or both, in relation to any one of the heavy and light chains, e.g., due to post-translational modifications resulting from the type of host cell in which the antibodies are expressed. For instance, Chinese Hamster Ovary (CHO) cells frequently cleave off a C-terminal lysine from antibody heavy chains.

[0102] In certain embodiments, the antigen binding proteins of the invention comprise (i) a first binding domain that specifically binds a first target antigen, (ii) a second binding domain that specifically binds to a second target antigen, and (iii) a human immunoglobulin Fc region, wherein one of the binding domains is positioned at the amino terminus of the Fc region and the other binding domain is positioned at the carboxyl terminus of the Fc region. In some such embodiments, each of the first and second binding domains comprises immunoglobulin variable regions. For instance, in certain embodiments, the first binding domain comprises a first light chain variable region (VL1) and a first heavy chain variable region (VH1) from an anti-first target antigen antibody and the second binding domain comprises a second light chain variable region (VL2) and a second heavy chain variable region (VH2) from an anti-second target antigen antibody.

[0103] As used herein, the term “Fc region” refers to the C-terminal region of an immunoglobulin heavy chain which may be generated by papain digestion of an intact antibody. The Fc region of an immunoglobulin generally comprises two constant domains, a CH2 domain and a CH3 domain, and optionally comprises a CH4 domain. In certain embodiments, the Fc region is an Fc region from an IgG1, IgG2, IgG3, or IgG4 immunoglobulin. In some embodiments, the Fc region comprises CH2 and CH3 domains from a human IgG1 or human IgG2 immunoglobulin. The Fc region may retain effector

function, such as C1q binding, complement dependent cytotoxicity (CDC), Fc receptor binding, antibody-dependent cell-mediated cytotoxicity (ADCC), and phagocytosis. In other embodiments, the Fc region may be modified to reduce or eliminate effector function as described in further detail herein.

[0104] In certain embodiments of the bispecific antigen binding proteins of the invention, the binding domain positioned at the amino terminus of the Fc region (i.e. the amino-terminal binding domain) is a Fab fragment fused to the amino terminus of the Fc region through a peptide linker described herein or through an immunoglobulin hinge region. An “immunoglobulin hinge region” refers to the amino acid sequence connecting the CH1 domain and the CH2 domain of an immunoglobulin heavy chain. The hinge region of human IgG1 is generally defined as the amino acid sequence from about Glu216 or about Cys226, to about Pro230. Hinge regions of other IgG isotypes may be aligned with the IgG1 sequence by placing the first and last cysteine residues forming inter-heavy chain disulfide bonds in the same positions and are determinable to those of skill in the art. In some embodiments, the amino-terminal binding domain is joined to the amino terminus of the Fc region through a human IgG1 hinge region. In other embodiments, the amino-terminal binding domain is joined to the amino terminus of the Fc region through a human IgG2 hinge region. In one embodiment, the amino-terminal binding domain (e.g. Fab fragment) is fused to the Fc region through the carboxyl terminus of the CH1 region of the Fab.

[0105] As used herein, the term “modified heavy chain” refers to a fusion protein comprising an immunoglobulin heavy chain, particularly a human IgG1 or human IgG2 heavy chain, and a functional antibody fragment (e.g. Fab) or portion thereof (e.g. immunoglobulin light chain or Fd fragment), wherein the fragment or portion thereof is fused at its N-terminus, optionally through a peptide linker, to the C-terminus of the heavy chain.

[0106] In some embodiments of the antigen binding proteins of the invention, the binding domain positioned at the carboxyl terminus of the Fc region (i.e. the carboxyl-terminal binding domain) is a Fab fragment. In such embodiments, the Fab is fused or otherwise connected to the carboxyl terminus of the Fc region (e.g. the carboxyl terminus of the CH3 domain) through a peptide linker through the amino terminus of the VH region of the Fab fragment. Thus, in one embodiment, the Fab is fused to an Fc region through the amino terminus of the VH region of the Fab such that the resulting fusion protein comprises, from N-terminus to C-terminus, a CH2 domain, a CH3 domain, a peptide linker, a VH region, and a CH1 region.

[0107] The peptide linker joining the Fc region to the carboxyl-terminal Fab can be any of the peptide linkers described herein. In particular embodiments, the peptide linker joining the Fc region to the carboxyl-terminal Fab fragment is at least 5 amino acids in length. In other embodiments, the peptide linker joining the Fc region to the carboxyl-terminal Fab fragment is at least 8 amino acids in length. Particularly suitable peptide linkers for joining the Fc region to the carboxyl-terminal Fab fragment are glycine-serine linkers, such as $(\text{Gly}_x\text{Ser})_n$ where $x=3$ or 4 and $n=2, 3, 4, 5$ or 6 . In one embodiment, the peptide linker connecting the Fc region to the carboxyl-terminal Fab fragment is a L10 $(\text{G}_4\text{S})_2$ linker (SEQ ID NO: 10). In another embodiment, the peptide linker connecting the Fc region to the carboxyl-terminal Fab fragment is a L9 or $\text{G}_3\text{SG}_4\text{S}$ linker (SEQ ID NO: 11).

[0108] In some embodiments of the bispecific antigen binding proteins of the invention in which the carboxyl-terminal binding domain is a Fab fragment, the binding domain positioned at the amino terminus of the Fc region (i.e. the amino-terminal binding domain) is also a Fab fragment. The amino-terminal Fab fragment can be fused to the amino terminus of the Fc region through a peptide linker or an immunoglobulin hinge region described herein. In some embodiments, the amino-terminal Fab fragment is joined to the amino terminus of the Fc region through a human IgG1 hinge region. In other embodiments, the amino-terminal Fab fragment is joined to the amino terminus of the Fc region through a human IgG2 hinge region. In one embodiment, the amino-terminal Fab fragment is fused to the Fc region through the carboxyl terminus of the CH1 region of the Fab.

[0109] In some embodiments, the bispecific antigen binding protein of the invention comprises a first antibody that specifically binds to a first target where one polypeptide chain (e.g. the heavy chain (VH2-CH1)) of a Fab fragment from a second antibody that specifically binds to a second target is fused to the carboxyl terminus of the heavy chain of the first antibody. The bispecific antigen binding protein in such embodiments also comprises a polypeptide chain containing the other half of the Fab fragment from the second antibody (e.g., the light chain (VL2-CL)). This format is referred to herein as the "IgG-Fab" format, and one embodiment of this type of molecule is shown schematically in Figure 1. Thus, in certain embodiments, the present invention includes a bispecific, multivalent antigen binding protein comprising: (i) a light chain from a first antibody, (ii) a heavy chain from the first antibody, wherein the heavy chain is fused at its carboxyl terminus through a peptide linker to a first polypeptide comprising VH-CH1 domains of a second antibody to form a modified heavy chain, and (iii) a second polypeptide comprising VL-CL domains of the second antibody. When dimerized, the bispecific antigen binding protein is a homohexamer

comprising two modified heavy chains, two light chains from the first antibody, and two polypeptide chains containing the other half of the Fab fragment from the second antibody (the Fd fragment). In one embodiment, the first polypeptide, which is fused to the carboxyl terminus of the heavy chain, comprises VH and CH1 domains from the second antibody, and the second polypeptide comprises VL and CL domains from the second antibody.

[0110] Charge pair mutations or complimentary amino acid substitutions as described herein can be introduced into the Fab regions of the first antibody (Fab 1) or second antibody (Fab 2) to promote correct heavy chain-light chain pairing. For instance, in some embodiments, the amino acid at EU position 38 of the VL domain in Fab 1 is replaced with a negatively-charged amino acid (e.g. glutamic acid) and the amino acid at EU position 39 of the VH domain in Fab 1 is replaced with a positively-charged amino acid (e.g. lysine). In other embodiments, the amino acid at EU position 38 of the VL domain in Fab 1 is replaced with a positively-charged amino acid (e.g. lysine) and the amino acid at EU position 39 of the VH domain in Fab 1 is replaced with a negatively-charged amino acid (e.g. glutamic acid). In certain embodiments, the amino acid at EU position 38 of the VL domain in Fab 2 is replaced with a negatively-charged amino acid (e.g. glutamic acid) and the amino acid at EU position 39 of the VH domain in Fab 2 is replaced with a positively-charged amino acid (e.g. lysine). In other embodiments, the amino acid at EU position 38 of the VL domain in Fab 2 is replaced with a positively-charged amino acid (e.g. lysine) and the amino acid at EU position 39 of the VH domain in Fab 2 is replaced with a negatively-charged amino acid (e.g. glutamic acid).

[0111] In embodiments in which the VH-CH1 region (i.e. Fd fragment) from the second antibody is fused to the heavy chain of the first antibody, the heavy chain from the first antibody comprises a S183E mutation (EU numbering), the light chain from the first antibody comprises a S176K mutation (EU numbering), the light chain from the second antibody comprises a S176E mutation (EU numbering), and the Fd region from the second antibody (which is fused to the C-terminus of the heavy chain from the first antibody) comprises a S183K mutation (EU numbering). In other embodiments, the heavy chain from the first antibody comprises a G44E mutation (EU) and S183E mutation (EU numbering), the light chain from the first antibody comprises a G100K mutation (EU) and S176K mutation (EU numbering), the light chain from the second antibody comprises a G100E mutation (EU) and S176E mutation (EU numbering), and the Fd region from the second antibody (which is fused to the C-terminus of the heavy chain from the first antibody) comprises a G44K mutation (EU) and S183K mutation (EU numbering). The charges in the foregoing examples

may be reversed so long as the charge on the corresponding light or heavy chain is also reversed so that the correct heavy/light chain pairs have opposite charges.

[0112] In one embodiment the present invention is directed to a bispecific, tetravalent antigen binding protein, comprising:

[0113] a) a first polypeptide comprising a first heavy chain of a first antibody comprising a first heavy chain variable region (VH1) and a first CH1 domain, wherein the first antibody specifically binds to a first antigen, and wherein the first heavy chain is fused through its C-terminus to the N-terminus of a polypeptide comprising a second heavy chain variable region of a second antibody (VH2), wherein the VH2 is fused through its C-terminus to the N-terminus of a second CH1 domain, and wherein the second antibody specifically binds to a second antigen; wherein

[0114] i) the VH1 or first CH1 domain comprises at least one amino acid substitution to introduce a positively charged amino acid at a residue selected from the group consisting of positions 39, 44, and 183 using EU numbering; and

[0115] ii) the VH2 or second CH1 domain comprises at least one amino acid substitution to introduce a negatively charged amino acid at a residue selected from the group consisting of a residue that corresponds to positions 39, 44, and 183 using EU numbering; and

[0116] b) a second polypeptide comprising a first light chain of the first antibody of a), wherein the first light chain comprises a first light chain variable region (VL1) and a first CL region; and wherein the VL1 or first CL domain comprises at least one amino acid substitution to introduce a negatively charged amino acid at a residue selected from the group consisting of positions 38, 100, and 176 using EU numbering; and

[0117] c) a third polypeptide comprising a second light chain of the second antibody of a), wherein the second light chain comprises a second light chain variable region (VL2) and a second CL region; and wherein the VL1 or first CL domain comprises at least one amino acid substitution to introduce a positively charged amino acid at a residue selected from the group consisting of positions 38, 100, and 176 using EU numbering.

[0118] “Corresponds to” as it pertains to the VH2 and second CH1 domain means that the amino acid residues of the VH2 and second CH1 domain are counted from the C-terminus of the first heavy chain if there is no linker. If there is a peptide linker, the amino acid residues of the VH2 and second CH1 domain are counted from the C-terminus of the peptide linker. In neither case are the amino acid residues counted from the N-terminus of the first heavy chain. Rather, for the VH2 and second CH1 domain, counting begins at the first amino acid

residue of the VH2 domain. The counting of amino acid residues is performed using the EU or AHo convention.

[0119] In certain embodiments: a) the VH1 or first CH1 domain comprises a mutation selected from the group consisting of Q39K, G44K, and S183K using EU numbering; b) the VH2 or second CH1 domain comprises a mutation selected from the group consisting of Q39E, G44E, and S183E using EU numbering; c) the VL1 or first CL domain comprises a mutation selected from the group consisting of Q38E, G100E, and S176E using EU numbering; and d) the VL2 or second CL domain comprises a mutation selected from the group consisting of Q38K, G100K, and S176K using EU numbering.

[0120] In certain embodiments: a) the first CH1 domain comprises a S183K mutation using EU numbering; b) the second CH1 domain comprises a S183E mutation using EU numbering; c) the first CL domain comprises a S176E mutation using EU numbering; and d) the second CL domain comprises a S176K mutation using EU numbering.

[0121] In certain embodiments: a) the VH1 comprises a Q39K mutation and the first CH1 domain comprises a S183K mutation using EU numbering; b) the VH2 comprises a Q39E mutation and the second CH1 domain comprises a S183E mutation using EU numbering; c) the VL1 comprises a Q38E mutation and the first CL domain comprises a S176E mutation using EU numbering; and d) the VL2 comprises a Q38K mutation and the second CL domain comprises a S176K mutation using EU numbering.

[0122] In certain embodiments: a) the first CH1 domain comprises G44K and S183K mutations using EU numbering; b) the second CH1 domain comprises G44E and S183E mutations using EU numbering; c) the first CL domain comprises G100E and S176E mutations using EU numbering; and d) the second CL domain comprises G100K and S176K mutations using EU numbering.

[0123] In one embodiment the present invention is directed to a bispecific, tetravalent antigen binding protein, comprising:

[0124] a) a first polypeptide comprising a first heavy chain of a first antibody comprising a first heavy chain variable region (VH1) and a first CH1 domain, wherein the first antibody specifically binds to a first antigen, and wherein the first heavy chain is fused through its C-terminus to the N-terminus of a polypeptide comprising a second heavy chain variable region of a second antibody (VH2), wherein the VH2 is fused through its C-terminus to the N-terminus of a second CH1 domain, and wherein the second antibody specifically binds to a second antigen; wherein

- [0125] i) the VH1 or first CH1 domain comprises at least one amino acid substitution to introduce a negatively charged amino acid at a residue selected from the group consisting of positions 39, 44, and 183 using EU numbering; and
- [0126] ii) the VH2 or second CH1 domain comprises at least one amino acid substitution to introduce a positively charged amino acid at a residue selected from the group consisting of a residue that corresponds to positions 39, 44, and 183 using EU numbering; and
- [0127] b) a second polypeptide comprising a first light chain of the first antibody of a), wherein the first light chain comprises a first light chain variable region (VL1) and a first CL region; and wherein the VL1 or first CL domain comprises at least one amino acid substitution to introduce a positively charged amino acid at a residue selected from the group consisting of positions 38, 100, and 176 using EU numbering; and
- [0128] c) a third polypeptide comprising a second light chain of the second antibody of a), wherein the second light chain comprises a second light chain variable region (VL2) and a second CL region; and wherein the VL1 or first CL domain comprises at least one amino acid substitution to introduce a negatively charged amino acid at a residue selected from the group consisting of positions 38, 100, and 176 using EU numbering.
- [0129] In certain embodiments: a) the VH1 or first CH1 domain comprises a mutation selected from the group consisting of Q39E, G44E, and S183E using EU numbering; b) the VH2 or second CH1 domain comprises a mutation selected from the group consisting of Q39K, G44K, and S183K using EU numbering; c) the VL1 or first CL domain comprises a mutation selected from the group consisting of Q38K, G100K, and S176K using EU numbering; and d) the VL2 or second CL domain comprises a mutation selected from the group consisting of Q38E, G100E, and S176E using EU numbering.
- [0130] In certain embodiments: a) the first CH1 domain comprises a S183E mutation using EU numbering; b) the second CH1 domain comprises a S183K mutation using EU numbering; c) the first CL domain comprises a S176K mutation using EU numbering; and d) the second CL domain comprises a S176E mutation using EU numbering.
- [0131] In certain embodiments: a) the VH1 comprises a Q39E mutation and the first CH1 domain comprises a S183E mutation using EU numbering; b) the VH2 comprises a Q39K mutation and the second CH1 domain comprises a S183K mutation using EU numbering; c) the VL1 comprises a Q38K mutation and the first CL domain comprises a S176K mutation using EU numbering; and d) the VL2 comprises a Q38E mutation and the second CL domain comprises a S176E mutation using EU numbering.

[0132] In certain embodiments: a) the first CH1 domain comprises G44E and S183E mutations using EU numbering; b) the second CH1 domain comprises G44K and S183K mutations using EU numbering; c) the first CL domain comprises G100K and S176K mutations using EU numbering; and d) the second CL domain comprises G100E and S176E mutations using EU numbering.

[0133] In one embodiment the present invention is directed to a bispecific, tetravalent antigen binding protein, comprising:

[0134] a) a first polypeptide comprising a first heavy chain of a first antibody comprising a first heavy chain variable region (VH1) and a first CH1 domain, wherein the first antibody specifically binds to a first antigen, and wherein the first heavy chain is fused through its C-terminus to the N-terminus of a polypeptide comprising a second heavy chain variable region of a second antibody (VH2), wherein the VH2 is fused through its C-terminus to the N-terminus of a second CH1 domain, and wherein the second antibody specifically binds to a second antigen; wherein

[0135] i) the VH1 or first CH1 domain comprises at least one amino acid substitution to introduce a charged amino acid at a residue selected from the group consisting of positions 39, 44, and 183 using EU numbering; and

[0136] ii) the VH2 or second CH1 domain comprises at least one amino acid substitution to introduce a charged amino acid at a residue selected from the group consisting of a residue that corresponds to positions 39, 44, and 183 using EU numbering, wherein the charge is the opposite of the substituted residue of the VH1 or first CH1 of the first heavy chain; and

[0137] b) a second polypeptide comprising a first light chain of the first antibody of a), wherein the first light chain comprises a first light chain variable region (VL1) and a first CL region; and wherein the VL1 or first CL domain comprises at least one amino acid substitution to introduce a charged amino acid at a residue selected from the group consisting of positions 38, 100, and 176 using EU numbering, wherein

[0138] the charge at position 38 is the opposite of the substituted residue of the VH1 or first CH1 of the first heavy chain at position 39; the charge at position 100 is the opposite of the substituted residue of the VH1 or first CH1 of the first heavy chain at position 44; the charge at position 176 is the opposite of the substituted residue of the VH1 or first CH1 of the first heavy chain at position 183; and

[0139] c) a third polypeptide comprising a second light chain of the second antibody of a), wherein the second light chain comprises a second light chain variable region (VL2) and a second CL region; and wherein the VL2 or second CL domain comprises at least one amino

acid substitution to introduce a charged amino acid at a residue selected from the group consisting of positions 38, 100, and 176 using EU numbering, wherein

[0140] the charge at position 38 is the opposite of the substituted residue of the VH2 or second CH1 of the second heavy chain at position 39; the charge at position 100 is the opposite of the substituted residue of the VH2 or second CH1 of the second heavy chain at position 44; the charge at position 176 is the opposite of the substituted residue of the VH2 or second CH1 of the second heavy chain at position 183.

[0141] In certain embodiments: a) the VH1 comprises a Q39E mutation and the first CH1 domain comprises a S183K mutation using EU numbering; b) the VH2 comprises a Q39K mutation and the second CH1 domain comprises a S183E mutation using EU numbering; c) the VL1 comprises a Q38K mutation and the first CL domain comprises a S176E mutation using EU numbering; and d) the VL2 comprises a Q38E mutation and the second CL domain comprises a S176K mutation using EU numbering.

[0142] In certain embodiments: a) the first CH1 domain comprises G44E and S183K mutations using EU numbering; b) the second CH1 domain comprises G44K and S183E mutations using EU numbering; c) the first CL domain comprises G100K and S176E mutations using EU numbering; and d) the second CL domain comprises G100E and S176K mutations using EU numbering.

[0143] In certain embodiments: a) the VH1 comprises a Q39K mutation and the first CH1 domain comprises a S183E mutation using EU numbering; b) the VH2 comprises a Q39E mutation and the second CH1 domain comprises a S183K mutation using EU numbering; c) the VL1 comprises a Q38E mutation and the first CL domain comprises a S176K mutation using EU numbering; and d) the VL2 comprises a Q38K mutation and the second CL domain comprises a S176E mutation using EU numbering.

[0144] In certain embodiments: a) the first CH1 domain comprises G44K and S183E mutations using EU numbering; b) the second CH1 domain comprises G44E and S183K mutations using EU numbering; c) the first CL domain comprises G100E and S176K mutations using EU numbering; and d) the second CL domain comprises G100K and S176E mutations using EU numbering.

[0145] In certain embodiments the first heavy chain is fused to the VH2 via a peptide linker. In certain embodiments the peptide linker comprises a sequence selected from the group consisting of (Gly₃Ser)₂, (Gly₄Ser)₂, (Gly₃Ser)₃, (Gly₄Ser)₃, (Gly₃Ser)₄, (Gly₄Ser)₄, (Gly₃Ser)₅, (Gly₄Ser)₅, (Gly₃Ser)₆, and (Gly₄Ser)₆. These sequences can also be written as GGGSGGGG (SEQ ID NO: 933), GGGGSGGGGS (SEQ ID NO: 934), GGGSGGGSGGGG

(SEQ ID NO: 935), GGGGSGGGGSGGGGS (SEQ ID NO: 936), GGGSGGGSGGGSGGGGS (SEQ ID NO: 937), GGGGSGGGGSGGGGSGGGGS (SEQ ID NO: 938), GGGSGGGSGGGSGGGSGGGGS (SEQ ID NO: 939), GGGGSGGGGSGGGGSGGGGSGGGGS (SEQ ID NO: 940), GGGSGGGSGGGSGGGSGGGSGGGGS (SEQ ID NO: 941), and GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS (SEQ ID NO: 942).

[0146] In one embodiment the present invention is directed to a method for preparing a bispecific, tetravalent antigen binding protein, comprising:

[0147] 1) co-expressing in a host cell:

[0148] a) a first polynucleotide wherein the first polynucleotide encodes a first polypeptide comprising a first heavy chain of a first antibody comprising a first heavy chain variable region (VH1) and a first CH1 domain, wherein the first antibody specifically binds to a first antigen, and wherein the first heavy chain is fused through its C-terminus to the N-terminus of a polypeptide comprising a second heavy chain variable region of a second antibody (VH2), wherein the VH2 is fused through its C-terminus to the N-terminus of a second CH1 domain, and wherein the second antibody specifically binds to a second antigen; wherein

[0149] i) the VH1 or first CH1 domain comprises at least one amino acid substitution to introduce a positively charged amino acid at a residue selected from the group consisting of positions 39, 44, and 183 using EU numbering; and

[0150] ii) the VH2 or second CH1 domain comprises at least one amino acid substitution to introduce a negatively charged amino acid at a residue selected from the group consisting of a residue that corresponds to positions 39, 44, and 183 using EU numbering; and

[0151] b) a second polynucleotide wherein the second polynucleotide encodes a second polypeptide comprising a light chain of the first antibody of a), wherein the light chain comprises a first light chain variable region (VL1) and a first CL region; and wherein the VL1 or first CL domain comprises at least one amino acid substitution to introduce a negatively charged amino acid at a residue selected from the group consisting of positions 38, 100, and 176 using EU numbering;

[0152] c) a third polynucleotide wherein the third polynucleotide encodes a third polypeptide comprising a light chain of the second antibody of a), wherein the light chain comprises a second light chain variable region (VL2) and a second CL region; and wherein the VL2 or second CL domain comprises at least one amino acid substitution to introduce a positively charged amino acid at a residue selected from the group consisting of positions 38, 100, and 176 using EU numbering;

[0153] 2) cultivating the host cell under conditions such that the polypeptides are produced;
and

[0154] 3) recovering from the host cell the antigen binding protein.

[0155] In one embodiment the present invention is directed to a method for preparing a bispecific, tetravalent antigen binding protein, comprising:

[0156] 1) co-expressing in a host cell:

[0157] a) a first polynucleotide wherein the first polynucleotide encodes a first polypeptide comprising a first heavy chain of a first antibody comprising a first heavy chain variable region (VH1) and a first CH1 domain, wherein the first antibody specifically binds to a first antigen, and wherein the first heavy chain is fused through its C-terminus to the N-terminus of a polypeptide comprising a second heavy chain variable region of a second antibody (VH2), wherein the VH2 is fused through its C-terminus to the N-terminus of a second CH1 domain, and wherein the second antibody specifically binds to a second antigen; wherein

[0158] i) the VH1 or first CH1 domain comprises at least one amino acid substitution to introduce a negatively charged amino acid at a residue selected from the group consisting of positions 39, 44, and 183 using EU numbering; and

[0159] ii) the VH2 or second CH1 domain comprises at least one amino acid substitution to introduce a positively charged amino acid at a residue selected from the group consisting of a residue that corresponds to positions 39, 44, and 183 using EU numbering; and

[0160] b) a second polynucleotide wherein the second polynucleotide encodes a second polypeptide comprising a first light chain of the first antibody of a), wherein the first light chain comprises a first light chain variable region (VL1) and a first CL region; and wherein the VL1 or first CL domain comprises at least one amino acid substitution to introduce a positively charged amino acid at a residue selected from the group consisting of positions 38, 100, and 176 using EU numbering; and

[0161] c) a third polynucleotide wherein the third polynucleotide encodes a third polypeptide comprising a second light chain of the second antibody of a), wherein the second light chain comprises a second light chain variable region (VL2) and a second CL region;. and wherein the VL1 or first CL domain comprises at least one amino acid substitution to introduce a negatively charged amino acid at a residue selected from the group consisting of positions 38, 100, and 176 using EU numbering;

[0162] 2) cultivating the host cell under conditions such that the polypeptides are produced;
and

[0163] 3) recovering from the host cell the antigen binding protein.

[0164] In one embodiment the present invention is directed to a method for preparing a bispecific, tetravalent antigen binding protein, comprising:

[0165] 1) co-expressing in a host cell:

[0166] a) a first polynucleotide wherein the first polynucleotide encodes a first polypeptide comprising a first heavy chain of a first antibody comprising a first heavy chain variable region (VH1) and a first CH1 domain, wherein the first antibody specifically binds to a first antigen, and wherein the first heavy chain is fused through its C-terminus to the N-terminus of a polypeptide comprising a second heavy chain variable region of a second antibody (VH2), wherein the VH2 is fused through its C-terminus to the N-terminus of a second CH1 domain, and wherein the second antibody specifically binds to a second antigen; wherein

[0167] i) the VH1 or first CH1 domain comprises at least one amino acid substitution to introduce a charged amino acid at a residue selected from the group consisting of positions 39, 44, and 183 using EU numbering; and

[0168] ii) the VH2 or second CH1 domain comprises at least one amino acid substitution to introduce a charged amino acid at a residue selected from the group consisting of a residue that corresponds to positions 39, 44, and 183 using EU numbering, wherein the charge is the opposite of the substituted residue of the VH1 or first CH1 of the first heavy chain; and

[0169] b) a second polynucleotide wherein the second polynucleotide encodes a second polypeptide comprising a light chain of the first antibody of a), wherein the light chain comprises a first light chain variable region (VL1) and a first CL region; and wherein the VL1 or first CL domain comprises at least one amino acid substitution to introduce a charged amino acid at a residue selected from the group consisting of positions 38, 100, and 176 using EU numbering, wherein

[0170] the charge at position 38 is the opposite of the substituted residue of the VH1 or first CH1 of the first heavy chain at position 39; the charge at position 100 is the opposite of the substituted residue of the VH1 or first CH1 of the first heavy chain at position 44; the charge at position 176 is the opposite of the substituted residue of the VH1 or first CH1 of the first heavy chain at position 183; and

[0171] c) a third polynucleotide wherein the third polynucleotide encodes a third polypeptide comprising a light chain of the second antibody of a), wherein the light chain comprises a second light chain variable region (VL2) and a second CL region; and wherein the VL1 or first CL domain comprises at least one amino acid substitution to introduce a positively charged amino acid at a residue selected from the group consisting of positions 38, 100, and 176 using EU numbering, wherein

[0172] the charge at position 38 is the opposite of the substituted residue of the VH2 or second CH1 of the second heavy chain at position 39; the charge at position 100 is the opposite of the substituted residue of the VH2 or second CH1 of the second heavy chain at position 44; the charge at position 176 is the opposite of the substituted residue of the VH2 or second CH1 of the second heavy chain at position 183;

[0173] 2) cultivating the host cell under conditions such that the polypeptides are produced; and

[0174] 3) recovering from the host cell the antigen binding protein.

[0175] Additionally or alternatively, correct heavy-light chain pairing may be facilitated by swapping the CH1 and CL domains in the carboxyl-terminal Fab binding domain. By way of example, the first polypeptide, which is fused to the carboxyl terminus of the heavy chain, may comprise a VL domain and CH1 domain from the second antibody, and the second polypeptide may comprise a VH domain and CL domain from the second antibody. In another embodiment, the first polypeptide, which is fused to the carboxyl terminus of the heavy chain, may comprise a VH domain and a CL domain from the second antibody, and the second polypeptide may comprise a VL domain and CH1 domain from the second antibody.

[0176] The heavy chain constant regions or the Fc regions of the bispecific antigen binding proteins described herein may comprise one or more amino acid substitutions that affect the glycosylation and/or effector function of the antigen binding protein. One of the functions of the Fc region of an immunoglobulin is to communicate to the immune system when the immunoglobulin binds its target. This is commonly referred to as “effector function.” Communication leads to antibody-dependent cellular cytotoxicity (ADCC), antibody-dependent cellular phagocytosis (ADCP), and/or complement dependent cytotoxicity (CDC). ADCC and ADCP are mediated through the binding of the Fc region to Fc receptors on the surface of cells of the immune system. CDC is mediated through the binding of the Fc with proteins of the complement system, e.g., C1q. In some embodiments, the bispecific antigen binding proteins of the invention comprise one or more amino acid substitutions in the constant region to enhance effector function, including ADCC activity, CDC activity, ADCP activity, and/or the clearance or half-life of the antigen binding protein. Exemplary amino acid substitutions (EU numbering) that can enhance effector function include, but are not limited to, E233L, L234I, L234Y, L235S, G236A, S239D, F243L, F243V, P247I, D280H, K290S, K290E, K290N, K290Y, R292P, E294L, Y296W, S298A, S298D, S298V, S298G, S298T, T299A, Y300L, V305I, Q311M, K326A, K326E, K326W, A330S, A330L, A330M,

A330F, I332E, D333A, E333S, E333A, K334A, K334V, A339D, A339Q, P396L, or combinations of any of the foregoing.

[0177] In other embodiments, the bispecific antigen binding proteins of the invention comprise one or more amino acid substitutions in the constant region to reduce effector function. Exemplary amino acid substitutions (EU numbering) that can reduce effector function include, but are not limited to, C220S, C226S, C229S, E233P, L234A, L234V, V234A, L234F, L235A, L235E, G237A, P238S, S267E, H268Q, N297A, N297G, V309L, E318A, L328F, A330S, A331S, P331S or combinations of any of the foregoing.

[0178] Glycosylation can contribute to the effector function of antibodies, particularly IgG1 antibodies. Thus, in some embodiments, the bispecific antigen binding proteins of the invention may comprise one or more amino acid substitutions that affect the level or type of glycosylation of the binding proteins. Glycosylation of polypeptides is typically either N-linked or O-linked. N-linked refers to the attachment of the carbohydrate moiety to the side chain of an asparagine residue. The tri-peptide sequences asparagine-X-serine and asparagine-X-threonine, where X is any amino acid except proline, are the recognition sequences for enzymatic attachment of the carbohydrate moiety to the asparagine side chain. Thus, the presence of either of these tri-peptide sequences in a polypeptide creates a potential glycosylation site. O-linked glycosylation refers to the attachment of one of the sugars N-acetylgalactosamine, galactose, or xylose, to a hydroxyamino acid, most commonly serine or threonine, although 5-hydroxyproline or 5-hydroxylysine may also be used.

[0179] In certain embodiments, glycosylation of the bispecific antigen binding proteins described herein is increased by adding one or more glycosylation sites, e.g., to the Fc region of the binding protein. Addition of glycosylation sites to the antigen binding protein can be conveniently accomplished by altering the amino acid sequence such that it contains one or more of the above-described tri-peptide sequences (for N-linked glycosylation sites). The alteration may also be made by the addition of, or substitution by, one or more serine or threonine residues to the starting sequence (for O-linked glycosylation sites). For ease, the antigen binding protein amino acid sequence may be altered through changes at the DNA level, particularly by mutating the DNA encoding the target polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

[0180] The invention also encompasses production of bispecific antigen binding protein molecules with altered carbohydrate structure resulting in altered effector activity, including antigen binding proteins with absent or reduced fucosylation that exhibit improved ADCC activity. Various methods are known in the art to reduce or eliminate fucosylation. For

example, ADCC effector activity is mediated by binding of the antibody molecule to the FcγRIII receptor, which has been shown to be dependent on the carbohydrate structure of the N-linked glycosylation at the N297 residue of the CH2 domain. Non-fucosylated antibodies bind this receptor with increased affinity and trigger FcγRIII-mediated effector functions more efficiently than native, fucosylated antibodies. For example, recombinant production of non-fucosylated antibody in CHO cells in which the alpha-1,6-fucosyl transferase enzyme has been knocked out results in antibody with 100-fold increased ADCC activity (*see Yamane-Ohnuki et al.*, Biotechnol Bioeng. 87(5):614-22, 2004). Similar effects can be accomplished through decreasing the activity of alpha-1,6-fucosyl transferase enzyme or other enzymes in the fucosylation pathway, e.g., through siRNA or antisense RNA treatment, engineering cell lines to knockout the enzyme(s), or culturing with selective glycosylation inhibitors (*see Rothman et al.*, Mol Immunol. 26(12):1113-23, 1989). Some host cell strains, e.g. Lec13 or rat hybridoma YB2/0 cell line naturally produce antibodies with lower fucosylation levels (*see Shields et al.*, J Biol Chem. 277(30):26733-40, 2002 and Shinkawa *et al.*, J Biol Chem. 278(5):3466-73, 2003). An increase in the level of bisected carbohydrate, e.g. through recombinantly producing antibody in cells that overexpress GnTIII enzyme, has also been determined to increase ADCC activity (*see Umana et al.*, Nat Biotechnol. 17(2):176-80, 1999).

[0181] In other embodiments, glycosylation of the bispecific antigen binding proteins described herein is decreased or eliminated by removing one or more glycosylation sites, e.g., from the Fc region of the binding protein. Amino acid substitutions that eliminate or alter N-linked glycosylation sites can reduce or eliminate N-linked glycosylation of the antigen binding protein. In certain embodiments, the bispecific antigen binding proteins described herein comprise a mutation at position N297 (EU numbering), such as N297Q, N297A, or N297G. In one particular embodiment, the bispecific antigen binding proteins of the invention comprise a Fc region from a human IgG1 antibody with a N297G mutation. To improve the stability of molecules comprising a N297 mutation, the Fc region of the molecules may be further engineered. For instance, in some embodiments, one or more amino acids in the Fc region are substituted with cysteine to promote disulfide bond formation in the dimeric state. Residues corresponding to V259, A287, R292, V302, L306, V323, or I332 (EU numbering) of an IgG1 Fc region may thus be substituted with cysteine. In one embodiment, specific pairs of residues are substituted with cysteine such that they preferentially form a disulfide bond with each other, thus limiting or preventing disulfide bond scrambling. In certain embodiments pairs include, but are not limited to, A287C and L306C, V259C and

L306C, R292C and V302C, and V323C and I332C. In particular embodiments, the bispecific antigen binding proteins described herein comprise a Fc region from a human IgG1 antibody with mutations at R292C and V302C. In such embodiments, the Fc region may also comprise a N297G mutation.

[0182] Modifications of the bispecific antigen binding proteins of the invention to increase serum half-life also may be desirable, for example, by incorporation of or addition of a salvage receptor binding epitope (e.g., by mutation of the appropriate region or by incorporating the epitope into a peptide tag that is then fused to the antigen binding protein at either end or in the middle, e.g., by DNA or peptide synthesis; *see, e.g.*, WO96/32478) or adding molecules such as PEG or other water soluble polymers, including polysaccharide polymers. The salvage receptor binding epitope preferably constitutes a region wherein any one or more amino acid residues from one or two loops of a Fc region are transferred to an analogous position in the antigen binding protein. In one embodiment, three or more residues from one or two loops of the Fc region are transferred. In one embodiment, the epitope is taken from the CH2 domain of the Fc region (e.g., an IgG Fc region) and transferred to the CH1, CH3, or VH region, or more than one such region, of the antigen binding protein. Alternatively, the epitope is taken from the CH2 domain of the Fc region and transferred to the CL region or VL region, or both, of the antigen binding protein. *See* International applications WO 97/34631 and WO 96/32478 for a description of Fc variants and their interaction with the salvage receptor.

[0183] The present invention includes one or more isolated nucleic acids encoding the bispecific antigen binding proteins and components thereof described herein. Nucleic acid molecules of the invention include DNA and RNA in both single-stranded and double-stranded form, as well as the corresponding complementary sequences. DNA includes, for example, cDNA, genomic DNA, chemically synthesized DNA, DNA amplified by PCR, and combinations thereof. The nucleic acid molecules of the invention include full-length genes or cDNA molecules as well as a combination of fragments thereof. In one embodiment, the nucleic acids of the invention are derived from human sources, but the invention includes those derived from non-human species, as well.

[0184] Relevant amino acid sequences from an immunoglobulin or region thereof (e.g. variable region, Fc region, etc.) or polypeptide of interest may be determined by direct protein sequencing, and suitable encoding nucleotide sequences can be designed according to a universal codon table. Alternatively, genomic or cDNA encoding monoclonal antibodies from which the binding domains of the bispecific antigen binding proteins of the invention

may be derived can be isolated and sequenced from cells producing such antibodies using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of the monoclonal antibodies).

[0185] An “isolated nucleic acid,” which is used interchangeably herein with “isolated polynucleotide,” is a nucleic acid that has been separated from adjacent genetic sequences present in the genome of the organism from which the nucleic acid was isolated, in the case of nucleic acids isolated from naturally- occurring sources. In the case of nucleic acids synthesized enzymatically from a template or chemically, such as PCR products, cDNA molecules, or oligonucleotides for example, it is understood that the nucleic acids resulting from such processes are isolated nucleic acids. An isolated nucleic acid molecule refers to a nucleic acid molecule in the form of a separate fragment or as a component of a larger nucleic acid construct. In one embodiment, the nucleic acids are substantially free from contaminating endogenous material. The nucleic acid molecule has been derived from DNA or RNA isolated at least once in substantially pure form and in a quantity or concentration enabling identification, manipulation, and recovery of its component nucleotide sequences by standard biochemical methods (such as those outlined in Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1989)). Such sequences are provided and/or constructed in the form of an open reading frame uninterrupted by internal non-translated sequences, or introns, that are typically present in eukaryotic genes. Sequences of non-translated DNA can be present 5' or 3' from an open reading frame, where the same do not interfere with manipulation or expression of the coding region. Unless specified otherwise, the left-hand end of any single-stranded polynucleotide sequence discussed herein is the 5' end; the left-hand direction of double-stranded polynucleotide sequences is referred to as the 5' direction. The direction of 5' to 3' production of nascent RNA transcripts is referred to as the transcription direction; sequence regions on the DNA strand having the same sequence as the RNA transcript that are 5' to the 5' end of the RNA transcript are referred to as “upstream sequences;” sequence regions on the DNA strand having the same sequence as the RNA transcript that are 3' to the 3' end of the RNA transcript are referred to as “downstream sequences.”

[0186] The present invention also includes nucleic acids that hybridize under moderately stringent conditions, and highly stringent conditions, to nucleic acids encoding polypeptides as described herein. The basic parameters affecting the choice of hybridization conditions and guidance for devising suitable conditions are set forth by Sambrook,, Fritsch, and Maniatis (1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold

Spring Harbor, N.Y., chapters 9 and 11; and Current Protocols in Molecular Biology, 1995, Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4), and can be readily determined by those having ordinary skill in the art based on, for example, the length and/or base composition of the DNA. One way of achieving moderately stringent conditions involves the use of a prewashing solution containing 5 x SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0), hybridization buffer of about 50% formamide, 6 x SSC, and a hybridization temperature of about 55°C (or other similar hybridization solutions, such as one containing about 50% formamide, with a hybridization temperature of about 42°C), and washing conditions of about 60°C, in 0.5 x SSC, 0.1% SDS. Generally, highly stringent conditions are defined as hybridization conditions as above, but with washing at approximately 68°C, 0.2 x SSC, 0.1% SDS. SSPE (1 x SSPE is 0.15M NaCl, 10 mM NaH₂PO₄, and 1.25 mM EDTA, pH 7.4) can be substituted for SSC (1 x SSC is 0.15M NaCl and 15 mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete. It should be understood that the wash temperature and wash salt concentration can be adjusted as necessary to achieve a desired degree of stringency by applying the basic principles that govern hybridization reactions and duplex stability, as known to those skilled in the art and described further below (*see, e.g.*, Sambrook *et al.*, 1989). When hybridizing a nucleic acid to a target nucleic acid of unknown sequence, the hybrid length is assumed to be that of the hybridizing nucleic acid. When nucleic acids of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the nucleic acids and identifying the region or regions of optimal sequence complementarity. The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5 to 10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, $T_m (^{\circ}\text{C}) = 2(\# \text{ of A} + \text{T bases}) + 4(\# \text{ of G} + \text{C bases})$. For hybrids above 18 base pairs in length, $T_m (^{\circ}\text{C}) = 81.5 + 16.6(\log_{10} [\text{Na}^+]) + 0.41(\% \text{ G} + \text{C}) - (600/\text{N})$, where N is the number of bases in the hybrid, and [Na⁺] is the concentration of sodium ions in the hybridization buffer ([Na⁺] for 1 x SSC = 0.165M). In one embodiment, each such hybridizing nucleic acid has a length that is at least 15 nucleotides (or at least 18 nucleotides, or at least 20 nucleotides, or at least 25 nucleotides, or at least 30 nucleotides, or at least 40 nucleotides, or at least 50 nucleotides), or at least 25% (or at least 50%, or at least 60%, or at least 70%, or at least 80%) of the length of the nucleic acid of the present invention to which it hybridizes, and has at least 60% sequence identity (or at least 70%, at least 75%, at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, 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%, or at least 99.5%) with the nucleic acid of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing nucleic acids when aligned so as to maximize overlap and identity while minimizing sequence gaps as described in more detail above.

[0187] Variants of the antigen binding proteins described herein can be prepared by site-specific mutagenesis of nucleotides in the DNA encoding the polypeptide, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the recombinant DNA in cell culture as outlined herein. However, antigen binding proteins comprising variant CDRs having up to about 100-150 residues may be prepared by *in vitro* synthesis using established techniques. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, e.g., binding to antigen. Such variants include, for example, deletions and/or insertions and/or substitutions of residues within the amino acid sequences of the antigen binding proteins. Any combination of deletion, insertion, and substitution is made to arrive at the final construct, provided that the final construct possesses the desired characteristics. The amino acid changes also may alter post-translational processes of the antigen binding protein, such as changing the number or position of glycosylation sites. In certain embodiments, antigen binding protein variants are prepared with the intent to modify those amino acid residues which are directly involved in epitope binding. In other embodiments, modification of residues which are not directly involved in epitope binding or residues not involved in epitope binding in any way, is desirable, for purposes discussed herein. Mutagenesis within any of the CDR regions and/or framework regions is contemplated. Covariance analysis techniques can be employed by the skilled artisan to design useful modifications in the amino acid sequence of the antigen binding protein. *See, e.g.,* Choulter, *et al.*, Proteins 41:475-484, 2000; Demarest *et al.*, J. Mol. Biol. 335:41-48, 2004; Hugo *et al.*, Protein Engineering 16(5):381-86, 2003; Aurora *et al.*, US Patent Publication No. 2008/0318207 A1; Glaser *et al.*, US Patent Publication No. 2009/0048122 A1; Urech *et al.*, WO 2008/110348 A1; Borrás *et al.*, WO 2009/000099 A2. Such modifications determined by covariance analysis can improve potency, pharmacokinetic, pharmacodynamic, and/or manufacturability characteristics of an antigen binding protein.

[0188] The nucleic acid sequences of the present invention. As will be appreciated by those in the art, due to the degeneracy of the genetic code, an extremely large number of nucleic acids may be made, all of which encode the CDRs (and heavy and light chains or other

components of the antigen binding proteins described herein) of the invention. Thus, having identified a particular amino acid sequence, those skilled in the art could make any number of different nucleic acids, by simply modifying the sequence of one or more codons in a way which does not change the amino acid sequence of the encoded protein.

[0189] The present invention also includes vectors comprising one or more nucleic acids encoding one or more components of the bispecific antigen binding proteins of the invention (e.g. variable regions, light chains, heavy chains, modified heavy chains, and Fd fragments). The term “vector” refers to any molecule or entity (e.g., nucleic acid, plasmid, bacteriophage or virus) used to transfer protein coding information into a host cell. Examples of vectors include, but are not limited to, plasmids, viral vectors, non-episomal mammalian vectors and expression vectors, for example, recombinant expression vectors. The term “expression vector” or “expression construct” as used herein refers to a recombinant DNA molecule containing a desired coding sequence and appropriate nucleic acid control sequences necessary for the expression of the operably linked coding sequence in a particular host cell. An expression vector can include, but is not limited to, sequences that affect or control transcription, translation, and, if introns are present, affect RNA splicing of a coding region operably linked thereto. Nucleic acid sequences necessary for expression in prokaryotes include a promoter, optionally an operator sequence, a ribosome binding site and possibly other sequences. Eukaryotic cells are known to utilize promoters, enhancers, and termination and polyadenylation signals. A secretory signal peptide sequence can also, optionally, be encoded by the expression vector, operably linked to the coding sequence of interest, so that the expressed polypeptide can be secreted by the recombinant host cell, for more facile isolation of the polypeptide of interest from the cell, if desired. For instance, in some embodiments, signal peptide sequences may be appended/fused to the amino terminus of any of the polypeptide sequences of the present invention. In certain embodiments, a signal peptide having the amino acid sequence of MDMRVPAQLLGLLLWLRGARC (SEQ ID NO: 943) is fused to the amino terminus of any of the polypeptide sequences of the present invention. In other embodiments, a signal peptide having the amino acid sequence of MAWALLLLTLLTQGTGSWA (SEQ ID NO: 944) is fused to the amino terminus of any of the polypeptide sequences of the present invention. In still other embodiments, a signal peptide having the amino acid sequence of MTCSPLLLTLIHCTGSWA (SEQ ID NO: 945) is fused to the amino terminus of any of the polypeptide sequences of the present invention. Other suitable signal peptide sequences that can be fused to the amino terminus of the polypeptide sequences described herein include: MEAPAQLLFLLLWLPDTTG (SEQ ID

NO: 946), MEWTWRVLFLVAAATGAHS (SEQ ID NO: 947), METPAQLLFLLLLWLPDTTG (SEQ ID NO: 948), METPAQLLFLLLLWLPDTTG (SEQ ID NO: 949), MKHLWFFLLLVAAPRWVLS (SEQ ID NO: 950), and MEWSWVFLFFLSVTTGVHS (SEQ ID NO: 951). Other signal peptides are known to those of skill in the art and may be fused to any of the polypeptide chains of the present invention, for example, to facilitate or optimize expression in particular host cells.

[0190] Typically, expression vectors used in the host cells to produce the bispecific antigen proteins of the invention will contain sequences for plasmid maintenance and for cloning and expression of exogenous nucleotide sequences encoding the components of the bispecific antigen binding proteins. Such sequences, collectively referred to as “flanking sequences,” in certain embodiments will typically include one or more of the following nucleotide sequences: a promoter, one or more enhancer sequences, an origin of replication, a transcriptional termination sequence, a complete intron sequence containing a donor and acceptor splice site, a sequence encoding a leader sequence for polypeptide secretion, a ribosome binding site, a polyadenylation sequence, a polylinker region for inserting the nucleic acid encoding the polypeptide to be expressed, and a selectable marker element. Each of these sequences is discussed below.

[0191] Optionally, the vector may contain a “tag”-encoding sequence, i.e., an oligonucleotide molecule located at the 5' or 3' end of the polypeptide coding sequence; the oligonucleotide tag sequence encodes polyHis (such as hexaHis), FLAG, HA (hemagglutinin influenza virus), myc, or another “tag” molecule for which commercially available antibodies exist. This tag is typically fused to the polypeptide upon expression of the polypeptide, and can serve as a means for affinity purification or detection of the polypeptide from the host cell. Affinity purification can be accomplished, for example, by column chromatography using antibodies against the tag as an affinity matrix. Optionally, the tag can subsequently be removed from the purified polypeptide by various means such as using certain peptidases for cleavage.

[0192] Flanking sequences may be homologous (i.e., from the same species and/or strain as the host cell), heterologous (i.e., from a species other than the host cell species or strain), hybrid (i.e., a combination of flanking sequences from more than one source), synthetic or native. As such, the source of a flanking sequence may be any prokaryotic or eukaryotic organism, any vertebrate or invertebrate organism, or any plant, provided that the flanking sequence is functional in, and can be activated by, the host cell machinery.

[0193] Flanking sequences useful in the vectors of this invention may be obtained by any of several methods well known in the art. Typically, flanking sequences useful herein will have

been previously identified by mapping and/or by restriction endonuclease digestion and can thus be isolated from the proper tissue source using the appropriate restriction endonucleases. In some cases, the full nucleotide sequence of a flanking sequence may be known. Here, the flanking sequence may be synthesized using routine methods for nucleic acid synthesis or cloning.

[0194] Whether all or only a portion of the flanking sequence is known, it may be obtained using polymerase chain reaction (PCR) and/or by screening a genomic library with a suitable probe such as an oligonucleotide and/or flanking sequence fragment from the same or another species. Where the flanking sequence is not known, a fragment of DNA containing a flanking sequence may be isolated from a larger piece of DNA that may contain, for example, a coding sequence or even another gene or genes. Isolation may be accomplished by restriction endonuclease digestion to produce the proper DNA fragment followed by isolation using agarose gel purification, Qiagen® column chromatography (Chatsworth, CA), or other methods known to the skilled artisan. The selection of suitable enzymes to accomplish this purpose will be readily apparent to one of ordinary skill in the art.

[0195] An origin of replication is typically a part of those prokaryotic expression vectors purchased commercially, and the origin aids in the amplification of the vector in a host cell. If the vector of choice does not contain an origin of replication site, one may be chemically synthesized based on a known sequence, and ligated into the vector. For example, the origin of replication from the plasmid pBR322 (New England Biolabs, Beverly, MA) is suitable for most gram-negative bacteria, and various viral origins (e.g., SV40, polyoma, adenovirus, vesicular stomatitis virus (VSV), or papillomaviruses such as HPV or BPV) are useful for cloning vectors in mammalian cells. Generally, the origin of replication component is not needed for mammalian expression vectors (for example, the SV40 origin is often used only because it also contains the virus early promoter).

[0196] A transcription termination sequence is typically located 3' to the end of a polypeptide coding region and serves to terminate transcription. Usually, a transcription termination sequence in prokaryotic cells is a G-C rich fragment followed by a poly-T sequence. While the sequence is easily cloned from a library or even purchased commercially as part of a vector, it can also be readily synthesized using known methods for nucleic acid synthesis.

[0197] A selectable marker gene encodes a protein necessary for the survival and growth of a host cell grown in a selective culture medium. Typical selection marker genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, tetracycline,

or kanamycin for prokaryotic host cells; (b) complement auxotrophic deficiencies of the cell; or (c) supply critical nutrients not available from complex or defined media. Specific selectable markers are the kanamycin resistance gene, the ampicillin resistance gene, and the tetracycline resistance gene. Advantageously, a neomycin resistance gene may also be used for selection in both prokaryotic and eukaryotic host cells.

[0198] Other selectable genes may be used to amplify the gene that will be expressed. Amplification is the process wherein genes that are required for production of a protein critical for growth or cell survival are reiterated in tandem within the chromosomes of successive generations of recombinant cells. Examples of suitable selectable markers for mammalian cells include dihydrofolate reductase (DHFR) and promoterless thymidine kinase genes. Mammalian cell transformants are placed under selection pressure wherein only the transformants are uniquely adapted to survive by virtue of the selectable gene present in the vector. Selection pressure is imposed by culturing the transformed cells under conditions in which the concentration of selection agent in the medium is successively increased, thereby leading to the amplification of both the selectable gene and the DNA that encodes another gene, such as one or more components of the bispecific antigen binding proteins described herein. As a result, increased quantities of a polypeptide are synthesized from the amplified DNA.

[0199] A ribosome-binding site is usually necessary for translation initiation of mRNA and is characterized by a Shine-Dalgarno sequence (prokaryotes) or a Kozak sequence (eukaryotes). The element is typically located 3' to the promoter and 5' to the coding sequence of the polypeptide to be expressed. In certain embodiments, one or more coding regions may be operably linked to an internal ribosome binding site (IRES), allowing translation of two open reading frames from a single RNA transcript.

[0200] In some cases, such as where glycosylation is desired in a eukaryotic host cell expression system, one may manipulate the various pre- or prosequences to improve glycosylation or yield. For example, one may alter the peptidase cleavage site of a particular signal peptide, or add prosequences, which also may affect glycosylation. The final protein product may have, in the -1 position (relative to the first amino acid of the mature protein) one or more additional amino acids incident to expression, which may not have been totally removed. For example, the final protein product may have one or two amino acid residues found in the peptidase cleavage site, attached to the amino-terminus. Alternatively, use of some enzyme cleavage sites may result in a slightly truncated form of the desired polypeptide, if the enzyme cuts at such area within the mature polypeptide.

[0201] Expression and cloning vectors of the invention will typically contain a promoter that is recognized by the host organism and operably linked to the molecule encoding the polypeptide. The term “operably linked” as used herein refers to the linkage of two or more nucleic acid sequences in such a manner that a nucleic acid molecule capable of directing the transcription of a given gene and/or the synthesis of a desired protein molecule is produced. For example, a control sequence in a vector that is “operably linked” to a protein coding sequence is ligated thereto so that expression of the protein coding sequence is achieved under conditions compatible with the transcriptional activity of the control sequences. More specifically, a promoter and/or enhancer sequence, including any combination of cis-acting transcriptional control elements is operably linked to a coding sequence if it stimulates or modulates the transcription of the coding sequence in an appropriate host cell or other expression system.

[0202] Promoters are untranscribed sequences located upstream (i.e., 5') to the start codon of a structural gene (generally within about 100 to 1000 bp) that control transcription of the structural gene. Promoters are conventionally grouped into one of two classes: inducible promoters and constitutive promoters. Inducible promoters initiate increased levels of transcription from DNA under their control in response to some change in culture conditions, such as the presence or absence of a nutrient or a change in temperature. Constitutive promoters, on the other hand, uniformly transcribe a gene to which they are operably linked, that is, with little or no control over gene expression. A large number of promoters, recognized by a variety of potential host cells, are well known. A suitable promoter is operably linked to the DNA encoding e.g., heavy chain, light chain, modified heavy chain, or other component of the bispecific antigen binding proteins of the invention, by removing the promoter from the source DNA by restriction enzyme digestion and inserting the desired promoter sequence into the vector.

[0203] Suitable promoters for use with yeast hosts are also well known in the art. Yeast enhancers are advantageously used with yeast promoters. Suitable promoters for use with mammalian host cells are well known and include, but are not limited to, those obtained from the genomes of viruses such as polyoma virus, fowlpox virus, adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, retroviruses, hepatitis-B virus and Simian Virus 40 (SV40). Other suitable mammalian promoters include heterologous mammalian promoters, for example, heat-shock promoters and the actin promoter.

[0204] Additional promoters which may be of interest include, but are not limited to: SV40 early promoter (Benoist and Chambon, 1981, *Nature* 290:304-310); CMV promoter (Thorsen et al., 1984, *Proc. Natl. Acad. U.S.A.* 81:659-663); the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto et al., 1980, *Cell* 22:787-797); herpes thymidine kinase promoter (Wagner et al., 1981, *Proc. Natl. Acad. Sci. U.S.A.* 78: 1444-1445); promoter and regulatory sequences from the metallothioneine gene Prinster et al., 1982, *Nature* 296:39-42); and prokaryotic promoters such as the beta-lactamase promoter (Villa-Kamaroff et al., 1978, *Proc. Natl. Acad. Sci. U.S.A.* 75:3727-3731); or the tac promoter (DeBoer et al., 1983, *Proc. Natl. Acad. Sci. U.S.A.* 80:21-25). Also of interest are the following animal transcriptional control regions, which exhibit tissue specificity and have been utilized in transgenic animals: the elastase I gene control region that is active in pancreatic acinar cells (Swift et al., 1984, *Cell* 38:639-646; Ornitz et al., 1986, *Cold Spring Harbor Symp. Quant. Biol.* 50:399-409; MacDonald, 1987, *Hepatology* 7:425-515); the insulin gene control region that is active in pancreatic beta cells (Hanahan, 1985, *Nature* 315: 115-122); the immunoglobulin gene control region that is active in lymphoid cells (Grosschedl et al., 1984, *Cell* 38:647-658; Adames et al., 1985, *Nature* 318:533-538; Alexander et al., 1987, *Mol. Cell. Biol.* 7: 1436-1444); the mouse mammary tumor virus control region that is active in testicular, breast, lymphoid and mast cells (Leder et al., 1986, *Cell* 45:485-495); the albumin gene control region that is active in liver (Pinkert et al., 1987, *Genes and Devel.* 1 :268-276); the alpha-feto-protein gene control region that is active in liver (Krumlauf et al., 1985, *Mol. Cell. Biol.* 5: 1639-1648; Hammer et al., 1987, *Science* 253:53-58); the alpha 1-antitrypsin gene control region that is active in liver (Kelsey et al., 1987, *Genes and Devel.* 1: 161-171); the beta-globin gene control region that is active in myeloid cells (Mogam et al, 1985, *Nature* 315:338-340; Kollias et al, 1986, *Cell* 46:89-94); the myelin basic protein gene control region that is active in oligodendrocyte cells in the brain (Readhead et al., 1987, *Cell* 48:703-712); the myosin light chain-2 gene control region that is active in skeletal muscle (Sani, 1985, *Nature* 314:283-286); and the gonadotropic releasing hormone gene control region that is active in the hypothalamus (Mason et al., 1986, *Science* 234: 1372-1378).

[0205] An enhancer sequence may be inserted into the vector to increase transcription of DNA encoding a component of the bispecific antigen binding proteins (e.g., light chain, heavy chain, modified heavy chain, Fd fragment) by higher eukaryotes. Enhancers are cis-acting elements of DNA, usually about 10-300 bp in length, that act on the promoter to increase transcription. Enhancers are relatively orientation and position independent, having

been found at positions both 5' and 3' to the transcription unit. Several enhancer sequences available from mammalian genes are known (e.g., globin, elastase, albumin, alpha-feto-protein and insulin). Typically, however, an enhancer from a virus is used. The SV40 enhancer, the cytomegalovirus early promoter enhancer, the polyoma enhancer, and adenovirus enhancers known in the art are exemplary enhancing elements for the activation of eukaryotic promoters. While an enhancer may be positioned in the vector either 5' or 3' to a coding sequence, it is typically located at a site 5' from the promoter. A sequence encoding an appropriate native or heterologous signal sequence (leader sequence or signal peptide) can be incorporated into an expression vector, to promote extracellular secretion of the antibody. The choice of signal peptide or leader depends on the type of host cells in which the antibody is to be produced, and a heterologous signal sequence can replace the native signal sequence. Examples of signal peptides are described above. Other signal peptides that are functional in mammalian host cells include the signal sequence for interleukin-7 (IL-7) described in US Patent No. 4,965,195; the signal sequence for interleukin-2 receptor described in Cosman et al., 1984, Nature 312:768; the interleukin-4 receptor signal peptide described in EP Patent No. 0367 566; the type I interleukin-1 receptor signal peptide described in U.S. Patent No. 4,968,607; the type II interleukin-1 receptor signal peptide described in EP Patent No. 0 460 846.

[0206] The expression vectors that are provided may be constructed from a starting vector such as a commercially available vector. Such vectors may or may not contain all of the desired flanking sequences. Where one or more of the flanking sequences described herein are not already present in the vector, they may be individually obtained and ligated into the vector. Methods used for obtaining each of the flanking sequences are well known to one skilled in the art. The expression vectors can be introduced into host cells to thereby produce proteins, including fusion proteins, encoded by nucleic acids as described herein.

[0207] In certain embodiments, nucleic acids encoding the different components of the bispecific antigen binding proteins of the invention may be inserted into the same expression vector. For instance, the nucleic acid encoding an anti-first target antigen light chain can be cloned into the same vector as the nucleic acid encoding an anti- first target antigen heavy chain. In such embodiments, the two nucleic acids may be separated by an internal ribosome entry site (IRES) and under the control of a single promoter such that the light chain and heavy chain are expressed from the same mRNA transcript. Alternatively, the two nucleic acids may be under the control of two separate promoters such that the light chain and heavy chain are expressed from two separate mRNA transcripts. In some embodiments, nucleic

acids encoding the anti- first target antigen light chain and heavy chain are cloned into one expression vector and the nucleic acids encoding the anti- second target antigen light chain and heavy chain are cloned into a second expression vector.

[0208] Similarly, for IgG-Fab bispecific antigen binding proteins, nucleic acids encoding each of the three components may be cloned into the same expression vector. In some embodiments, the nucleic acid encoding the light chain of the IgG-Fab molecule and the nucleic acid encoding the second polypeptide (which comprises the other half of the C-terminal Fab domain) are cloned into one expression vector, whereas the nucleic acid encoding the modified heavy chain (fusion protein comprising a heavy chain and half of a Fab domain) is cloned into a second expression vector. In certain embodiments, all components of the bispecific antigen binding proteins described herein are expressed from the same host cell population. For example, even if one or more components is cloned into a separate expression vector, the host cell is co-transfected with both expression vectors such that one cell produces all components of the bispecific antigen binding proteins.

[0209] After the vector has been constructed and the one or more nucleic acid molecules encoding the components of the bispecific antigen binding proteins described herein has been inserted into the proper site(s) of the vector or vectors, the completed vector(s) may be inserted into a suitable host cell for amplification and/or polypeptide expression. Thus, the present invention encompasses an isolated host cell comprising one or more expression vectors encoding the components of the bispecific antigen binding proteins. The term “host cell” as used herein refers to a cell that has been transformed, or is capable of being transformed, with a nucleic acid and thereby expresses a gene of interest. The term includes the progeny of the parent cell, whether or not the progeny is identical in morphology or in genetic make-up to the original parent cell, so long as the gene of interest is present. A host cell that comprises an isolated nucleic acid of the invention, in one embodiment operably linked to at least one expression control sequence (e.g. promoter or enhancer), is a “recombinant host cell.”

[0210] The transformation of an expression vector for an antigen binding protein into a selected host cell may be accomplished by well-known methods including transfection, infection, calcium phosphate co-precipitation, electroporation, microinjection, lipofection, DEAE-dextran mediated transfection, or other known techniques. The method selected will in part be a function of the type of host cell to be used. These methods and other suitable methods are well known to the skilled artisan, and are set forth, for example, in Sambrook et al., 2001, *supra*.

[0211] A host cell, when cultured under appropriate conditions, synthesizes an antigen binding protein that can subsequently be collected from the culture medium (if the host cell secretes it into the medium) or directly from the host cell producing it (if it is not secreted). The selection of an appropriate host cell will depend upon various factors, such as desired expression levels, polypeptide modifications that are desirable or necessary for activity (such as glycosylation or phosphorylation) and ease of folding into a biologically active molecule.

[0212] Exemplary host cells include prokaryote, yeast, or higher eukaryote cells. Prokaryotic host cells include eubacteria, such as Gram-negative or Gram-positive organisms, for example, *Enterobacteriaceae* such as *Escherichia*, e.g., *E. coli*, *Enterobacter*, *Erwinia*, *Klebsiella*, *Proteus*, *Salmonella*, e.g., *Salmonella typhimurium*, *Serratia*, e.g., *Serratia marcescans*, and *Shigella*, as well as *Bacillus*, such as *B. subtilis* and *B. licheniformis*, *Pseudomonas*, and *Streptomyces*. Eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for recombinant polypeptides. *Saccharomyces cerevisiae*, or common baker's yeast, is the most commonly used among lower eukaryotic host microorganisms. However, a number of other genera, species, and strains are commonly available and useful herein, such as *Pichia*, e.g. *P. pastoris*, *Schizosaccharomyces pombe*; *Kluyveromyces*, *Yarrowia*; *Candida*; *Trichoderma reesia*; *Neurospora crassa*; *Schwanniomyces*, such as *Schwanniomyces occidentalis*; and filamentous fungi, such as, e.g., *Neurospora*, *Penicillium*, *Tolypocladium*, and *Aspergillus* hosts such as *A. nidulans* and *A. niger*.

[0213] Host cells for the expression of glycosylated antigen binding proteins can be derived from multicellular organisms. Examples of invertebrate cells include plant and insect cells. Numerous baculoviral strains and variants and corresponding permissive insect host cells from hosts such as *Spodoptera frugiperda* (caterpillar), *Aedes aegypti* (mosquito), *Aedes albopictus* (mosquito), *Drosophila melanogaster* (fruitfly), and *Bombyx mori* have been identified. A variety of viral strains for transfection of such cells are publicly available, e.g., the L-1 variant of *Autographa californica* NPV and the Bm-5 strain of *Bombyx mori* NPV.

[0214] Vertebrate host cells are also suitable hosts, and recombinant production of antigen binding proteins from such cells has become routine procedure. Mammalian cell lines available as hosts for expression are well known in the art and include, but are not limited to, immortalized cell lines available from the American Type Culture Collection (ATCC), including but not limited to Chinese hamster ovary (CHO) cells, including CHOK1 cells (ATCC CCL61), DXB-11, DG-44, and Chinese hamster ovary cells/-DHFR (CHO, Urlaub *et al.*, Proc. Natl. Acad. Sci. USA 77: 4216, 1980); monkey kidney CV1 line transformed by

SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, (Graham *et al.*, J. Gen Virol. 36: 59, 1977); baby hamster kidney cells (BHK, ATCC CCL 10); mouse sertoli cells (TM4, Mather, Biol. Reprod. 23: 243-251, 1980); monkey kidney cells (CV1 ATCC CCL 70); African green monkey kidney cells (VERO-76, ATCC CRL-1587); human cervical carcinoma cells (HELA, ATCC CCL 2); canine kidney cells (MDCK, ATCC CCL 34); buffalo rat liver cells (BRL 3A, ATCC CRL 1442); human lung cells (W138, ATCC CCL 75); human hepatoma cells (Hep G2, HB 8065); mouse mammary tumor (MMT 060562, ATCC CCL51); TRI cells (Mather *et al.*, Annals N.Y Acad. Sci. 383: 44-68, 1982); MRC 5 cells or FS4 cells; mammalian myeloma cells, and a number of other cell lines. In certain embodiments, cell lines may be selected through determining which cell lines have high expression levels and constitutively produce bispecific antigen binding proteins of the present invention. In another embodiment, a cell line from the B cell lineage that does not make its own antibody but has a capacity to make and secrete a heterologous antibody can be selected. CHO cells are host cells in some embodiments for expressing the bispecific antigen binding proteins of the invention.

[0215] Host cells are transformed or transfected with the above-described nucleic acids or vectors for production of bispecific antigen binding proteins and are cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. In addition, novel vectors and transfected cell lines with multiple copies of transcription units separated by a selective marker are particularly useful for the expression of antigen binding proteins. Thus, the present invention also provides a method for preparing a bispecific antigen binding protein described herein comprising culturing a host cell comprising one or more expression vectors described herein in a culture medium under conditions permitting expression of the bispecific antigen binding protein encoded by the one or more expression vectors; and recovering the bispecific antigen binding protein from the culture medium.

[0216] The host cells used to produce the antigen binding proteins of the invention may be cultured in a variety of media. Commercially available media such as Ham's F10 (Sigma), Minimal Essential Medium ((MEM), (Sigma), RPMI-1640 (Sigma), and Dulbecco's Modified Eagle's Medium ((DMEM), Sigma) are suitable for culturing the host cells. In addition, any of the media described in Ham *et al.*, Meth. Enz. 58: 44, 1979; Barnes *et al.*, Anal. Biochem. 102: 255, 1980; U.S. Patent Nos. 4,767,704; 4,657,866; 4,927,762; 4,560,655; or 5,122,469; WO90103430; WO 87/00195; or U.S. Patent Re. No. 30,985 may be used as culture media for the host cells. Any of these media may be supplemented as necessary with hormones

and/or other growth factors (such as insulin, transferrin, or epidermal growth factor), salts (such as sodium chloride, calcium, magnesium, and phosphate), buffers (such as HEPES), nucleotides (such as adenosine and thymidine), antibiotics (such as GentamycinTM drug), trace elements (defined as inorganic compounds usually present at final concentrations in the micromolar range), and glucose or an equivalent energy source. Any other necessary supplements may also be included at appropriate concentrations that would be known to those skilled in the art. The culture conditions, such as temperature, pH, and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

[0217] Upon culturing the host cells, the bispecific antigen binding protein can be produced intracellularly, in the periplasmic space, or directly secreted into the medium. If the antigen binding protein is produced intracellularly, as a first step, the particulate debris, either host cells or lysed fragments, is removed, for example, by centrifugation or ultrafiltration. The bispecific antigen binding protein can be purified using, for example, hydroxyapatite chromatography, cation or anion exchange chromatography, or affinity chromatography, using the antigen(s) of interest or protein A or protein G as an affinity ligand. Protein A can be used to purify proteins that include polypeptides that are based on human $\gamma 1$, $\gamma 2$, or $\gamma 4$ heavy chains (Lindmark *et al.*, J. Immunol. Meth. 62: 1-13, 1983). Protein G is recommended for all mouse isotypes and for human $\gamma 3$ (Guss *et al.*, EMBO J. 5: 15671575, 1986). The matrix to which the affinity ligand is attached is most often agarose, but other matrices are available. Mechanically stable matrices such as controlled pore glass or poly(styrenedivinyl)benzene allow for faster flow rates and shorter processing times than can be achieved with agarose. Where the protein comprises a CH3 domain, the Bakerbond ABXTM resin (J. T. Baker, Phillipsburg, N.J.) is useful for purification. Other techniques for protein purification such as ethanol precipitation, Reverse Phase HPLC, chromatofocusing, SDS-PAGE, and ammonium sulfate precipitation are also possible depending on the particular bispecific antigen binding protein to be recovered.

[0218] In some embodiments, the invention provides a pharmaceutical composition comprising one or a plurality of the bispecific antigen binding proteins of the invention together with pharmaceutically acceptable diluents, carriers, excipients, solubilizers, emulsifiers, preservatives, and/or adjuvants. Pharmaceutical compositions of the invention include, but are not limited to, liquid, frozen, and lyophilized compositions.

“Pharmaceutically-acceptable” refers to molecules, compounds, and compositions that are

non-toxic to human recipients at the dosages and concentrations employed and/or do not produce allergic or adverse reactions when administered to humans. In certain embodiments, the pharmaceutical composition may contain formulation materials for modifying, maintaining or preserving, for example, the pH, osmolarity, viscosity, clarity, color, isotonicity, odor, sterility, stability, rate of dissolution or release, adsorption or penetration of the composition. In such embodiments, suitable formulation materials include, but are not limited to, amino acids (such as glycine, glutamine, asparagine, arginine or lysine); antimicrobials; antioxidants (such as ascorbic acid, sodium sulfite or sodium hydrogen-sulfite); buffers (such as borate, bicarbonate, Tris-HCl, citrates, phosphates or other organic acids); bulking agents (such as mannitol or glycine); chelating agents (such as ethylenediamine tetraacetic acid (EDTA)); complexing agents (such as caffeine, polyvinylpyrrolidone, beta-cyclodextrin or hydroxypropyl-beta-cyclodextrin); fillers; monosaccharides; disaccharides; and other carbohydrates (such as glucose, mannose or dextrans); proteins (such as serum albumin, gelatin or immunoglobulins); coloring, flavoring and diluting agents; emulsifying agents; hydrophilic polymers (such as polyvinylpyrrolidone); low molecular weight polypeptides; salt-forming counterions (such as sodium); preservatives (such as benzalkonium chloride, benzoic acid, salicylic acid, thimerosal, phenethyl alcohol, methylparaben, propylparaben, chlorhexidine, sorbic acid or hydrogen peroxide); solvents (such as glycerin, propylene glycol or polyethylene glycol); sugar alcohols (such as mannitol or sorbitol); suspending agents; surfactants or wetting agents (such as pluronics, PEG, sorbitan esters, polysorbates such as polysorbate 20, polysorbate 80, triton, tromethamine, lecithin, cholesterol, tyloxapal); stability enhancing agents (such as sucrose or sorbitol); tonicity enhancing agents (such as alkali metal halides, sodium or potassium chloride, mannitol sorbitol); delivery vehicles; diluents; excipients and/or pharmaceutical adjuvants. Methods and suitable materials for formulating molecules for therapeutic use are known in the pharmaceutical arts, and are described, for example, in REMINGTON'S PHARMACEUTICAL SCIENCES, 18th Edition, (A.R. Genrmo, ed.), 1990, Mack Publishing Company.

[0219] In some embodiments, the pharmaceutical composition of the invention comprises a standard pharmaceutical carrier, such as a sterile phosphate buffered saline solution, bacteriostatic water, and the like. A variety of aqueous carriers may be used, e.g., water, buffered water, 0.4% saline, 0.3% glycine and the like, and may include other proteins for enhanced stability, such as albumin, lipoprotein, globulin, etc., subjected to mild chemical modifications or the like.

[0220] Exemplary concentrations of the bispecific antigen binding proteins in the formulation may range from about 0.1 mg/ml to about 180 mg/ml or from about 0.1 mg/mL to about 50 mg/mL, or from about 0.5 mg/mL to about 25 mg/mL, or alternatively from about 2 mg/mL to about 10 mg/mL. An aqueous formulation of the antigen binding protein may be prepared in a pH-buffered solution, for example, at pH ranging from about 4.5 to about 6.5, or from about 4.8 to about 5.5, or alternatively about 5.0. Examples of buffers that are suitable for a pH within this range include acetate (e.g. sodium acetate), succinate (such as sodium succinate), gluconate, histidine, citrate and other organic acid buffers. The buffer concentration can be from about 1 mM to about 200 mM, or from about 10 mM to about 60 mM, depending, for example, on the buffer and the desired isotonicity of the formulation.

[0221] A tonicity agent, which may also stabilize the antigen binding protein, may be included in the formulation. Exemplary tonicity agents include polyols, such as mannitol, sucrose or trehalose. In one embodiment the aqueous formulation is isotonic, although hypertonic or hypotonic solutions may be suitable. Exemplary concentrations of the polyol in the formulation may range from about 1% to about 15% w/v.

[0222] A surfactant may also be added to the antigen binding protein formulation to reduce aggregation of the formulated antigen binding protein and/or minimize the formation of particulates in the formulation and/or reduce adsorption. Exemplary surfactants include nonionic surfactants such as polysorbates (e.g. polysorbate 20 or polysorbate 80) or poloxamers (e.g. poloxamer 188). Exemplary concentrations of surfactant may range from about 0.001% to about 0.5%, or from about 0.005% to about 0.2%, or alternatively from about 0.004% to about 0.01% w/v.

[0223] In one embodiment, the formulation contains the above-identified agents (i.e. antigen binding protein, buffer, polyol and surfactant) and is essentially free of one or more preservatives, such as benzyl alcohol, phenol, m-cresol, chlorobutanol and benzethonium chloride. In another embodiment, a preservative may be included in the formulation, e.g., at concentrations ranging from about 0.1% to about 2%, or alternatively from about 0.5% to about 1%. One or more other pharmaceutically acceptable carriers, excipients or stabilizers such as those described in Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980) may be included in the formulation provided that they do not adversely affect the desired characteristics of the formulation.

[0224] Therapeutic formulations of the bispecific antigen binding protein are prepared for storage by mixing the bispecific antigen binding protein having the desired degree of purity with optional physiologically acceptable carriers, excipients or stabilizers (Remington's

Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980)), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients, or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid and methionine; preservatives (such as octadecyldimethylbenzyl ammonium chloride; hexamethonium chloride; benzalkonium chloride, benzethonium chloride; phenol, butyl or benzyl alcohol; alkyl parabens such as methyl or propyl paraben; catechol; resorcinol; cyclohexanol; 3-pentanol; and m-cresol); low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, histidine, arginine, or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, maltose, or dextrans; chelating agents such as EDTA; sugars such as sucrose, mannitol, trehalose or sorbitol; salt-forming counter-ions such as sodium; metal complexes (e.g., Zn-protein complexes); and/or non-ionic surfactants such as TWEEN™, PLURONICS™ or polyethylene glycol (PEG).

[0225] In one embodiment, a suitable formulation of the claimed invention contains an isotonic buffer such as a phosphate, acetate, or TRIS buffer in combination with a tonicity agent, such as a polyol, sorbitol, sucrose or sodium chloride, which tonicifies and stabilizes. One example of such a tonicity agent is 5% sorbitol or sucrose. In addition, the formulation could optionally include a surfactant at 0.01% to 0.02% wt/vol, for example, to prevent aggregation or improve stability. The pH of the formulation may range from 4.5-6.5 or 4.5 to 5.5. Other exemplary descriptions of pharmaceutical formulations for antigen binding proteins may be found in US 2003/0113316 and US patent no. 6,171,586, each incorporated herein by reference in its entirety.

[0226] The formulation herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. For example, it may be desirable to further provide an immunosuppressive agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

[0227] The active ingredients may also be entrapped in microcapsule prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsule and poly-(methylmethacrylate) microcapsule, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles and nanocapsules) or in macroemulsions. Such

techniques are disclosed in Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980).

[0228] Suspensions and crystal forms of antigen binding proteins are also contemplated. Methods to make suspensions and crystal forms are known to one of skill in the art.

[0229] The formulations to be used for *in vivo* administration must be sterile. The compositions of the invention may be sterilized by conventional, well known sterilization techniques. For example, sterilization is readily accomplished by filtration through sterile filtration membranes. The resulting solutions may be packaged for use or filtered under aseptic conditions and lyophilized, the lyophilized preparation being combined with a sterile solution prior to administration.

[0230] The process of freeze-drying is often employed to stabilize polypeptides for long-term storage, particularly when the polypeptide is relatively unstable in liquid compositions. A lyophilization cycle is usually composed of three steps: freezing, primary drying, and secondary drying (*see* Williams and Polli, Journal of Parenteral Science and Technology, Volume 38, Number 2, pages 48-59, 1984). In the freezing step, the solution is cooled until it is adequately frozen. Bulk water in the solution forms ice at this stage. The ice sublimates in the primary drying stage, which is conducted by reducing chamber pressure below the vapor pressure of the ice, using a vacuum. Finally, sorbed or bound water is removed at the secondary drying stage under reduced chamber pressure and an elevated shelf temperature. The process produces a material known as a lyophilized cake. Thereafter the cake can be reconstituted prior to use.

[0231] The standard reconstitution practice for lyophilized material is to add back a volume of pure water (typically equivalent to the volume removed during lyophilization), although dilute solutions of antibacterial agents are sometimes used in the production of pharmaceuticals for parenteral administration (*see* Chen, Drug Development and Industrial Pharmacy, Volume 18: 1311-1354, 1992).

[0232] Excipients have been noted in some cases to act as stabilizers for freeze-dried products (*see* Carpenter *et al.*, Volume 74: 225-239, 1991). For example, known excipients include polyols (including mannitol, sorbitol and glycerol); sugars (including glucose and sucrose); and amino acids (including alanine, glycine and glutamic acid).

[0233] In addition, polyols and sugars are also often used to protect polypeptides from freezing and drying-induced damage and to enhance the stability during storage in the dried state. In general, sugars, in particular disaccharides, are effective in both the freeze-drying

process and during storage. Other classes of molecules, including mono- and di-saccharides and polymers such as PVP, have also been reported as stabilizers of lyophilized products.

[0234] For injection, the pharmaceutical formulation and/or medicament may be a powder suitable for reconstitution with an appropriate solution as described above. Examples of these include, but are not limited to, freeze dried, rotary dried or spray dried powders, amorphous powders, granules, precipitates, or particulates. For injection, the formulations may optionally contain stabilizers, pH modifiers, surfactants, bioavailability modifiers and combinations of these.

[0235] Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the bispecific antigen binding protein, which matrices are in the form of shaped articles, e.g., films, or microcapsule. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Patent No. 3,773,919), copolymers of L-glutamic acid and γ ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the Lupron DepotTM (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods. When encapsulated polypeptides remain in the body for a long time, they may denature or aggregate as a result of exposure to moisture at 37°C, resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered to be intermolecular S-S bond formation through thio-disulfide interchange, stabilization may be achieved by modifying sulfhydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

[0236] The formulations of the invention may be designed to be short-acting, fast-releasing, long-acting, or sustained-releasing as described herein. Thus, the pharmaceutical formulations may also be formulated for controlled release or for slow release.

[0237] Specific dosages may be adjusted depending on conditions of disease, the age, body weight, general health conditions, sex, and diet of the subject, dose intervals, administration routes, excretion rate, and combinations of drugs. Any of the above dosage forms containing

effective amounts are well within the bounds of routine experimentation and therefore, well within the scope of the instant invention.

[0238] The bispecific antigen binding protein is administered by any suitable means, including parenteral, subcutaneous, intraperitoneal, intrapulmonary, and intranasal, and, if desired for local treatment, intralesional administration. Parenteral infusions include intravenous, intraarterial, intraperitoneal, intramuscular, intradermal or subcutaneous administration. In addition, the bispecific antigen binding protein is suitably administered by pulse infusion, particularly with declining doses of the antigen binding protein. In one embodiment the dosing is given by injections, intravenous or subcutaneous injections, depending in part on whether the administration is brief or chronic. Other administration methods are contemplated, including topical, particularly transdermal, transmucosal, rectal, oral or local administration e.g. through a catheter placed close to the desired site. In one embodiment, the antigen binding protein of the invention is administered intravenously in a physiological solution at a dose ranging between 0.01 mg/kg to 100 mg/kg at a frequency ranging from daily to weekly to monthly (e.g. every day, every other day, every third day, or 2, 3, 4, 5, or 6 times per week), a dose ranging from 0.1 to 45 mg/kg, 0.1 to 15 mg/kg or 0.1 to 10 mg/kg at a frequency of once per week, once every two weeks, or once a month.

[0239] As used herein, the term “treating” or “treatment” is an intervention performed with the intention of preventing the development or altering the pathology of a disorder. Accordingly, “treatment” refers to both therapeutic treatment and prophylactic or preventative measures. Those in need of treatment include those already diagnosed with or suffering from the disorder or condition as well as those in which the disorder or condition is to be prevented. “Treatment” includes any indicia of success in the amelioration of an injury, pathology or condition, including any objective or subjective parameter such as abatement, remission, diminishing of symptoms, or making the injury, pathology or condition more tolerable to the patient, slowing in the rate of degeneration or decline, making the final point of degeneration less debilitating, or improving a patient’s physical or mental well-being. The treatment or amelioration of symptoms can be based on objective or subjective parameters, including the results of a physical examination, self-reporting by a patient, neuropsychiatric exams, and/or a psychiatric evaluation.

[0240] The bispecific antigen binding proteins of the invention are useful for detecting target antigen(s) in biological samples and identification of cells or tissues that express the target antigen(s).

[0241] The bispecific antigen binding proteins described herein can be used for diagnostic purposes to detect, diagnose, or monitor diseases and/or conditions associated with the target antigen(s). Also provided are methods for the detection of the presence of the target antigen(s) in a sample using classical immunohistological methods known to those of skill in the art (e.g., Tijssen, 1993, Practice and Theory of Enzyme Immunoassays, Vol 15 (Eds R.H. Burdon and P.H. van Knippenberg, Elsevier, Amsterdam); Zola, 1987, Monoclonal Antibodies: A Manual of Techniques, pp. 147-158 (CRC Press, Inc.); Jalkanen et al., 1985, J. Cell. Biol. 101:976-985; Jalkanen et al., 1987, J. Cell Biol. 105:3087-3096). The detection of either target can be performed *in vivo* or *in vitro*.

[0242] Diagnostic applications provided herein include use of the antigen binding proteins to detect expression of target antigen(s). Examples of methods useful in the detection of the presence of the receptor include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA).

[0243] For diagnostic applications, the antigen binding protein typically will be labeled with a detectable labeling group. Suitable labeling groups include, but are not limited to, the following: radioisotopes or radionuclides (e.g., ^3H , ^{14}C , ^{15}N , ^{35}S , ^{90}Y , ^{99}Tc , ^{111}In , ^{125}I , ^{131}I), fluorescent groups (e.g., FITC, rhodamine, lanthanide phosphors), enzymatic groups (e.g., horseradish peroxidase, β -galactosidase, luciferase, alkaline phosphatase), chemiluminescent groups, biotinyl groups, or predetermined polypeptide epitopes recognized by a secondary reporter (e.g., leucine zipper pair sequences, binding sites for secondary antibodies, metal binding domains, epitope tags). In some embodiments, the labeling group is coupled to the antigen binding protein via spacer arms of various lengths to reduce potential steric hindrance. Various methods for labeling proteins are known in the art and may be used.

[0244] In another embodiment, the bispecific antigen binding protein described herein can be used to identify a cell or cells that express target antigen(s). In a specific embodiment, the antigen binding protein is labeled with a labeling group and the binding of the labeled antigen binding protein to target antigen(s) is detected. In a further specific embodiment, the binding of the antigen binding protein to target antigen(s) is detected *in vivo*. In a further specific embodiment, the bispecific antigen binding protein is isolated and measured using techniques known in the art. See, for example, Harlow and Lane, 1988, Antibodies: A Laboratory Manual, New York: Cold Spring Harbor (ed. 1991 and periodic supplements); John E. Coligan, ed., 1993, Current Protocols In Immunology New York: John Wiley & Sons.

[0245] Examples

[0246] Bispecific antigen binding proteins were prepared with a subset of the anti-TNF α and anti-TL1A antibodies. In some embodiments of this IgG-Fab format, a polypeptide comprising a VH-CH1 domain from a second antibody is fused through a peptide linker to the carboxyl- terminus of the heavy chain of a first antibody to form a modified heavy chain. A polypeptide comprising the remaining domains of the Fab fragment from the first antibody (i.e. a VL-CL domain) is co-expressed with the light chain of the first antibody and the modified heavy chain to produce the complete molecule. Assembly of the full molecule creates a tetravalent binding protein having two antigen binding domains against a first antigen located on the amino terminal side of a dimerized immunoglobulin Fc region and two antigen binding domains against a second antigen located on the carboxyl terminal side of the dimerized Fc region.

[0247] The TNF α /TL1A IgG-Fab consists of two antigen binding domains, one directed against TNF α and the other against TL1A. The DNA molecules encoding TNF α /TL1A IgG-Fab molecules contain fragments encoding an anti- TNF α (or anti- TL1A) antibody light chain, an anti- TNF α (or anti-TL1A) antibody heavy chain in which the C-terminus is fused to (i) an anti-TL1A (or anti- TNF α) antibody light chain or (ii) an anti-TL1A (or anti-TNF α) Fd (VH-CH1), and a third polypeptide comprising the other half of the Fab fragment to complete the carboxy-terminal binding domain (e.g. (i) an anti-TL1A (or anti- TNF α) Fd or (ii) an anti-TL1A (or anti- TNF α) antibody light chain. The IgG-Fab bispecific molecules contain charge pair mutations introduced into CH1 and CL domains of each Fab region (Fab 1 and Fab 2 as illustrated in Figure 3). The charge pairs are designed to allow preferential assembly of anti-TNFAR light chain/VHCH1(Fd) pair and anti-TL1A light chain/VHCH1 (Fd) pair. As an additional approach to promote correct pairing of the light chain/VHCH1 (Fd) pair, for a subset of the IgG-Fab molecules generated, the CL and CH1 regions in the carboxyl-terminal Fab (i.e. Fab 2) were swapped such that the polypeptide fused to the carboxyl-terminal region of the heavy chain of the second antibody comprised VL and CH1 regions from the first antibody and the second polypeptide comprised VH and CL regions from the first antibody. See molecules listed in Tables 4 and 6. The DNA molecules were generated by synthesized gBlocks and cloned into the pTT5.1 vector. These expression vectors were used to transfect and express the TNF α /TL1A bispecific molecules in human 293-6E cells. 144 different IgG-Fab bispecific molecules were generated. The full sequences for each molecule are set forth in Table 4.

[0248] The IgG-Fab molecules were purified using affinity captured by MabSelect SuRe chromatography (GE Life Sciences, Piscataway, NJ) using a Large Format Autosampler

(LFAS, Amgen, Inc., Thousand Oaks, CA). Clarified, conditioned media was loaded onto a 1 mL HiTrap MabSelect SuRe column (GE Life Sciences, Piscataway, NJ) equilibrated with Dulbecco's phosphate buffered saline without divalent cations (D-PBS, Life Technologies, Grand Island, NY). MabSelect columns were washed with 8 column volumes of D-PBS and eluted with 100 mM acetic acid, pH 3.6. When protein A eluates had an absorbance above 5 mAU at 280 nm, the eluent was directly loaded onto a HiTrap Desalting column (GE Life Sciences, Piscataway, NJ) and developed with 1.2 column volumes of 10 mM sodium acetate, 150 mM NaCl, pH 5.0. When desalting eluates had an absorbance above 3 mAU at 280 nm, sample collection was triggered and fractions were collected in 96-well deepwell blocks to a maximum of 2 mL each. Sample purity was determined by Caliper LabChip analysis under reducing (with 2% 2-mercaptoethanol) and non-reducing (with 25 mM iodoacetamide) conditions. Analytical SEC was carried out using a Zenix-C SEC-300 column (Sepax Technologies, Newark, DE) with an isocratic elution in 50 mM sodium phosphate, 250 mM NaCl, pH 6.9 over 8'.

[0249] The IgG-Fab molecules were tested for their expressability (titer and recovery) and activity. The results are shown in Figures 17-23 and in Table 6.

[0250] TL1A activity assay was performed using TF-1 NF- κ B reporter cell line. In brief, 30 ng/ml (EC90) of human or cynomolgus monkey TL1A was incubated with 10^4 TF-1 NF- κ B reporter cells in the presence of serially diluted anti-TL1A antibodies or TL1A/TNF- α bispecific molecules in 96-well plate at 37 °C overnight. Each well was supplemented with 50 μ l of Steady-glo Luciferase testing solution (Promega). Plate was covered and incubated while shaking for 10 minutes. Luciferase activity was analyzed by microbeta reader.

[0251] TNF α activity assay was performed using TF-1 NF- κ B reporter cell line. In brief, 1 ng/ml (EC90) of human or cynomolgus monkey TNF- α was incubated with 10^4 TF-1 NF- κ B reporter cells in the presence of a serially diluted anti-TNF- α antibodies or TL1A/TNF α bispecific molecules in 96-well plate at 37 °C overnight. 50 μ l of Steady-glo Luciferase testing solution (Promega) was added to each well. Plate was covered and incubated while shaking for 10 minutes. Luciferase activity was analyzed by microbeta reader.

Table 4 – Sequence Listing

iPS	Ab	Type	
1PS: 376597	001_Adalimumab_IgG.001_3B3v2_VH_CH1 (S183E)	NA	GATATCCAAATGACA CAATCACCATCGTCG CTTTCAGCGTCTGTT GGCGACCGTGTGACG ATTACCTGTCGCGG TCCAGGGAATCCGG AATTACCTCGCATGG TATCAGCAAAAACCC GGAAAAGCACCGAAG CTCCTGATCTATGCC GCCTCGACTCTTCAG AGTGGTGTCCTCGTCG AGGTTTAGCGGGTCC GGGTACGGTACGGAC TTTACTCTCACAAAT TCCAGCCTGCAGCCC GAAGATGTAGCTACC TATTACTGCCAGAGA TACAACCGAGCCCT TACACATTCGGACAA GGGACAAAAGTCGAG ATCAAGCGTACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGAAC TGCC TCTGTTGTGTGCC TG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCCGAG GAGAGTGTACACAGAG CAGGACAGCAAGGAC
			GAAATTGTGTTGACG CAGTCTCCAGGCACC CTGTCTTTGTCTCCA GGGAAAAGAGCCACC CTCTCCTGCAGGGCC AGTCAGAGTGTTAGA AGCAGTTACTTAGCC TGGTACCAGCAGAAA CCTGGCCAGGCTCCC AGGCTCCTCATCTAT GGTGCA TC CAGCAGG GCCACTGGCATCCCA GACAGGTTCA GTGGC AGTGGTCTGGGACA GACTTCACTCTCACC ATCAGCAGACTGGAG CCTGAAGATTTTGCA GTGTA TTA CTGTCAG CAGTATGGTAGCTCA CCTACCTTCGGCCAA GGACACGACTGGAG ATTAACGAACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGTACCGCC TCTGTTGTGTGCC TG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCCGAG GAGAGTGTACACAGAG CAGGACAGCAAGGAC
			GAGGTACAAC TGGTGGAATCAGGTGGAGGTTTGGTGCA GCCGGGAG ATCGCTCAGGCTTAGCTGTGCGGCATCGGGGTTTACTTTCGATGATT ATCGGATGCAT TGGGTCCGGCAAGCGCTGAAAAGGGCTCGAGTGG GTTTCCGCCATTACGTGGAATAGCGGACACATCGATTATGCAGACAG TGTGGAGGCAGATTCACAATCTCAGAGACAATGCTAAGAACAGCC TGTA CTTT CAGATGAAC TCACTTTCGCGCGGAAGATACCGCCGTATAC TACTGCGCCAAAGTCTCCTACTTGTCTACAGCTTTCGTGCTCGACTA TTGGGTCAAGGAACGTTGGTCA CCGTCTCTAGTGCC TCCACCAAGG GCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGACCTCTTGGG GGCACAGCGGCCCTGGGCTGCC TGGTCAAGGACTACTTCCCCGAACC GGTGACGGTGTCTGTGGAAC TCA GGGCCCTGACCAGCGGCGTGCACA CCTTCCCCGGCTGTCTTACAGTCTCTCAGGACTCTACTCCCTCAAAAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG CAACGTGAATCA CAAGCCCCAGCAACACCAAGGTGGACAAGAAA GTTG AGCCCAAAATCTTGTGACAAAAC TCA CACATGCCACCGTGCCCCAGCA CCTGAACTCCTGGGGGACCGTCAGTCTTCTCTCTTCCCCCCAAAACC CAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGG TGGTGACGTGAGCCACGAAGACCCCTGAGGTC AAGTTC AACTGGTAC GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACC GTTGTGT CAGCGTCTCTCACCGTCTCTGC ACCAGACTGGCTGAATGGCAAGGAGTACAAGTGC AAGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAAGG GCAGCCCCGAGAAACCA CAGGTGTACACCCCTGCCCCCATCCCCGGAGG AGATGACCAAGAAC CAGGTCA GCCCTGACCTGCC TGGTCAAAGGCTTC TATCC CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA GAA CAACTACAAGACCA CGCCTCCCGTGTGCTGGACTCCGACGGCTCCT TCTTCCCTCTATAGCAAAGCTCACCGTGGACA AAGACAGGTGGCAGCAG GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGACCTCTCCCTGTCTCCGGGTGGTGGCGGATCGG GAGGTGGCGGATCC CAGGTGCAGTTACAGCAGTCGGGCGCAGGACTG TTGAAGCCTTCGGAGACCC TGTCCCTCACCTGCGCTGTCCA TGGTGG GTCTTTCAGTGGTTACTACTGGAAC TGGATTTCGCCAGCCACCAGGGA AGGGCTAGAGTGGATTGGGAAATCAATCATGTCTGGAAACACCAAC TACAACCCGTCCCTCAAGAGTCGAGTCACCATATCATTAGACACGTC

			AGCACCTACAGCCTC GAAAGCACCCCTGACG CTGAGCAAAAGCAGAC TACGAGAAAACACAAA GTCACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	AGCACCTACAGCCTC AAGAGCACCCCTGACG CTGAGCAAAAGCAGAC TACGAGAAAACACAAA GTCACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	CAAGAACCAGTTCTCCCTGACGCTGACCTCTGTGACCGCCGCGGACA CGGCTGTGTATTACTGTGCGAGAGGATATTGTAGAAGTACCACCTGC TACTTTGACTACTGGGCCAGGAACCCCTAGTACCGTCTCCTCAGC CTCCACCAAGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGA GCACCTCTGGGGCACAGGCCCCCTGGGCTGCCTGTTCAAGGACTAC TTCCCCGAACCGGTGACGGTGTCTGTGAACTCAGGCGCCCTGACCCAG CGGCTGCACACCTTCCCCGGCTGTCTTACAGTCTCAGGACTCTACT CCCTCGAGAGCGTGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAG ACCTACATCTGCAACGTGAATCACAAAGCCCAGCAACACCAAGGTGGA CAAGAAAGTTGAGCCCCAAATCTTGT
			SEQ ID NO:1	SEQ ID NO:2	SEQ ID NO:3
AA			DIQMTQSPSSLSASV GDRVITITCRASQ GIR NYLAWYQQKPGKAPK LLIYAASTLQSGVPS RFSGSGGTDFTLTI SSLQPEDVATYYCQR YNRAPYTFGQGTKVE IKRTVAAPSVFI FPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLESTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGE C	EIVLTQSPGTL LSLP GERATLSCRASQSVR SSYLAWYQQKPGQAP RLLIYGASSRATGIP DRFSGSGGTDFTLT ISRLEPEDFAVYYCQ QYGS SPTFGQGRLE IKRTVAAPSVFI FPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLKSTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGE C	EVQLVESGGGLVQPGRSLRLS CAASGFTFDDYAMHWVRQAPGKGLEW VSAITWNSGHIDYADSV EGRFTISRDNAKNSLYLQMNSLRAEDTAVY YCAKVSYLSTASSLDYWGQGT LVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLKS VVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQ YGSTRYCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQ VYITLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMEALHNHYTQKSLSLSPGSGSGGGSQVQLQQSGAGL LKPSETLSLTCAVHGGSFSGY YWNWIRQPPGKGLEWIGEINHAGNTN YNPSLKSRTVISLDTSKNQFSLT LTVSVAADTAVVYCARGYCRSTTC YFDYWGQGT LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLESVVTVPS SSLGTQ TYICNVNHKPSNTKVDKKVEPKSC
			SEQ ID NO:4	SEQ ID NO:5	SEQ ID NO:6
NA			GATATCCAAAATGACA CAATCACCATCGTCG CTTTCAGCGTCTGTT GGCAGCCGTGTGACG ATTACCTGTCGCGCG TCCCAGGGAATCCGG AATTACCTCGCATGG TATCAGCAAAAACCC GGAAAAGCACCCGAAG CTCCTGATCTATGCC	GACATCCAGATGACC CAGTCTCCATCCTCC CTGTCTGCATCTGTA GGAGACAGAGTCACC ATCACTTGCCGGGCA AGTCAGAGCATTAAC AACTATTAAATTGG TATCAGCAGAGACCA GGGAAAGCCCCCTAAG CTCCTGATCTATGCT	GAGGTACAAC TGGTGGAATCAGGTGGAGGTTTGGTGACGCCGGGAG ATCGCTCAGGCTTAGCTGTGCGGCATCGGGGTTTACTTTCGATGATT ATGCGATGCATTGGGTCCGGCAAGCGCCTGGAAAAGGGCTCGAGTGG GTTTCCGCCATTACGTGGAATAGCGGACACATCGATTATGCAGACAG TGTGGAGGGCAGATTCACAATCTCACGAGACAAATGCTAAGAACAGCC TGTA CTTCAGATGAATCACTCACTTCGCGCGGAAGATACCGCCGTATAC TACTGCGCCAAAGTCTCCTACTTGTCTACAGCTTCGTCGCTCGACTA TTGGGGTCAAGGAACGTTGGTCACCGTCTCTAGTGCCTCCACCAAGG GCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGG GGCACAGCGGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCCGAAAC

			NYLAWYQQKPGKAPK LLIYAASTLQSGVPS RFSGSGGTDFTLTI SSLQPEDVATYYCQR YNRAPYTFGQGTKVE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSYSLESTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEN	NYLNWYQQRP GKAPK LLIYAASSLQSGVPS RFSGSGGTDFTLTI SSLQPEDFATYYCQQ SYSTPRTFGQGTKLE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSYSLKSTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEN	SEQ ID NO:10 GATA TCCAAATGACA CAATCACCATCGTCG CTTT CAGCGTCTGTT GGCGACCGTGTGACG ATTACCTGTCGCGCG TCCCAGGGAATCCGG AATTACCTCGCATGG TATCAGCAAAAACCC GGAAAAGCACCCGAAG CTCCTGATCTATGCC GCCTCGACTCTTCAG AGTGGTGTGCCGTGCG AGGTTTAGCGGGTCC GGGTCAGGTACGGAC TTTACTCTCACAATT TCCAGCCTGCAGCCC GAAGATGTAGCTACC TATTACTGCCAGAGA TACAACCGAGCGCCT TACACATTCCGACAA GGGACAAAAGTCGAG ATCAAGCGTACGGTG GCTGCACCATCTGTC	003_Ada1imumab_Igg.001_23B3_VH4_VH_CH1 (S1 83E)	1PS: 376605
			SEQ ID NO:10 GATA TCCAAATGACA CAATCACCATCGTCG CTTT CAGCGTCTGTT GGCGACCGTGTGACG ATTACCTGTCGCGCG TCCCAGGGAATCCGG AATTACCTCGCATGG TATCAGCAAAAACCC GGAAAAGCACCCGAAG CTCCTGATCTATGCC GCCTCGACTCTTCAG AGTGGTGTGCCGTGCG AGGTTTAGCGGGTCC GGGTCAGGTACGGAC TTTACTCTCACAATT TCCAGCCTGCAGCCC GAAGATGTAGCTACC TATTACTGCCAGAGA TACAACCGAGCGCCT TACACATTCCGACAA GGGACAAAAGTCGAG ATCAAGCGTACGGTG GCTGCACCATCTGTC	SEQ ID NO:11 GACATCCAGATGACC CAGTCTCCAAGCTCC CTGTCTGCGTCTGTG GGCGATAGGGTCACC ATCACTTG CAGGTCC AGCCAGAGTGTGTTA TACAGCTCCAACAAT AAGAACTACTTAGTT TGGTACCAGCAGAAA CCAGGAAAAGTTCCCT AAACTGCTCATTTAC TGGGCATCTACCCGG GAATCCGGGGTCCCT AGTCGATT CAGTGGC AGCGGGTCTGGGACA GATTTCACTCTCACC ATCAGCAGCCTGCAG CCTGAAGATGTGGCA ACTTATTACTGT CAG CAATATTATAAGACT CCTCTCACTTTCGGC GGAGGGACCAAGGTG GAGATCAAACGAACG	SEQ ID NO:12 GAGGTACAAC TGGTGGAATCAGGTGGAGGTTTGGTGCAGCCGGGAG ATCGCTCAGGCTTAGCTGTGCGGCATCGGGGTTTACTTTCGATGATT ATGCGGATGCATTGGGTCCGGCAAGCGCTGGA AAAAGGGCTCGAGTGG GTTTCCGCCATTACGTGGAATAGCGGACACATCGATTATGCAGACAG TGTGGAGGGCAGATTCACAATCTCACGAGACAAATGCTAAGAACAGCC TGTA CCTTCAGATGAAC TCACTCACTTCGCGGGAAGATACCGCCGTATAC TACTGCGCCAAAAGTCTCCTACTTGTCTACAGCTTCGTGCTCGACTA TTGGGGTCAAGGAAACGTTGGTCACCGTCTCTAGTGCCCTCCACCAAGG GCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGG GGCACAGCGGCCCTGGGCTGCCGTGGTCAAGGACTACTTCCCCGAACC GGTGACGGTGTCGTGGAAC TCAAGCCTCAGCGCCCTGACCAGCGCGTG CACA CCTTCCCGGTGTCTACAGTCTCTCAGGACTCTACTCCTCAA AAGC GTG GTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG CAACGTGAATCACAAGCCAGCAACACCAAGGTGGACAGAAAAGTTG AGCCCCAAATCTTGTGACAAA AACTCACACATGCCACCCGTGCCAGCA CCTGAAC TCC TGGGGGACCGTCAGTCTTCCTCTTCCCCCAAACC CAAGGACACCC TCA TGATCTCCCGGACCCCTGAGGTCA CATGCGTGG TGGTG GACGTGAGCCACGAA GACCCCTGAGGTCAAGTCAACTGGTAC GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAAGCCGTGTGAGGA GCAGTACGGCAGCAGTACCGTTGTGT CAGCGTCC TCA CCGTCTCTGC ACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGG GCAGCCCCGAGAACCA CAGGTGTACACCTTGCCCCCATCCCCGGAGG		

		TTCAATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGAAGTGC TCTGTTGTGTGCCTG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCCGAG GAGAGTGTACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC GAAAGCACCCCTGACG CTGAGCAAAAGCAGAC TACGAGAAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGAGAGTGT	GTGGCTGCACCATCT GTCTTCACTTCCCG CCATCTGATGAGCAG TTGAAAATCTGGTACC GCCTCTGTTGTGTC CTGCTGAATAACTTC TATCCCAGAGAGGCC AAAGTACAGTGGAAG GTGGATAACGCCCTC CAATCGGGTAAC TTC CAGGAGAGTGT CACA GAGCAGGACAGCAAG GACAGCACCTACAGC CTCAAGAGCACCC TG ACGCTGAGCAAAAGCA GACTACGAGAAAACAC AAAGTCTACGCC TGC GAAGTCACCCATCAG GGCCTGAGCTCGCCC GTCACAAAAGAGCTTC AACAGGGGAGAGTGT	AGATGACCAAGAAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTC TATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA GAACAACTACAAGACCACGCCCTCCCGTGTGGACTCCGACGGCTCCT TCTTCTCTATAGCAAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGACCTCTCCCTGTCTCCGGTGGTGGCGGATCGG GAGGTGGCGGATCCCAGGTACAGTTGCAGGAGTCAGGTCAGGACTG GTGAAGCCCTCGGAGACCCTCTCACTCACCTGTACCATCTCCGGGGA CAGTGTCTTACCAACAGTGTTCCTTGGAAC TGGA TTAGGCAGCCCC CAGGGAAGGCCCTTGAGTGATAGGAAGGACATACACAGTCCAAG TGGTATAATGATTA TGCAGTTTCTCTGAAAAAGTCGAGTAACCATCAG CCCAGACACATCCAAGAACCAAGTTTCTCTGAAAGCTGAAGCTCTGTGA CTGCCGCGACACGGCTGTGTATTACTGTGCAAGAGAGGATGGGGAT AGTACTACCGCTACGGTATG GACGTCTGGGGCCAAAGGACCACGGT CACCGTCTCCTCAGCCTCCACCAAGGCCCATCGGTC TCCCCCTGG CACCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGC CTGGTCAAGGACTACTTCCCCGAAACCGGTGACGGTGTCTG TGGAACTC AGCGCCCTGACCAGCGCGGTGCACACCTTCCCGGCTGTCTCTACAGT CCTCAGGACTCTACTCCCTCGAGAGCGTGTGACCGTGCCTCCAGC AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAG CAACACCAAGGTGGACAAGAAAAGTTGAGCCCCAAATCTTGT
		SEQ ID NO:13	SEQ ID NO:14	SEQ ID NO:15
AA		DIQMTQSPSSLSASV GDRVITICRASQGIR NYLAWYQQKPGKAPK LLIYAASTLQSGVPS RFGSGSGTDFTLT I SSLQPEDVATYYCQR YNRAPYTFGQGTKVE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLESTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGE C	DIQMTQSPSSLSASV GDRVITICRSSQSVL YSSNNKNYLVWYQQK PGKVPKLLIYWASTR ESGVPSRFSGSGSGT DFTLTISSLQPEDVA TYYCQQYYKTPLTFG GGTKVEIKRTVAAPS VFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGNS QESVTEQDSKDSYS LKSTLTLSKADYEKH KVYACEVTHQGLSSP VTKSFNRGEC	EVQLVESGGGLVQPGPGRSLRLSCAASGFTFFDDYAMHWVRQAPGKGLEW VSAITWNSGHIDYADSV EGRFTISRDNAKNSLYLQMNSLRAEDTAVY YCAKVSYLESTASSLDYWGQGT LVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLKS VVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDNLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVY TLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTT PTPVLDSGSEFFLYSKLTVDKSRWQQ GNVFCSSVMHEALHNHYTQKSLSLSPGGGGSGGSQVQLQESGPG L VKPSETLSLTCTISGDSVSTNSVAWN WIRQPPGKGLEWIGRTYYRSK WYNDYAVSLKSRVTISPDT SKNQFSLKLSVTAADTAVYYCAREDDGD SYRYRGMDVWGQGT TTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSL ESVTVTPSS SLGTQTYICNVNHKPSNTKVDKKVEPKSC

			AGCTATCTGAGCCTG ACGCTTGAGCAGTGG AAGTCCACAGAAGC TACAGCTGCCAGGTC ACGCATGAAGGGAGC ACCGTGAGAAAGACA GTGGCCCCTACAGAA TGTTCA	CTGAGCAAAGCAGAC TACGAGAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	GGCCAGGGAACCCTAGTCACCGTCTCCTCAGCCTCCACCAAGGGCCC ATCGGTCTTCCCCCTGGCACCCCTCTCCAAGAGCACCTCTGGGGGCA CAGCGCCCTGGGTGCCCTGGTCAAGGACTACTTCCCCGAACCCGGTG ACGGTGTCTGTGAACTCAGGCGCCCTGACCAGGGCGTGACACACCTT CCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCGAGAGCGTGG TGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAAC GTGAATCACAAGCCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGT
			SEQ ID NO:19	SEQ ID NO:20	SEQ ID NO:21
AA			QSVLTQPPSVSGAPG QRVTISCTGSSSNIG AGYDVHWYQQFPGTA PKLLIQGNSNRPSGV PDRFSGSKSGTSASL AITGLQAEDEADYYC QSYDSSLSGSVFGGG TKLTVLGQPKAAPSV TLFPPSSEELQANKA TLVCLISDFYPGAVT VAWKADSSPVKAGVE TTTPSKQSNNKYAAE SYLSLTPEQWKSHRS YSCQVTHEGSTVEKT VAPTECS	EIVLTQSPGTLSLSP GERATLSCRASQSVR SSYLAWYQQKPGQAP RLLIYGASSRATGIP DRFSGSGGTDFTLT ISRLEPEDFAVYYCQ QYSSPTFGQGTGLE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLKSTLT LSKADYEEKHKVYACE VTHQGLSSPVTKSFN RGECL	EVQLVQSGAEVKKPESLIKISCKTSEYFTSYWIGWVRQMPGKGLEW MGI IYLGDS DTRYSPSFQGV TISADKSI STAYLQWSSLKASD TAMY YCARSNWGLDYGQGTLLVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLKSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPELLG GPSVFLFPPKPKD TLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSYRCVS VLTVLHQDWLNGKEYKCKVSNKALP A PIEKTISKAKGQPREPQVY TLPSPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYK TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGGSGGGGQVQLQSSGAGLLK PSE TLSLTCAVHGGSFSGYYWNWIRQPPPGKGLEWIGE INHAGNTNYP SL KSRVTISLDTSKNQFSLT LTSVTAADTAVYICARGYCRSTTCYFDYW GQGTLLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSL ESVVTVPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSC
			SEQ ID NO:22	SEQ ID NO:23	SEQ ID NO:24
NA	005_VH_CH1 (S183E) 3.2_IgG.001_9C8	1PS: 376613	CAGTCTGTGCTGACG CAGCCGCCCTCAGTG TCTGGGGCCCCAGGG CAGAGGTCACCATC TCCTGCAC TGGGAGC AGTTCCAACATCGGG GCAGGTTATGATGTA CACTGGTACCAGCAG TTTCCAGGAACAGCC CCCCAACTCCTCATC CAAGGTAACAGCAAT CGGCCCTCAGGGGTC	GACATCCAGATGACC CAGTCTCCATCCTCC CTGTCTGCATCTGTA GGAGACAGAGTCACC ATCACTTGCCGGGCA AGTCAGAGCATTAAC AACTATTTAAATTGG TATCAGCAGAGACCA GGGAAAGCCCCCTAAG CTCCTGATCTATGCT GCATCCAGTTTGCAA AGTGGGGTCCCATCA	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAGCCCGGGA GTCTCTGAAGATCTCCTGTAA GACTTCTGAATACAGCTTTACCAGCT ACTGGATCGGCTGGGTGCCCCAGATGCCCGGGAAGGCCCTGGAGTGG ATGGGATCATCTATCTTGGTGACTCAGATACCAGATACAGCCCCTC CTTCCAAGGCCAGGTCA CCACTCTCAGCCGACAAGTCCATCAGTACC CCTACCTGCAGTGAGCAGCCTGAAGGCCCTCGGACACCGCCATGTAT TACTGTGCGAGAAAGTA ACTGGGTCTTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTCTCTAGTGCCCTCACCAAGGCCCATCGGTCTTCC CCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTG GGCTGCCCTGGTCAAGGACTACTTCCCCGAAACCGGTGACGGTGTCTG GAACTCAGCGCCCTGAC CAGCGGCGTGACACACCTTCCCGGCTGTCC TACAGTCCCTCAGGACTCTACTCCCTCAAAAAGCGTGTGACCGTGCCC

		CCTGACCGATTCTCT GGCTCCAAGTCTGGC ACCTCAGCCTCCCTG GCCATCACTGGGCTC CAGGCTGAGGATGAG GCTGATTATTACTGC CAGTCCTATGACAGC AGCCTGAGTGGTTCG GTGTTGGCGGAGGG ACCAAGCTGACCGTC CTAGGTCAGCCCCAAG GCTGCCCCCTCGGTC ACTCTGTTCCCGCCC TCCTCTGAGGAGCTT CAAGCCAACAAGGCC ACACTGGTGTGTCTC ATAAGTGACTTCTAC CCGGAGCCCGTGACA GTGGCCTGGAAGGCA GATAGCAGCCCGTC AAGCGGGAGTGGAG ACCACCACACCCCTCC AAACAAAGCAACAAC AAGTACGGGCGCGAG AGCTATCTGAGCCTG ACGCCTGAGCAGTGG AAGTCCCACAGAAGC TACAGCTGCCAGGTC ACGCATGAAGGGAGC ACCGTGGAAGAACA GTGGCCCTTACAGAA TGTTCA	AGGTTCAGTGGCAGT GGATCTGGGACAGAT TTCACTCTACCCATC AGCAGTCTGCAACCT GAAGATTTTGCAACT TACTACTGTCAACAG AGTTACAGTACCCCT CGGACGTTGCGCCAA GGACCAAGCTGGAA ATCAAAACGAACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGTACCGCC TCTGTTGTGTGCCTG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAAGTG GATAACGCCCTCCAA TCGGGTAAC TCCCAG GAGAGTGTCA CAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC AAGAGCACCCCTGACG CTGAGCAAAAGCAGAC TACGAGAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAA GCCAGCAACACCAAGGTGGACAAAGAAAGTTGAGCCCCAAATCTTGTG ACAAAACTCACACATGCCCACCGTGCCAGACACCTGAACTCCTGGGG GGACCGTCAGTCTTCTCTTCCCCCCCCAAAAACCAAGGACACCCCTCAT GATCTCCGGACCCCTGAGGTACATGCGTGGTGGTGACGTGAGCC ACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAG GTGCATAATGCCAAGACAAAGCCGTGTGAGGAGCAGTACGGCAGCAC GTACCGTTGTGTACGCTCCTCACCGTCTGACCCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCC CCCATCGAGAAACCATCTCCAAGCCAAAAGGCAGCCCCGAGAACC ACAGGTGTACACCTGCCCCCATCCCCGGAGGAGATGACCAAGAAACC AGGTCAGCCTGACCTGCCCTGGTCAAAGGCTTCTATCCCAGCGACATC GCCGTGAGTGGGAGAGCAATGGGAGCCGGAGAAACAATA CAAAGAC CACGCCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCA AGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGAACGTCTTCTCA TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAAGAGAG CCTCTCCCTGTCTCCGGGTGGTGGCGGATCGGGAGTGGCGGATCCC AGGTGCAGCTGCAGAGTCTGGGCCAGGACTGGTGAAGCC TTCGGAG ACCTGTCTCCCTCACCTGCAC TGTCTCTGGTGGCTCCA TCAGTAGTTA CTTCTGGAGCTGGATTCTGGCAGCCCCCAGGTAAGGACTGGAGTGGA TTGGCTATATCTATTACAGTGGGCAGACCAATAACACCCCTCCCTC AAGAGTCGAGTCACCATATCAATAGACACACGTCCAAGAACCA GTTCTC CCTGAAGCTGAGCTCTGTGACCGCTGCGGACACGGCCGTGATTACT GTGCGAGAGAAAAC TGGGAGCTACTACGGCTTTGACTACTGGGGCCAG GGAACCTGGTCACCGTCTCCTCAGCCTCCACCAAGGCCCATCGGT CTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG CCCTGGGCTGCC TGGTCAAGGACTACTTCCCCGAACCGGTGACGGTG TCGTGGAAC TCAAGCGCCCTGACCAAGCGGCTGCACACCTTCCC GGC TGTCC TACAGTCC TCAAGGACTCTACTCCCTCGAGAGCGTGGTGACCG TGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT CACAAAGCC CAGCAACACCAAGGTGGACAAAGAAAGTTGAGCCCCAAATC TTGT
		SEQ ID NO:25	SEQ ID NO:26	SEQ ID NO:27
	AA	QSVLTQPPSVSGAPG QRVTISCTGSSSNIG AGYDVHWYQQFPGTA PKLLIQGNSNRPSGV	DIQMTQSPSSLASV GDRV TITCRASQ SIN NYLNWYQQRPGKAPK LLIYAASSLQSGVPS	EVQLVQSGAEVKKPGESLKISKCTSEYSFTSYWIGWVRQMPKGLEW MGI IYLGDS DTRYSPSFQGV TISADKSI STAYLQWSSLKASDTAMY YCARSNWGLDYGQGT LVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLKSVVTVP

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		TCC TCTGAGGAGCTT CAAGCCAAACAAGCC ACACTGGTGTGTCTC ATAAGTGACTTCTAC CCGGAGCCCGTGACA GTGGCCTGGAAGGCA GATAGCAGCCCCGTC AAGCGGGAGTGGAG ACCAACACACCCCTCC AAACAAAGCAACAAC AAGTACGGGCCGAG AGCTATCTGAGCCTG ACGCCTGAGCAGTGG AAGTCCACAGAAAGC TACAGCTGCCAGGTC ACGCATGAAGGGAGC ACCGTGAGAAAGACA GTGGCCCCTACAGAA TGTTCA	CCATCTGATGAGCAG TTGAAATCTGGTACC GCC TCTGTTGTGTGC CTGCTGAATAACTTC TATCCAGAGAGGCC AAAGTACAGTGG AAG GTGGATAACGCCCTC CAATCGGGTA ACTCC CAGGAGAGTGT CACA GAGCAGGACAGCAAG GACAGCACCTACAGC CTCAAGAGCACCC TG ACGCTGAGCAAAGCA GACTACGAGAAACAC AAAGTCTACGCC TGC GAAGTCACCCCATCAG GGCCTGAGCTCGCCC GTCACAAAGAGCTTC AACAGGGGAGAGTGT	CACGCTCCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCA AGCTCACCGTGGAACAAGAGCAGGTGGCAGCAGGGAAACGTCTTCTCA TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAAGAG CCTCTCCCTGTCTCCGGGTGGTGGCGGATCGGGAGGTGGCGGATCCC AGGTACAGTTGCAGGAGTCAGTCCAGGACTGGTGAAGCCCTCGGAG ACCTCTCACTCACCTGTACCATCTCCGGGACAGTGTCTCTACCAA CAGTGTGCTTGAACTGGATTAGGCAGCCCCCAGGAAAGGCCTTG AGTGGATAGGAAGGACATACTACAGGTCCAAGTGGTATAATGATTAT GCAGTTTCTCTGAAAAGTCGAGTAACCATCAGCCCCAGACATCCAA GAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGCCGCGACACGG CTGTGATTACTGTGCAAGAGAGGATGGGGATAGCTACTACCGCTAC GGTATGGACGCTCTGGGCCAAAGGACCACCGTCACCGTCTCCTCAGC CTCCACCAAGGCCCATCGGTCTTCCCTGGCACCCCTCCTCCAAGA GCACCTCTGGGGCACAGCGGCCCTGGGCTGCC TGTCAAGGACTAC TTCCCCGAACCGGTGACGGTGTCTGTGAACTCAGGCGCCCTGACCAG CGCGTGCACACCTTCCCGGCTGTCTCTACAGTCTCAGGACTCTACT CCCTCGAGAGCGTGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAG ACCTACATCTGCAACGTGAATCACAAAGCCCAGCAACACCAAGGTGGA CAAGAAAGTTGAGCCCCAAATCTTGT
		SEQ ID NO: 31	SEQ ID NO: 32	SEQ ID NO: 33
AA		QSVLTQPPSVSGAPG QRVTISCTGSSSNIG AGYDVHWYQQFFGTA PKLLIQNSNRPSGV PDRFSGSKGTSASL AITGLQAEDEADYYC QSYDSSLSGSVFGGG TKLTVLGQPKAAPSV TLFPPSSEELQANKA TLVCLISDFYPGAVT VAWKADSSPVKAGVE TTTPSKQSNNKYAAE SYLSLTPEQWKSHRS YSCQVTHEGSTVEKT VAPTECS	DIQMTQSPSSLSASV GDRV TITCRSSQSVL YSSNNKNYLVWYQQK PGKVPKLLIYWASTR ESGVPSRFSGSGSGT DFTLTISSLQPEDVA TYYCQQYYKTPLTFG GGTKVEIKRTVAAPS VFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGNS QESVTEQDSKDS TYS LKSTLTLSKADYEKH KVYACEVTHQGLSSP VTKSFNRGEC	EVQLVQSGAEVKKPGESLKISCKTSEYFTSYWIGWVRQMPGKGLEW MGI IYLGSDSDTRYSPSFQGQVTI SADKSI STAYLQWSSLKASDTAMY YCARSNWGLDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLKSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPAPEL LG GPSVFLFPPKPKD TLMISRTPETCVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVY TLPSPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGSGSGGSQVQLQESGPGLVKPS E TLSLTCTISGDSVSTNSVAWNWIRQPPGKGLEWIGRTY YRSKWYNDY AVSLKSRVTISPDTSKNQFSLKLSVTAADTAVYYCAREDGDSYYRY GMDVWGQGT TVTVSSASTKGPSVFPLAPSSKSTSGTAAIGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLESVTVTPSSSLGTQ TYICNVNHKPSNTKVDKKVEPKSC
		SEQ ID NO: 34	SEQ ID NO: 35	SEQ ID NO: 36

1PS: 376621	007_3B3v2_IgG.001_Ada1Imumab_VH_CH1 (S183E)	NA	GAAATTGTGTTGACG CAGTCTCCAGGCACC CTGTCTTTGTCTCCA GGGAAAGAGCCACC CTCTCCTGCAGGGCC AGTCAGAGTGTTAGA AGCAGTTACTTAGCC TGGTACCAGCAGAAA CCTGGCCAGGCTCCC AGGCTCCTCATCTAT GGTGCAATCCAGCAGG GCCACTGGCATCCCA GACAGGTTCAGTGGC AGTGGGTCTGGGACA GACTTCACTCTCACC ATCAGCAGACTGGAG CCTGAAGATTTTGCA GTGTATTACTGTCTAG CAGTATGGTAGCTCA CCTACCTTCGGCCAA GGGACACGACTGGAG ATTAAACGAACGGTG GCTGCACCAATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGTACCGCC TCTGTTGTGTGCCTG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCCAG GAGAGTGTACACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC GAGAGCACCCCTGACG CTGAGCAAAAGCAGAC	GATATCCAAAATGACA CAATCACCATCGTCG CTTTCAGCGTCTGTT GGGACCCGTGTGACG ATTACCTGTCGCGCG TCCCAGGGAATCCGG AATTACCTCGCATGG TATCAGCAAAAACCC GGAANAAGCACCGAAG CTCCTGATCTATGCC GCCTCGACTCTTTCAG AGTGGTGTGCCGTGG AGGTTTAGCGGGTCC GGTTCAGGTACGGAC TTTACTCTCACAATT TCCAGCCTGCAGCCC GAAGATGTAGCTACC TATTACTGCCAGAGA TACAACCGAGCGCCT TACACATTCGGACAA GGGACAAAAGTCGAG ATCAAGCGTACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGAACCTGCC TCTGTTGTGTGCCTG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCCAG GAGAGTGTACACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC AAGAGCACCCCTGACG CTGAGCAAAAGCAGAC	CAGGTGCAGTTACAGCAGTCGGGGCGCAGGACTGTTGAAAGCCTTTCGGA GACCCGTCTCCCTCACCTGCGCTGTCCATGGTGGGTCTTTCAGTGGTT ACTACTGGAACCTGGATCCGCCAGCCACACAGGGAAGGGCTAGAGTGG ATTGGGGAAATCAATCATGTCTGGAACACCAACTACAACCCGTCCCT CAAGAGTCGAGTCACCATATCATATTAGACACGTCCAAGAACCAAGTTCT CCCTGACGCTGACCTCTGTGACCGCGCGGACACGGCTGTGTATTAC TGTGCGAGAGGATATTGTAGAAGTACCACCTGCTACTTTGACTACTG GGCCAGGGAACCTAGTCAACCGTCTCTCAGCCTCCACCAAGGGCC CATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGC ACAGCGGCCCTGGGCTGCCGTGGTCAAGGACTACTTCCCCGAACCGGT GACGGTGTCTGTGGAACCTCAGGGGCCCTGACCAGGGCGTGCAACCT TCCCCGCTGTCTACAGTCTCTCAGGACTCTACTCCCTCAAAAGCGTG GTGACCCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAA CGTGAATCACAAAGCCCAACAACACCAAGGTGGACAAGAAAGTTGAGC CCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCT GAACTCCTGGGGGACCGTCAGTCTTCTCTTCTTCCCCCAAAACCCAA GGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGG TGGACGTGAGCCACGAAGACCCCTGAGGTCAAAGTTCAACTGGTACGTG GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGTGTGAGGAGCA GTACGGCAGCACGTACCGTTGTGTCAAGCTCCTCACCGTCTGCACC AGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGTCTCCAACAAA GCCCTCCCAGCCCCCATCGAGAAAAACCATCTCCAAGCCAAAGGGCA GCCCCGAGAACCAAGGTGTACACCCCTGCCCCCATCCCGGAGGAGA TGACCAAGAACCAAGTTCAGCCTGACCTGCCCTGGTCAAAGGCTTCTAT CCCAGCAGCATCGCCGTGGAGTGGAGAGCAATGGCAGCCCGAGAA CAACTACAAGACCAAGCCCTCCCGTGTGCTGGACTCCGACGGCTCCTTCT TCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG AACGTCTTCTCATGTCTCCGTGATGCATGAGGCTCTGCACAACCACTA CACGCAGAAGAGCCCTCTCCCTGTCTCCGGGTGGTGGCGGATCGGGAG GTGGCGGATCCGAGGTACAACCTGGTGAATCAGGTGGAGGTTTGGTG CAGCCGGGAGATCGCTCAGGCTTAGCTGTCCGGCATCGGGGTTTAC TTTTCGATGATTATGCGATGCATTTGGGTCCGGCAAGCGCCTGGAAGAAG GGCTCGAGTGGGTTTCCGCCATTACGTGGAATAGCGGACACATCGAT TATGCAGACAGTGTGGAGGGCAGATTCACAATCTCACGAGACAAATGC TAAGAACAAGCCCTGTACCTTCAGATGAACCTCACTTCGCGCGGAAGATA CCGCCGTATACTACTGCGGCCAAAGTCTCCTACTTGTCTACAGCTTCG TCGCTCGACTATTGGGGTCAAGGAACGTTGGTCAACCGTCTCTAGTGC
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		TACGAGAAACACAAA GTCTACGCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	TACGAGAAACACAAA GTCTACGCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	CTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGA GCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC TTCCCCGAACCGGTGACGGTGTCTGTGAACCTCAGGCGCCCTGACCCAG CGGCTGCACACCTTCCCCGGCTGTCTACAGTCTCAGGACTCTACT CCCTCGAGAGCGTGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAG ACCTACATCTGCAACGTGAATCACAAAGCCCAGCAACACCAAGGTGGA CAAGAAAGTTGAGCCCCAAATCTTGT
		SEQ ID NO:37	SEQ ID NO:38	SEQ ID NO:39
AA		EIVLTQSPGTLISLSP GERATLSCRASQSVR SSYLAWYQQKPGQAP RLLIYGASSRATGIP DRFSGSGTDFTLT ISRLEPEDFAVYYCQ QYGSSTFFGQGTRLE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLESTLT LSKADYEKHKVYACE VTHQG LSSPVTKSFN RGEN	DIQMTQSPSSLSASV GDRVITITCRASQGIR NYLAWYQQKPGKAPK LLIYAASTLQSGVPS RFSGSGTDFTLTI SSLQPEDVATYYCQR YNRAPYTFGQGTKVE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLKSTLT LSKADYEKHKVYACE VTHQG LSSPVTKSFN RGEN	QVQLQQSGAGLLKPSSETLSLTCAVHGGSFSGYYWNWIRQPPGKGLEW IGEINHAGNTNYPNPSLKSRVTISLDTSKNQFSLTLTSVTAADTAVYY CARGYCRSTTCYFDYWGGQTLTVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSKSV VTVPSSSLGTQYICNVNHPKPSNTKVDKKVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGEVHNNAKTKPCEEQYGSYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMEALHNHYTQKSLSLSPGGSGGGSEVQLVESGGGLV QPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSAITWNSGHID YADSVTEGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAKVSYLSTAS SLDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLESVTVTPSSSLGTQ TYICNVNHPKPSNTKVDKKVEPKSC
		SEQ ID NO:40	SEQ ID NO:41	SEQ ID NO:42
		GAAATTGTGTTGACG CAGTCTCCAGGCACC CTGTCTTTGTCTCCA GGGAAAGAGCCACC CTCTCCTGCAGGGCC AGTCAGAGTGTTAGA AGCAGTTACTTAGCC TGGTACCAGCAGAAA CCTGGCCAGGCTCCC AGGCTCCTCATCTAT GGTGATCCAGCAGG GCCACTGGCATCCCA GACAGGTTCAGTGGC	CAGTCTGTGCTGACG CAGCCGCCCTCAGTG TCTGGGGCCCCAGGG CAGAGGGTCACCATC TCCTGCACTGGGAGC AGTTCCAACATCGGG GCAGGTTATGATGTA CACTGGTACCAGCAG TTTCCAGGAACAGCC CCCAAAC TCCTCATC CAAGGTAACAGCAAT CGGCCCTCAGGGGTC CCTGACCCGATTCTCT	CAGGTGCAGTTACAGCAGTCGGGGCGCAGGACTGTTGAAGCCTTCGGA GACCCGTGCCCTCACCTGCGCTGTCCATGGTGGTCCCTCAGTGGTT ACTACTGGAACTGGATCCGCCAGCCACAGGGAAGGGCTAGAGTGG ATTGGGGAATCAATCATGCTGGAACACCAACTACAACCCGTC CCT CAAGAGTCGAGTCACCATATCATTAGACACGTC CAAGAACAGTTCT CCCTGACGCTGACCTCTGTGACCGCGCGGACACGGCTGTGTATTAC TGTGCGAGAGGATAATTGTAAGAGTACCACCTGCTACTTTGACTACTG GGCCAGGGAACCTAGTCACCGTCTCCTCAGCCTCCACCAAGGGCC CATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGC ACAGCGCCCTGGGCTGCCGTGGTCAAGGACTACTTCCC GAACCGGT GACGGTGTCTGTGGAAC TCAGGCGCCCTGACCAGCGGCGTGACACCT TCCCGGCTGTCTACAGTCTCTCAGGACTCTACTCCCTCAAAAGCGTG GTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAA
	008 3B3v2 1gG.001 3.2 _VH_CH1 (S183E) _	1PS: 376625		

	AGTGGGTCTGGGACA GACTTCACTCTCACC ATCAGCAGACTGGAG CCTGAAGATTTTGCA GTGTATTACTGTCTAG CAGTATGGTAGCTCA CCTACCTTCGGCCAA GGGACACGACTGGAG ATTAAACGAACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGTACCGCC TCTGTTGTGTGCCCTG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCCAG GAGAGTGTACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC GAGAGCACCCCTGACG CTGAGCAAAGCAGAC TACGAGAAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	GGCTCCAAGTCTGGC ACCTCAGCCTCCCCTG GCCATCACTGGGCTC CAGGCTGAGGATGAG GCTGATTATTACTGC CAGTCCCTATGACAGC AGCCTGAGTGGTTCTG GTGTTCCGGCGGAGGG ACCAAGCTGACCGTC CTAGGTACGCCCAAG GCTGCCCTCCTCGGTC ACTCTGTTCCCAGCCC TCCTCTGAGGAGCTT CAAGCCAAACAAGGCC ACACTGGTGTGTCCTC ATAAGTGACTTCTAC CCGGGAGCCGTGACA GTGGCCTGGAAGGCA GATAGCAGCCCCGTC AAGCGGGAGTGGAG ACCACCAACCCCTCC AAACAAAGCAACAAC AAGTACGCGGCCAAG AGCTATCTGAGCCTG ACGCCTGAGCAGTGG AAGTCCCACAGAAGC TACAGCTGCCAGGTC ACGCATGAAGGGAGC ACCGTGAGAAAGACA GTGGCCCCCTACAGAA TGTTCA	CGTGAATCACAAAGCCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGC CCAAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCCAGCACCTT GAACTCCTGGGGACCGCTCAGTCTTCTCTTCCCCCCCCAAAACCCCAA GGACACCTCATGATCTCCCGGACCCCTGAGGTCAAGTTCAACTGGTACGTG TGACCGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTG GACGGCTGGAGGTGCATAATGCCAAGACAAAGCCGTGTGAGGAGCA GTACGGCAGCACGTACCGTTGTGTCTCAGCGTCTCACCGTCCCTGCACC AGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA GCCCTCCCAGCCCCCATCGAGAAAAACCATCTCCAAGCCAAAAGGGCA GCCCCGAGAACACAGGTGTACACCCCTGCCCTCCCATCCCGGAGGAGA TGACCAAGAACCAAGTCAAGCTGACCTGACCTGCCCTGGTCAAAGGCTTCTAT CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAA CAACTACAAGACCAACGCCCTCCCGTGTGCTGGACTCCGACGGCTCCTTCT TCCTCTATAGCAAAGCTCACCGTGGACAAGACAGCAGGTGGCAGCAGGGG AACGTCTTCTCATGTCTCCGTGATGCATGAGGCTCTGCACAACCACTA CACGCAAGAGCCCTCTCCCTGTCTCCGGGTGGTGGCGGATCGGGAG GTGGCGGATCCGAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAA AAGCCCCGGGAGTCTCTGAAGATCTCCTGTAAAGACTTCTGAATACAG CTTTACCAGCTACTGGATCGGCTGGGTGGTGCCAGATGCCCGGAAAAG GCCTGGAGTGGATGGGATCATCTATCTTGGTGACTCAGATACCAGA TACAGCCCCGTCTTCCAAGGCCAGGTCAACCATCTCAGCCGACAAGTC CATCAGTACCGCCTACCTGCAGTGGAGCAGCCTGAAGGCCCTCGGACA CCGCCATGTATTACTGTGCGAGAAAGTAACTGGGTCTTGACTACTGG GGCCAGGGAACCCCTGGTCACCGTCTCTAGTGCCCTCCACCAAGGCCCC ATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCA CAGCGGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCCGAACCGGTG ACGGTGTCTGTGGAACCTCAGGCGCCCTGACCAGCGCGTGCACACCTT CCCGGCTGTCCCTACAGTCCCTCAGGACTCTACTCCCTCGAGAGCGTGG TGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAAC GTGAATCACAAAGCCCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGT
	SEQ ID NO:43	SEQ ID NO:44	SEQ ID NO:45
AA	EIVLTQSPGTLISLP GERATLSCRASQSVR SSYLAWYQQKPGQAP RLLIYGASSRATGIP DRFSGSGGTDFTLT	QSVLTQPPSVSGAPG QRVTISCTGSSSNIG AGYDVHWYQQFPGTA PKLLIQGNSNRPSGV PDRFSGSKSGTSASL	QVQLQQSGAGLLKPSSETLSLTCAVHGGSFSGYYWNWIRQPPGKGLEW IGEINHAGNTNYPNPSLKSRVTISLDTSKNQFSLTLTSVTAADTAVYY CARGYCRSTTCYFDYWQGQTLTVVSSASTKGPSVFPIAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLKSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTPPCPAP

			ISRLEPEDFAVYYCQ QYGSPTFGQTRLE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLESTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEN	AITGLQAEDEADYYC QSYDSSLSGSVFGGG TKLTVLGQPKAAPSV TLFPPSSEELQANKA TLVCLISDFYPGAVT VAWKADSSPVKAGVE TTTPSKQSNNKYAAK SYLSLTPEQWKSHRS YSCQVTHEGSTVEKT VAPTECS	ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVTDKSRWQQG NVFSCSVMEALHNHYTQKSLSLSPGGSGGGSEVQLVQSGAEVK KPGESLKISCKTSEYSFYSYWI GWRQMPGKGLEWMGI IYLGSDSDTR YSPSFQGQVTISADKSI STAYLQWSSSLKASDTAMYICARSNWGLDYW GQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSQVHTTTPAVLQSSGLYSLESVVTVFPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSC
			SEQ ID NO:46	SEQ ID NO:47	SEQ ID NO:48
		009_9c8_1gg.001_Ada1imumab_VH_CH1 (S183E)	NA	CAGGTGCAGCTGCAGGAGTCGGGGCCAGGACTGGTGAAGCCTTCGGA GACCCGTGCCCTCACCTGCACGTGCTCTCTGGTGGCTCCATCAGTAGTT ACTTCTGGAGCTGGATCCGGCAGCCCCCAGGTAAGGGACTGGAGTGG ATTGGCTATATCTATTACAGTGGCAGACCACCAATAACAACCCCTCCCT CAAGAGTCGAGTCACCATATCAATAGACACAGTCACAAGAACAGTTCT CCCTGAAGCTGAGCTCTGTGACCGCTGCGGACACAGGCCGTGTATTAC TGTCGAGAGAAACTGGGAGCTACTACGGCTTTGACTACTGGGCCA GGGAACCCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGCCCATCGG TCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGTGCCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGT GTCGTGGAACCTCAGCGCCCTGACCAGCGCGGTGCACACCTTCCCCGG CTGTCTACAGTCTCTAGGACTCTACTCCCTCAAAAGCGTGTGACC GTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAA TCACAAGCCCCAGCAACACCAAGGTGGACAAAGAAAGTTGAGCCCCAAAT CTTGTGACAAAACCTCACACATGCCACCGTCCCGACGACCTGAACCTC CTGGGGGACCGTCAGTCTTCTCTTCCCCCCCCAAAACCCAAAGGACAC CCTCATGATCTCCCGACCCCTGAGGTCACATGCGTGGTGGTGACG TGAGCCACGAAACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGTGAGGAGCAGTACGG CAGCACGTACCGTTGTGTACGCTCCTCACCGTCCCTGCACCCAGGACT GGCTGAATGGCAAGGAGTACAAAGTGCAAGGTCTCCAACAAAAGCCCTC CCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGCAGCCCCG AGAACACAGGTGTACACCCCTGCCCCCATCCCCGGGAGGAGATGACCA AGAACCCAGGTCAGCCTGACCTGCCCTGGTCAAGGCTTCTATCCCAGC GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTA CAAGACCAAGCCTCCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTCT	

		TCTGTTGTGTGCCTG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAAGTG GATAACGCCCTCCAA TCGGGTAACTCCCG GAGAGTGTACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC GAGAGCACCTGACG CTGAGCAAAAGCAGAC TACGAGAAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	TCTGTTGTGTGCCTG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAAGTG GATAACGCCCTCCAA TCGGGTAACTCCCG GAGAGTGTACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC AAGAGCACCTGACG CTGAGCAAAAGCAGAC TACGAGAAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	ATAGCAAGCTCACCGTGGACAAAGAGCAGGTGGCAGCAGGGGAAACGTC TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCA GAAAGACCTCTCCCTGTCTCCGGTGGTGGCGGATCGGAGGTGGCG GATCCGAGGTACAACTGGTGGAAATCAGGTGGAGGTTTGGTGCAGCCG GGGAGATCGCTCAGGCTTAGCTGTGCGGCATCGGGGTTTACTTTCGA TGATTATGCGATGCATTGGGTCCGGCAGCGCCTGGAATAAGGGCTCG AGTGGGTTTCCGCCATTACGTGGAATAGCGGACACATCGATTATGCA GACAGTGTGGAGGGCAGATTCACAATCTCACGAGACAAATGCTAAGAA CAGCCTGTACCTTCAGATGAACTCACTTCGCGCGGAAAGATACCGCCG TATACTACTGCGCCAAAAGTCTCCTACTTGTCTACAGCTTCGTCGCTC GACTATTGGGGTCAAGGAAAGTTGGTCAACCGTCTCTAGTGCCCTCCAC CAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCT CTGGGGCACAGCGGCCCTGGGCTGCCGTGTCAGGACTACTTCCCC GAACCGGTGACGGTGTCTGTGGAACTCAGGGCCCTGACCAGCGCGGT GCACACCTTCCCGCTGTCTACAGTCTCAGGACTCTACTCCCTCG AGAGCGTGTGACCGTCCCCCTCCAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAAGCCCAGCAACACCAAGGTGGACAAGAA AGTTGAGCCCAAATCTTGT	SEQ ID NO:49	SEQ ID NO:50	SEQ ID NO:51
	AA	DIQMTQSPSSLSASV GDRVITITCRASQIN NYLNWYQQRP GKAPK LLIYAASSLQSGVPS RFSGSGGTDFTLTI SSLQPEDFATYYCQQ SYSTPRTFGQGTKLE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLESTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEC	DIQMTQSPSSLSASV GDRVITITCRASQIR NYLAWYQQKPGKAPK LLIYAAS TLQSGVPS RFSGSGGTDFTLTI SSLQPEDVATYYCQR YNRAPYTFGQGTKVE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLKSTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEC	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYFWSWIRPPGKGLEW IGYIYSGQTKYNPSLKSRTVISIDTSKNQFSLKLSVTAADTAVYY CARETGSYYGFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLKSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFFLYSKLTVDKSRWQQGNV FSCSVMH EALHNHYTQKSLSLSPGSGGGGGSEVQLVESGGGLVQP GRSLRLSCAASGFTFDDYAMHWVRQAPKGLEWVSAITWNSGHIDYA DSVEGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAKVS YLSTASSL DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSL ESVVTVPSSSLGTQTY ICNVNHKPSNTKVDKKVEPKSC	SEQ ID NO:52	SEQ ID NO:53	SEQ ID NO:54

1PS: 376633	010_9C8_1gG.001_3.2_VH_CH1 (S183E)	NA	GACATCCAGATGACC CAGTCTCCATCCTCC CTGTCTGCACTGTGA GGAGACAGAGTCACC ATCACTTGCCGGCA AGTCAGAGCATTAAC AACTATTTAAATTGG TATCAGCAGAGACCA GGGAAAGCCCCTAAG CTCCTGATCTATGCT GCATCCAGTTTGCAA AGTGGGGTCCCATCA AGGTTCAGTGGCAGT GGATCTGGGACAGAT TTCACCTCACCATC AGCAGTCTGCAACCT GAAGATTTTGCAACT TACTACTGTCAACAG AGTTACAGTACCCCT CGGACGTTCGGCCAA GGGACCAAGCTGGAA ATCAAAACGAACGGTG GCTGCACCATCTGTC TTCATCTTCCCCGCA TCTGATGAGCAGTTG AAATCTGGTACCGCC TCTGTTGTGTGCCTG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCCAG GAGAGTGTACACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC GAGAGCACCCCTGACG CTGAGCAAAAGCAGAC	CAGTCTGTGCTGACG CAGCCGCCCTCAGTG TCTGGGGCCCCAGGG CAGAGGGTCACCATC TCCTGCACTGGGAGC AGTTCCAACATCGGG GCAGGTTATGATGTA CACTGGTACCAGCAG TTTCCAGGAACAGCC CCCAAACCTCCTCATC CAAGGTAACAGCAAT CGGCCCTCAGGGGTC CCTGACCCGATTCTCT GGCTCCAAGTCTGGC ACCTCAGCCTCCCTG GCCATCACTGGGCTC CAGGCTGAGGATGAG GCTGATTATTACTGC CAGTCCCTATGACAGC AGCCTGAGTGTTGCG GTGTTCCGGCGGAGGG ACCAAGCTGACCGTC CTAGGTCAGCCCAAG GCTGCCCCCTCGGTC ACTCTGTTCCCGCCC TCCTCTGAGGAGCTT CAAGCCAACAAGGCC ACACTGGTGTGTC ATAAGTGACTTCTAC CCGGAGCCGTGACA GTGGCCTGGAAGGCA GATAGCAGCCCCGTC AAGCGGGAGTGGAG ACCACCACACCTCC AAACAAAAGCAACAAC AAGTACGGGCCCAAG AGCTATCTGAGCCTG	CAGGTGCAGCTGCAGGAGTCGGGGCCCAGGACTGGTGAAAGCCTTCGGA GACCCGTGTCCTCACCTGCACGTGTCTCTGGTGGCTCCATCAGTAGTT ACTTCTGGAGCTGGATCCGGCAGCCCCCAGGTAAGGGACTGGAGTGG ATTGGCTATATCTATTACAGTGGGAGACCAAAATACAACCCCTCCCT CAAGAGTCGAGTCACCATATCAATAGACACGTCCAAGAACAGTTCT CCCTGAAGCTGAGCTCTGTGACCCGTGCGGACACCGGCCGTGTATTAC TGTGCGAGAGAAACTGGGAGCTACTACGGCTTTGACTACTGGGGCCA GGGAACCTTGGTCACCGTCTCCTCAGCCTCCACCAAGGCCCATCGG TCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGT GTCGTGGAACCTCAGGGCCCCGTGACCAGCGGCGTGACACCTTCCCGG CTGTCCCTACAGTCCCTCAGGACTCTACTCCCTCAAAAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAA TCACAAGCCCCAGCAACACCAAGGTGGACAAAGAAAGTTGAGCCCCAAAT CTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAACCTC CTGGGGGACCGTCAGTCTTCTCTCTTCCCCCCAAAACCCAAAGGACAC CCTCATGATCTCCCGACCCCTGAGGTCAATGCGTGGTGGTGGACG TGAGCCACGAAGACCCCTGAGGTCAAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGTGAGGAGCAGTACGG CAGCACGTACCCTGTGTGTCAGCGTCTCACCGTCTGACACGAGACT GGCTGAATGGCAAGGAGTACAAAGTGCAAGGTCTCCAACAAAGCCCTC CCAGCCCCCATCGAGAAAACCATCTCCAAAAGCCAAAGGGCAGCCCCG AGAACACAGGTGTACACCCCTGCCCCCATCCGGGAGGAGATGACCA AGAACCCAGTCAAGCTGACCTGACCTGCCCTGGTCAAAGCTTCTATCCCAGC GACATCGCCGTGGAGTGGAGAGCAATGGGCAGCCGGAGAACAACTA CAAGACCAAGCTCCCGTGTGCTGGACTCCGACGGCTCCTTCTTCTCTCT ATAGCAAGCTCACCGTGGACAAAGAGCAGGTGGCAGCAGGGGAAACGTC TTCTCATGTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCA GAAGAGCCTCTCCCTGTCTCCGGGTGGTGGCGGATCGGGAGGTGGCG GATCCGAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCC GGGAGTCTCTGAAGATCTCCTGTAAAGACTTCTGAATACAGCTTTAC CAGCTACTGGATCGGCTGGGTGCGCCAGATCCCCGGGAAAGGCCTGG AGTGGATGGGATCATCTATCTTGGTGACTCAGATACCAGATACAGC CCGTCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAAGTCCATCAG TACCGCCTACCTGCAGTGGAGCAGCCTGAAGGCCTCGGACACCGCCA TGTAATTACTGTCCGAGAAGTAACTGGGTCTTGACTACTGGGGCCAG GGAACCTTGGTCACCGTCTCTAGTGCCCTCCACCAAGGCCCATCGGT
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		TACGAGAAACACAAA GTCTACGCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	ACGCCTGAGCAGTGG AAGTCCACAGAAGC TACAGCTGCCAGGTC ACGATGAAGGGAGC ACCGTGAGAAAGACA GTGGCCCCCTACAGAA TGTTCA	CTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGTGGGGGCACAGCGG CCCTGGGCTGCCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTG TCGTGAACTCAGCGGCCCTGACCAAGCGGCTGCACACCTTCCCCGGC TGTCCTACAGTCTCTCAGGACTCTACTCTCCCTCGAGAGCGTGGTGACCG TGCCCTCCAGAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT CACAAAGCCAGCAACACCAAGGTGGACAAAGAAAGTTGAGCCCCAAATC TTGT
		SEQ ID NO:55	SEQ ID NO:56	SEQ ID NO:57
AA		DIQMTQSPSSLSASV GDRVITITCRASQIN NYLNWYQQRP GKAPK LLIYAASSLQSGVPS RFGSGSGTDFTLTI SSLQPEDFATYYCQQ SYSTPRTFGQGTKLE IKRTVAAPSVFI FPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLESTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEC	QSVLTQPPSVSGAPG QRVTISCTGSSSNIG AGYDVHWYQQFPGTA PKLLIQNSNRPSGV PDRFSGSKSGTSASL AITGLQAEDEADYYC QSYDSSLSGSVFGGG TKLTVLGQPKAAPSV TLFPPSSEELQANKA TLVCLISDFYPGAVT VAWKADSSPVKAGVE TTTPSKQSNNKYAAK SYLSLTPEQWKSHRS YSCQVTHEGSTVEKT VAPTECS	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYFWSWIRQPPGKGLEW IGYIYYSGQTKYNPSLKSRVTISIDTSKNQFSKLSSVTAADTAVYY CARETGSYYGFDYWGGTTLVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLKSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMEALHNHYTQKSLSLSPGSGSGGSEVQLVQSGAEVKKP GESLKISCKTSEYSFTSYWIGWVRQMPGKGLEWMGIIYLGDS DTRY S PSFQGQVTISADKSI STAYLQWSSLKASDTAMY YCARSNWGLD YWGQ GTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSL ESVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSC
		SEQ ID NO:58	SEQ ID NO:59	SEQ ID NO:60
		GACATCCAGATGACC CAGTCTCCAAGCTCC CTGTCTGCGTCTGTG GGCGATAGGGTCACC ATCACTTGCAGGTCC AGCCAGAGTGTGTTA TACAGCTCCAACAAT AAGAACTACTTAGTT TGGTACCAGCAGAAA CCAGGAAAGGTTCCCT AAACTGCTCATTAC TGGGCATCTACCCGG GAATCCGGGGTCCCT	GATATCCAAATGACA CAATCACCATCGTCG CTTTCAGCGTCTGTT GGCGACCGTGTGACG ATTACCTGTCGCGCG TCCCAGGGAATCCGG AATTACCTCGCATGG TATCAGCAAAAACCC GGA AAAGCACCCGAAG CTCCTGATCTATGCC GCCTCGACTCTTCAG AGTGGTGTGCCGTCG AGGTTTAGCGGGTCC	CAGGTACAGTTGCAGGAGTCAGGTCCAGGACTGGTGAAGCCCTCGGA GACCCCTCACTACCTGTACCATCTCCGGGGACAGTGTCTCTACCA ACAGTGTTCCTTGAACTGGATCAGGCAGCCCCCAGGAAAGCCCTT GAGTGGATAGGAAGGACATAC TACAGGTCCAAGTG GTATAATGATTA TGCAGTTTCTCTGAAAAGTCGAGTAACCATCAGCC CAGACATCCA AGAAC CAGTTCTCCCTGAAAGCTGAGCTCTGTGACTGCCCGGACACG GCTGTGTA TTA CTGTGCAAGAGAGGATGGG GATAGCTACTACCGCTA CGGTA TG GACGTCTGGGGCCAAAGGAC CACGGTCACCGTCTCCTCAG CCTCCACCAAGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAG AGCACCTCTGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCTGTGGAAC T CAGGGCCCCCTGACCA GCGGCGTGCAACACCTTCCCCGGCTGTCTCTACAGTCCCTCAGGACTCTAC TCCCTCAAAAGCGTGGTGACCCGTGCCCTCCAGCAGCTTGGGCACCCA
		011_23B3_VH4_IgG.001_A dal'imunab_VH_CH1 (S183F)		
!PS: 376637				

	AGTCGATTCA GTGGC AGCGGTCTGGGACA GATTTCAC TCTCAC C ATCAGCAGCCTGCAG CCTGAAGATGTGGCA ACTTATTACTGT CAG CAATATTATAAGACT CCTCTCACTTTCGGC GGAGGGACCAAGGTG GAGATCAAACGAACG GTGGCTGCACCATCT GTCTTCATCTTCCCG CCATCTGATGAGCAG TTGAAAATCTGGTACC GCCCTCTGTTGTGTG CTGCTGAATAACTTC TATCCAGAGAGGCC AAAGTACAGTGGAAG GTGGATAACGCCCTC CAATCGGGTAAC TCC CAGGAGAGTGT CACA GAGCAGGACAGCAAG GACAGCACC TACAGC CTCGAGAGCACCCCTG ACGCTGAGCAAAGCA GACTACGAGAAAACAC AAAGTCTACGCC TGC GAAGTCACCCCATCAG GGCCTGAGCTCGCCC GTCACAAAGAGCTTC AACAGGGGAGAGTGT	GGGTCAGGTACGGAC TTTACTCTCACAATT TCCAGCCTGCAGCCC GAAGATGTAGCTACC TATTACTGCCAGAGA TACAACCGAGCGCCT TACACATTTCGGACAA GGGACAAAAGTCGAG ATCAAAGCTACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGA ACTGCC TCTGTTGTGTGCC TG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAGTG GATAACGCCCTCCAA TCGGGTAACTCCCAG GAGAGTGT CACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC AAGAGCACCC TGACG CTGAGCAAAGCAGAC TACGAGAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAAGACTTCAAC AGGGGAGAGTGT	GACCTACATCTGCAACGTGAATCACAAAGCC CAGCAACACCAAGGTGG ACAAGAAAAGTTGAGCCCAAATCTTTGTGACAAAAC TCAACACATGCCCA CCGTGCCAGCACCTGAAC TCTGGGGGACCGTCA GTCTTCCCTCTT CCCCCAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGG TCACATGCGTGTGTGGACGTGAGCCACGAAGACCC TGAGGTCAAG TTCAA ACTGGTACGTGGACGGCGTGGAGGTGCATAA TGCCAAAGACAAA GCCGTGTGAGGAGCAGTACGGCAGCACGTACC GTTGTGT CAGCGTCC TCACCGTCTGCAC CAGGACTGGCTGAATGGCAAGGAGTACAAAGTGC AAGGTCTCCAA CAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTC CAAAGCCAAAGG CAGCCCCGAGAACCA CAGGTGTACACCCCTGCCCC CATCCGGGAGAGATGACCAAAGAACCAAGTCA GCCTGACCTGACCTGCCTG GTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAA TGGCAGCCGGAGAACAACTACAAGAC CACGCCCTCCCGTGTGGA CT CCGACGGCTCCTTCTTCTCTCTATAGCAAAGCTCACCCGTGGACAAAGAGC AGGTGGCAGCAGGGGAACGTCTTCTCATGTCTCCGTGATGCATGAGGC TCTGCACAA CCACTACACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTG GTGGCGGATCGGGAGGTGGCGGATCCGAGGTACAACTGCTGGAATCA GGTGGAGGTTTGGTGACGCCGGGAGATCGCTCAGGCTTAGCTGTGC GGCATCGGGGTTTACTTTTCGATGATTATGCGGATGCATTGGGTCCGGC AAGCGCTGGA AAAAGGCTCGAGTGGGTTTCCGCCATTACGTGGAAT AGCGGACACATCGATTATGCAGACAGTGTGGAGGCGAGATTCA CAAT CTCACGAGACAATGCTAAGAACAGCCTGTACCTTCAGATGA ACTCAC TTGCGCGGAAAGATACCGCCGTATACTACTGCGCCAAAAGTCTCCTAC TTGTCTACAGCTTCGTGCTCGCTCGACTATTGGGGTCAAGGAACGTTGGT CACCGTCTCTAGTGCCCTCCACCAAGGCCCATCGGTCTTCCCCCTGG CACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGC CTGGTCAAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGA ACTC AGCGCCCTGACCAGCGGGCTGCACACCTTCCCGGTGTCTCTACAGT CCTCAGGACTCTACTCCCTCGAGAGCGTGGTGACCGTGCCCTCCAGC AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCCAG CAACACCAAGGTGGACAAAGAAAGTTGAGCCCCAAAATCTTGT
	SEQ ID NO: 61	SEQ ID NO: 62	SEQ ID NO: 63
AA	DIQMTQSPSSLSASV GDRVITITCRSSQSVL YSSNNKNYLVWYQQK PGKVPKLLIYWASTR ESGVPSRFSGSGST	DIQMTQSPSSLSASV GDRVITITCRASQGIR NYLAWYQQKPGKAPK LLIYAASTLQSGVPS RFSGSGSGTDFTLTI	QVQLQESGPGLVKPSETLSLTCTISGDSVSTNSVAWNWIRQPPGKGL EWIGRTYYRSKWINDYAVSLKSRVTISPDTSKNQFSLKLSVTAADT AVYYCAREDGDSYYRYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY SLKSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTHCP

			DFTLTISLQPEDVA TYYCQQYYKTPLTFG GGTKVEIKRTVAAPS VFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGNS QESVTEQDSKDSYYS LESTLTLSKADYEKH KVYACEVTHQGLSSP VTKSFNRGEC	SSLQPEDVATYYCQR YNRAPYTFGQGTKVE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSYSLKSTLT LSKADYEHKHYACE VTHQGLSSPVTKSFN RGEC	PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKC KVSNAKALPAIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVSCVMHEALHNYHTQKSLSLSPPGGSGGGSEVQLVES GGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSAITWN SGHIDYADSVGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAKVS LSTASSLDYWGGTTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLESVVTVPS SLGTQTYICNVNHHKPSNTKVDKKVEPKSC
			SEQ ID NO: 64	SEQ ID NO: 65	SEQ ID NO: 66
			GACATCCAGATGACC CAGTCTCCAAGCTCC CTGTCTGCCGTCTGTG GGCGATAGGGTCACC ATCACTTGCAGGTCC AGCCAGAGTGTGTTA TACAGCTCCAACAAT AAGAACTACTTAGTT TGGTACCAGCAGAAA CCAGGAAAGGTTCCCT AAACTGCTCATTTAC TGGGCATCTACCCGG GAATCCGGGGTCCCT AGTCGATTCAAGTGGC AGCGGGTCTGGGACA GATTTCACTCTCACC ATCAGCAGCCTGCAG CCTGAAAGATGTGGCA ACTTATTACTGTCCAG CAATATTATAAGACT CCTCTCACTTTCGGC GGAGGACCAAGGTG GAGATCAAAACGAACG GTGGCTGCACCATCT GTCTTCATCTTCCCG CCATCTGATGAGCAG	CAGTCTGTGCTGACG CAGCCGCCCTCAGTG TCTGGGGCCCCAGGG CAGAGGGTCACCATC TCCTGCACTGGGAGC AGTTCCAACATCGGG GCAGGTTATGATGTA CACTGGTACCAGCAG TTTCCAGGAACAGCC CCCAAACCTCCTCATC CAAGGTAAACAGCAAT CGGCCCTCAGGGTC CCTGACCGATTCTCT GGCTCCAAGTCTGGC ACCTCAGCCTCCCTG GCCATCACTGGGCTC CAGGCTGAGGATGAG GCTGATTATTACTGC CAGTCCATGACAGC AGCCTGAGTGGTTCCG GTGTTCCGGCGGAGGG ACCAAGCTGACCGTC CTAGGTCAGCCCCAAG GCTGCCCCCTCGGTC ACTCTGTTCCCGCCC TCCTCTGAGGAGCTT	CAGGTACAGTTGCAGGAGTCAGGTCCAGGACTGGTGAAGCCCTCGGA GACCCCTCACTACCTGTACCATCTCCGGGGACAGTGTCTCTACCA ACAGTGTTCCTTGAACTGGATCAGGCAGCCCCCAGGAAAGGCCCTT GAGTGGATAGGAAGGACATACATACAGGTCCAAGTGGTATAATGATTA TGCAGTTTCTCTGAAAAGTCGAGTAACCATCAGCCCAGACACATCCA AGAAACCAGTTCTCCCTGAAAGCTGAGCTCTGTGACTGCCCGGCACACG GCTGTGTAATTAAGTGTGCAAGAGAGGATGGGATAGCTACTACCGCTA CGGTAATGGACGCTCTGGGGCCAAAGGACACACGGTCACCGTCTCCCTCAG CCTCCACCAAGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAG AGCACCTCTGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCCTGACCA GCGGCGTGACACACCTTCCCGGCTGTCTACAGTCTCAGGACTCTAC TCCCTCAAAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAGCCAGCAACACCAAGGTGG ACAAGAAAAGTTGAGCCCCAAATCTTGTGACAAAACCTCACACATGCCCA CCGTGCCCCAGCACCTGAACCTCCTGGGGGACCCGTCACTTCCCTCTT CCCCCAAACCCAAAGACACCCCTCATGATCTCCCGACCCCTGAGG TCACATGCCGTGGTGGTGACGTGAGCCACGAAGACCCCTGAGGTCAAG TTCAACTGGTACGTGGACGGCGGTGGAGGTGCATAATGCCAAGACAAA GCCGTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTGTACGGTCC TCACCGTCTCTGCACCCAGGACTGGCTGAATGGCAAGGAGTACAAAGTGC AAGGTCTCCAAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTC CAAAGCCAAAGGCAGCCCCCGAGAACCAACAGGTGTACACCCCTGCCCC CATCCCGGAGGAGATGACCAAGAACCAAGGTGAGCCTGACCTGCCCTG GTCAAAGGCTTCTATCCAGCGGACATCGCCGTGGAGTGGAGAGCAAA TGGGCAGCCGGAGAACAACTACAAGACCACGCCCTCCCGTCTGGACT

012_23B3_VH4_1g.001_3.2_VH_CH1 (S183E)

NA

		TTGAAATCTGGTACC GCCTCTGTTGTGTGC CTGCTGAATAACTTC TATCCCAGAGAGGCC AAAGTACAGTGAAG GTGGATAACGCCCTC CAATCGGGTAACTCC CAGGAGAGTGCACA GAGCAGGACAGCAAG GACAGCACCTACAGC CTCGAGAGCACCCCTG ACGCTGAGCAAAAGCA GACTACGAGAAACAC AAAGTCTACGCCCTGC GAAGTCACCCATCAG GGCCTGAGCTCGCCC GTCACAAAAGAGCTTC AACAGGGGAGAGTGT	CAAGCCAAACAAGGCC ACACTGGTGTGTCTC ATAAGTGACTTCTAC CCGGAGCCGTGACA GTGGCCTGGAAGCA GATAGCAGCCCCGTC AAGCGGGAGTGGAG ACCACCAACCCCTCC AAACAAAAGCAACAAC AAGTACGCGGCCAAG AGCTATCTGAGCCTG ACGCCTGAGCAGTGG AAGTCCCACAGAAGC TACAGCTGCCAGGTC ACGCATGAAGGGAGC ACCGTGGAGAAGACA GTGGCCCCTACAGAA TGTTCA	CCGACGGCTCCTTCTTCCCTCTATAGCAAGCTCACCCGTGGACAAAGAGC AGGTGGCAGCAGGGGAACGTCTTCTCATGTCTCCGTGATGCATGAGGC TCTGCACAAACCATAACACGCAGAAAGAGCCTCTCCTGTCTCCGGGTG GTGGCGGATCGGGAGGTGGCGGATCCGAGGTGCAGCTGTCAGTCT GGAGCAGAGGTGAAAAAGCCCGGGAGTCTCTGAAGATCTCCTGTAA GACTTCTGAATAACAGCTTTACCAGTACTGGATCGGCTGGGTGCGCC AGATGCCCCGGAAAAGCCCTGGAGTGGATGGGATCATCTATCTTGGT GACTCAGATACCAGATACAGCCCGTCCCTTCCAAGGCCAGGTCACCCAT CTCAGCCGACAAGTCCATCAGTACCGCCTACCTGCAGTGGAGCAGCC TGAAGCCTCGGACACCGCCATGTATTACTGTGCGAGAAGTAACTGG GGTCTTGACTACTGGGGCCAGGAAACCCTGGTCACCGTCTCTAGTGC CTCCACCAAGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGA GCACCTCTGGGGCACAGCGGCCCTGGGCTGCCCTGGTCAAGGACTAC TTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCCTGACCCAG CGCGTGCACACCTTCCCGGCTGTCCTACAGTCCCTCAGGACTCTACT CCCTCGAGAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAG ACCTACATCTGCAACGTGAATCACAAAGCCCAGCAACACCAAGGTGGA CAAGAAAGTTGAGCCCAAATCTTGT
		SEQ ID NO:67	SEQ ID NO:68	SEQ ID NO:69
AA		DIQMTQSPSSLSASV GDRVITITCRSSQSVL YSSNNKNYLVWYQQK PGKVPKLLIYWASTR ESGVPSRFSGSGSGT DFTLTISSLQPEDVA TYYCQQYYKTPLTFG GGTKVEIKRTVAAPS VFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGNS QESVTEQDSKDSSTYS LESTLTLSKADYEKH KVYACEVTHQGLSSP VTKSFNRGEC	QSVLTQPPSVSGAPG QRVTISCTGSSSNIG AGYDVHWYQQFPGTA PKLLIQNSNRPSGV PDRFSGSKSGTSASL AITGLQAEDEADYYC QSYDSSLSGSVFGGG TKLTVLGQPKAAPSV TLFPPSSEELQANKA TLVCLISDFYPGAVT VAWKADSSPVKAGVE TTTPSKQSNNKYAAK SYLSLTPEQWKSHRS YSCQVTHEGSTVEKT VAPTECS	QVQLQESGPGLVKPSETLSLTCTISGDSVSTNSVANNWIRQPPGKGL EWIGRTYRYSKWYNDYAVSLKSRVTISPDTSKNQFSLKLSVTAADT AVYYCAREDDGDSYYRYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY SLKSVVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTHCP PCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKC KVSNKALPAPIEKTIISKAKGQPREPQVYITLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGGGSEVQLVQS GAEVKKPGESLKISCKTSEYSFTSYWIGWVRQMPGKGLEWMGIIYLG DSDTRYSPSFQGGQVTISADKSI STAYLQWSSLKASDTAMYICARSNW GLDYGWQGGLVTTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLESVTVTPSSSLGTQ TYICNVNHKPSNTKVDKKVEPKSC
		SEQ ID NO:70	SEQ ID NO:71	SEQ ID NO:72

1PS: 376645	013_Adalimumab_CK(S176K)_Fc_3B3v2_VH_CH1(S183F)	NA	GAAATTGTGTTGACG CAGTCTCCAGGCACC CTGTCTTTGTCTCCA GGGAAAGAGCCACC CTCTCCTGCAGGGCC AGTCAGAGTGTTAGA AGCAGTTACTTAGCC TGGTACCAGCAGAAA CCTGGCCAGGCTCCC AGGCTCCTCATCTAT GGTGCAATCCAGCAGG GCCACTGGCATCCCA GACAGGTTCAGTGGC AGTGGGTCTGGGACA GACTTCACCTCACC ATCAGCAGACTGGAG CCTGAAGATTTTGCA GTGTATTACTGTGAG CAGTATGGTAGCTCA CCTACCTTCGGCCAA GGGACACGACTGGAG ATTAAACGAACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGTACCGCC TCTGTTGTGTGCCCTG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCCCAG GAGAGTGTACACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC AAGAGCACCCCTGACG CTGAGCAAAAGCAGAC	GAGGTACAACTGGTGGAAATCAGGTGGAGGTTTGGTGCAGCCGGGGAG ATCGCTCAGGCTTAGCTGTGCGGCATCGGGGTTTACTTTCGATGATT ATGCGATGCAATGGGTCCGGCAAGCGCCTGGAATAAGGGCTCGAGTGG GTTTCCGCCATTACGTGGAATAGCGGACACATCGATTATGCAGACAG TGTGGAGGGCAGATTCACAATCTCACGAGACAATGCTAAGAACAGCC TGTAACCTTCAGATGAACCTCACTTCGCGCGGAAGATACCGCCGTATAC TACTGCGCCAAAAGTCTCCTACTTGTCTACAGCTTCGTCGCTCGACTA TTGGGTCAAAGGAACGTTGGTCACCGTCTCTAGTACGGTGGCTGCAC CATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAAATCTGGA ACTGCCCTCTGTTGTGTGCCCTGCTGAATAACTTCTATCCAGAGAGGC CAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCC AGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC AAGAGCACCCCTGACGCTGAGCAAAAGCAGACTACGAGAAAACACAAAGT CTACGCCCTGCCAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAA AGAGCTTCAACAGGGGAGAGTGTGACAAAACCTCACACATGCCCACCG TGCCCAGCACCTGAACTCCTGGGGGACCGTCAGTCTTTCCTCTTCCC CCCCAAAACCCAAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCA CATGCGTGGTGGTGACGTGAGCCACGAAGACCCCTGAGGTCAAAGTTC AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAAGCC GTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTGTGTCAGCGTCCCTCA CCGTCTTGCAACCAGACTGGCTGAAATGGCAAAGGAGTACAAGTGCAAG GTCTCCAACAAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAAGGCAGCCCCGAGAACCAAGGTGTACACCCCTGCCCCCAT CCCGGGAGGAGATGACCAAGAACCAAGTCAAGCTGACCTGACCTGGTGC AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAAACAACTACAAGACCAACGCTCCCGTGTGGACTCCG ACGGCTCCTTCTTCCCTCTATAGCAAAGCTCACCGTGGACAAGAGCAGG TGGCAGCAGGGGAACGTCTTCTCATGTCTCCGTGATGCATGAGGCTCT GCACAAACCACTACACGCAGAAAGACCTCTCCCTGTCTCCGGGTGGTG GCGGATCGGAGGTGGCGGATCCCAAGTCCAGGTGCAGTTACAGCAGTCGGGC GCAGGACTGTTGAAGCCTTCGGAGACCCGTGTCCCTCACCTGCGCTGT CCATGGTGGGTCCCTTCAGTGGTTACTACTGGAACCTGGATTCCGCCAGC CACCAAGGAAGGGCTAGAGTGGATTGGGAAATCAATCATGCTGGA AACACCAACTACAACCCGTCCCTCAAGAGTCGAGTCACCATATCATTT AGACACGTCCAAGAACCAAGTTCTCCCTGACGCTGACCTCTGTGACCG CCGGGACACGGCTGTGTATTACTGTGCGAGAGGATATTGTAGAAGT ACCACCTGCTACTTTGACTACTGGGGCCAGGGAACCCCTAGTCACCGT	GATATCCAAATGACA CAATCACCATCGTCG CTTTCAGCGTCTGTT GGGACCGTGTGACG ATTACCTGTCGCGG TCCCAGGGAATCCGG AATTACCTCGCATGG TATCAGCAAAAACCC GGAAAAAGCACCGAAG CTCCTGATCTATGCC GCCTCGACTCTTCAG AGTGGTGTGCCGTGG AGGTTAGCGGTCC GGTCAAGTACGGAC TTTACTCTCACAATT TCCAGCCTGCAGCCC GAAGATGTAGCTACC TATTACTGCCAGAGA TACAAACGAGCGCCT TACACATTCCGACAA GGGACAAAAGTCGAG ATCAAAGCGTGCCTCC ACCAAGGCCCATCG GTCTTCCCCCTGGCA CCCTCCTCCAAGAGC ACCTCTGGGGCACA GCGGCCCTGGGCTGC CTGGTCAAGGACTAC TTCCCCGAACCGGTG ACGGTGTCTGTGAAC TCAGGCGCCCTGACC AGCGCGGTGCACACC TTCCCCGGCTGTCCTA CAGTCTCAGGACTC TACTCCCTCGAAAGC GTGGTGACCGTGCCC TCCAGCAGCTTGGGC
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		TACGAGAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGAGAGTGT	CTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCT CCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCCTGGTC AAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAATCAGGCGC CCTGACCAGCGGTGCACACCTTCCCGGCTGTCTACAGTCTCTCAG GACTCTACTCCCTCGAGAGCGTGTGACCGTGCCCTCCAGCAGCTTG GGCACCAGACCTACATCTGCAACGTGAATCACAAAGCCCAGCAACAC CAAGGTGGACAAAGAAAGTTGAGCCCCAAAATCTTGT	ACCCAGACCTACATC TGCAACGTGAATCAC AAGCCAGCAACACC AAGGTGGACAAGAAA GTTGAGCCCCAAATCT TGT
		SEQ ID NO: 73	SEQ ID NO: 74	SEQ ID NO: 75
AA		EIVLTQSPGTLISLSP GERATLSCRASQSVR SSYLAWYQQKPGQAP RLLIYGASSRATGIP DRFSGSGTDFTLT ISRLEPEDFAVYYCQ QYGSSTFFGQGRLE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLKSTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEC	EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEW VSAITWNSGHIDYADSVVEGRFTISRDNAKNSLYLQMNSLRAEDTAVY YCAKVSYLESTASSLDYWGGQTLTVTSSTVAAPSVFIAPPSEQLKSG TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL KSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECDKTHTCPP CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGGSGGGSVQLQQSG AGLLKPSSETLSLTCAVHGGSFSGYYWNWIRQPPGKGLEWIGEINHAG NTNYPNPSLKSRVTISLDTSKNQFSLTLTSVTAADTAVYYCARGYCRS TTCYFDYWGGQTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHFFPAVLQSSGLYSLESVVTVPSSSL GTQTYICNVNHPKPSNTKVDKKVEPKSC	DIQMTQSPSSLSASV GDRVITITCRASQGIR NYLAWYQQKPKKAPK LLIYAASTLQSGVPS RFGSGSGTDFTLTI SSLQPEDVATYYCQR YNRAPYTFGQGTKVE IKRASTKGPSVFPLA PSSKSTSGGTAALGC LVKDYFFPEPVTVSWN SGALTSGVHFFPAVL QSSGLYSLESVVTVP SSSLGTQTYICNVNH KPSNTKVDKKVEPKS C
		SEQ ID NO: 76	SEQ ID NO: 77	SEQ ID NO: 78
		GACATCCAGATGACC CAGTCTCCATCCTCC CTGTCTGCATCTGTA GGAGACAGAGTCACC ATCACTTGCCGGGCA AGTCAGAGCATTAAC AACTATTAAATTGG TATCAGCAGAGACCA GGGAAAGCCCCTAAG CTCCTGATCTATGCT GCATCCAGTTTGCAA AGTGGGTCCCATCA AGGTTCAGTGGCAGT	GAGGTACAACTGGTGGAATCAGGTGGAGGTTTGGTGCAGCCGGGGAG ATCGCTCAGGCTTAGCTGTGCGGCATCGGGGTTTACTTTCGATGATT ATGCCGATGCATTGGTCCGGCAAGCGCCTGGAAAAGGGCTCGAGTGG GTTTCCGCCATTACGTGGAATAGCGGACACATCGATTATGCAGACAG TGTGGAGGCAGATTCACAATCTCACGAGACAATGCTAAGAACAGCC TGTAACCTTCAGATGAACTCACCTTCGCGCGGAAGATACCGCCGTATAC TACTGCGCCAAAAGTCTCCTACTTGTCTACAGCTTCGTCGCTCGACTA TTGGGGTCAAGGAACGTTGGTCACCGTCTCTAGTACGGTGGCTGCAC CATCTGTCTTCACTCTCCCGCCATCTGATGAGCAGTTGAAAATCTGGA ACTGCCCTCTGTTGTGTGCCCTGCTGAATAACTTCTATCCAGAGAGGC CAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAACTCCC AGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC AAGAGCACCCCTGACGCTGAGCAAAAGCAGACTACGAGAAAACACAAAGT	GATATCCAAATGACA CAATCACCATCGTCG CTTTCAGCGTCTGTT GGCAGCCGTGTGACG ATTACCTGTCGCGCG TCCCAGGGAATCCGG AATTACCTCGCATGG TATCAGCAAAAACCC GGAAAAGCACCCGAAG CTCCTGATCTATGCC GCCTCGACTCTTCAG AGTGGTGTGCCGTG AGGTTTAGCGGGTCC
		NA		
1PS: 376651	014 Adalimumab_CK (S176))_Fc_9C8_VH_CH1 (S183F)			

		GGATCTGGGACAGAT TTCACTCTCACCATC AGCAGTCTGCAACCT GAAGATTTTGCAACT TACTACTGTCAACAG AGTTACAGTACCCCT CGGACGTTCCGCCAA GGGACCAAGCTGGAA ATCAAAACGAACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGTACCGCC TCTGTTGTGTGCCGTG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCCAG GAGAGTGTACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC AAGAGCACCCCTGACG CTGAGCAAAAGCAGAC TACGAGAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	CTACGCCCTGCGAAGTCA AGAGCTTCAACAGGGAGAGTGTGACAAAACTCACACATGCCCCACCG TGCCCAGCACCTGAACCTCCTGGGGGACCGTACGTCTTCTCTTCCC CCCAAAACCCAAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCA CATGCGTGGTGGACGCTGAGCCACGAAGACCCCTGAGGTCAAGTTC AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCC GTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTGTCAAGCGTCCCTCA CCGTCTCTGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAAGTGC GTCTCCAACAAAGCCCTCCAGACCCCATCGAGAAAAACCATCTCCAA AGCCAAAAGGCAGCCCCGAGAACACACAGGTGTACACCCCTGCCCCCAT CCCGGAGGAGATGACCAAGAACCAAGTCAAGCTGACCTGACCTGCCTGGTC AAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGAGAGCAATGG GCAGCCGGAGAAACAACTACAAAGACCAAGCCCTCCCGTGTGACTCCG ACGGCTCCTTCTTCTCTCTATAGCAAGCTCACCGTGGACAAAGACAGG TGGCAGCAGGGAACTCTTCTCATGTCTCCGTGATGCATGAGGCTCT GCACAACTACTACACGCAGAAAGACCTCTCCCTGTCTCCGGGTGGTG GCGGATCGGGAGGTGGCGGATCCAGGTGCAGCTGCAGGAGTCGGGC CCAGGACTGGTGAAAGCTTCGGAGACCCCTGTCCCTCACCTGCACCTGT CTCTGGTGGCTCCATCAGTAGTTACTTCTGGAGCTGGATTTCGGCAGC CCCCAGGTAAGGACTGGAGTGGATTGGCTATATCTATTACAGTGGG CAGACCAAATACAAACCCCTCCCTCAAGAGTCGAGTCACCATATCAAT AGACACGTCCAAAGAACCAAGTCTCCCTGAAGCTGAGCTCTGTGACCG CTGCGGACACGGCCGTGTATTACTGTGCGAGAGAAACTGGGAGCTAC TACGGCTTTGACTACTGGGGCCACAGGGAACCCCTGGTCACCCGTCTCCTC AGCCTCCACCAAGGCCCATCGGTCTTCCCGCTGGCACCCCTCCTCCA AGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCCTGGTCAAGGAC TACTTCCCCGAAACCGGTGACGGTGTCTGTGAACTCAGCGCCCTGAC CAGCGCGTGCACACCTTCCCGGCTGTCTCTACAGTCCCTCAGGACTCT ACTCCCTCGAGAGCGTGTGACCCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAGCCCAAGCAACACCAAGGT GGACAAAGAAAGTTGAGCCCCAAAATCTTGT	SEQ ID NO: 79	SEQ ID NO: 80	SEQ ID NO: 81
AA		DIQMTQSPSSLSASV GDRVITTCRASQ NYLNWYQQRP LLIYAASSLQSGVPS RFSGSGSGTDFTLT	EVQLVESGGGLVQ VSAITWNSGHIDYAD YCAKVSYLSTASSLDYWGQ TASVVCLLNFFYP KSTLTLSKADYEK HVKVYACEVTHQGLSSPVTKSFNRGEC	DIQMTQSPSSLSASV GDRVITTCRASQ NYLAWYQQKPGKAPK LLIYAASTLQSGVPS RFSGSGSGTDFTLT		

			SSLQPEDFATYYCQQ SYSTPRTFGQTKLE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLKSTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEN	CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGGSGSGGSQVQLQESG PGLVKPSETLSLTCTVSGGSISSYFWSWIRQPPGKGLEWIGIYIYSG QTKYNPSSLKSRVTISIDTSKNQFSLKLSVTAADTAVYYCARETGSY YGFDPYWGQTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHFFPAVLQSSGLYSLESVVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC	SSLQPEDVATYYCQR YNRAPYTFGQGTKVE IKRASTKGPSVFPLA PSSKSTSGGTAALGC LVKDYFFPEPVTVSWN SGALTSGVHFFPAVL QSSGLYSLESVVTVP SSSLGTQTYICNVNH KPSNTKVDKKVEPKS C
			SEQ ID NO:82	SEQ ID NO:83	SEQ ID NO:84
	015_Adalimumab_CK(s176K)_Fc_23B3_VH4_VH_CH1(s183E)	NA	GACATCCAGATGACC CAGTCTCCAAGCTCC CTGTCTGCCGTCTGTG GGCGATAGGGTCACC ATCACTTGCAGGTCC AGCCAGAGTGTGTTA TACAGCTCCAACAAT AAGAACTACTTAGTT TGGTACCAGCAGAAA CCAGGAAAGGTTCCCT AAACTGCTCATTTAC TGGGCATCTACCCGG GAATCCGGGGTCCCT AGTCGATTCAGTGGC AGCGGGTCTGGGACA GATTTCACCTCACC ATCAGCAGCCTGCAG CCTGAAGATGTGGCA ACTTATTACTGTCAG CAATATATAAGACT CCTCTCACTTTCGGC GGAGGACCAAGGTG GAGATCAAAACGAACG GTGGCTGCACCATCT GTCTTCATCTTCCCG CCATCTGATGAGCAG	GAGGTACAACTGGTGGAATCAGGTGGAGGTTTGGTGCAGCCGGGGAG ATCGCTCAGGCTTAGCTGTGCGGCATCGGGGTTTACTTTCGATGATT ATGCCGATGCATTGGGTCCGGCAAGCGCCTGGAAAAGGGCTCGAGTGG GTTTCCGCCATTACGTGGAATAGCGGACACATCGATTATGCAGACAG TGTGGAGGCAGATTCACAATCTCACGAGACAAATGCTAAGAACAGCC TGTAACCTTCAGATGAACCTCACTTCGGCGGGAAGATACCGCCGTATAC TACTGCGCCAAAAGTCTCCTACTTGTCTACAGCTTCGTCGCTCGACTA TTGGGGTCAAGGAACGTTGGTCAACCGTCTCTAGTACGGTGGCTGCAC CATCTGTCTTCACTCTTCCCGCCATCTGATGAGCAGTTGAAAATCTGGA ACTGCCCTCTGTTGTGTGCCCTGCTGAATAACTTCTATCCAGAGAGGC CAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAACTCCC AGGAGAGTGTCA CAGAGCAGGACAGCAAGCAAGGACAGCACCTACAGCCTC AAGAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAAACACAAAAGT CTACGCCCTGCGAAGTCACCCCATCAGGGCCTGAGCTCGCCCGTCACAA AGAGCTTCAACACAGGGGAGAGTGTGACAAAACCTCACACATGCCCACCG TGCCCAAGCACCTGAACTCCTGGGGGACCGTCAGTCTTCTCTTCCC CCCAAAACCCAAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCA CATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAAGTTC AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAAGCC GTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTGTGTCAGCGTCCCTCA CCGTCCCTGCACCCAGGACTGGCTGAA TGGCAAGGAGTACAAAGTGCAAG GTCTCCAACAAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAAGGCGAGCCCGGAGAAACCA CAGGTGTACACCCCTGCCCCCAT CCCCGGGAGGAGATGACCAAGAACCAAGGT CAGCCTGACCTGCCCTGGTC AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAAACAACTACAAGACCACGCTCCCGTGGTGGACTCCG	GATATCCAAATGACA CAATCACCATCGTCG CTTTCAGCGTCTGTT GGCGACCGTGTGACG ATTACCTGTCGCGG TCCCAGGGAATCCGG AATTACCTGTCGCGG TATCAGCAAAAACCC GGA AAAACCCGAAG CTCCTGATCTATGCC GCCTCGACTCTTCAG AGTGGTGTCCGTCG AGGTTAGCGGTCC GGTCAGGTACGGAC TTTACTCTACAATT TCCAGCCTGCAGCCC GAAGATGTAGCTACC TATTACTGCCAGAGA TACAACCGAGCGCCT TACACATTCCGACAA GGGACAAAAGTCGAG ATCAAGCGTGCCTCC ACCAAGGCCCATCG GTCTTCCCCCTGGCA CCCTCCTCCAAGAGC ACCTCTGGGGGCACA

		TTGAAATCTGGTACC G CCTCTGTTGTGTGC CTGCTGAATAAACTTC TATCCCAGAGAGGCC AAAGTACAGTGGAAG GTGGATAACGCCCTC CAATCGGGTAACTCC CAGGAGAGTGTACACA GAGCAGGACAGCAAG GACAGCACCTACAGC CTCAAGAGCACCCCTG ACGCTGAGCAAAAGCA GACTACGAGAAACAC AAAGTCTACGCCCTGC GAAGTCACCCATCAG GGCCTGAGCTCGCCC GTCACAAAAGAGCTTC AACAGGGAGAGTGT	ACGGCTCCTTCTTCCCTCTATAGCAAAGCTCACCGTGGACAAAGAGCAGG TGGCAGCAGGGGAACGTCTTCTCATGTCTCCGTGATGCATGAGGCTCT GCACAACCACTACACGACAGAGAGCCTCTCCCTGTCTCCGGTGGTG GCGGATCGGAGGTGGCGGATCCCAGGTACAGTTGCAGGAGTCAGGT CCAGGACTGTTAAGCCCTCGGAGACCCCTCTCACTACCTGTACCAT CTCCGGGACAGTGTCTCTACCAACAGTGTGCTTGGAACCTGGATTA GGCAGCCCCAGGAAAGCCCTTGAGTGGATAGGAAGGACATACTAC AGGTCCAAGTGGTAAATGATTATGCAGTTTCTCTGAAAAGTCGAGT AACCATCAGCCCCAGACACATCCAAGAACCAAGTTCTCCCTGAAGCTGA GCTCTGTGACTGCCGCGGACACGGCTGTGATTACTGTGCAAGAGAG GATGGGATAGCTACTACCGCTACGGTATGGACGTCTGGGGCCAAGG GACCACGGTCACCGTCTCTCAGCCTCCACCAGGGCCCATCGGTCT TCCCCCTGGACCCCTCCTCCAAGAGCACCTCTGGGGCACAGCGGCC CTGGGCTGCCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTC GTGGAACCTCAGCGCCCTGACCAGCGGCTGCACACCTTCCC GGCTG TCCTACAGTCCTCAGGACTCTACTCCCTCGAGAGCGTGGTGACCCGTG CCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCA CAAGCCCAGCAACACCAAGGTGGACAAAGAAAGTTGAGCCCCAAATCTT GT	GCGGCCCTGGGCTGC CTGGTCAAGGACTAC TTCCCCGAACCGGTG ACGGTGTCTGTGAAC TCAGGCGCCCTGACC AGCGCGTGCACACC TTCCCCGGCTGTCCTA CAGTCCCTCAGGACTC TACTCCCTCGAAAGC GTGGTGACCGTGCCC TCCAGCAGCTTGGGC ACCCAGACCTACATC TGCAACGTGAATCAC AAGCCCAGCAACACC AAGGTGGACAAAGAA GTTGAGCCCCAAATCT TGT
		SEQ ID NO:85	SEQ ID NO:86	SEQ ID NO:87
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		SEQ ID NO:88	SEQ ID NO:89	SEQ ID NO:90

1PS: 376659	016_3.2_CL(S176K)_Fc_3B3v2_VH_CH1(S183E)	NA	GAAATTGTGTTGACG CAGTCTCCAGGCACC CTGTCTTTGTCTCCA GGGAAAGAGCCACC CTCTCCTGCAGGGCC AGTCAGAGTGTTAGA AGCAGTTACTTAGCC TGGTACCAGCAGAAA CCTGGCCAGGCTCCC AGGCTCCTCATCTAT GGTGCAATCCAGCAGG GCCACTGGCATCCCA GACAGGTTCAGTGGC AGTGGGTCTGGGACA GACTTCACCTCTCACC ATCAGCAGACTGGAG CCTGAAGATTTTGCA GTGTATTACTGTCTAG CAGTATGGTAGCTCA CCTACCTTCGGCCAA GGGACACGACTGGAG ATTAAACGAACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGTACCGCC TCTGTTGTGTGCCCTG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCCCAG GAGAGTGTACACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC AAGAGCACCCCTGACG CTGAGCAAAAGCAGAC	GAGGTGCAGCTGGTG GTCTCTAAAGATCTC ACTGGATCGGCTGGT ATGGGGATCATCTAT CTTCCAAGGCCAGGT CCTACCTGCAGTGGAG TACTGTGCGAGAAGTA CCTGGTACCCGTCTCT TGTTCCCCCCTCCTCT GTGTGTCTGATCAGTGA GAAGGCAGATGGCAGC CCTCCAAAACAGAGCA CTGACGCCCCGAGCAG CACGCATGAAGGGAGCA GTTCAGACAAAACACT CTGGGGGACCGTCA CCTCATGATCTCCCGA TGAGCCACGAAGACCC GTGGAGGTGCATAA CAGCACGTACCCGTT GGCTGAATGGCAAGGA CCAGCCCCCATCGAGA AGAACCAACAGGTGT AGAACCACAGGTGTAC AGAACCAAGTCAAGCT GACATCGCCGTGGAGT CAAGACCACGCCCTCC ATAGCAAGCTCACCCTG TTCTCATGCTCCGTGAT GAAGAGCCTCTCCCTGT GATCCCAGGTGCAGTTA TCGGAGACCCCTGTCC TGGTTACTACTGGAAC AGTGGAATTGGGAAATC TCCCTCAAGAGTCGAGT GTTCTCCCTGACGCTGA ATTACTGTGCGAGAGGA TACTGGGGCCAGGGAAC	GAGGTGCAGCTGGAG GTCTGTAAAGATCTCT ACTGGATCGGCTGGTG ATGGGGATCATCTAT CTTCCAAGGCCAGGT CCTACCTGCAGTGGAG TACTGTGCGAGAAGTA CCTGGTACCCGTCTCT TGTTCCCCCCTCCTCT GTGTGTCTGATCAGTGA GAAGGCAGATGGCAGC CCTCCAAAACAGAGCA CTGACGCCCCGAGCAG CACGCATGAAGGGAGCA GTTCAGACAAAACACT CTGGGGGACCGTCA CCTCATGATCTCCCGA TGAGCCACGAAGACCC GTGGAGGTGCATAA CAGCACGTACCCGTT GGCTGAATGGCAAGGA CCAGCCCCCATCGAGA AGAACCAACAGGTGT AGAACCACAGGTGTAC AGAACCAAGTCAAGCT GACATCGCCGTGGAGT CAAGACCACGCCCTCC ATAGCAAGCTCACCCTG TTCTCATGCTCCGTGAT GAAGAGCCTCTCCCTGT GATCCCAGGTGCAGTTA TCGGAGACCCCTGTCC TGGTTACTACTGGAAC AGTGGAATTGGGAAATC TCCCTCAAGAGTCGAGT GTTCTCCCTGACGCTGA ATTACTGTGCGAGAGGA TACTGGGGCCAGGGAAC	CAGTCTGTGCTGACG CAGCCGCCCTCAGTG TCTGGGGCCCCAGGG CAGAGGTCACCATC TCCTGCACCTGGGAGC AGTTCCAAACATCGGG GCAGGTTATGATGTA CACTGGTACCAGCAG TTTCCAGGAACAGCC CCCAAACCTCCTCATC CAAGGTAAACAGCAAT CGGCCCTCAGGGGTC CCTGACCGATTCTCT GGTCCAAAGTCTGGC ACCTCAGCCTCCCTG GCCATCACTGGGCTC CAGGCTGAGGATGAG GCTGATTATTACTGC CAGTCCATATGACAGC AGCCTGAGTGGTTCG GTGTTCGGCGGAGGG ACCAAAGCTGACCGTC CTAGGTGCCCTCCACC AAGGGCCCCATCGGTC TTCCCCCTGGCACCC TCCTCCAAAGAGCAC TCTGGGGGCACAGCG GCCCTGGGCTGCCCTG GTCAAAGACTACTTC CCCGAACCCGGTGACG GTGTCTGTGAACTCA GGCGCCCTGACCCAGC GGCGTGCACACCTTC CCGGCTGTCCCTACAG TCCTCAGGACTCTAC TCCCTCGAAAGCGTG GTGACCCGTGCCCTCC
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			TACGAGAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	GGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTG GGGGCACAGCGGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCCGAA CCGGTGACGGTGTCGTGAACTCAGCGCCCTGACCAAGCGCGTGCA CACCTTCCCGGCTGTCTACAGTCTCTCAGGACTCTACTCCCTCGAGA GCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATC TGCAACGTGAATCACAAAGCCAGCAACACCAAGGTGGACAAGAAAGT TGAGCCCCAAATCTTGT	AGCAGCTTGGGCACC CAGACCTACATCTGC AACGTGAATCACAAAG CCCAGCAACACCAAG GTGGACAAAGAAAGTT GAGCCCCAAATCTTGT
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	AA		EIVLTQSPGTLISLSP GERATLSCRASQSVR SSYLAWYQQKPGQAP RLLIYGASSRATGIP DRFSGSGTDFTLT ISRLEPEDFAVYYCQ QYGSSTFFGQGRLE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLKSTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEN	EVQLVQSGAEVKKPGESLKISCKTSEYSFYSYWGVRQMPGKGLEW MGI IYLGDS DTRYSPSFQGQVTI SADKSI STAYLQWSSLKASDTAMY YCARSNWGLDYWGQGLVTIVSSQPKANPTVTLFPPSSEELQANKATL VCLISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAAKSYLS LTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECSDKTHHTCPPCPAPEL LGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMEALHNHYTQKSLSLSPGGGGSGGSQVQLQQSGAGLLKP SETLSLTCAVHGGSFSGYYWNWIRQPPGKLEWIGEINHAGNTNYP SLKSRVTISLDTSKNQFSLTLTSVTAADTAVYYCARGYCRSTTCYFD YWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSGLYSLESVVTVPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKSC	QSVLTQPPPSVSGAPG QRVTISCTGSSSNIG AGYDVHWYQQFPGTA PKLLIQNSNRPSGV PDRFSGSKSGTSASL AITGLQAEDEADYYC QSYDSSLSGSVFGGG TKLTVLGASTKGPSV FPLAPSSKSTSGGTA ALGCLVKDYFPEPVT VSWNSGALTSGVHTF PAVLQSSGLYSLESV VTVPSSSLGTQTYIC NVNHHKPSNTKVDKKV EPKSC
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1PS: 376665	017_3.2 CL(S176K)_Fc_9 C8_VH_CH1(S183E)	NA			

		GGATCTGGGACAGAT TTCACTCTCACCATC AGCAGTCTGCAACCT GAAGATTTTGCAACT TACTACTGTCAACAG AGTTACAGTACCCCT CGGACGTTCCGGCCAA GGGACCAAGCTGGAA ATCAAAACGAACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGTACCGCC TCTGTTGTGTGCCCTG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCCAG GAGAGTGTACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC AAGAGCACCCCTGACG CTGAGCAAAAGCAGAC TACGAGAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	CACGCA TG AAGGAGCACCGTGGAGAA GACAGTGGCCCCCTACAGAAT GTTCAGACAAAACTCACACATGCCCAACCGTGCCCAAGCACCTGAACTC CTGGGGACCCGTAGTCTTCTCTTCCCCCAAACCCAAAGACAC CCTCATGATCTCCCGACCCCTGAGGTCACATGCGTGGTGGACG TGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAA TGCCAAAGACAAAGCCGTGTGAGGAGCAGTACGG CAGCACGTACCGTTGTGTGTCAGCGTCTCACCGTCTTGCAACCAGGACT GGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTC CCAGCCCCCATCGAGAAAAACCATCTCCAAGCCAAAGGCAGCCCCG AGAAACCACAGGTGTACACCCCTGCCCCCATCCCGGAGGAGATGACCA AGAAACCAGGTCA GCCCTGACCTGCCCTGGTCAAAGGCTTCTATCCCAGC GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAACAACTA CAAGACCACGCCCTCCCGTGTCTGGACTCCGACGGCTCCTTCTTCCCTCT ATAGCAAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCA GAAGAGCCTCTCCCTGTCTCCGGGTGGTGGCGGATCGGGAGGTGGCG GATCCCAGGTGCAGCTGCAGGAGTCCGGGCCAGGACTGGTGAAGCCT TCGGAGACCCCTGTCCCTCACCTGCATGTCTCTGTGTGGCTCCATCAG TAGTTACTTCTGGAGCTGGATTCCGGCAGCCCCCAGGTAAGGACTGG AGTGGATTGGCTATA TCTATTACAGTGGCAGACCAATAACAACCCC TCCCTCAAGAGTCGAGTCACCATATCAATAGACACGTCCAAGAAACCA GTTCTCCCTGAAAGCTGAGCTCTGTGACCGCTGCGGACACGGCCGTGT ATTACTGTGCGAGAGAAACTGGGAGCTACTACGGCTTTGACTACTGG GGCCAGGGAACCCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCC ATCGGCTTTCGCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGCA CAGCGGCCCTGGGCTGCCGTGTTCAAGGACTACTTCCCCGAACCGGTG ACGGTGTCGTGGAAC TCAAGCGCCCTGACCAGCGCGTGCACACCTT CCCCGCTGTCTACAGTCTCTCAGGACTCTACTCCCTCGAGAGCGTGG TGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAAC GTGAATCACAAAGCCCAGCAACACCAAGGTGGACAAAGAAAGTTGAGCC CAAA TCTTGT	SEQ ID NO: 97	SEQ ID NO: 98	SEQ ID NO: 99
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			SSLQPEDFATYYCQQ SYSTPRTFGQTKLE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLKSTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEN	LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMEALHNHYTQKSLSLSPGSGGSGGSQVQLQESGPGLVKP SETLSLTCTVSGGSISSYFWSWIRQPPGKLEWIGIYIYSGQTKYNP SLKSRVTISIDTSKNQFSLLKLSVTAADTAVYYCARETGSYYGFDYW GQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLESVTVTPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSC	AITGLQAEDEADYYC QSYDSSLSGSVFGGG TKLTVLGASTKGPSV FPLAPSSKSTSGGTA ALGCLVKDYFPEPVT VSWNSGALTSGVHTF PAVLQSSGLYSLESV VTVPSSSLGTQTYIC NVNHHKPSNTKVDKKV EPKSC
			SEQ ID NO:100	SEQ ID NO:101	SEQ ID NO:102
	018_3.2_CL(S176K)_Fc_23B3_VH4_VH_CH1(S183E)	NA	GACATCCAGATGACC CAGTCTCCAAGCTCC CTGTCTGCGTCTGTG GGCGATAGGGTCACC ATCACTTGCAGGTCC AGCCAGAGTGTTTA TACAGCTCCAACAAT AAGAACTACTTAGTT TGGTACCAGCAGAAA CCAGGAAAGGTTCCCT AAACTGCTCATTAC TGGGCATCTACCCGG GAATCCGGGGTCCCT AGTCGATTCAGTGGC AGCGGGTCTGGGACA GATTTCACCTCACC ATCAGCAGCCTGCAG CCTGAAGATGTGGCA ACTTATTACTGTCAG CAATATTAAGACT CCTCTCACTTTCGGC GGAGGACCAAGGTG GAGATCAAAACGAACG GTGGCTGCACCATCT GTCTTCATCTTCCCG CCATCTGATGAGCAG	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCCGGGGA GTCTCTGAAGATCTCCTGTAAGACTTCTGAATACAGCTTTACCAGCT ACTGGATCGGCTGGTGCGCCAGATGCCGGGAAAGGCCCTGGAGTGG ATGGGGATCATCTATCTTGGTGACTCAGATACCAGATACAGCCCCGTC CTTCCAAGGCCAGGTCAACATCTCAGCCGACAAAGTCCATCAGTACCG CCTACCTGCAGTGGAGCAGCCTGAAGGCTCGGACACCGCCCATGTAT TACTGTGCGAGAAGTAACCTGGGCTCTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTCTCTAGTCAAGCCCAAGCCCAACCCCACTGTCACTC TGTTCCCGCCCTCCTCTGAGGAGCTCCAAGCCCAACAAGGCCACACTA GTGTGCTGATCAGTGACTTCTACCCGGAGCTGTGACAGTGGCCTG GAAGGCAGATGGCAGCCCCGTCAAGCGGGAGTGGAGACCACCAAAAC CCTCCAACAGAGCAACAACAAGTACGCGGCCAAGAGCTACCTGAGC CTGACGCCCGAGCAGTGGAAGTCCCAAGAACTACAGCTGCCAGGT CACGCATGAAGGGAGCACCGTGAGAGAAGACAGTGGCCCCTACAGAAAT GTTCAGACAAAACCTCACACATGCCCAACCGTGCCAGCACCTGAACCTC CTGGGGGACCGTCAGTCTTCCTCTTCCCCCCTCAAAACCCAAAGGACAC CCTCATGATCTCCCGACCCCTGAGGTCACATGCGTGGTGGACG TGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGTGAGGAGCAGTACGG CAGCACGTACCCTGTGTGTCAGCGTCCCTCACCGTCTGCACCGGACT GGCTGAATGGCAAGGAGTACAAAGTGCAAGGTCTCCAACAAAGCCCTC CCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGCAGCCCCG AGAAACCACAGGTGTACACCTTGCCCTCCCATCCCGGAGGAGATGACCA AGAAACCAGGTCAAGCTGACCTGCCCTGGTCAAAGGCTTCTATCCCAGC GACATCGCCGTGAGTGGAGAGCAATGGCAGCCGAGAGAAACAATA CAAGACCACGCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCCTCT	CAGTCTGTCTGACG CAGCCGCCCTCAGTG TCTGGGGCCCCAGGG CAGAGGGTCACCATC TCCTGCACTGGGAGC AGTTCCAAACATCGGG GCAGGTTATGATGTA CACTGTACCAGCAG TTTCCAGGAACAGCC CCCAAACTCCTCATC CAAGGTAACAGCAAT CGGCCCTCAGGGGTC CCTGACCGATTCTCT GGTCCAAAGTCTGGC ACCTCAGCCTCCCTG GCCATCACTGGGCTC CAGGCTGAGGATGAG GCTGATTATTACTGC CAGTCCCTATGACAGC AGCCTGAGTGGTTCG GTGTTGGGGGAGGG ACCAAGCTGACCGTC CTAGGTGCCCTCCACC AAGGGCCCATCGGTC TTCCCCCTGGCACCC TCCTCCAAGAGCAC

		TTGAAATCTGGTACC GCC TCTGTTGTGTGC CTGCTGAATAAACTTC TATCCCAGAGAGGCC AAAGTACAGTGAAG GTGGATAACGCCCTC CAATCGGGTAACTCC CAGGAGAGTGCACA GAGCAGGACAGCAAG GACAGCACCTACAGC CTCAAGAGCACCCCTG ACGCTGAGCAAAAGCA GACTACGAGAAACAC AAAGTCTACGCCCTGC GAAGTACCCCATCAG GGCCTGAGCTCGCCC GTCACAAAAGAGCTTC AACAGGGAGAGTGT	ATAGCAAGCTCACCGTGGACAAAGAGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAACCACTACACGCA GAAGAGCCTCTCCCTGTCTCCGGGTGGTGGCGATCGGAGGTGGCG GATCCCAGGTACAGTTGCAGGAGTCAGGTCCAGGACTGGTGAAGCCC TCGGAGACCCCTCTCACTCACCTGTACCATCTCCGGGACAGTGTCTC TACCAACAGTGTGCTTGGAAC TGGATTAGGCAGCCCCCAGGGAAG GCCTTGAGTGGATAGGAAGGACATATA CAGGTCCAAGTGGTATAAT GATTATGCAGTTTCTGAAAAGTCGAGTAACCATCAGCCCAGACAC ATCCAAGAAACCA GTTCTCCCTGAAGCTGAGCTCTGTGACTGCCGCGG ACACGGCTGTGTA TTACTGTGCAAGAGAGGATGGGATAGCTACTAC CGTACGGTATGGACGCTCTGGGCCAAGGACCA CGGTCAACCGTCTC CTCAGCCCTCACCAAGGCCCATCGGTCTTCCCCCTGGCACCCCTCCT CCAAAGACACCTCTGGGGCACAGCGGCCCTGGGCTGCC TGGTCAAG GACTACTTCCCCGAACCGGTGACGGTGTCTGTGGA ACTCAGGCGCCCT GACCAGCGCGTGCA CACCTTCCC GGCTGTCTCTACAGTCTCAGGAC TCTACTCCCTCGAGAGCGTGTGACCGTGCCCTCCAGCAGCTTGGGC ACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAA GGTGGACAAAGATTGAGCCCCAAATCTTGT	TCTGGGGGCACAGCG GCC TGGGCTGCCCTG GTCAAGGACTACTTC CCCGAA CCGGTGACG GTGTCGTGGA ACTCA GGGCCCTGACCAGC GGCGTGCACACCTTC CCGGCTGTCC TACAG TCCTCAGGACTCTAC TCCCTCGAAAGCGTG GTGACCGTGCCCTCC AGCAGCTTGGGCACC CAGACCTACATCTGC AACGTGAATCACAAG CCCAGCAACACCAAG GTGGACAAAGAA GTT GAGCCCCAAATCTTGT
		SEQ ID NO:103	SEQ ID NO:104	SEQ ID NO:105
	AA	DIQMTQSPSSLSASV GDRVITITCRSSQSVL YSSNNKNYLVWYQQK PGKVPKLLIYWASTR ESGVPSRFSGSGSGT DFTLTISLQPEDVA TYYCQQYYKTPLTFG GGTKVEIKRTVAAPS VFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGNS QESVTEQDSKDS TYS LKSTLTLSKADYEKH KVYACEVTHQGLSSP VTKSFNRGEC	EVQLVQSGAEVKKPGESLKISCKTSEYFTSYWIGWVRQMPKGLEW MGI IYLGDS DTRYSPSFQGQVTISADKSI STAYLQWSSSLKASDTAMY YCARSNWGLDYWGQGT LVTVSSQPKANPTVTLFPPSSEELQANKATL VCLISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAAKS YLS LTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECSDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYK TTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMH EALHNHYTQKSLSLSPGGGGSGGSQVQLQESGPGLVKP SETLSLTCTISGDSVSTNSVAWNWIRQPPGKGLEWIGRTYYRSKWYN DYAVSLKSRVTISPDTSKNQFSLKLSSTAAADTAVYYCARE DGD SY Y RYGMDVWGQGT TTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLESVVTVPSSSLG TQTYICNVNHKPSNTKVDKKVEPKSC	QSVLTQPPSVSGAPG QRVTISCTGSSSNIG AGYDVHWYQQFPGTA PKLLIQGNSNRPSGV PDRFSGSKSGTSASL AITGLQAEDEADYYC QSYDSSLSGSVFGGG TKLTVLGASTKGPSV FPLAPSSKSTSGGTA ALGCLVKDYFPEPVT VSWNSGALTSGVHTF PAVLQSSGLYSLESV VTVPSSSLGTQTYIC NVNHKPSNTKVDKKV EPKSC
		SEQ ID NO:106	SEQ ID NO:107	SEQ ID NO:108

1PS: 376673	019_3B3v2_CK(S176K)_Fc_Ada1immunab_VH_CH1(S183F)	NA	GATATCCAAATGACA CAATCACCATCGTCG CTTTCAGCGTCTGTT GGCGACCGTGTGACG ATTACCTGTCGCGG TCCCAGGGAATCCGG AATTACCTCGCATGG TATCAGCAAAAACCC GGAAAAGCACCGAAG CTCCTGATCTATGCC GCCTCGACTCTTCAG AGTGGTGTCCTGTCG AGGTTTAGCGGTCC GGGTCAAGTACGGAC TTTACTCTCACAAAT TCCAGCCTGCAGCCC GAAGATGTAGCTACC TATTACTGCCAGAGA TACAACCGAGCCCT TACACATTGGACAA GGGACAAAAGTCGAG ATCAAGCGTACGGTG GCTGCACCATCTGTC TTCATCTTCCCCCA TCTGATGAGCAGTTG AAATCTGGAAC TGCC TCTGTTGTGTCCTG CTGAATAACTTCTAT CCCAGAGAGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCCCAG GAGAGTGTACACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC AAGAGCACCCCTGACG CTGAGCAAAAGCAGAC	CAGGTGCAGTTACAGCAGTCGGGCGCAGGACTGTTGAAGCCTTTCGGA GACCCCTGTCCCTCACCTGCGCTGTCCATGGTGGTCCCTTCAGTGGTT ACTACTGGAAC TGGATTGCGCAGCCACCAGGAAAGGGCTAGAGTGG ATTGGGGAAATCAATCATGCTGGAAACACCAACTACAACCCGTCCCT CAAAGATCGAGTCACCATATCATTAGACACGTC CAAGAACCAGTTCT CCCTGACGCTGACCTCTGTGACCGCGCGGACACGGCTGTGTATTAC TGTCGAGAGGATATTGTAGAAGTACCACCTGCTACTTTGACTACTG GGCCAGGGAACCTAGTCACCGTCTCCTCAACGGTGGCTGCACCAT CTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAAATCTGGAACT GCC TCTGTTGTGCTGCTGCTGAATAACTTCTATCCAGAGAGGCCAA AGTACAGTGGAAGGTGGATAACGCCCTCCAAATCGGGTAACTCCCAGG AGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAAG AGCACCCTGACGCTGAGCAAAAGCAGACTACGAGAAACACAAAAGTCTA CGCCTGCCAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGA GCTTCAACAGGGGAGAGTGTGACAAAAC TCAACATGCCACCCGTGC CCAGCACCTGAACTCCTGGGGACCGTCAGTCTTTCCTCTTCCCCC AAAACCCCAAGGACACCC TCATGATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGACGTGAGCCACGAAACCCCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGTG TGAGGAGCAGTACGGCAGCACGTACC GTTGTGTCA GCGTCC TCACCG TCCTGCAC CAGGACTGGCTGAA TGGCAAAGGAGTACAAGTGCAAGTCTC TCCAACAAAAGCCCTCCCAGCCCCCATCGAGAAAAACCATCTCCAAAGC CAAAGGCAGCCCCGAGAAC CACAGGTGTACACCTGCCCCCATCCC GGGAGGAGATGACCAAGAAC CAGGTCA GCTGACCTGCCCTGGTCAAA GGCTTC TATCCAGCGACATCGCCGTGGAGTGGAGAGCAATGGGCA GCCGGAGAA CAACTACAAGACCA CGCCTCCCGTGTGGACTCCGACG GCTCCTTCTTCC TCTATAGCAAAGCTCACCGTGGACAAGACAGGTGG CAGCAGGGGAACGCTTCTCATGTCTCCGTGATGCATGAGGCTCTGCA CAACCACTACACGCAGAAAGCCCTCTCCCTGTCTCCGGGTGGTGGCG GATCGGAGGTGGCGGATCCGAGGTACAAC TGGTGAATCAGGTGGA GGTTTGGTGCAGCCGGGAGATCGCTCAGGCTTAGCTGTGCGGCATC GGGGTTTACTTTTCGATGATTATGCGATGCAT TGGGTCCGGCAAGCGC CTGGAAAAGGCTCGAGTGGGTTTCCGCCATTACGTGGAATAGCGGA CACATCGATTATGCAGACAGTGTGGAGGGCAGATTCACAATCTCACG AGACAA TGCTAAGAACAGCCTGTACCTTCAGATGAAC TCACTTCGCG CGGAAGATA CCGCCGTATACTACTGCGCCAAAGTCTCCTACTTGTCT ACAGCTTCGTCGCTCGACTATTGGGGTCAAGGAACGTTGGTCA CCGT	GAAATTGTGTTGACG CAGTCTCCAGGCACC CTGTCTTTGTCTCCA GGGAAAAGAGCCACC CTCTCCTGCAGGGCC AGTCAGAGTGTTAGA AGCAGTTACTTAGCC TGGTACCAGCAGAAA CCTGGCCAGGCTCCC AGGCTCCTCATCTAT GGTGCA TCCAGCAGG GCCACTGGCATCCCA GACAGGTTCAGTGGC AGTGGGTCTGGGACA GACTTCAC TCTCACC ATCAGCAGACTGGAG CCTGAAGATTTTGCA GTGATTACTGT CAG CAGTATGGTAGCTCA CCTACCTTCGGCCAA GGGACACGACTGGAG ATTAAA CAGACCCTCC ACCAAGGCCCATCG GTCTTCCCCCTGGCA CCCTCCTCCAAGAGC ACCTCTGGGGCACA GCGGCCCTGGGCTGC CTGGTCAAGGACTAC TTCCCCGAACCCGTG ACGGTGTCTGTGAAC TCAGGCGCCCTGACC AGCGGCGTGCA CACC TTCCCCGGCTGTCCTA CAGTCTCAGGACTC TACTCCCTCGAAAGC GTGGTGACCGTGCCC TCCAGCAGCTTGGGC
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		TACGAGAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGAGAGTGT	CTCTAGTGCCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCT CCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCCTGGTC AAGGACTACTTCCCCGAACCGGTGACGGTGTGCGTGAACCTCAGGCGC CCTGACCAGCGGTGCACACCTTCCCCGGCTGTCTACAGTCCTCAG GACTCTACTCCCTCGAGAGCGTGTGACCGTGCCCTCCAGCAGCTTG GGCACCAGACCTACATCTGCAACGTGAATCACAAAGCCCAGCAACAC CAAGGTGGACAAAGAAAGTTGAGCCCCAAAATCTTGT	ACCCAGACCTACATC TGCAACGTGAATCAC AAGCCAGCAACACC AAGGTGGACAAGAAA GTTGAGCCCCAAATCT TGT
		SEQ ID NO:109	SEQ ID NO:110	SEQ ID NO:111
AA		DIQMTQSPSSLSASV GDRVITITCRASQGIR NYLAWYQQKPGKAPK LLIYAASTLQSGVPS RFGSGSGTDFTLTI SSLQPEDVATYYCQR YNRAPYTFGQGTKVE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLKSTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEN	QVQLQQSGAGLLKPSSETLSLTCAVHGGSFSGYYWNWIRQPPGKGLEW IGEINHAGNTNYPNPSLKSRVTISLDTSKNQFSLTLTSVTAADTAVYY CARGYCRSTTCYFDYWGGQLVTVSSSTVAAPSVFIFPPSDEQLKSGT ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLK STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECDKHTTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW QQGNVFCSCVMHEALHNYHQKLSLSLSPGGSGGGSEVQLVESGG GLVQPGRSRLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVAITWNSG HIDYADSVETRFTISRDNAKNSLYIQMNSLRAEDTAVYYCAKVSYLS TASSLDYWGGQLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLESVVTVPSSSL GTQTYICNVNHPKPSNTKVDKKVEPKSC	EIVLTQSPGTLSLSP GERATLSCRASQSVR SSYLAWYQQKPGQAP RLLIYGASSRATGIP DRFSGSGSDFTLT ISRLEPEDFAVYYCQ QYSSPTFGQTRLR IKRASTKGPSVFPLA PSSKSTSGGTAALGC LVKDYFPEPVTVSWN SGALTSGVHTFPAVL QSSGLYSLESVVTVP SSSLGTQTYICNVNH KPSNTKVDKKVEPKS C
		SEQ ID NO:112	SEQ ID NO:113	SEQ ID NO:114
		CAGTCTGTGCTGACG CAGCCGCCCTCAGTG TCTGGGGCCCCAGGG CAGAGGGTCACCATC TCCTGCAC TGGGAGC AGTTCCCAACATCGGG GCAGGTTATGATGTA CACTGGTACCAGCAG TTTCCAGGAACAGCC CCCCAAACTCCTCATC CAAGGTAAACAGCAAT CGGCCCTCAGGGGTC CCTGACCGATTCTCT	CAGGTGCAGTTACAGCAGTCGGGGCGCAGGACTGTTGAAGCCTTCGGA GACCCGTGTCCTCACCTGCGCTGTCCATGGTGGTCTCTCAGTGTT ACTACTGGAAC TGGATTCCGCCAGCCACCAGGAAGGGCTAGAGTGG ATTGGGGAAATCAATCATGCTGGAACACCAACTACAACCCGTCCCT CAAGAGTCGAGTCACCATATCATTAGACACGTCCAAGAACCAAGTTCT CCCTGACGCTGACCTCTGTGACCGCGCGGACACGGCTGTGTATTAC TGTGCGAGAGGATATTGTAGAAGTACCACCTGCTACTTTGACTACTG GGCCAGGGAACCTAGTCACCGTCTCCTCAACGGTGGCTGCACCAT CTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAC T GCCCTCTGTTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAA AGTACAGTGGAAGGTGGATAACGCCCTCCAAATCGGGTAACTCCCCAGG AGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAAG AGCACCCCTGACGCTGAGCAAAAGCAGACTACGAGAAACACAAAAGTCTA	GAAATTGTGTTGACG CAGTCTCCAGGCACC CTGTCTTTGTCTCCA GGGAAAAGAGCCACC CTCTCCTGCAGGGCC AGTCAGAGTGTTAGA AGCAGTTACTTAGCC TGGTACCAGCAGAAA CCTGGCCAGGCTCCC AGGCTCCTCATCTAT GGTGCA TCAGCAGG GCCACTGGCATCCCA GACAGGTTCAGTGGC
		NA		
!PS: 376679	020_3B3v2_CK (S176K)_Fc _3.2_VH_CH1 (S183E)			

		GGCTCCAAGTCTGGC ACCTCAGCCTCCCTG GCCATCACTGGGCTC CAGGCTGAGGATGAG GCTGATTATTACTGC CAGTCCATATGACAGC AGCCTGAGTGGTTCCG GTGTTCCGGGAGGG ACCAAGCTGACCGTC CTAGGTCAGCCCAAG GCTGCCCTTCGGTC ACTCTGTTCCCGCCC TCCTCTGAGGAGCTT CAAGCCAAACAAGGCC ACACTGGTGTGTCCTC ATAAGTGACTTCTAC CCGGGAGCCGTGACA GTGGCCTGGAAGGCA GATAGCAGCCCCGTC AAGCGGGAGTGGAG ACCAACACACCTCC AAACAAAGCAACAAC AAGTACGGGCCAAG AGCTATCTGAGCCTG ACGCCTGAGCAGTGG AAGTCCCACAGAAGC TACAGCTGCCAGGTC ACGCATGAAGGGAGC ACCGTGAGAAAGACA GTGGCCCCTACAGAA TGTTCA	CGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGA GCTTCAACAGGGGAGAGTGTGACAAAACCTCACACATGCCCCACCGTGC CCAGCACCTGAACCTCCTGGGGACCGTCAGTCTTTCCTCTTCCCCCCC AAAACCCAAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGACCTGAGCCACGAAGACCCCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGAGACAAAGCCGTG TGAGGAGCAGTACGGCAGCACGTACCGTTGTGTGTCAGCGTCCTCACCG TCCTGCACCCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTC TCCAAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGC CAAAGGCAGCCCCGAGAACCACAGGTGTACACCCCTGCCCCCATCCC GGGAGGAGATGACCAAGAACCAAGTCAAGCTGACCTGCCCTGGTCAAA GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCA GCCGGAGAAACAATAAGACCAACGCTCCCGTGTGCTGGACTCCGACG GCTCCTTCTTCCCTCTATAGCAAGCTCACCGTGGACAAGCAGGTTGG CAGCAGGGGAACGTCTTCTCATGTCTCCGTGATGCATGAGGCTCTGCA CAACCACTACACGCAAGAGAGCCTCTCCCTGTCTCCGGGTGGTGGCG GATCGGGAGGTGGCGGATCCGAGGTGCAGCTGGTGCAGTCTGGAGCA GAGTGAAAAAGCCCCGGGAGTCTCTGAAGATCTCCTGTAAGACTTC TGAATACAGCTTTACCAGCTACTGGATCGGCTGGGTGGCCAGATGC CCGGAAAGCCCTGGAGTGGATGGGATCATCTATCTTGGTGACTCA GATACCAGATACAGCCCGTCTTCCAAGCCAGGTCAACCATCTCAGC CGACAAAGTCCATCAGTACCGCCTACCTGCAGTGGAGCAGCCCTGAAGG CCTCGGACACCGCCATGTATTACTGTGCGAGAAGTAAC TGGGTCTT GACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCTAGTGCCTCCAC CAAAGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCT CTGGGGGCACAGCGGCCCTGGGCTGCCGTGCTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCTGTGGAAC TCAAGCGCCCTGACCAAGCGCGT GCACACCTTCCCCGGCTGTCTCTACAGTCCCTCAGGACTCTACTCCCTCG AGAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAGCCCAACACCAAGGTGGACAAGAA AGTTGAGCCCCAAATCTTGT	AGTGGGTCTGGGACA GACTTCAC TCTCACC ATCAGCAGACTGGAG CCTGAA GATTTTGCA GTGTATTACTGT CAG CAGTATGGTAGCTCA CCTACCTTCGGCCAA GGGACACGACTGGAG ATTAAACGAGCCTCC ACCAAGGGCCCATCG GTCTTCCCCCTGGCA CCCTCCTCCAAGAGC ACCTCTGGGGCACA GCGGCCCTGGGCTGC CTGGTCAAGGACTAC TTCCCCGAACCCGTG ACGGTGTCTGTGGAAC TCAGGCGCCCTGACC AGCGGCGTGCACACC TTCCCCGGCTGTCCTA CAGTCCCTCAGGACTC TACTCCCTCGAAAGC GTGTGACCGTGCCC TCCAGCAGCTTGGGC ACCCAGACCTACATC TGCAACGTGAATCAC AAGCCCAGCAACACC AAGGTGACAAGAAA GTTGAGCCCCAAATCT TGT
		SEQ ID NO:115 QSVLTQPPSVSGAPG QRVTISCTGSSSNIG AGYDVHWYQQFPGTA PKLLIQGNSNRPSGV PDRFSGSKSGTSASL	SEQ ID NO:116 QVQLQQSGAGLLKPSETLSLTCAVHGGSFSGYYWNWIRQPPKGLEW IGEINHAGNTNYPNPSLKS RVTISLDTSKNQFSLTILTSVTAADTAVYY CARGYCRSTTCYFDYWGQGT LVTVSSSTVAAPSVFI FPPSDEQLKSGT ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLK STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC DKTHTCPPC	SEQ ID NO:117 EIVLTQSPGTL SLSP GERATLSCRASQSVR SSYLAWYQQKPGQAP RLLIYGASSRATGIP DRFSGSGSGTDFTLT

			AITGLQAEDEADYYC QSYDSSLSGSVFGG TKLTVLGQPKAAPSV TLFPPSSEELQANKA TLVCLISDFYPGAVT VAWKADSSPVKAGVE TTTTPSKQSNNKYAAK SYLSLTPEQWKSHRS YSCQVTHEGSTVEKT VAPTECS	PAPELLGGPSVFLFPPKPKD WYVDGVEVHNAKTKPCEEQY SNKALPAPIEKTISKAKGQ GFYPSDIAVEWESNGQPEN QQGNVFC SVMHEALHNHYT EVKKPGESLKISCKTSEYS DTRYSPSFQGVTTISADKSI DYWGQGLTVTVSSASTKGP EPVTVSWNSGALTSGVHTF ICNVNHPKPSNTKVDKKV SEQ ID NO:118	SEQ ID NO:119	ISRLPEDEFAVYQC QYGSSTFFGQGRLE IKRASTKGPSVFPLA PSSKSTSGGTAALGC LVKDYFFPEPVTVSWN SGALTSGVHTFPAVL QSSGLYSLESVVTVP SSSLGTQTYICNVNH KPSNTKVDKKVEPKS C
			GATATCCAAATGACA CAATCACCATCGTCG CTTTCAGCGTCTGTT GGGACCGTGTGACG ATTACCTGTCGCGG TCCCAGGGAATCCGG AATTACCTCGCATGG TATCAGCAAAAACCC GGAAAAGCACCGAAG CTCCTGATCTATGCC GCCTCGACTCTTCAG AGTGGTGTGCCGTGG AGGTTTAGCGGGTCC GGGTCAGGTACGGAC TTTACTCTCACAAATT TCCAGCCTGCAGCCC GAAGATGTAGCTACC TATTACTGCCAGAGA TACAAACCGAGCGCCT TACACATTCCGGACAA GGGACAAAAGTCGAG ATCAAGCGTACGGTG GCTGCACCATCTGTC TTCATCTTCCCCGCA TCTGATGAGCAGTTG AAATCTGGAACTGCC	CAGGTGCAGCTGCAGGAGT GACCCGTCTCCCTCACCT ACTTCTGGAGCTGGATT ATTGGCTATATCTATTAC CAAGAGTCGAGTCACCAT CCCTGAAGCTGAGCTCT TGTCGAGAGAAAAC GGGAACCTGGTCACCGT TCATCTTCCCGCCATCT GTTGTGTGCTGTGAATA GTGGAAGGTGGATAAC TCACAGACGAGACAGCA CTGACGCTGAGCAAAAG CGAAGTCACCCATCAGG ACAGGGGAGAGTGTGAC CCTGAACTCCTGGGGGAC CAAGGACACCCCTCATG TGGTGGACGTGAGCCAC GTGGACGGCGTGGAGGT GCAGTACGGCAGCACGT ACCAAGGACTGGCTGAAT AAAGCCCTCCAGCCCCC GCAGCCCCGAGAACCA AGATGACCAAGAACCA TATCCCAGCGACATCGC GAACAACTACAAGACCA	SEQ ID NO:120	GACATCCAGATGACC CAGTCTCCATCCTCC CTGTCTGCATCTGTA GGAGACAGAGTCACC ATCACTTGCCGGCA AGTCAGAGCATTAAC AACTATTTAAATTGG TATCAGCAGAGACCA GGGAAAAGCCCCTAAG CTCCTGATCTATGCT GCATCCAGTTTGCAA AGTGGGTCCCATCA AGGTTCAGTGGCAGT GGATCTGGGACAGAT TTCACCTCACCATC AGCAGCTGCAACCT GAAGATTTTGCAACT TACTACTGTCAACAG AGTTACAGTACCCCT CGGACGTTCGGCCAA GGGACCAAGCTGGAA ATCAAAACGAGCCTCC ACCAAGGCCCATCG GTCTTCCCCCTGGCA CCCTCCTCCAAGAGC ACCTCTGGGGGCACA

		TCTGTTGTGTGCCTG CTGAATAACTTCTAT CCCAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCAG GAGAGTGCACAGAG CAGACAGCAAGGAC AGCACCTACAGCCTC AAGAGCACCTGACG CTGAGCAAAAGCAGAC TACGAGAAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	TCTTCCTCTATAGCAAGCTCACCGTGGACAAAGAGCAGGTGGCAGCAG GGGAACGTCTTCTCATGTCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGAGAGCCCTCTCCCTGTCTCCGGTGGTGGCGGATCGG GAGTGGCGGATCCGAGGTACAACCTGGTGAATCAGGTGAGGTTTG GTGAGCCGGGAGATCGCTCAGGCTTAGCTGTGCGGCATCGGGGTT TACTTTCGATGATTATGCGATGCATTGGGTCCGGCAAGCCCTGGAA AAGGGCTCGAGTGGGTTTCCGCCATTACGTGGAATAGCGGACACATC GATTATGCAGACAGTGTGGAGGCAGATTCACAATCTCACGAGACAA TGCTAAGAAACAGCCTGTACCTTCAGATGAACCTCACTTCGCGCGGAAG ATACCGCCGTATACTACTGCGCCAAAAGTCTCCTACTGTCTACAGCT TCGTGCTCGACTATTGGGGTCAAGGAACTTGGTCAACCGTCTCTAG TGCCCTCACCAAGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCA AGAGCACCTCTGGGGCACAGCGGCCCTGGGCTGCCCTGGTCAAGGAC TACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCCTGAC CAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCCTCAGGACTCT ACTCCCTCGAGAGCGTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAAGCCCAGCAACACCAAGGT GGACAAAGAAAGTTGAGCCCAAATCTTGT	GCGGCCCTGGGCTGC CTGGTCAAGGACTAC TTCCCCGAACCGGTG ACGGTGTCTGTGAAC TCAGGCGCCCTGACC AGCGCGTGCACACC TTCCCCGGCTGTCCTA CAGTCTCAGGACTC TACTCCCTCGAAAGC GTGGTGACCGTGCCC TCCAGCAGCTTGGGC ACCCAGACCTACATC TGCAACGTGAATCAC AAGCCCAGCAACACC AAGGTGGACAAAGAA GTTGAGCCCCAAATCT TGT
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		SEQ ID NO:124	SEQ ID NO:125	SEQ ID NO:126

1PS: 376689	022_9C8_CR(S176K)_Fc_3.2_VH_CH1(S183F)	NA	CAGTCTGTGCTGACG CAGCCGCCCTCAGTG TCTGGGCCCCAGGG CAGAGGTCACCATC TCCTGCAC TGGGAGC AGTTCCAACATCGGG GCAGGTTATGATGTA CACTGGTACCAGCAG TTTCCAGGAACAGCC CCCAAACTCCTCATC CAAGGTAACAGCAAT CGGCCCTCAGGGGTC CCTGACCGATTCTCT GGTCCAAGTCTGGC ACCTCAGCCTCCCTG GCCATCACTGGGCTC CAGGCTGAGGATGAG GCTGATTA TTA CTGC CAGTCCTATGACAGC AGCCTGAGTGGTTCG GTGTTGGCGGAGGG ACCAAGCTGACCGTC CTAGGTCAGCCC AAG GCTGCCCCCTCGGTC ACTCTGTTCCCGCCC TCCTCTGAGGAGCTT CAAGCCAA CAAGGCC ACACTGGTG TGTCTC ATAAGTGACTTCTAC CCGGAGCCG TGACA GTGGCCTGGAAGGCA GATAGCAGCCCCGTC AAGCGGGAGTGGAG ACCAACACACCTCC AAACAAAGCAACAAC AAGTACGGGCCAAG AGCTATCTGAGCCTG	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTG GTGAAGCCTTCGGA GACCC TGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGTAGTT ACTTCTGGAGCTGGATTTCGGCAGCCCCCAGGTAAGGACTGGAGTGG ATTGGCTATA TCTATTACAGTGGGCAGACCAAATACAA CCCCCTCCCT CAAGAGTCGAGTCACCATATCAATAGACACGTC CAAGAACCAGTTCT CCCTGAAAGCTGAGCTCTGTGACCGCTGCGGACACGCGCTGTATTAC TGTGCGAGAGAAACTGGGAGCTACTACGGCTTTGACTACTGGGGCCA GGGAACCTGGTCACCGTCTCCTCAACGGTGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCCTCT GTTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACA GTGGAAGGTGGATAACGCCCTCCAA TCGGGTAACTCCCAGGAGAGTG TCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAAGAGCACCC CTGACGCTGAGCAAAAGCAGACTACGAGAAACACAAAGTCTACGCCTG CGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGTGACAAAACTCACACATGCCACCGTGCC CAGCA CCTGAACTCCTGGGGGACCGTCA GTCTTCTCTTCCCCC CAAAACC CAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGG TGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAAGTTCAACTGGTAC GTGGACGGCGTGAGGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCA GCGTCCTCACCGTCCCTGC ACCAGGACTGGCTGAATGGCAAGGAGTACAAAGTCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAAGCCAAAGG GCAGCCCCGAGAACCAACAGGTGTACACCCCTGCCCCATCCCGGAGG AGATGACCAAGAAC CAGGTACGCTGACCTGACCTGGTCAAAGGCTTC TATCCCAGCGACATCGCCGTGGAGTGGAGAGCAATGGCAGCCGGA GAACAACTACAAGACCA CGCCTCCCGTGTGACTCCGACGGCTCCT TCTTCCCTCTATAGCAAGCTCACCGTGGACAAAGACAGGTGGCAGCAG GGGAACGTCTTCTCATGTCTCCGTGATGCATGAGGCTCTGCACAA CCA CTACACGCAGAAAGCCCTCTCCCTGTCTCCGGGTGGTGGCGGATCGG GAGGTGGCGGATCCGAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTG AAAAAGCCCCGGAGTCTCTGAAGATCTCCTGTGAAGACTTCTGAATA CAGCTTTACAGCTACTGGATCGGCTGGGTGCGCCAGATGCCCGGGA AAGCCCTGGAGTGGATGGGATCATCTATCTTGGTGACTCAGATACC AGATACAGCCCGTCC TTCCAAGGCCAGGTCA CCACTCTCAGCCGACAA GTCCATCAGTACCGCCTACCTGCAGTGGAGCAGCCTGAAGGCCCTCGG ACACCGCCATGTATTACTGTGCGGAGAAGTAACTGGG GTCTTGACTAC TGGGGCCAGGGAACCC TGGTCACCGTCTCTAGTGCCCTCCACCAAGGG	GACATCCAGATGACC CAGTCTCCATCCTCC CTGTCTGCATCTGTA GGAGACAGAGTCACC ATCACTTGCCGGCA AGTCAGAGCATTAAC AACTATTTAAATTGG TATCAGCAGAGACCA GGGAAAGCCCCTAAG CTCCTGATCTATGCT GCATCCAGTTTGCAA AGTGGGGTCCCATCA AGGTTCAGTGGCAGT GGATCTGGGACAGAT TTCAC TCTCACCATC AGCAGTCTGCAACCT GAAGATTTTGCAACT TACTACTGTCAACAG AGTTACAGTACCCCT CGGACGTTCCGCCAA GGGACCAAGCTGGAA ATCAAAACGAGCCTCC ACCAAGGCCCATCG GTCTTCCCCCTGGCA CCCTCCTCCAAGAGC ACCTCTGGGGCACA GCGGCCCTGGGCTGC CTGGTCAAGGACTAC TTCCCCGAACCCGTG ACGGTGTCTGTGAAC TCAGGCGCCCTGACC AGCGGCTGCACACC TTCCCCGGCTGTCCTA CAGTCTCAGGACTC TACTCCCTCGAAAGC GTGGTGACCGTGCCC TCCAGCAGCTTGGGC
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		ACGCCTGAGCAGTGG AAGTCCCACAGAAAGC TACAGCTGCCAGGTC ACGCATGAAGGGAGC ACCGTGGAAGAAGACA GTGGCCCCTACAGAA TGTTCA	CCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTG GGG GCACAGCGGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCCGAACCG GTGACGGTGTCGTGAACTCAGCGCCCTGACCAAGCGGCTGCACAC CTTCCCCGGCTGTCTACAGTCCCTCAGGACTCTACTCCCTCGAGAGCG TGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC AACGTGAATCACAAAGCCCAGCAACACCAAGGTGGACAAAGAAAGTTGA GCCCCAAATCTTGT	ACCCAGACCTACATC TGCAACGTGAATCAC AAGCCAGCAACACC AAGGTGGACAAAGAA GTTGAGCCCCAAATCT TGT
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		AGYDVHWYQQFPGTA	CARETGSYYGF D YWGQTLVTVSSTVAAPS VFIFPPSDEQLKSGTAS	NYLNWYQQRP GKAPK
		PKLLIQGNSNRPSGV	VVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLKST	LLIYAASSLQSGVPS
		PDRFSGSKSGTSASL	LTL SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC DKHTTCPPCPA	RFGSGSGTDFTLTI
		AITGLQAEDEADYYC	PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY	SSLQPEDFA TYYCQQ
		QSYDSSLSGSVFGGG	VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN	SYSTPRRTFGQGTKLE
		TKLTVLGQPKAAPSV	KALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGF	IKRASTKGPSVFPLA
		TLFPSSSEELQANKA	YPSDIAVEWESNGQPENNYKTTTPV L DSDGSFFLYSKLTV D KSRWQQ	PSSKSTSGGTAALGC
		TLVCLISDFYPGAVT	GNVFSCSVMEALHNHYTQKSLSLSPGGSGGGSEVQLVQSGAEV	LVKDYFFPEPVTVSWN
NA		VAWKADSSPVKAGVE	KKPGESLKISCKTSEYSFTSYWIGWVRQMPGKGLEWMGI IYLGDSDT	SGALTSGVHTFPAVL
		TTTPSKQSNNKYAAK	RYSPSFQGGQVTISADKSI STAYLQWSSLKASDTAMY YCARSNWGLDY	QSSGLYSLESVVTVP
		SYLSLTPEQWKSHRS	WGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFFPEP	SSSLGTQTYICNVNH
		YSCQVTHEGSTVEKT	VTVSWNSGALTSGVHTFPAVLQSSGLYSLESVVTVPSSSLGTQTYIC	KPSNTKVDKKVEPKS
		VAPTECS	NVNHKPSNTKVDKKVEPKSC	C
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		CTTTCAGCGTCTGTT	ACAGTGTGCTTGGA ACTGGATTAGGCAGCCCCCAGGAAAGGCCTT	CTGTCTGCCGTCTGTG
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		ATTACCTGTCGCGCG	TGCAGTTTCTCTGAAAAGTCGAGTAACCATCAGCC CAGACACATCCA	ATCACTTCAGGTCC
		TCCCAGGGAATCCGG	AGAA CCA GTTCTCCCTGAAGCTGAGCTCTGTGACTGCCCGGACACG	AGCCAGAGTGTGTTA
		AATTACCTCGCATGG	GCTGTGTATTACTGTGCAAGAGAGGATGGG GATAGCTACTACCGCTA	TACAGCTCCAACAAT
		TATCAGCAAAAACCC	CGGTATGGACGTCTGGGGCCAAAGGACCACGGTCA CCGTCTCCTCAA	AAGAACTACTTAGTT
		GGAAAAGCACCCGAAG	CGGTGGCTGCACCATCTGTCTTT CATCTTCCCGCCATCTGATGAGCAG	TGGTACCAGCAGAAA
		CTCCTGATCTATGCC	TTGAAATCTGGA ACTGCCCTCTGTGTGTGCC TGTGAATAACTTCTA	CCAGGAAAAGGTTCCCT
		GCCTCGACTCTTCAG	TCCCAGAGAGGCCAAAGTACAGTGG AAGTGGA TAACGCCCTCCCAAT	AAACTGCTCATTTAC
		AGTGGTG TCCCGTCG	CGGGTAACTCCCAGGAGAGTGT CACAGAGCAGGACAGCAAGGACAGC	TGGGCATCTACCCGG
		AGGTTTAGCGGGTCC	ACCTACAGCCTCAAGAGCACCCCTGACGCTGAGCAAAAGCAGACTACGA	GAA TCCGGG GTCCT
1PS: 376693	023_23B3_VH4_CK (S176K) Fc_Ada1 ₁ umab_VH_CH1 (S183E)			

		GGGTCAGGTACGGAC TTTACTCTCACAATT TCCAGCCTGCAGCCC GAAGATGTAGCTACC TATTACTGCCAGAGA TACAACCGAGCGCCT TACACATTCCGACAA GGGACAAAAGTCGAG ATCAAGCGTACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGAAC TGCC TCTGTTGTGTGCCTG CTGAATAACTTCTAT CCCAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCCAG GAGAGTGTACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC AAGAGCACCCCTGACG CTGAGCAAAGCAGAC TACGAGAAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	GAAACACAAAGTCTACGCCCTGCCAAGTCACCCATCAGGGCCTGAGCT CGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTGACAAAACTCAC ACATGCCACCGTGCCAGCACCTGAACCTCCTGGGGACCGTCAGT CTTCCCTCTTCCCCCAAACCCAAAGACACCCCTCATGATCTCCCGGA CCCCTGAGGTCACATGCGTGTGTTGAGCTGAGCCACGAAGACCCCT GAGGTCAAAGTTCAACTGTGTACGTGGACGGCGTGGAGTGCATAATGC CAAGACAAAAGCCGTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTG TCAGCGTCCCTCACCGTCCCTGCACCAAGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAA AACCATCTCAAAGCCAAAGGGCAGCCCCGAGAACCCACAGGTGTACA CCCTGCCCCCATCCCGGAGGAGATGACCAAAGAACAGGTCAGCCTG ACCTGCCCTGTTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTG GGAGAGCAATGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCG TGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCCGTG GACAAGAGCAGGTGGCAGCAGGGGAACGTCCTTCTCATGCTCCGTGAT GCATGAGGCTCTGCACAAACCAC TACACGCAGAAAGAGCCTCTCCCTGT CTCCGGGTGTTGGCGGATCGGGAGGTGGCGGATCCGAGGTACAACTG GTGGAATCAGGTGGAGGTTTGGTGACGCCGGGAGATCGCTCAGGCT TAGCTGTGCGGCATCGGGGTTTACTTTCGATGATTATGCGATGCATT GGGTCCGGCAAGCGCTGGAAAAGGCTCGAGTGGGTTTCCGCCATT ACGTGGAATAGCGGACACATCGATTATGCAGACAGTGTGGAGGGCAG ATTCACAATCTCACGAGACAAATGCTAAGAACAGCCTGTACCTTCAGA TGAAC TCACTTCGCGGGAAGATACGCCGTATACTACTGCGCCAAA GTCTCCTACTTGTCTACAGCTTCGTGCTCGACTATTGGGGTCAAGG AACGTTGGTCACCGTCTCTAGTGCC TCCACC AAGGCCCATCGGTCT TCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCC CTGGGCTGCCGTGGTCAAGGACTACTTCCCCGAACCGGTACGGTGTC GTGGAAC TCAAGCGCCCTGACCAAGCGCGTGCACACCTTCCCGCTG TCCTACAGTCTCTCAGGACTCTACTCCCTCGAGAGCGTGGTGACCCGTG CCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCA CAAGCCCAGCAACACCAAGGTGGACAAAGAAAGTTGAGCCCCAAATCTT GT	AGTCGATT CAGTGGC AGCGGGTCTGGGACA GATTTACTCTCACC ATCAGCAGCCTGCAG CCTGAAGATGTGGCA ACTTATTACTGT CAG CAATATTATAAGACT CCTCTCACTTTCGGC GGAGGGACCAAGGTG GAGATCAAACGAGCC TCCACCAAAGGCCCA TCGGTCTTCCCCCTG GCACCC TCTCCAAG AGCACCTCTGGGGC ACAGCGGCCCTGGGC TGCC TGGTCAAAGGAC TACTTCCCCGAACCG GTGACGGTGTCTGTG AACTCAGGCGCCCTG ACCAGCGCGTGCAC ACCTTCCCGGCTGTC CTACAGTCTCTCAGGA CTCTACTCCCTCGAA AGCGTGGTGACCGTG CCCTCCAGCAGCTTG GGCACCCAGACCTAC ATCTGCAACGTGAAT CACAAAGCCAGCAAC ACCAAGGTGGACAA AAAAGTTGAGCCCCAA TCTTGT
		SEQ ID NO:133	SEQ ID NO:134	SEQ ID NO:135
AA	QVQLQESGPGLVKPSSETLSLTCTISGDSVSTNSVAWNWIRQPPGKGL EWIGRTYYRSKWINDYAVSLKSRVTISPDTSKNQFSLKLSVTAADT AVYYCAREDGDSYYRYGMDVWGQGTVTVSSITVAAPSVFIFPPSDEQ LLIYAASTLQSGVPS	DIQMTQSPSSLSASV GDRVITITCRASQ GIR NYLAWYQQKPKAPK	DIQMTQSPSSLSASV GDRVITITCRSSQSVL YSSNNKNYLVWYQQK	PGKVPKLLIYWASTR

			RFSGSGGTDFTLTI SSLQPEDVATYYCQR YNRAPYTFGQTKVE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLKSTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEN	TYSLKSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNYTQKSLSLSPGSGSGGGSEVQL VESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSAI TWNSGHIDYADSVETRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAK VSYLSTASSLDYWGQGTLLVTVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLESVVTV PSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSC	ESGVPSRFSGSGGT DFTLTISSLQPEDVA TYYCQQYYKTPLTFG GGTKVEIKRASTKGP SVFPLAPSSKSTSGG TAALGCLVKDYFPEP VTVSWNSGALTSGVH TFPAVLQSSGLYSLE SVVTVPSSSLGTQTY ICNVNHHKPSNTKVDK KVEPKSC
			SEQ ID NO:136	SEQ ID NO:137	SEQ ID NO:138
	024_23B3_VH4_CK(S176K)_Fc_3.2_VH_CH1(S183E)	NA	CAGTCTGTGCTGACG CAGCGGCCCTCAGTG TCTGGGGCCCCAGGG CAGAGGTCACCATC TCCTGCACTGGGAGC AGTTCCAACATCGGG GCAGGTTATGATGTA CACTGGTACCAGCAG TTTCCAGGAACAGCC CCCCAACTCCTCATC CAAGGTAACAGCAAT CGGCCCTCAGGGGTC CCTGACCGATTCTCT GGCTCCAAGTCTGGC ACCTCAGCCTCCCTG GCCATCAC TGGGCTC CAGGCTGAGGATGAG GCTGATTATTACTGC CAGTCCCTATGACAGC AGCCTGAGTGGTTCTG GTGTTGCGCGGAGGG ACCAAGCTGACCGTC CTAGGTCAGCCCAAG GCTGCCCCCTCGGTC ACTCTGTTCCCGCCC	CAGGTACAGTTGCAGGAGTCAGGTCCAGGACTGGTGAAGCCCTCGGA GACCTCTCACTACCTGTACCATCTCCGGGACAGTGTCTCTACCA ACAGTGTTCCTTGGAACTGGATTAGGCAGCCCCCAGGGAAAAGCCCTT GAGTGGATAGGAAGACATACTACAGGTCCAAGTGGTATAATGATTA TGCAAGTTTCTGTGAAAAGTCGAGTAACCATCAGCCCCAGACATCCA AGAACCAAGTTCTCCCTGAAGCTGAGCTCTGTGACTGCCGCGGACACG GCTGTGATTACTGTGCAAGAGAGGATGGGGATAGCTACTACCGCTA CGGTATGGACGTC TGGGGCCAAAGGACCACCGTCACCGTCTCCTCAA CGGTGGCTGCACCATCTGTCTTTCATCTTCCCGCCATCTGATGAGCAG TTGAAAATCTGGAACTGCCCTCTGTGTGTGCCCTGCTGAATAACTTCTA TCCCAGAGAGGCCAAAGTACAGTGGAAAGTGGATAACGCCCTCCAAT CGGGTAACTCCAGGAGAGTGTACAGAGACGAGCAGCAAGACAGCAGC ACCTACAGCCTCAAGAGCACCCCTGACGCTGAGCAAAAGCAGACTACGA GAAACACAAAAGTCTACGCCCTGCCAAGTCACCCATCAGGGCCTGAGCT CGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTGACAAAACCTCAC ACATGCCCACCGTGCCCAGCACCTGAACCTCCTGGGGGACCGTCAGT CTTCCCTCTTCCCCCAAACCCAAAGACACCCCTCATGATCTCCCGGA CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCT GAGGTCAAGTTCAACTGTTACGTGGACGGCGTGGAGGTGCATAATGC CAAGACAAAAGCCGTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTG TCAGCGTCCTCACCGTCCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGTCTCCAAACAAAGCCCTCCAGCCCCCATCGAGAA AACCATCTCCAAAGCCAAAGGGCAGCCCCCGAGAAACACAGGTGTACA CCCTGCCCCCATCCCGGAGGAGATGACCAAGAACCAAGTCAGCCTG ACCTGCCCTGGTCAAAGGCTTCTATCCCAAGCAGACATCGCCGTGGAGTG	GACATCCAGATGACC CAGTCTCCAAGCTCC CTGTCTGCGTCTGTG GGCGATAGGTCACC ATCACTTGCAGGTCC AGCCAGAGTGTGTTA TACAGCTCCAACAAT AAGAACTACTTAGTT TGGTACCAGCAGAAA CCAGGAAAAGGTTCC AAACTGCTCATTTAC TGGCATCTACCCGG GAATCCGGGTCCCT AGTCGATTCAGTGGC AGCGGTCTGGGACA GATTTCACTCTCACC ATCAGCAGCCTGCAG CCTGAAGATGTGGCA ACTTATTACTGTGAG CAATA TTATAAGACT CCTCTCACTTTCGGC GGAGGACCAAAGTG GAGATCAAACGAGCC TCCACCAAGGCCCA TCGGTCTTCCCCCTG

		T CCTTCTGAGGAGCTT CAAGCCAAACAAGGCC ACACTGGTGTGTCTC ATAAGTGACTTCTAC CCGGAGCCCGTGACA GTGGCCTGGAAGGCA GATAGCAGCCCCGTC AAGCGGGAGTGGAG ACCACCACACCCCTCC AAACAAAGCAACAAC AAGTACGGGCCAAG AGCTATCTGAGCCTG ACGCCTGAGCAGTGG AAGTCCCACAGAAGC TACAGCTGCCAGGTC ACGCATGAAGGGAGC ACCGTGAGAGAAACA GTGGCCCCTACAGAA TGTTCA	GGAGAGCAATGGGCAGCCGGAGAAACAATAAGACCACGCCTCCCG TGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCCGTG GACAAAGACAGGTGGCAGCAGGGAAACGTCTTCTCATGCTCCGTGAT GCATGAGGCTCTGCACAAACCACATACACGCAGAAAGAGCCTCTCCCTGT CTCCGGGTGCTGCCGATCGGGAGTGCGGATCCGAGGTGCAGCTG GTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGAGTCTCTGAAAGAT CTCCTGTAAGACTTCTGAATACAGCTTTACCAGCTACTGGATCGGCT GGTGCGCCAGATGCCCGGGAAGGCCCTGGAGTGGATGGGATCATC TATCTTGGTGACTCAGATACCAGATACAGCCCGTCCTTCCAAGGCCA GGTCACCATCTCAGCCGACAAGTCCATCAGTACCGCTACCTGCAGT GGAGCAGCCTGAAGGCCTCGGACACCGCATGTATTACTGTGCGAGA AGTAACTGGGCTCTTGACTACTGGGGCCAGGAACCCCTGGTCACCGT CTCTAGTGCCCTCCACCAAGGCCCATCGGTCTTCCCCCTGGACCCCT CCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTC AAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAGCGGTGCACACCTTCCCGGCTGTCTACAGTCCCTCAG GACTCTACTCCCTCGAGAGCGTGTGTGACCGTGCCCTCCAGCAGCTTG GGCACCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAC CAAGGTGGACAAAGAAAGTTGAGCCCCAAAATCTTGT	GCACCCCTCCTCCAAG AGCACCTCTGGGGGC ACAGCGCCCTGGGC TGCTTGGTCAAGGAC TACTTCCCCGAACCG GTGACGGTGTCTGG AACTCAGGCGCCCTG ACCAGCGCGTGCAC ACCTTCCCCGGCTGC CTACAGTCTCAGGA CTCTACTCCCTCGAA AGCGTGGTGACCGTG CCCTCAGCAGCTTG GGACCCAGACCTAC ATCTGCAACGTGAAT CACAAAGCCAGCAAC ACCAAGGTGGACAA AAAGTTGAGCCCCAAA TCTTGT
		SEQ ID NO:139 QSVLTQPPSVSGAPG QRVTISCTGSSSNIG AGYDVHWYQQFFP PKLLIQGNSNRPSGV PDRFSGSKGTSASL AITGLQAEDEADYYC QSYDSSLSGSVF TKLTVLGQPKAAPSV TLFPPSSEELQANKA TLVCLISDFYPGAVT VAWKADSSPVKAGVE TTTPSKQSNNKYAAK SYLSLTPEQWKSHRS YSCQVTHEGSTVEKT VAPTECS	SEQ ID NO:140 QVQLQESGPGLVKPS EWIGRTYYRSKWYND AVYYCAREDGDSYYR LKSGTASVVCLLNNF TYSLSKSTLTLSKAD TCPPCPAPELLGGPS EVKFNWYVDGVEVHN YKCKVSNKALPAPIE TCLVKGFYPSDIAVE DKSRWQQQGNVFS VQSGAEVKKPGESL YLGDS DTRYSPSFQ SNWGLDYWGQGLTV KDYFPEPVTVSWNS GTQTYICNVNHHKPS	SEQ ID NO:141 DIQMTQSPSSLSASV GDRVITTCRSSQSVL YSSNNKNYLVWYQQK PGKVPKLLIYWASTR ESGVPSSRFSGSGST DFTLTISSLQPEDVA TYYCQQYYKTPLTFG GGTKVEIKRASTKGP SVFPLAPSSKSTSGG TAALGCLVKDYFPEP VTVSWNSGALTSGVH TFPAVLQSSGLYSLE SVVTVPSSSLGTQTY ICNVNHHKPSNTKVDK KVEPKSC
	AA	SEQ ID NO:142	SEQ ID NO:143	SEQ ID NO:144

1PS: 376703	025_Adalimumab_IgG.001_3B3v2_VH_CK(S176E)	NA	GATATCCAAATGACA CAATCACCATCGTCG CTTTCAGCGTCTGTT GGCGACCGTGTGACG ATTACCTGTCGCGG TCCAGGGAATCCGG AATTACCTCGCATGG TATCAGCAAAAACCC GGAAAAGCACCGAAG CTCCTGATCTATGCC GCCTCGACTCTTCAG AGTGGTGTCCTGTCG AGGTTTAGCGGGTCC GGGTCAGGTACGGAC TTTACTCTCACAAATT TCCAGCCTGCAGCCC GAAGATGTAGCTACC TATTACTGCCAGAGA TACAACCGAGCGCCT TACACATTGGACAA GGGACAAAAGTCGAG ATCAAGCGTACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGAAC TGCC TCTGTTGTGTGCC TG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCCA G GAGAGTGTACACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC GAAAGCACCCCTGACG CTGAGCAAAAGCAGAC	GAGGTACAACTGGTGGAAATCAGGTGGAGGTTTGTTGTCAGCCGGGGAG ATCGCTCAGGCTTAGCTGTGCGGCATCGGGGTTTACTTTCGATGATT ATCGGATGCATTGGTCCGGCAAGCGCCTGGA AAAAGGCTCGAGTGG GTTTCCGCCATTACGTGGAATAGCGGACACATCGATTATGCAGACAG TGTGGAGGGCAGATTCACAATCTCACGAGACAATGCTAAGAACAGCC TGTA CCTTCAGATGAAC TCACTTCGCGCGGAAGATACCGCCGTATAC TACTGCGCCAAA GTCTCCTACTTGTCTACAGCTTCGTCGCTCGACTA TTGGGTC AAGGAACGTTGGTCA CCGTCTCTAGTGCCCTCCACCAAGG GCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGACACCTCTGGG GGCACAGCGCCCTGGGCTGCC TGGTCAAGGACTACTTCCCGAACC GGTGACGGTGTCGTGGAAC TCAAGGCCCTGACCAAGCGGCTGCACA CCTTCCCCGGCTGTCTACAGTCTCTCAGGACTCTACTCCCTCAAAAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGCACCCAGACCTACATCTG CAACGTGAATCACAAGCCCAGCAACACCAAGTGGACAAAGAA GTTG AGCCCAAATCTTGTGACAAAAC TCAACATGCCACCGTGCCCAGCA CCTGA ACTCTCTGGGGGACCGTCA GTCTTCTCTTCCCCCAA AAC CAAGGACACCCCTCATGATCTCCCGGACCCCTGAGT CACATGCGTGG TGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAA GTTCAACTGGTAC GTGGACGGCGTGAGGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACC GTTGTGTCA GCGTCTCACCCTCCTGC ACCAGGACTGGCTGAATGGCAAAGGATACAA GTGCAAGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAGCCCAAAGG GCAGCCCCGAGAACCA CAGGTGTACACCCCTGCCCATCCCCGGAGG AGATGACCAAGAAC CAGGTACGCTGACCTGCC TGGTCAAAGGCTTC TATCCCA GCGACATCGCCGTGGAGTGGAGAGCAATGGCAGCCGGA GAACAACTACAAGACCA CGCCTCCGTGCTGGACTCCGACGGCTCCT TCTTCCCTCTATAGCAAGCTCACCGTGGACAAAGACAGGTGGCAGCAG GGGAACGTCTTCTCATGTCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAAGCCCTCTCCCTGTCTCCGGGTGGTGGCGGATCGG GAGGTGGCGGATCCCAGGTGCAGTTACAGCAGTCGGGCGCAGGACTG TTGAAGCCTTCGGAGACCCGTGTCCCTCACCTGCGCTGTCCA TGGTGG GTCCCTTCAGTGGTTACTACTGGAAC TGGAATTCGCCAGCCACAGGGA AGGGCTAGAGTGGATTGGGAAATCAATCATGTGTGAAACACCCAAC TACAACCCGTCCCCTCAAGAGTCGAGTCACCATATCATTAGACACGTC CAAGAACCAGTTCTCCCTGACGCTGACCTCTGTGACCGCCGCGGACA CGGCTGTGTATTACTGTGCGAGAGGATATTGTAGAAGTACCACTGC TACTTTGACTACTGGGGCCAGGGAACCTTAGTCA CCGTCTCTCAAC	GAAATTGTGTTGACG CAGTCTCCAGGCACC CTGTCTTTGTCTCCA GGGAAAAGAGCCACC CTCTCCTGCAGGGCC AGTCAGAGTGTTAGA AGCAGTTACTTAGCC TGGTACCAGCAGAAA CCTGGCCAGGCTCCC AGGCTCCTCATCTAT GGTGCA TCCAGCAGG GCCACTGGCATCCCA GACAGGTTCAGTGGC AGTGGGTCTGGGACA GACTTCAC TCTCACC ATCAGCAGACTGGAG CCTGAAGATTTTGCA GTGTATTACTGT CAG CAGTATGGTAGCTCA CCTACCTTCGGCCAA GGGACACGACTGGAG ATTA AACGAGCCTCC ACCAAGGCCCATCG GTCTTCCCCCTGGCA CCCTCCTCCAAGAGC ACCTCTGGGGCACA GCGGCCCTGGGCTGC CTGGTCAAGGACTAC TTCCCCGAACCGGTG ACGGTGTCTGGAAC TCAGGCGCCCTGACC AGCGGCGTGCA CACC TTCCCCGGCTGTCC TA CAGTCTCAGGACTC TACTCCCTCAA AAGC GTGGTGACCGTGCCC TCCAGCAGCTTGGGC
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		TACGAGAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGAGAGTGT	TGTGGCTGCACCATCTGTCTTCAATCTTCCCGCCATCTGATGAGCAGT TGAATCTGGAACTGCCCTCTGTTGTGTGCCCTGCTGAATAACTTCTAT CCCAGAGAGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAATC GGTAACTCCAGGAGAGTGTCAAGAGCAGACAGCAAGGACAGCA CCTACAGCCTCGAAAAGCACCCCTGACGCTGAGCAAAGCAGACTACGAG AAACACAAAGTCTACGCCCTGCGAAGTCACCCATCAGGGCCTGAGCTC GCCCCGCACAAAAGAGCTTCAACAGGGGAGAGTGT	ACCCAGACCTACATC TGCAACGTGAATCAC AAGCCAGCAACACC AAGTGGACAAGAAA GTTGAGCCCAAATCT TGT
		SEQ ID NO:145	SEQ ID NO:146	SEQ ID NO:147
AA		DIQMTQSPSSLSASV GDRVITTCRASQGIR NYLAWYQQKPGKAPK LLIYAASTLQSGVPS RFGSGSGTDFTLT SSLQPEDVATYYCQR YNRAPYTFGQGTKVE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLESTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEN	EVQLVESGGGLVQPGRSRLRLSCAASGFTFDDYAMHWVRQAPGKGLEW VSAITWNSGHIDYADSVEGRFTISRDNAKNSLYLQMNSLRAEDTAVY YCAKVSYLEASTASLLDYWGQGLVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLKS VVTVPSSSLGTQYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMEALHNHYTQKSLSLSPGGSGGGSQVQLQQSGAGL LKPSSETLSLTCAVHGGSFGYYWNWIRQPPGKGLEWIGEINHAGNTN YNPSLKSRVTISLDTSKNQFSLTLTTSVTAADTAVYYCARGYCRSTTC YFDYWGQGLVTVSSITVAAPSVFIFPPSDEQLKSGTASVVCLLNIFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLESTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC	EIVLTQSPGTLSLSP GERATLSCRASQSVR SSYLAWYQQKPGQAP RLLIYGASSRATGIP DRFSGSGSGTDFTLT ISRLEPEDFAVYYCQ QYGSSTFFGQGRLE IKRASTKGPSVFPLA PSSKSTSGGTAALGC LVKDYFPEPVTVSWN SGALTSGVHTFPAVL QSSGLYSLKSVVTVP SSSLGTQYICNVNH KPSNTKVDKKVEPKS C
		SEQ ID NO:148	SEQ ID NO:149	SEQ ID NO:150
		GATATCCAAATGACA CAATCACCATCGTCG CTTTCAGCGTCTGTT GGCGACCGTGTGACG ATTACCTGTCGCGCG TCCCAGGGAATCCGG AATTACCTCGCATGG TATCAGCAAAAACCC GGAAGAAGCACCGAAG CTCCTGATCTATGCC GCCTCGACTCTTCAG AGTGGTGTGCCGTCG AGGTTTAGCGGGTCC	GAGGTACAACTGGTGGAAATCAGGTGGAGGTTTGGTGCAGCCCGGGGAG ATCGCTCAGGCTTAGCTGTGCGGCATCGGGGTTTACTTTCGATGATT ATGCGATGCATTGGGTCCGGCAAGCGCCTGGAAAAGGGCTCGAGTGG GTTTCCGCCATTACGTGGAATAGCGGACACATCGATTATGCAGACAG TGTGGAGGCAGATTCACAATCTCACGAGACAATGCTAAGAACAGCC TGTAACCTTCAGATGAACCTCACTTCGCGCGGAAGATACCGCCGTATAC TACTGCGCCAAAAGTCTCCTACTTGTCTACAGCTTCGTCGCTCGACTA TTGGGGTCAAGGAACGTTGGTCACCGTCTCTAGTGCCTCCACCAAGG GCCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGG GGCACAGCGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCCGAACC GGTGACGGTGTCTGTGGAACCTCAGGCGCCCTGACCAAGCGGCGTGACAC CCTTCCCGGCTGTCTACAGTCCCTCAGGACTCTACTCCCTCAAAAGC GTGGTGACCGTGCCCTCCAGCAGCCTTGGGCACCCAGACCTACATCTG	GACATCCAGATGACC CAGTCTCCATCCTCC CTGTCTGCATCTGTA GGAGACAGAGTCACC ATCACTTGCCGGCA AGTCAGAGCATTAAC AACTATTTAAATTGG TATCAGCAGAGACCA GGGAAAAGCCCCTAAG CTCCTGATCTATGCT GCATCCAGTTTGCAA AGTGGGCTCCCATCA AGGTTCAGTGGCAGT

		GGGTCAAGTACGGAC TTTACTCTCACAATT TCCAGCCTGCAGCCC GAAGATGTAGCTACC TATTACTGCCAGAGA TACAACCGAGCGCCT TACACATTCCGACAA GGGACAAAAGTCGAG ATCAAGCGTACGGTG GCTGCACCATCTGTC TTCAATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGAACCTGCC TCTGTTGTGTGCCCTG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCCAG GAGAGTGCACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC GAAAGCACCCCTGACG CTGAGCAAAAGCAGAC TACGAGAAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	CAACGTGAATCACAAAGCCAGCAACACCAAGGTGGACAAAGAAAGTTG AGCCCAAATCTTTGTGACAAAACCTCACACATGCCACCCGTTGCCCCAGCA CCTGAACCTCCTGGGGGACCGTCACTCTTCTCCTCTTCCCGCCAAAACC CAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTG TGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAAGTTCAACTGGTAC GTGGACGGCGTGGAGGTGCATAAATGCCAAGACAAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCAAGCTCTCACCCTCCTGCTGC ACCAGGACTGGCTGAATGGCAAGAGTACAAAGTGCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAAGG GCAGCCCCGAGAACACACAGGTGTACACCCCTGCCCCCATCCCGGAGG AGATGACCAAGAACCCAGGTCAAGCTGACCTGACCTGGTCAAAGGCTTC TATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA GAACAACTACAAAGACACGCCCTCCCGTGTGCTGGACTCCGACGGCTCCT TCTTCCCTCTATAGCAAGCTCACCGTGGACAAAGACAGGTGGCAGCAG GGGAACGTCTTCTCATGTCTCCGTGATGATGAGGCTCTGCACAAACCA CTACACGCAGAAAGACCTCTCCCTGTCTCCGGGTGGTGGCGGATCGG GAGGTGGCGGATCCCAGGTGCAGCTGCAGGAGTCGGGCCAGGACTG GTGAAGCCTTCGGAGACCCCTGTCCCTCACCTGCACCTGTCTCTGGTGG CTCCATCAGTAGTTACTTCTGGAGCTGGATTTCGGCAGCCCCCAGGTA AGGGACTGGAGTGGATTGGCTATATCTATTAACAGTGGCAGACCAAA TACAACCCCTCCCTCAAGAGTCGAGTCACCATATCAATAGACACGTC CAAGAACCCAGTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCGGACA CGGCCGTGATTAATCTGTGCGAGAGAAACTGGAGCTACTACGGCTTT GACTACTGGGGCCAGGAAACCCTGGTCACCGTCTCCTCAACTGTGGC TGACACCATCTGTCTTTCATCTTCCCGCCATCTGATGAGCAGTTGAAAT CTGGAACTGCCCTCTGTTGTGTGCTGCTGAAATAACTTCTATCCCAGA GAGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAA CTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACA GCCTCGAAAGCACCCCTGACGCTGAGCAAAAGCAGACTACGAGAAACAC AAAGTCTACGCCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCCGT CACAAAGAGCTTCAACAGGGGAGAGTGT	SEQ ID NO:151	SEQ ID NO:152	SEQ ID NO:153
AA		DIQMTQSPSSLSASV GDRVITTCRASQGIR NYLAWYQQKPGKAPK LLIYAASTLQSGVPS RFSGSGSGTDFTLTI	EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKLEW VSAITWNSGHIDYADSVVEGRFTISRDNAKNSLYLQMNSLRAEDTAVY YCAKVSYSLTASSLDYWGGQTLTVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLKS VVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA	DIQMTQSPSSLSASV GDRVITTCRASQIN NYLNWYQQRP GKAPK LLIYAASSLQSGVPS RFSGSGSGTDFTLTI		

			SSLQPEDVATYYCQR YNRAPYTFGQGTKVE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLESTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEC	PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDSFFLYSKLTVDKSRWQQ GNVFSQVMHEALHNHYTQKSLSLSPGGSGGGSQVQLQESGPGL VKPSETLSLTCTVSGGSISSYFWSWIRQPPGKGLEWIGIYYISGQTK YNPSLKSRVTISIDTSKNQFSKLSSLSSVTAADTAVYYCARETGSYYGF DYWGQGLTVTSSTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP EAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLESTLTLSKADYEKH KVYACEVTHQGLSSPVTKSFNRGEC	SSLQPEDFATYYCQQ SYSTPRTFGQGTKLE IKRASTKGPSVFPLA PSSKSTSGGTAALGC LVKDYFFPEPVTVSWN SGALTSGVHTFPAVL QSSGLYSLKSVVTVP SSSLGTQTYICNVNH KPSNTKVDKKVEPKS C
			SEQ ID NO:154	SEQ ID NO:155	SEQ ID NO:156
	027_Ada1imab_1gg.001_23B3_VH4_VH_CK(S176E)	NA	GATATCCAAATGACA CAATCACCATCGTCG CTTTCAGCGTCTGTT GGGACCGTGTGACG ATTACCTGTCGCGG TCCCAGGGAATCCGG AATTACCTCGCATGG TATCAGCAAAAACCC GGAAGAAGCACCGAAG CTCCTGATCTATGCC GCCTCGACTCTTCAG AGTGGTGTGCCGTGG AGGTTTAGCGGGTCC GGGTCAGGTACGGAC TTTACTCTCACAAATT TCCAGCCTGCAGCCC GAAGATGTAGCTACC TATTACTGCCAGAGA TACAACCGAGCGCCT TACACATTCCGGACAA GGGACAAAAGTCGAG ATCAAGCGTACGGTG GCTGCACCATCTGTC TTCATCTTCCCCGCA TCTGATGAGCAGTTG AAATCTGGAACTGCC	GAGGTACAACTGGTGGAAATCAGGTGGAGGTTTGGTGCAGCCGGGGAG ATCGCTCAGGCTTAGCTGTGCGGCATCGGGGTTTACTTTCGATGATT ATGCGATGCATTGGGTCCGGCAAGCGCCTGGAAAAGGGCTCGAGTGG GTTTCCGCCATTACGTGGAATAGCGGACACATCGATTATGCAGACAG TGTGGAGGCAGATTCACAATCTCACGAGACAAATGCTAAGAACAGCC TGTAACCTTCAGATGAATCACTTCGCGCGGAAGATACCGCCGTATAC TACTGCGCCAAAAGTCTCCTACTTGTCTACAGCTTCGTCGCTCGACTA TTGGGGTCAAGGAACGTTGGTCAACCGTCTCTAGTGCCCTCCACCAAGG GCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGG GGCACAGCGGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCCGAACC GGTGACGGTGTCTGTGGAACCTCAGGCGCCCTGACCAAGCGCGTGCACA CCTTCCCGGCTGTCTACAGTCTCAGTCCCTCAGGACTCTACTCCCTCAAAAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG CAACGTGAATCAAAAGCCCAAGCAACACCAAGGTGGACAAAGAAAGTTG AGCCCAAATCTTGTGACAAAACCTCACACATGCCACCCGTGCCAGCA CCTGAACCTCTGGGGGACCGTCACTCTCTCTTCCCCCCAAAACC CAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGG TGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAAGTTCAACTGGTAC GTGGACGGCGTGGAGGTGCATAAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTACAGCTCCTCACCGTCCCTGC ACCAGGACTGGCTGAATGGCAAGGATACAAAGTGCAAGGTC'TCCCAAC AAAGCCCTCCAGCCCCCATCGAGAAAAACCATCTCCAAAAGCCAAAGG GCAGCCCCGAGAACCAACAGGTGTACACCCCTGCCCCCATCCCGGAGG AGATGACCAAGAACCAAGGTACGCCTGACCTGCCCTGGTCAAAGGCTTC TATCCCAGCGACATCGCCGTGGAGTGGAGAGCAATGGCAGCCCGGA GAACAACTACAAAGACACGCCCTCCCGTGTGGACTCCGACGGCTCCT	GACATCCAGATGACC CAGTCTCCAAGCTCC CTGTCTGCCGTCTGTG GGCGATAGGTCACC ATCACTTGCAGTCC AGCCAGAGTGTGTTA TACAGCTCCAACAAT AAGAACTACTTAGTT TGGTACCAGCAGAAA CCAGGAAAAGGTTCCCT AAACTGCTCATTTAC TGGGCATCTACCCGG GAATCCGGGTCCTCT AGTCGATTCAGTGGC AGCGGTCTGGGACA GATTTCACTCTCACC ATCAGCAGCCTGCAG CCTGAAAGATGTGGCA ACTTATTACTGTCTAG CAATATTATAAGACT CCTCTCACTTTTCGGC GGAGGACCAAGGTG GAGATCAAACGAGCC TCCACCAAGGGCCCA TCGGTCTTCCCCCTG GCACCCCTCTCTCCAAG

		TCTGTTGTGTGCCTG CTGAATAACTTCTAT CCCAGAGAGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCCAG GAGAGTGCACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC GAAAGCACCCTGACG CTGAGCAAAAGCAGAC TACGAGAAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	TCTTCCTCTATAGCAAGCTCACCGTGGACAAAGAGCAGGTGGCAGCAG GGGAACGTCTTCTCATGTCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGAGAAAGCCTCTCCCTGTCTCCGGTGGTGGCGGATCGG GAGTGGCGGATCCCAGGTACAGTTGCAGGAGTCAGGTCCAGGACTG GTGAAGCCCTCGGAGACCCTCTCACTCACCTGTACCATCTCCGGGA CAGTGTCTCTACCAACAGTGTGCTTGAACTGGATTAGGCAGCCCC CAGGAAAAGCCTTGAGTGGATAGGAAGGACATATAcAGGTCCAAG TGGTATAATGATTATGcAGTtTCTCTGAAAAGTCGAGTAACCATCAG CCCAGACACATCCAAGAAcCAGtTCTCCCTGAAGCTGAGCTCTGTGA CTGCCGCGGACACGGCTGTGTATTACTGTGCAAGAGAGATGGGAT AGCTACTACCGCTACGGTATGGACGTCTGGGGCCAAAGGACACAGGT CACCGTCTCCTCAACTGTGGCTGCACCATCTGTCTTCACTTCCCCG CATCTGATGAGCAGTTGAAATCTGGAActGCCCTCTGTGTGTGCTG CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGA TAACGCCCTCCAATCGGTAActCCcAGGAGAGTGTcACAGAGCAGG ACAGCAAGGACAGCACCTACAGCCTCGAAAGCACCCCTGACGCTGAGC AAAGCAGACTACGAGAAAACACAaAGTCTAcGCCCTGCGAAAGTcACCCA TCAGGGCCTGAGCTCGCCCGTcACAaAGAGCTTCAACAGGGGAGAGT GT	AGCACCTCTGGGGC ACAGCGCCCTGGGC TGCTGTGTCaAGGAC TACTTCCCCGAACCG GTACGGTGTCTGTG AACTCAGGGCCCTG ACCAGCGCGTGCAC ACCTTCCCGGCTGTC CTACAGTCTCAGGA CTCTACTCCCTCAAA AGCGTGGTGACCGTG CCCTCCAGCAGCTTG GGACCCAGACCTAC ATCTGCAACGTGAAT CACAAAGCCAGCAAC ACCAAGGTGGACAAg AAAGTTGAGCCCCAA TCTTGT
		SEQ ID NO:157	SEQ ID NO:158	SEQ ID NO:159
AA		DIQMTQSPSSLSASV GDRVITTCRASQGIR NYLAWYQQKPGKAPK LLIYAASTLQSGVPS RFGSGSGTDFTLT SSLQPEDVATYYCQR YNRAPYTFGQGTKVE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLESTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGE	EVQLVESGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKLEW VSAITWNSGHIDYADSVVEGRFTISRDNAKNSLYLQMNSLRAEDTAVY YCAKVSYLSTASSLDYWGGQGLVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLKS VVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMEALHNHYTQKSLSLSPGGGGGGGSQVQLQESGPG VKPSETLSLTCTISGDSVSTNSVAWNWIRQPPGKGLEWIGRTYYSK WYNDYAVSLKSRVTISPDTSKNQFSLKSSVTAADTAVYYCAREDDG SYRYGMDVWGQGTVTVSSVAAPSVFIFPPSDEQLKSGTASVVCL LNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLESTLT KADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	DIQMTQSPSSLSASV GDRVITTCRSSQSVL YSSNNKNYLVWYQQK PGKVPKLLIYWASTR ESGVPSPRFSGSGST DFTLTISSLQPEDVA TYYCQQYYKTPLTFG GGTKVEIKRASTKGP SVFPLAPSSKSTSGG TAALGCLVKDYFPEP VTVSWNSGALTSGVH TFPAVLQSSGLYSLK SVVTVPSSSLGTQTY ICNVNHKPSNTKVDK KVEPKSC
		SEQ ID NO:160	SEQ ID NO:161	SEQ ID NO:162
NA	NA	CAGTCTGTGCTGACG	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGA	GAAATTGTGTTGACG

		CAGCCGCCCTCAGTG TCTGGGCCCCCAGGG CAGAGGTACACATC TCCTGCAC TGGGAGC AGTTCCAACATCGGG GCAGGTTATGATGTA CACTGGTACCAGCAG TTTCCAGGAACAGCC CCCAAACTCCTCATC CAAGGTAACAGCAAT CGGCCCTCAGGGGTC CCTGACCGATTCTCT GGCTCCAAGTCTGGC ACCTCAGCCTCCCTG GCCATCAC TGGGCTC CAGGCTGAGGATGAG GCTGATTATTACTGC CAGTCCATATGACAGC AGCCTGAGTGGTTCG GTGTTCGGCGGAGGG ACCAAGCTGACCGTC CTAGGT CAGCCCAAG GCTGCCCCCTCGGTC ACTCTGTTCCCGCCC TCCCTCTGAGGAGCTT CAAGCCAAACAAGGCC ACACTGGTGTGTC TC ATAAGTGACTTCTAC CCGGGAGCCGTGACA GTGGCCTGGAAGGCA GATAGCAGCCCGTC AAGCGGGAGTGGAG ACCACCACACCCCTCC AAACAAAGCAACAAC AAGTACGCGGCCGAG AGCTATCTGAGCCTG ACGCCTGAGCAGTGG	GTCTCTGAAGATCTCCTGTAGACTTCTGAATACAGCTTTACCAGCT ACTGGATCGGCTGGGTGCGCCAGATGCCCGGAAAGGCCCTGGAGTGG ATGGGATCATCTATCTTGGTGACTCAGATACCA GATACAGCCCGTC CTTCCAAGGCCAGGTCACCATCTCAGCCGACAAAGTCCATCAGTACCG CCTACCTGCAGTGGAGCAGCCTGAAGGCCCTCGGACACCGCCATGTAT TACTGTGCGAGAAAGTAACTGGGGTCTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTCTCTAGTGCCCTCCACC AAGGCCCATCGGTCTTCC CCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGCACAGCGGCCCTG GGCTGCC TGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTG GAACTCAGGCGCCCTGACCAGCGGCGTGCA CACCTTCCCGCTGTCC TACAGTCTCAGGACTCTACTCCTCAA AAGCGTGGTGACCGTGCCC TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAA GCCCAGCAACACCAAGGTGGACAAAGAA GTTGAGCCCAAATCTTGTG ACAAAACTCACATGCCCCACCGTGCCCCAGCACCTGA ACTCCTGGGG GGACCGTCAGTCTTCTCTTCCCCCAA AACCACCAAGGACACCCCTCAT GATCTCCCGACCCCTGAGGTCA CATGCGTGGTGGTGACGTGAGCC ACGAAGACCCCTGAGGTCAAAGTTCAA CTGGTACGTGGACGGCGTGGAG GTGCATAATGCCAAGACAAAGCCGTGTGAGGAGCAGTACGGCAGCAC GTACCGTTGTGT CAGCGTCCCTCACCGTCTCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCC CCCATCGAGAAAACCATCTCCA AAGCCAAAGGCAGCCCCGAGAACC ACAGGTGTACACCCCTGCCCCCATCCCGGAGGAGATGACCAAGAACC AGGTCAGCCTGACCTGCC TGTGTCAAAGGCTTCTATCCAGCGACATC GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGACA AACTACAAGAC CACGCCCTCCCGTGTGGACTCCGACGGCTCCTTCTCTCTATAGCA AGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA TGCTCCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA GAG CCTCTCCCTGTCTCCGGTGGTGGCGGATCGGGAGGTGGCGGATCCC AGGTGCAGTTACAGCAGTCGGGCGCAGGACTGTTGAAGCCTTCGGGAG ACCCGTGTCCCTCACCTGCGCTGTCCATGGTGGTCCCTTCAGTGGTTA CTACTGGA ACTGGATTTCGCCAGCCACCAAGGAAGGGCTAGAGTGGA TTGGGGAAATCAATCATGCTGGAAAACACCAACTACAACCCGTCCC TC AAGAGTCGAGTCACCATATCATTAGACACAGTCCAAGAACCA GTTCTC CCTGACGCTGACCTCTGTGACCGCGCGGACACGGCTGTGTATTACT GTGCGAGAGGATATTGTAGAAGTACCACCTGCTACTTTGACTACTGG GGCCAGGGAACCCTAGTCACCGTCTCCTCAA ACTGTGGCTGCACCATC TGTC TT CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGA ACTG	CAGTCTCCAGGCACC CTGTCTTTTGTCTCCA GGGAAAGAGCCACC CTCTCCTGCAGGGCC AGTCAGAGTGTTAGA AGCAGTTACTTAGCC TGGTACCAGCAGAAA CCTGGCCAGGCTCCC AGGCTCCTCATCTAT GGTGCA TC CAGCAGG GCCACTGGCATCCCCA GACAGGTT CAGTGGC AGTGGTCTGGGACA GACTTCACTCTCACC ATCAGCAGACTGGAG CCTGAA GATTTTGCA GTGTATTACTGT CAG CAGTATGGTAGCTCA CCTACCTTCGGCCAA GGGACACGACTGGAG ATTAACGAGCCTCC ACCAAGGGCCCATCG GTCTTCCCCCTGGCA CCCTCCTCCAAGAGC ACCTCTGGGGCACA GCGGCCCTGGGCTGC CTGGTCAAGGACTAC TTCCCGAACC GG TG ACGGTGTCTGTGGAAC TCAGGCGCCCTGACC AGCGCGTGCACACC TTCCCGGCTGTCC TA CAGTCCTCAGGACTC TACTCCCTCAAAAGC GTGGTGACCGTCCCC TCCAGCAGCTTGGG
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			AAGTCCACAGAAAGC TACAGCTGCCAGGTC ACGCATGAAGGAGC ACCGTGAGAAAGACA GTGGCCCCTACAGAA TGTTCA	CCTCTGTTGTGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAA GTACAGTGGAAGTGGATAAACGCCCTCCAATCGGGTAACTCCCAGGA GAGTGTCACAGACAGACAGCAAGACAGACACCTACAGCCTCGAAA GCACCCTGACGCTGAGCAAAAGCAGACTACGAGAAACACAAAGTCTAC GCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCCGTACAAAAGAG CTTCAACAGGGAGAGTGT	TGCAACGTGAATCAC AAGCCCAGCAACACC AAGGTGACAAAGAAA GTTGAGCCCCAAATCT TGT
			SEQ ID NO:163	SEQ ID NO:164	SEQ ID NO:165
AA			QSVLTQPPSVSGAPG QRVTISCTGSSSNIG AGYDVHWYQQFPGTA PKLLIQGNSNRPSGV PDRFSGSKGTSASL AITGLQAEDEADYYC QSYDSSLGSVFGGG TKLTVLGQPKAAPSV TLFPPSSEELQANKA TLVCLISDFYPGAVT VAWKADSSPVKAGVE TTTPSKQSNNKYAAE SYLSLTPEQWKSHRS YSCQVTHEGSTVEKT VAPTECS	EVQLVQSGAEVKKPGESLKISCKTSEYSFTSYWIGWVRQMPKGLEW MGI IYLGDSDTRYSPSFQGGVTISADKSI STAYLQWSSLKASDTAMY YCARSNWGLDYWGQGLVTVSSASTKGPSVFFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLKSVVTVTP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTI SKAKGQPREPQVYITLPPSRSEEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGGSGGGSQVQLQQSGAGLLKPSE TLSLTCAVHGGSFSGYYWNWIRQPPPKGLEWIGEINHAGNTNYPNPSL KSRVTISLDTSKNQFSLTILTSVTAADTAVYYCARGYCRSTTCYFDYW GQGTLVTVSSTVAAPSVFI FPPSDEQLKSGTASVVCLLNNFYPREAK VQWKVDNALQSGNSQESVTEQDSKDSYSTLESTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC	EIVLTQSPGTLSLSP GERATLSCRASQSVR SSYLAWYQQKPGQAP RLLIYGASSRATGIP DRFSGSGSGTDFTLT ISRLEPEDFAVYYCQ QYGSSTPFGQGRLE IKRASTKGPSVFPLA PSSKSTSGGTAALGC LVKDYFPEPVTVSWN SGALTSGVHTFPAVL QSSGLYSLKSVVTVTP SSSLGTQTYICNVNH KPSNTKVDKKVEPKS C
			SEQ ID NO:166	SEQ ID NO:167	SEQ ID NO:168
			CAGTCTGTGCTGACG CAGCCGCCCTCAGTG TCTGGGCCCCCAGGG CAGAGGTCACCATC TCCTGCACTGGGAGC AGTTCCAACATCGGG GCAGGTTATGATGTA CACTGGTACCAGCAG TTTCCAGGAACAGCC CCCCAACTCCTCATC CAAGGTAACAGCAAT CGGCCCTCAGGGGTC CCTGACCGATTCTCT GGCTCCAAAGTCTGGC	GAGGTGCAGCTGGTGAGTCTGGAGCAGAGGTGAAAAAGCCCCGGGA GTCTCTGAAGATCTCCTGTAAAGACTTCTGAATACAGCTTTACCAGCT ACTGGATCGGCTGGGTGCGCCAGATGCCCGGAAAGGCCCTGGAGTGG ATGGGGATCATCTATCTTGGTGACTCAGATACCAAGATACAGCCCCGTC CTTCCAAGGCCAGGTCACCATCTCAGCCGACAAAGTCCATCAGTACCG CCTACCTGCAGTGGAGCAGCCTGAAGGCCCTCGGACACCGCCATGTAT TACTGTGCGAGAAAGTAACTGGGTCTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTCTCTAGTGCC TCCACCAAGGCCCATCGGTC TTCC CCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTG GGCTGCCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTG GAAC TCAGGCGCCCTGACCAGCGCGGTGCACACCTTCCC GGCTGTCC TACAGTCTCAGGACTCTACTCCCTCAAAAGCGTGGTGACCGTGCCCC TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAA GCCCAGCAACACCAAGGTGGACAAAGAAAGTTGAGCCCCAAATCTTGTG	GACATCCAGATGACC CAGTCTCCATCCTCC CTGTCTGCATCTGTA GGAGACAGAGTCACC ATCACTTGCCGGGCA AGTCAGAGCATTAAC AACTATTTAAATTGG TATCAGCAGAGACCA GGGAAAGCCCCCTAAG CTCCTGATCTATGCT GCATCCAGTTTGCAA AGTGGGTTCCCATCA AGGTTCAGTGGCAGT GGATCTGGGACAGAT
			029_3.2_1gg.001_9c8_VH_C K(S176E)		
			!PS: 376725		
			NA		

		ACCTCAGCCTCCCTG GCCATCACTGGGCTC CAGGCTGAGGATGAG GCTGATTATTACTGC CAGTCC TATGACAGC AGCCTGAGTGGTTCG GTGTTCCGGCGGAGGG ACCAAGCTGACCGTC CTAGGTCAGCCCCAAG GCTGCCCTTCGGTC ACTCTGTTCCCGCCC TCCTCTGAGGAGCTT CAAGCCAAACAAGGCC ACACTGGTGTGTCTC ATAAGTGACTTCTAC CCGGAGCCGTGACA GTGGCCTGGAAGGCA GATAGCAGCCCGTC AAGCGGGAGTGGAG ACCACCAACCCCTCC AAACAAAGCAACAAC AAGTACGCGCGCGAG AGCTATCTGAGCCTG ACGCCTGAGCAGTGG AAGTCCCACAGAAGC TACAGCTGCCAGGTC ACGCATGAAGGGAGC ACCGTGAGAAAGACA GTGGCCCTTACAGAA TGTTCA	ACAAAACTCACACATGCCACACCGTGCCCGCAGCACCTGAACCTCCTGGGG GGACCGTCAGTCTTCTCTTCCCCCAAACCCAAAGGACACCCCTCAT GATCTCCCGACCCCTGAGGTACATGCGTGTGTTGGAGCTGAGCC ACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAG GTGCATAATGCCAAGACAAAGCCGTTGTAGGAGCAGTACGGCAGCAC GTACCGTTGTGTACGCTCCTCACCGTCTGTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAAACAAAGCCCTCCAGCC CCCATCGAGAAACCATCTCCAAAGCCAAAGGCAGCCCCGAGAAACC ACAGGTGTACACCTGCCCTCCCATCCCGGGAGGAGATGACCAAGAACC AGGTCAGCCTGACCTGCCCTGGTCAAAGGCTTCTATCCAGCGACATC GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAAGAC CACGCCCTCCCGTGTGACTCCGACGGCTCCTTCTTCTCTATAGCA AGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGAACTCTTCTCA TGCTCCGTGATGCATGAGGCTCTGCACAACTACTACCGCAGAAAGAG CCTCTCCCTGTCTCCGGTGTGTGGCGATCGGGAGGTGGCGGATCCC AGGTGCAGCTGCAGGAGTCCGGCCCAAGGACTGGTGAAGCCTTCGGAG ACCCGTGCCCTCACCTGCACGTGTCTCTGGTGGCTCCATCAGTAGTTA CTTCTGGAGCTGGATTTCGGCAGCCCCCAGGTAAGGACTGGAGTGGA TTGGCTATATCTATTACAGTGGGCAGACCAAATACAACCCCTCCCCTC AAGAGTCGAGTCACCATATCAATAGACACAGTCCAAGAACCACTTCTC CCTGAAGCTGAGCTCTGTGACCGCTGCGGACACGGCCGTGTATTACT GTGCGAGAGAAACTGGGAGCTACTACGGCTTTGACTACTGGGGCCAG GGAACCCCTGGTCACCGTCTCCTCAACTGTGGCTGCACCATCTGTCTT CATCTTCCCGCCATCTGATGAGCAGTTGAAAATCTGGAACCTGCCTCTG TTGTGTGCCCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAG TGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGT CACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCGAAAGCACCC TGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCCCTGC GAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCAACAAAGAGCTTCAA CAGGGGAGAGTGT	TTCACTCTCACCATC AGCAGTCTGCAACCT GAAGATTTTGCAACT TACTACTGTCAACAG AGTTACAGTACCCCT CGGACGTTTCGGCCAA GGGACCAAGCTGGAA ATCAAAACGAGCCTCC ACCAAGGGCCCATCG GTCTTCCCCCTGGCA CCCTCCTCCAAAGAGC ACCTCTGGGGGCACA GCGGCCCTGGGCTGC CTGGTCAAGGACTAC TTCCCCGAACCGGTG ACGGTGTCTGTGGAAC TCAGGGCGCCCTGACC AGCGCGTGCACACC TTCCCCGGCTGTCCCTA CAGTCTCAGGACTC TACTCCCTCAAAAGC GTGGTGACCGTGCCC TCCAGCAGCTTGGGC ACCCAGACCTACATC TGCAACGTGAATCAC AAGCCCAGCAACACC AAGGTGACAAAGAAA GTTGAGCCCCAAATCT TGT
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			QSYDSSLGSVFGGG TKLTVLGQPKAAPSV TLFPPSSEELQANKA TLVCLISDFYPGAVT VAWKADSSPVKAGVE TTTPSKQSNNKYAAE SYLSLTPEQWKSHRS YSCQVTHEGSTVEKT VAPTECS	VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPAP PIEKTI SKAKGQPREPQVYTLPPSR EEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPG GGSGGQVQLQESGPGLVK PSE TLSLTCTVSGGSISSYFWSWIRQPPGKGLEWIGIYIYSGQT KYNPSL KSRVTISIDTSKNQFS LSKLSSVTAADTA VYYCARETGSYYGFDYWGQ GTLVTVSSTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQ WKVDNALQSGNSQESVTEQDSKDSTYSLEST LTLTKADYEKHKVYAC EVTHQGLSSPVTKSFNRGEC	SYSTPRTFGQGTKLE IKRASTKGPSVFPLA PSSKSTSGGTAALGC LVKDYFFPEPVT VSWN SGALTS GVHTFFPAVL QSSGLYSLKSVV TVP SSSLGTQTYICNV NH KPSNTKVDKKVEPKS C
			SEQ ID NO:172	SEQ ID NO:173	SEQ ID NO:174
			CAGTCTGTGCTGACG CAGCCGCCCTCAGTG TCTGGGCCCCAGGG CAGAGGTCACCATC TCCTGCAC TGGGAGC AGTTCCAA CATCGGG GCAGGTTATGATGTA CACTGGTAC CAGCAG TTTCCAGGAACAGCC CCCAAACTCCTCATC CAAGGTAACAGCAAT CGGCCCTCAGGGGTC CCTGACCGATTCTCT GGCTCCAAGTCTGGC ACCTCAGCCTCCCTG GCCATCAC TGGGCTC CAGGCTGAGGATGAG GCTGATTATTACTGC CAGTCC TATGACAGC AGCCTGAGTGGTTCG GTGTTCCGGCGGAGGG ACCAAGCTGACCGTC CTAGGT CAGCCCCAAG GCTGCCCCCTCGGTC ACTCTGTTCCCGCCC TCCCTCTGAGGAGCTT CAAGCCAA CAAGGCC	GAGGTGCAGCTGGTG CAGTCTGGAGCAGAGGT GAAAAAGCCCCGGGA GTCTCTGAAGATCTC CTGTAAAGACTTCTGA ATAACAGCTTTAC CAGCT ACTGGATCGGCTGG GTGCGCCAGATGCCG GGAAGGCCCTGGAGTG G ATGGGATCATCTATC TTGGTGACTCAGATA CCAGATACAGCCCCGTC CTTCCAAAGGCCAGGT CACCATCTCAGCCGACA AGTCCCATCAGTACCCG CCTACCTGCAGTGGAG CAGCCTGAAGGCCCTC GGACACCGCCATGTAT TACTGTGCGAGAA GTAACTGGGTCTTGACT ACTGGGCCAGGGAAC CCTGGTCACCGTCTC TAGTGCCCTCCACCA AGGCCCATCGGTCTTCC CCCTGGCACCCCTCCT CCAAGAGCACCTCTG GGGGCACAGCGGCCCTG GGCTGCCCTGGTCA AGGACTACTTCCCCGA AACCGGTGACGGTGT CGTG GAACTCAGGCGCCCT GACCAGCGCGTGCA CACACCTTCCC GGCTGTCC TACAGTCTCAGGACT CTACTCCCTCAA AAGCGTGGTGACCCGT GCCCC TCCAGCAGCTTGGG CACCCAGACCTACAT CTGCAACGTGAATCA CAA GCCCAGCAACACCA AGGTGGACAAAGATT GAGCCCCAAATCTTGTG ACAAAACTCACACA TCCCCACCGTGCCCC AGCACCTGAACCTCCT GGGG GGACCGTCAGTCTT CCTCTTCCCCCAA AACCCAGGACACCCCTCAT GATCTCCCGGACCC CTGAGGTCACATGCGT GGTGGACGTGAGCC ACGAAGACCCCTG AGGTCAAGTTCAACT GGTACGTGGACGGCGT GGAG GTGCAATAATGCCA AGACAAAGCCGTGTG AGGAGCAGTACGGCAG CAC GTACCGTTGTGT CAGCGTCCCTCAC CGTCCCTGCACCCAGG ACTGGCTGA ATGGCAAGGAGTACA AGTGCAAGGTCTCCA AACAAAGCCCTCC CAGCC CCCATCGAGAAAA CCATCTCCAAAGCCAA AGGCGAGCCCCGAGAA ACC ACAGGTGTACACCC TGCCCCCATCCCCG GAGGAGATGACCAAGA ACC AGGTCAGCCTGAC CTGCCCTGGTCA AAGGCTTCTATCC CAGCGACATC GCCGTGGAGTGGG AGAGCAATGGG CAGCCGAGAAC TACAAG CACGCTCCCGT GCTGGACTCCGAC GGCTCCTTCTTCT CTATAGCA AGCTCACCGTGGACA AGAGCAGGTGGCAG GGGAACGTCCTTCTCA	

030_3.2_IgG.001_23B3_VH4_VH_CK(S176F)

NA

1PS:376729

		ACACTGGTGTGTCTC ATAAGTGACTTCTAC CCGGAGCCGTGACA GTGGCCTGGAAGGCA GATAGCAGCCCGTC AAGCGGGAGTGGAG ACCACCACACCCCTCC AAACAAAGCAACAAC AAGTACGGGCCGAG AGCTATCTGAGCCTG ACGCCTGAGCAGTGG AAGTCCCACAGAAAGC TACAGCTGCCAGGTC ACGCATGAAGGGAGC ACCGTGGAAGAAGACA GTGGCCCTTACAGAA TGTTCA	TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAAGAG CCTCTCCCTGTCTCCGGGTGGTGGCGGATCGGGAGGTGGCGGATCCC AGGTACAGTTGCAGAGTCAGGTCCAGGACTGGTGAAGCCCTCGGAG ACCCCTCTCACTCACCTGTACCATCTCCGGGGACAGTGTCTCTACCAA CAGTGTGCTTGAACTGGATTAGGCAGCCCCCAGGAAAGGCCCTTG AGTGGATAGGAAGGACATACTACAGGTCCAAAGTGGTATAATGATTAT GCAGTTTCTCTGAAAAAGTCGAGTAACCATCAGCCCAGACACATCCAA GAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGCCGCGGACACGG CTGTGTATTACTGTGCAAGAGAGGATGGGGATAGCTACTACCGCTAC GGTATGACGTCTGGGGCCAAAGGACCACGGTCACCGTCTCCTCAAC TGTGGCTGCACCATCTGTCTTCACTCTTCCGCCATCTGATGAGCAGT TGAAATCTGGAACCTGCCCTCTGTTGTGTGCCCTGCTGAATAACTTCTAT CCCAGAGAGCCAAAAGTACAGTGAAGTGGAAGTGATAACGCCCTCCAATC GGTAACTCCAGGAGAGTGTCAAGAGCAGGACAGCAAGGACAGCA CCTACAGCCTCGAAAAGCACCCCTGACGCTGAGCAAAGCAGACTACGAG AAACACAAAGTCTACGCCCTGCGAAGTCACCCCATCAGGGCCTGAGCTC GCCCCGCACAAAAGAGCTTCAACAGGGGAGAGTGT	ACAGCGGCCCTGGGC TGCTTGGTCAAGGAC TACTTCCCGAACC GTACGGTGTCTGG AACTCAGCGCCCTG ACCAGCGGTGCAC ACCTTCCCGGTGTC CTACAGTCTCAGGA CTCTACTCCCTCAAA AGCGTGGTGACCGTG CCCTCCAGCAGCTTG GGACCCAGACCTAC ATCTGAAACGTGAAT CACAAAGCCAGCAAC ACCAAAGGTGACAAG AAAGTTGAGCCCCAAA TCTTGT
		SEQ ID NO:175	SEQ ID NO:176	SEQ ID NO:177
AA		QSVLTQPPSVSGAPG QRVTISCTGSSSNIG AGYDVHWYQQFPGTA PKLLIQGNSNRPSGV PDRFSGSKGTSASL AITGLQAEDEADYYC QSYDSSLSGSVFGGG TKLTVLGQPKAAPSV TLFPPSSEELQANKA TLVCLISDFYPGAVT VAWKADSSPVKAGVE TTTTPSKQSNNKYAAE SYLSLTPEQWKSHRS YSCQVTHEGSTVEKT VAPTECS	EVQLVQSGAEVKKPGESLKISCKTSEYSFYSYTWIGVVRQMPGKGLEW MGI IYLGDS DTRYSPSFQGQVTI SADKSI STAYLQWSSLKASDTAMY YCARSNWGLDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLKSVVTVTP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELIG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTTPVLDSDGSFFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGSGSGGGSQVQLQESGPGLVKPSSE TSLTCTISGDSVSTNSVAWNWIRQPPGKGLEWIGRTYYRSKWYNDY AVSLKSRVTISPDTSKNQFSLKLSVSTAADTAVYYCAREDGDSYYRY GMDVWGQGTTVTVSSSTVAAPSVFIFPPSDEQLKSGTASVVCLLNIFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLESTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC	DIQMTQSPSSLSASV GDRVITITCRSSQSVL YSSNNKNYLVWYQQK PGKVPKLLIYWASTR ESGVPSRFSGSGSGT DFTLTISSLQPEDVA TYYCQQYYKTPLTFG GGTKVEIKRASTKGP SVFPLAPSSKSTSGG TAALGCLVKDYFPEP VTVSWNSGALTSGVH TFPAVLQSSGLYSLK SVVTVPSSSLGTQTY ICNVNHKPSNTKVDK KVEPKSC
		SEQ ID NO:178	SEQ ID NO:179	SEQ ID NO:180

1PS: 376733	031_3B3v2_IgG.001_Ada1Imumab_VH_CK(S176E)	NA	GAAATTGTGTTGACG CAGTCTCCAGGCACC CTGTCTTTGTCTCCA GGGAAAGAGCCACC CTCTCCTGCAGGGCC AGTCAGAGTGTTAGA AGCAGTTACTTAGCC TGGTACCAGCAGAAA CCTGGCCAGGCTCCC AGGCTCCTCATCTAT GGTGCAATCCAGCAGG GCCACTGGCATCCCA GACAGGTTCAGTGGC AGTGGGTCTGGGACA GACTTCACCTCTCACC ATCAGCAGACTGGAG CCTGAAGATTTTGCA GTGTATTACTGTCTAG CAGTATGGTAGCTCA CCTACCTTCGGCCAA GGGACACGACTGGAG ATTAAACGAACGGTG GCTGCACCATCTGTC TTCATCTTCCC GCCA TCTGATGAGCAGTTG AAATCTGGTACCGCC TCTGTTGTGTGCCCTG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCCAG GAGAGTGTACACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC GAGAGCACCCCTGACG CTGAGCAAAAGCAGAC	CAGGTGCAGTTACAGCAGTCGGGCGCAGGACTGTTGAAGCCTTTCGGA GACCCCTGTCCCTCACCTGCGCTGTCCATGGTGGTCCCTTCAGTG GTT ACTACTGGAAC TGGATCCGCCAGCCACCAGGAAAGGGCTAGAGTGG ATTGGGGAAATCAATCATGCTGGAACACCAACTACAACCCGTCCCT CAAGAGTCGAGTCACCATATCATTAGACACGTC CAAGAACCAGTTCT CCCTGACGCTGACCTCTGTGACCGCGCGGACACGGCTGTGTATTAC TGTGCGAGAGGATATTGTAGAAGTACCACCTGCTACTTTGACTACTG GGCCAGGGAACCCTAGTCACCGTCTCCTCAGCCTCCACCAAGGGCC CATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGCC ACAGCGCCCTGGCTGCC TGGTCAAGGACTACTTCCCCGAACCGGT GACGGTGTCTGGAACTCAGGCGCCCTGACCAGCGGCTGCACACCT TCCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAAAAAGCGTG GTGACCGTGCCCTCCAGCAGCTTGGCACCCAGACCTACATCTGCAA CGTGAA TCACAAAGCCAGCAACACCAAGTGGACAAAGAAAGTTGAGC CCAAATCTTGTGACAAAAC TCAACATGCCACCGTGCCCAGCACCT GAACTCCTGGGGACCGTCA GTCTTCTCTTCCCCCAAACCCAA GGACACCCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGG TGGACGTGAGCCACGAAGACCCCTGAGGTCAAAGTTCAA CTGGTACGTG GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGTGTGAGGAGCA GTACGGCAGCACGTACC GTTGTGTCAGCGTCTCACCGTCTTGCAACC AGGACTGGCTGAATGGCAAGGAGTACAAAGTGC AAAGTCTCCAACAAA GCCCCCAGCCCCCATCGAGAAAA CCACTCCAAGGCCAAAGGGCA GCCCCGAGAACCAAGGTGTACACCTGCCCCCATCCCCGGAGGAGA TGACCAAGAACCAAGGTCA GCTCAGCCTGACCTGCC TGGTCAAAGCTTCTAT CCCAGCGACATCGCCGTGGAGTGGAGAGACAAATGGCAGCCCGGAGAA CAACTACAAGACCA CGCTCCCGTGTGACTCCGACGGCTCCTTCT TCCCTCTATAGCAAGCTCACCCGTGGACAAAGACAGGTGGCAGCAGGGG AACGTCTTCTCATGTCTCCGTGATGCATGAGGCTCTGCACAACCACTA CACGCAGAAAGACCTCTCCCTGTCTCCGGGTGGTGGCGGATCGGGAG GTGGCGGATCCGAGGTACA ACTGGTGGATCAGGTGGAGGTTTGGTG CAGCCGGGAGATCGCTCAGGCTTAGCTGTGCGGCATCGGGGTTTAC TTTTCGATGATTATGCGATGCATTTGGGTCCGGCAAGCGCCTGGA AAAAG GGCTCGAGTGGGTTTCCGCCATTACGTGGAATAGCGGACACATCGAT TATGCAGACAGTGTGGAGGGCAGATTCACAA TCTCACGAGACAAATGC TAAGAAACAGCCTGTACCTTCAGATGAAC TCACTTCGCGCGGAAGATA CCGCCGTATACTACTGCGCCAAAAGTCTCCTACTTGTCTACAGCTTCG TCGCTCGACTATTGGGGTCAAGGAACGTTGGTCA CCGTCTCTAGTAC	GATATCCAAATGACA CAATCACCATCGTCG CTTTCAGCGTCTGTT GGGACCGTGTGACG ATTACCTGTCGCGG TCCCAGGGAATCCGG AATTACCTCGCATGG TATCAGCAAAAACCC GGAAAAAGCACCGAAG CTCCTGATCTATGCC GCCTCGACTCTTCAG AGTGGTGTGCCGTGG AGGTTAGCGGTCC GGTCAGGTACGGAC TTTACTCTCACAATT TCCAGCCTGCAGCCC GAAGATGTAGCTACC TATTACTGCCAGAGA TACAAACGAGCGCCT TACACATTCCGACAA GGGACAAAAGTCGAG ATCAAAGCTGCCCTCC ACCAAGGCCCATCG GTCTTCCCCCTGGCA CCCTCCTCCAAGAGC ACCTCTGGGGCACA GCGGCCCTGGGCTGC CTGGTCAAGGACTAC TTCCCCGAACCGGTG ACGGTGTCTGTGAAC TCAGGCGCCCTGACC AGCGGCGTGCACACC TTCCCCGGCTGCC TA CAGTCTCAGGACTC TACTCCCTCAAAAGC GTGGTGACCGTGCCC TCCAGCAGCTTGGGC
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			TACGAGAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGAGAGTGT	TGTGGCTGCACCATCTGTCTTCAATCTTCCCGCCATCTGATGAGCAGT TGAATCTGGAACCTGCCCTCTGTTGTGTGCTGCTGAATAACTTCTAT CCCAGAGAGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC GGTAACTCCAGGAGAGTGTCAAGAGCAGACAGCAAGGACAGCA CCTACAGCCTCGAAAAGCACCCCTGACGCTGAGCAAAGCAGACTACGAG AAACACAAAGTCTACGCCCTGCGAAGTCACCCATCAGGGCCTGAGCTC GCCCCGCACAAAAGAGCTTCAACAGGGGAGAGTGT	ACCCAGACCTACATC TGCAACGTGAATCAC AAGCCAGCAACACC AAGTGGACAAGAAA GTTGAGCCCCAAATCT TGT
			SEQ ID NO:181	SEQ ID NO:182	SEQ ID NO:183
AA			EIVLTQSPGTLISLSP GERATLSCRASQSVR SSYLAWYQQKPGQAP RLLIYGASSRATGIP DRFSGSGTDFTLT ISRLEPEDFAVYYCQ QYGSSTFFGQGRLE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLESTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEN	QVQLQQSGAGLLKPSSETLSLTCAVHGGSFSGYYWNWIRQPPGKGLEW IGEINHAGNTNYPNPSLKSRVTISLDTSKNQFSLTLTSVTAADTAVYY CARGYCRSTTCYFDYWGGQTLVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLKSV VTVPSSSLGTQYIICNVNHHKPSNTKVDKKVEPKSCDKHTHTCPPCPAP ELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMHREALHNHYTQKSLSLSPGGSGGGSEVQLVESGGGLV QPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSAITWNSGHID YADSVTEGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAKVSYLSTAS SLDYWGQGLTVTVSSITVAAPSVFIFPPSDEQLKSGTASVVCLLNIFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLESTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC	DIQMTQSPSSLSASV GDRVITITCRASQGIR NYLAWYQQKPKKAPK LLIYAASTLQSGVPS RFSGSGSGTDFTLTI SSLQPEDVATYYCQR YNRAPYTFGQGTKVE IKRASTKGPSVFPLA PSSKSTSGGTAALGC LVKDYFPEPVTVSWN SGALTSGVHTFPAVL QSSGLYSLKSVVTVP SSSLGTQYICNVNH KPSNTKVDKKVEPKS C
			SEQ ID NO:184	SEQ ID NO:185	SEQ ID NO:186
			GAAATTGTTTGACG CAGTCTCCAGGCACC CTGTCTTTGTCTCCA GGGAAAGAGCCACC CTCTCCTGCAGGGCC AGTCAGAGTGTTAGA AGCAGTTACTTAGCC TGGTACCAGCAGAAA CCTGGCCAGGCTCCC AGGCTCCTCATCTAT GGTGATCCAGCAGG GCCACTGGCATCCCA GACAGGTTCAGTGGC	CAGGTGCAGTTACAGCAGTCGGGGCGCAGGACTGTTGAAGCCTTCGGA GACCCGTGTCCTCACCTGCGCTGTCCATGGTGGTCTCTCAGTGTT ACTACTGGAACCTGGATCCGCCAGCCACCAGGAAGGGCTAGAGTGG ATTGGGGAAATCAATCATGCTGGAACACCAACTACAACCCGTCCCT CAAGAGTCGAGTCACCATATCATGCTGGAACACCAACTACAACCCGTCT CCCTGACGCTGACCTCTGTGACCGCGCGGACACGGCTGTGTATTAC TGTGCGAGAGGATATTGTAGAAGTACCACCTGCTACTTTGACTACTG GGCCAGGGAACCTAGTCACCGTCTCCTCAGCCTCCACCAAGGGCC CATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGC ACAGCGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCCGAACCGGT GACGGTGTCTGGAACTCAGGCGCCCTGACCAAGCGGCTGCACACCT TCCCGGCTGTCTACAGTCCCTCAGGACTCTACTCCCTCAAAAAGCGTG GTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAA	CAGTCTGTGCTGACG CAGCCGCCCTCAGTG TCTGGGGCCCCAGGG CAGAGGGTCACCATC TCCTGCACTGGGAGC AGTTCCAACATCGGG GCAGGTTATGATGTA CACTGTACCAGCAG TTTCCAGGAACAGCC CCCAAACTCCTCATC CAAGGTAACAGCAAT CGGCCCTCAGGGGTC CCTGACCGATTCTCT
!PS: 376739	032_3B3v2_1gG.001_3.2_	VH _{CL} (S176E)	NA		

			AGTGGGTCTGGGACA GACTTCACTCTCACC ATCAGCAGACTGGAG CCTGAAGATTTTGCA GTGTATTACTGTCAG CAGTATGGTAGCTCA CCTACCTTCGGCCAA GGGACACGACTGGAG ATTAAACGAACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGTACCGCC TCTGTTGTGTGCCCTG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAAC TCCCAG GAGAGTGTACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC GAGAGCACCTGACG CTGAGCAAAAGCAGAC TACGAGAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	CGTGAATCACAAAGCCAGCAACACCAAGGTGGACAAAGAAAGTTGAGC CCAAAATCTTTGTGACAAAACTCACACATGCCCACCCGTGCCAGCACCT GAACTCCTGGGGACCGTCAGTCTTCTCTTCCCTCCCAAAACCCAA GGACACCCCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGG TGGACGTGAGCCACGAAGACCCCTGAGGTCAAAGTTCAACTGGTACGTG GACGGCTGGAGGTGCATAAATGCCAAGACAAAAGCCGTGTGAGGAGCA GTACGGCAGCACGTACCGTTGTGTCAAGCTCTCACCGTCTCTGCACC AGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA GCCCTCCCAGCCCCCATCGAGAAAAACCATCTCCAAGCCAAAGGGCA GCCCGAGAAACCAAGGTGTACACCTGCCCCCATCCCGGAGGAGA TGACCAAGAAACCAAGGTACGCCCTGACCTGCCCTGTTCAAGGCTTCTAT CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAA CAACTACAAGACACGCCCTCCGTGCTGGACTCCGACGGCTCCTTCT TCCTCTATAGCAAGCTCACCGTGGACAAAGACAGGTGGCAGCAGGGG AACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTA CACGCAGAAAGCCTCTCCCTGTCTCCGGGTGGTGGCGGATCGGGAG GTGGCGGATCCGAGGTGCAGCTGTTGCAGTCTGGAGCAGAGGTGAAA AAGCCCGGGAGTCTCTGAAGATCTCCTGTAAAGACTTCTGAATACAG CTTTACCAGCTACTGGATCGGCTGGGTGGCGCCAGATGCCCGGAAAG GCCTGGAGTGGATGGGATCATCTATCTTGGTACTCAGATACCAAGA TACAGCCCGTCTTCAAAGGCCAGGTCAACCATCTCAGCCGACAAAGTC CATCAGTACCGCTACCTGCACTGAGTGAGCAGCTGAAGCCTCGGACA CCGCCATGTATTACTGTGCGAGAAAGTAACTGGGGTCTTGACTACTGG GGCCAGGAAACCCCTGGTCAACCGTCTCTAGTCAAGCCCAAGCCCAACCC CACTGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTCCAAGCCAAACA AGGCCACACTAGTGTGTCTGATCAGTGACTTCTACCCGGGAGCTGTG ACAGTGGCCTGGAAGGCAGATGGCAGCCCGCTCAAGCGGAGTGA GACCAACCAACCCCTCAAACACAGACAAACAAGTACGCGGCCGAGA GCTACCTGAGCCTGACGCCCGAGCAGTGGAAGTCCACAGAAAGCTAC AGCTGCCAGGTACGCATGAAGGGAGCACCGTGGAGAAAGACAGTGGC CCCTACAGAAATGTTCA	SEQ ID NO:187	SEQ ID NO:188	SEQ ID NO:189
AA	EIVLTQSPGTLISLSP GERATLSCRASQSVR SSYLAWYQQKPGQAP RLLIYGASSRATGIP DRFSGSGSDFTLT	QVQLQQSGAGLLKPSETLSLTCAVHGGSFSGYYWNWIRQPPKGLEW IGELINHAGNTNYPNPSLKSRVTISLDTSKNQFSLTILTSVTAADTAVYY CARGYCRSTTCYFDYWGQGTSLTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLKSV VTPVSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP	QSVLTQPPPSVSGAPG QRVTI SCTGSSSNIG AGYDVHWYQQFPGTA PKLLIQGNSNRPSGV PDRFSGSKSGTSASL				

			ISRLEPEDFAVYYCQ QYGSPTFGQTRLE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLESTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEN	ELGGPSVFLFPPPKDKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMEALHNHYTQKSLSLSPGSGSGGSEVQLVQSGAEVK KPGESLKISKCTSEYSFTSYWIGWVRQMPGKGLEWMGIIYLGDSDDR YSPSFQGGVTISADKSI STAYLQWSSLKASDTAMYCARSNWGLDYYW GQGTLVTVSSQPKANPTVTLFPPSSEELQANKATLVCLISDFYPGAV TVAWKADGSPVKAGVETTKPSKQSNNKYAESYLSLTPEQWKSHRSY SCQVTHEGSTVEKTVAPTECS	AITGLQAEDEADYYC QSYDSSLSGSVFGGG TKLTVLGASTKGPSV FPLAPSSKSTSGGTA ALGCLVKDYFPEPVT VSWNSGALTSGVHTF PAVLQSSGLYSLKSV VTVPSSSLGTQTYIC NVNHKPSNTKVDKKV EPKSC
			SEQ ID NO:190	SEQ ID NO:191	SEQ ID NO:192
	033_9c8_1Ig.001_Ada1Imumab_VH_CK (S176E)	NA	GACATCCAGATGACC CAGTCTCCATCCTCC CTGTCTGCATCTGTA GGAGACAGAGTCACC ATCACTTGCCGGGCA AGTCAGAGCATTAAAC AACTATTAAATTGG TATCAGCAGAGACCA GGGAAAGCCCCTAAG CTCCTGATCTATGCT GCATCCAGTTTGCAA AGTGGGTCCCATCA AGGTTCAGTGGCAGT GGATCTGGGACAGAT TTCACCTCTACCATC AGCAGCTGC AACCT GAAGATTTTGCAACT TACTACTGTCAACAG AGTTACAGTACCCCT CGGACGTTCGGCCAA GGGACCAAGCTGGAA ATCAAAACGAACGGTG GCTGCACCATCTGTC TTCATCTTCCCCGCA TCTGATGAGCAGTTG AAATCTGGTACCGCC	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGA GACCCCTGTCCCTCACCTGCAC TGTCTCTGGTGGCTCCATCAGTAGTT ACTTCTGGAGCTGGATCCGGCAGCCCCCAGGTAAGGACTGGAGTGG ATTGGCTATATCTATTACAGTGGGAGACCAATAACAACCCCTCCCT CAAGAGTCGAGTCACCATATCAATAGACACGTCCAAGAACCAAGTTCT CCCTGAAGCTGAGCTCTGTGACCCGTGCGGACACGGCCGTGTATTAC TGTCGAGAGAAACTGGGAGCTACTACGGCTTTGACTACTGGGCCA GGGAACCTGGTCACCGTCTCCTCAGCCTCCACCAAGGCCCATCGG TCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGCTGCCGTGTC AAGGACTACTTCCCGAACCGGTGACGGT GTCGTGGAACTCAGGCGCCCTGACCAAGCGGTGCACACCTTCCCCGG CTGTCC TACAGTCC TCAGGACTCTACTCCTCAAAAAGCGTGTGACC GTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAA TCACAAAGCCAGCAACACCAAGGTGGACAAAGAAAGTTGAGCCCCAAAT CTTGTGACAAAAC TCAACATGCCACCCGTCGCCAGCACCTGAAC T C CTGGGGGACCGTCAGTCTTCTCTTCCCCC AAAACCCAAAGGACAC CCTCATGATCTCCCGACCCCTGAGGTCACATGCGTGGTGGACG TGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAAGCCGTGTGAGGAGCAGTACGG CAGCACGTACCGTTGTGT CAGCGTCTCACCCTGCTGCACCGGACT GGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTC CCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAAGGCAGCCCCG AGAAACCAAGGTGTACACCCCTGCCCCCATCCGGGAGGAGATGACCA AGAAACCAAGGTGAGCCTGACCTGCCCTGGTCAAAGGCTTCTATCCCAGC GACATCGCCGTGAGTGGGAGAGCAATGGCAGCCGGAGAAACAATA CAAGACACGCCCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTCT	GATATCCAAATGACA CAATCACCATCGTCG CTTTCAGCGTCTGTT GGCAGCCGTGTGACG ATTACCTGTCCGCG TCCCAGGGAATCCGG AATTACCTCGCATGG TATCAGCAAAAACCC GGAAAAGCACCGAAG CTCCTGATCTATGCC GCCTCGACTCTTCAG AGTGGTGTCCCGTCC AGGTTAGCGGTCC GGGTCAGGTACGGAC TTTACTCTACAATT TCCAGCCTGCAGCCC GAAGATGTAGCTACC TATTACTGCCAGAGA TACAACCGAGCGCCT TACACATTCCGACAA GGGACAAAAGTCGAG ATCAAGCGTGCCTCC ACCAAGGCCCATCG GTCTTCCCCCTGGCA CCCTCCTCCAAGAGC ACCTCTGGGGGCACA

		TCTGTTGTGTGCCTG CTGAATAACTTCTAT CCCAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCAG GAGAGTGCACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC GAGAGCACCTGACG CTGAGCAAAAGCAGAC TACGAGAAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	ATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCA GAAGAGCCTCTCCCTGTCTCCGGGTGGTGGCGATCGGAGGTGGCG GATCCGAGGTACAACTGTTGGAATCAGGTGGAGGTTTGGTGCAGCCG GGGAGATCGCTCAGCCTTAGCTGTGCGGCATCGGGGTTTACTTTCGA TGATTATGCGATGCATTGGTCCGGCAAGCGCCTGGAAAAGGGCTCG AGTGGGTTTCCGCCATTACGTGGAATAGCGGACACATCGATTATGCA GACAGTGTGAGGGCAGATTCACAATCTCACGAGACAATGCTAAGAA CAGCCTGTACCTTCAGATGAACCTCACTTCGCGCGGAAGATACCGCCG TATACTACTGCGCCAAAGTCTCCTACTTGTCTACAGCTTCGTCGCTC GACTATTGGGTCAAAGGAACGTTGGTCACCGTCTCTAGTACTGTGGC TGCACCATCTGTCTTCACTTCCCGCCATCTGATGAGCAGTTGAAAT CTGGAACCTGCCCTCTGTTGTGTGCTGCTGAATAACTTCTATCCCCAGA GAGGCCAAAGTACAGTGGAAGTGGATAACGCCCTCCAATCGGGTAA CTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACA GCCTCGAAAAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAAACAC AAAGTCTACGCCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCCGT CACAAAGAGCTTCAACAGGGGAGAGTGT	GCGGCCCTGGGCTGC CTGGTCAAGGACTAC TTCCCCGAACCGGTG ACGGTGTCTGTGAAC TCAGGCGCCCTGACC AGCGCGTGCACACC TTCCCCGGCTGTCCTA CAGTCTCAGGACTC TACTCCCTCAAAAGC GTGGTGACCGTGCCC TCCAGCAGCTTGGGC ACCCAGACCTACATC TGCAACGTGAATCAC AAGCCCAGCAACACC AAGGTGGACAAAGAA GTTGAGCCCCAAATCT TGT
		SEQ ID NO:193	SEQ ID NO:194	SEQ ID NO:195
AA		DIQMTQSPSSLSASV GDRVITICRASQGIN NYLNWYQQRP GKAPK LLIYAASSLQSGVPS RFSGSGGTDFTLTI SSLQPEDFATYYCQQ SYSTPRTFGQTKLE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLESTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEN	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYFWSWIRQPPKGLEW IGYIYYSGQTKYNPSLKSRTVISIDTSKNQFS LKLSVTAADTAVYY CARETGSYYGFDYWGGQTLTVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLKSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYITLPPSRREMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMH EALHNHYTQKSLSLSPGGGGGGGSEVQLVESGGGLVQP GRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSAITWNSGHIDYA DSVEGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAKVSYLSTASSL DYWGQGTLVTVSSTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLESTLTLSKADYEKHK KVYACEVTHQGLSSPVTKSFNRGEC	DIQMTQSPSSLSASV GDRVITICRASQGIR NYLAWYQQRP GKAPK LLIYAASTLQSGVPS RFSGSGGTDFTLTI SSLQPEDVATYYCQR YNRAPYTFGQTKVE IKRASTKGPSVFPLA PSSKSTSGGTAALGC LVKDYFPEPVTVSWN SGALTSGVHTFP AVL QSSGLYSLKSVVTV SSSLGTQTYICNVNH KPSNTKVDKKVEPKS C
		SEQ ID NO:196	SEQ ID NO:197	SEQ ID NO:198

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		TACGAGAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGAGAGTGT	CACTCTGTTCCCGCCCTCCTCTGAGGAGCTCCAAGCCAACAAAGGCCA CACTAGTGTGTCTGATCAGTGACTTCTACCCGGGAGCTGTGACAGTG GCCTGGAAGCAGATGGCAGCCCGCTCAAGCGGGAGTGGAGACCAC CAAACCTTCCAAACAGAGCAACAACAAGTACGGCGCGAGAGCTACC TGAGCCTGACGCCCGAGCAGTGGAAGTCCACAGAAAGCTACAGCTGC CAGGTCACGCATGAAGGGAGCACCGTGGAGAAAGACAGTGGCCCCCTAC AGAA TGTTCA	AGCAGCTTGGGCACC CAGACCTACATCTGC AACGTGAATCACAAAG CCCAGCAACACCAAG GTGGACAAAGAAAGTT GAGCCCCAAATCTTGT
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AA		DIQMTQSPSSLSASV GDRVITTCRASQ SIN NYLNWYQQRP GKAPK LLIYAASSLQSGVPS RFGSGSGTDFTLTI SSLQPEDFATYYCQQ SYSTPRTFGQGTKLE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLESTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN R GEC	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYFWSWIRQPPGKGLEW IGYIYYSGQTKYNPSLKSRVTISIDTSKNQFSLKLSSTVAADTAVYY CARETGSYYGF D YWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSQVHTFPAVLQSSGLYSLKSVVT VPSSSLGTQYIICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMEALHNHYTQKSLSLSPGGSGGGSEVQLVQSGAEVKKP GESLKI SCKTSEYSFTSYWIGWVRQMPGKGLEWMGI IYLGDS DTRY S PSFQGGQVTISADKSI STAYLQWSSLKASDTAMY YCARSNWGLD YWGQ GTLVTVSSQPKANPTVTLFPPSS EELQANKATLVCLISDFYPGAVTV AWKADGSPVKAGVETTTKPSKQSN NKYAAESYLSLTPEQWKSHRSYSC QVTHEGSTVEKTVAPTECS	QSVLTQPPPSVSGAPG QRVTISCTGSSSNIG AGYDVHWYQQFPGTA PKLLIQNSNRPSGV PDRFSGSKSGTSASL AITGLQAEDEADYYC QSYDSSLSGSVFGGG TKLTVLGASTKGPSV FPLAPSSKSTSGGTA ALGCLVKDYFPEPVT VSWNSGALTSGVHTF PAVLQSSGLYSLKSV VTVPSSSLGTQYIC NVN HKPSNTKVDKKV EPKSC
		SEQ ID NO:202	SEQ ID NO:203	SEQ ID NO:204
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		035_23B3_VH4_IgG.001_A dalimnab_VH_CK(s176E)	NA	
!PS: 376755				

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			ESGVPSRFSGSGGT DFTLTISSLQPEDVA TYYCQQYYKTPLTFG GGTKVEIKRTVAAPS VFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGNS QESVTEQDSKDSYTS LESTLTLISKADYEKH KVYACEVTHQGLSSP VTKSFNRGEC	SLKSVTVPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCP PCPAPELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDLNGKEYKC KVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGGGGSEVQLVES GGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSAITWN SGHIDYADSVETRFTISRDNAKNSLYLQMNLSLRAEDTAVYYCAKVS LSTASSLDYWGQGTLLVTVSSTVAAPSVFI FPPSDEQLKSGTASVVCL LNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYTSLESTLTL KADYEKHKVYACEVTHQGLSPVTKSFNRGEC	RFSGSGTGDTFTLTI SSLQPEDVATYYCQR YNRAPYTFGQGTKVE IKRASTKGPSVFPLA PSSKSTSGGTAALGC LVKDYFPEPVTVSWN SGALTSGVHTFFPAVL QSSGLYSLKSVVTVP SSSLGTQTYICNVNH KPSNTKVDKKVEPKS C
			SEQ ID NO:208	SEQ ID NO:209	SEQ ID NO:210
		036_23B3_VH4_1g_001_3.2_VH_CL(S176F)	GACATCCAGATGACC CAGTCTCCAAGCTCC CTGTCTGCGTCTGTG GGCGATAGGTCACC ATCACTTGCAGGTCC AGCCAGAGTGTTTA TACAGCTCCAACAAT AAGAACTACTTAGTT TGGTACCAGCAGAAA CCAGGAAAGGTTCCCT AAACTGCTCATTTAC TGGGCATCTACCCGG GAATCCGGGGTCCCT AGTCGATTCAAGTGGC AGCGGGTCTGGGACA GATTTCACCTCACC ATCAGCAGCCTGCAG CCTGAAGATGTGGCA ACTTATTACTGTCAG CAATATTATAAGACT CCTCTCATTTCGGC GGAGGGACCAAGGTG GAGATCAAAACGAACG GTGGCTGCACCATCT GTCTTTCATCTTCCCG	CAGGTACAGTTGCAGGAGTCAGGTCCAGGACTGGTGAAGCCCTCGGA GACCTCTCACTACCTGTACCATCTCCGGGACAGTGTCTCTACCA ACAGTGTTCCTTGGAACTGGATCAGGCAGCCCCCAGGAAAGCCCTT GAGTGGATAGGAAGACATACTACAGGTCCAAGTGGTATAATGATTA TGCAAGTTTCTCTGAAAAGTCGAGTAAACCATCAGCCCCAGACATCCA AGAAACCAAGTTCTCCCTGAAGCTGAGCTCTGTGACTGCCGCGACACG GCTGTGATTACTGTGCAAGAGAGGATGGGGATAGCTACTACCGCTA CGGTATGGACGCTCTGGGGCCAAAGGACCACCGTCACCGTCTCCTCAG CCTCCACCAAGGCCCATCGGTCTTCCCTGGCACCCCTCCTCCAAG AGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCGTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTGCTGGAACCTCAGGCGCCCTGACCA GGGGGTGCACACCTTCCCGGCTGTCTACAGTCTCAGGACTCTAC TCCCTCAAAAAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCACAAAGCCAGCAACACCAAGGTGG ACAAAGAAAGTTGAGCCCCAAATCTTGTGACAAAACTCACACATGCCCA CCGTGCCCAGCACCTGAACCTCCTGGGGGACCGTCAGTCTTCCCTCTT CCCCCAAAACCCAAAGGACACCCCTCATGATCTCCCGACCCCTGAGG TCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAG TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAA GCCGTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTGTCAAGCTCC TCACCGTCCTGCAACCAAGACTGGCTGAATGGCAAGGAGTACAAGTGC AAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTC CAAAAGCCAAAGGCAGCCCCCGAGAACCAAGGTGTACACCCCTGCCCC CATCCCGGAGGAGATGACCAAGAACCAAGGTGAGCCTGACCTGCCCTG GTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAA	CAGTCTGTGCTGACG CAGCCGCCCTCAGTG TCTGGGGCCCCAGGG CAGAGGTCACCATC TCCTGCACCTGGGAGC AGTTCCAAACATCGGG GCAGGTTATGATGTA CACTGGTACCAGCAG TTTCCAGGAACAGCC CCCAAACTCCTCATC CAAGGTAAACAGCAAT CGGCCCTCAGGGGTC CCTGACCGATTCTCT GGCTCCAAGTCTGGC ACCTCAGCCTCCCTG GCCATCAGTGGGCTC CAGGCTGAGGATGAG GCTGATTATTACTGC CAGTCCATATGACAGC AGCCTGAGTGGTTCTG GTGTTTCGGCGGAGGG ACCAAGCTGACCGTC CTAGGTGCCCTCCACC AAGGCCCATCGGTC TTCCCCCTGGCACCC

		CCATCTGATGAGCAG TTGAAATCTGGTACC GCCCTGTGTGTGC CTGCTGAATAACTTC TATCCAGAGAGGCC AAAGTACAGTGGAAG GTGGATAACGCCCTC CAATCGGGTAACTCC CAGGAGAGTGTACACA GAGCAGGACAGCAAG GACAGCCTACAGC CTCGAGAGCACCCCTG ACGCTGAGCAAAAGCA GACTACGAGAAACAC AAAGTCTACGCCTGC GAAGTCACCCATCAG GGCCTGAGCTCGCCC GTCACAAAGAGCTTC AACAGGGGAGAGTGT	TGGGAGCCGGAGAACTACAAGACCACGCTCCCGTGCTGGACT CCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAAGAGC AGGTGGCAGAGGGAACTCTTCTCATGCTCCGTGATGATGAGGC TCTGCACAACTACACGCAGAGAGCCCTCTCCCTGTCTCCGGGTG GTGGCGGATCGGAGGTGGCGGATCCGAGGTGCAGCTGGTGAGTCT GGAGCAGAGTGAATAAGCCCGGGAGTCTCTGAAGATCTCCTGTAA GACTTCTGAATACAGCTTTACCAGCTACTGGATCGGCTGGGTGGCC AGATGCCCGGAAAGCCCTGGAGTGATGGGATCATCTATCTTGGT GACTCAGATACCAGATACAGCCCCGTCTTCCAAGGCCAGGTACCCAT CTCAGCCGACAAAGTCCATCAGTACCGCCTACCTGCAGTGGAGCAGCC TGAAAGCCTCGGACACCGCCATGTATTACTGTGCGAGAAAGTAACTGG GGTCTTGACTACTGGGGCCAGGGAACCTGGTCACCGTCTCTTAGTCA GCCCAGGCCAAACCCACTGTCACTCTGTTCGCCCTCCTCTGAGG AGTCCAAGCCAAACAAGGCCACACTAGTGTCTGTGATCAGTGACTTC TACCCGGGAGCTGTGACAGTGGCCTGGAAGGCAGATGGCAGCCCCGT CAAGCGGGAGTGGAGACCAACCAACCTCCAAACAGAGCAACAACA AGTACGGCGCCGAGAGCTACCTGAGCCTGACGCCCGAGCAGTGGAAG TCCCACAGAAAGCTACAGCTGCCAGGTACGCATGAAGGGAGCACCGT GGAGAAAGACAGTGGCCCCCTACAGAAATGTTCA	TCTCTCAAAGAGCACC TCTGGGGGCACAGCG GCCCTGGGCTGCCCTG GTCAAAGGACTACTTC CCCGAACCGGTGACG GTGTCTGTGAACTCA GGCGCCCTGACCAGC GGGTGCACACCTTC CCGGCTGTCCCTACAG TCCTCAGGACTCTAC TCCCTCAAAGCGTG GTGACCGTGCCCTCC AGCAGCTTGGGCACC CAGACCTACATCTGC AACGTGAATCACAAG CCCAGCAACACCAAG GTGGACAAAGAAAGTT GAGCCCAAATCTTGT
		SEQ ID NO:211	SEQ ID NO:212	SEQ ID NO:213
	AA	DIQMTQSPSSLSASV GDRVITITCRSSQSVL YSSNNKNYLVWYQQK PGKVPKLLIYWASTR ESGVPSRFSGSGSGT DFTLTISSLQPEDVA TYYCQQYYKTPLTFG GGTKVEIKRTVAAPS VFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGNS QESVTEQDSKDSSTYS LESTLTLSKADYEKH KVYACEVTHQGLSSP VTKSFNRGEC	QVQLQESGPGLVKPSSETLSLTCTISGDSVSTNSVAWNWI EWIGRTYYRSKWINDYAVSLKSRVTISPDTSKNQFSLKLS AVYYCAREDDGDSYYRYGMDVWGQGTIVTVSSASTKGPSV STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SLKSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDK PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNG KVSNKALPAPIEKTI VKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT RWQQGNVFCSCVMHEALHNHYTQKSLSLSPGGSGGGSEVQLV GAEVKKPGESLKISCKTSEYSFTSYWIGWVRQMPGKGLEWMGI DSDTRYSPSFQGGQVTISADKSI GLDYWGQGTIVTVSSQPKANPTVTILFPPSSEELQANKATLVCLIS YPGAVTVAWKADGSPVKAGVETTKPKSKQSNNKYA SHRSYSCQVTHEGSTVEKTVAPTECS	QSVLTQPPPSVSGAPG QRVTISCTGSSSNIG AGYDVHWYQQFPGTA PKLLIQGNSNRPSGV PDRFSGSKSGTSASL AITGLQAEDEADYYC QSYDSSLSGSVFGGG TKLTVLGASTKGPSV FPLAPSSKSTSGGTA ALGCLVKDYFPEPVT VSWNSGALTSGVHTF PAVLQSSGLYSLKSV VTVPSSSLGTQTYIC NVNHKPSNTKVDKKV EPKSC
		SEQ ID NO:214	SEQ ID NO:215	SEQ ID NO:216

1PS: 376765	037_Adalimumab_CK(S176K)_Fc_3B3v2_VH_CK(S176E)	NA	GAGGTACAACTGGTGGAAATCAGGTGGAGGTTTGGTGCCAGCCGGGGAG ATCGCTCAGGCTTAGCTGTGCGGCATCGGGGTTTACTTTCGATGATT ATCGATGCATTGGGTCCGGCAAGCGCCTGGAAGGGCTCGAGTGG GTTTCCGCCATTACGTGGAATAGCGGACACATCGATTATGCAGACAG TGTGGAGGCAGATTCACAATCTCACGAGACAATGCTAAGAACAGCC TGTAACCTTCAGATGAACTCACTTCGCGCGGAAGATACCGCCGTATAC TACTGCGCCAAAAGTCTCCTACTTGTCTACAGCTTCGTCGCTCGACTA TTGGGTCAAAGAAACGTTGGTCAACCCTCTCTAGTACGGTGGCTGCAC CATCTGTCTTCATCTTCCCGCCATCTGTATGAGCAGTTGAAATCTGGA ACTGCCCTGTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGC CAAGTACAGTGGAAAGTGGATAACGCCCTCCAATCGGGTAACTCCC AGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC AAGAGCACCCCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGT CTACGCCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCAAA AGAGCTTCAACAGGGGAGAGTGTGACAAAACACTACACATGCCCACCG TGCCACGACCTGAACCTCCTGGGGGACCGTCAGTCTTCCCTCTTCCC CCCCAAAACCAAGGACACCCCTCATGATCTCCCCGACCCCTGAGGTCA CATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTC AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAAGCC GTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTGTCAAGCTCCTCA CCGTCCGTGCACCAGGACTGGCTGAAATGGCAAGGAGTACAAGTGCAAG GTCGCCAAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAAACCAAGGTGTACACCCCTGCCCCCAT CCCCGGAGGAGATGACCAAGAACCAAGTCAGCCTGACCTGCCCTGGTC AAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGAGAGCAATGG GCAGCCGGAGAACAACTACAAAGACCACGCCCTCCCGTGTCTGGACTCCG ACGGCTCCCTTCTTCTCTATAGCAAGCTCACCGTGGAACAAGAGCAGG TGGCAGCAGGGAAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCT GCACAAACCACTACACGCAGAAGAGCCTCTCCCCTGTCTCCGGGTGGTG GCGGATCGGGAGGTGGCGGATCCCAGGTGCAGTTACAGCAGTCGGGC GCAGGACTGTTGAAGCCTTGCGAGACCCCTGTCCCCTACCTGCGCTGT CCATGGTGGGTCCCTTCAGTGGTTACTACTGGAACCTGGATTCCGCCAGC CACCAGGGAAGGGCTAGAGTGGATTGGGGAATCAATCATGCTGGA AACACCAACTACAACCCGTCCTCAAGAGTCGAGTCACCATATCATTT AGACACGTCCAAGAACCAGTTCTCCCCTGACGCTGACCTCTGTGACCG CCGGGACACGGCTGTGTATTACTGTGCGAGAGGATATTGTAGAAGT ACCACCTGCTACTTTGACTACTGGGGCCAGGGAACCCTAGTCACCGT
			GAAATTGTGTTGACG CAGTCTCCAGGCACC CTGTCTTTGTCTCCA GGGAAAAGAGCCACC CTCTCCTGCAGGGCC AGTCAGAGTGTTAGA AGCAGTTACTTAGCC TGGTACCAGCAGAAA CCTGGCCAGGCTCCC AGGCTCCTCATCTAT GGTGCATCCAGCAGG GCCACTGGCATCCCA GACAGGTTCAGTGGC AGTGGGTCTGGGACA GACTTCACTCTCACC ATCAGCAGACTGGAG CCTGAAGATTTTGCA GTGTATTACTGTGAG CAGTATGGTAGCTCA CCTACCTTCGGCCAA GGACACGACTGGAG ATTAAAACGAGCCTCC ACCAAGGCCCATCG GTCTTCCCCCTGGCA CCCTCCTCCAAGAGC ACCTCTGGGGCACA GCGGCCCTGGGCTGC CTGGTCAAGGACTAC TTCCCCGAACCGGTG ACGGTGTGCTGGAAC TCAGGCGCCCTGACC AGCGGCGTGCAACACC TTCCCGGCTGTCCCTA CAGTCCTCAGGACTC TACTCCCTCAAAAGC GTGGTGACCGTGCCC TCCAGCAGCTTGGGC
			GATATCCAAATGACA CAATCACCATCGTCG CTTTCAGCGTCTGTT GGGACC GTGTGACG ATTACCTGTCGCGG TCCCAGGGAATCCGG AATTACCTCGCATGG TATCAGCAAAAACCC GGAAAAGCACCCGAAG CTCCTGATCTATGCC GCCTCGACTCTTCAG AGTGGGTGTCCTCG AGGTTAGCGGTCC GGTCAGGTACGGAC TTTACTCTCACAATT TCCAGCCTGCAGCCC TCCAGCAGCTTGGGC

		CTCCTCAACTGTGGCTGCACCATCTGTCTTTCACTTCCCGCCATCTG ATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGCTGCTGAAT AACTTCTATCCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACGC CCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCA AGGACAGCACCTACAGCCTCGAAAGCACCCCTGACGCTGAGCAAAAGCA GACTACGAGAAACACAAAGTCTACGCCCTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	ACCCAGACCTACATC TGCAACGTGAATCAC AAGCCAGCAACACC AAGGTGGACAAAGAAA GTTGAGCCCCAAATCT TGT	ACCCAGACCTACATC TGCAACGTGAATCAC AAGCCAGCAACACC AAGGTGGACAAAGAAA GTTGAGCCCCAAATCT TGT	ACCAGACCTACATC TGCAACGTGAATCAC AAGCCAGCAACACC AAGTGGACAAAGAAA GTTGAGCCCCAAATCT TGT
		SEQ ID NO:217	SEQ ID NO:218	SEQ ID NO:219	
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		SEQ ID NO:220	SEQ ID NO:221	SEQ ID NO:222	
NA	038 Adalimumab CR (S176) K_Fc_9C8_VH_CR (S176E)	GAGGTACAACTGGTGGAAATCAGGTGGAGGTTTGGTGCAGCCGGGAG ATCGCTCAGGCTTAGCTGTGCGGCATCGGGGTTTACTTTCGATGATT ATGCGATGCATTGGGTCCGGCAAGCGCCTGGAAGGCTCGAGTGG GTTTCCGCCATTACGTGGAATAGCGGACACATCGATTATGCAGACAG TGTGGAGGCGAGATTCACAATCTCACGAGACAAATGCTAAGAACAGCC TGTAACCTTCAGATGAACCTCACTTCGCGCGGAAGATACCGCCGTATAC TACTGCGCCAAAAGTCTCCTACTTGTCTACAGCTTCGTCGCTCGACTA TTGGGGTCAAGGAAACGTTGGTCACCGTCTCTAGTACGGTGGCTGCAC CATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAAATCTGGA ACTGCCCTCTGTTGTGCGCTGCTGAATAACTTCTATCCAGAGAGGC CAAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCC AGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC AAGAGCACCCCTGACGCTGAGCAAAAGCAGACTACGAGAAACACAAAGT	GACATCCAGATGACC CAGTCTCCATCCTCC CTGTCTGCATCTGTA GGAGACAGAGTCACC ATCACTTGCCGGGCA AGTCAGAGCATTAAC AACTATTTAAATTGG TATCAGCAGAGACCA GGGAAAGCCCTAAG CTCCTGATCTATGCT GCATCCAGTTTGCAA AGTGGGTCCCATCA AGGTTTCAGTGGCAGT	GATATCCAAATGACA CAATCACCATCGTCG CTTTCAGCGTCTGTT GGCAGCCGTGTGACG ATTACCTGTCCGCGG TCCCAGGGAATCCGG AATTACCTCGCATGG TATCAGCAAAAACCC GGAAAAGCACCCGAAG CTCCTGATCTATGCC GCCTCGACTCTTCAG AGTGGTGTGCCGTG AGGTTTAGCGGGTCC	

1PS: 376770

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			CPAPELLGGPSVFLFPPKPKD ¹ TLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTTPPVLDSGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGGSGGGSQVQLQESG PGLVKPSETLSLTCTVSGGSISSYFWSWIRQPPGKGLEWIGYIYYSG QTKYNPSLKS ⁴ RV ⁵ TI ⁶ SIDTSKNQ ⁷ FS ⁸ LK ⁹ LSSV ¹⁰ TAAD ¹¹ TA ¹² VY ¹³ CARE ¹⁴ TGS ¹⁵ Y YGF ¹⁶ DYWGQ ¹⁷ TL ¹⁸ TV ¹⁹ SS ²⁰ TV ²¹ AA ²² PS ²³ VF ²⁴ IF ²⁵ PP ²⁶ SD ²⁷ EQ ²⁸ LK ²⁹ SG ³⁰ TAS ³¹ VV ³² CL ³³ LN ³⁴ NF YPREAKVQ ³⁵ WK ³⁶ VD ³⁷ NALQ ³⁸ SG ³⁹ NSQ ⁴⁰ ES ⁴¹ SV ⁴² TEQ ⁴³ DS ⁴⁴ SKD ⁴⁵ ST ⁴⁶ YS ⁴⁷ LE ⁴⁸ ST ⁴⁹ LT ⁵⁰ LSKAD ⁵¹ Y EKHKVYACEV ⁵³ THQ ⁵⁴ GL ⁵⁵ SP ⁵⁶ VT ⁵⁷ KS ⁵⁸ FN ⁵⁹ R ⁶⁰ GEC	SSLQPEDFATYYCQQ SYSTPRTFGQGTKLE IKRASTKGPSVFPLA PSSKSTSGGTAALGC LVKDYFFPEPVT ⁶¹ SV ⁶² WN SGALTSGVHT ⁶³ FP ⁶⁴ AVL QSSGLYSLS ⁶⁵ ES ⁶⁶ V ⁶⁷ TVP SSSLGTQ ⁶⁸ TY ⁶⁹ IC ⁷⁰ NV ⁷¹ NH KPSNTKVDKK ⁷² VE ⁷³ PKS C	SSLQPEDVATYYCQR YNRAPYTFGQGTKVE IKRASTKGPSVFPLA PSSKSTSGGTAALGC LVKDYFFPEPVT ⁷⁵ SV ⁷⁶ WN SGALTSGVHT ⁷⁷ FP ⁷⁸ AVL QSSGLYSLS ⁷⁹ ES ⁸⁰ V ⁸¹ TVP SSSLGTQ ⁸² TY ⁸³ IC ⁸⁴ NV ⁸⁵ NH KPSNTKVDKK ⁸⁶ VE ⁸⁷ PKS C
			SEQ ID NO:226	SEQ ID NO:227	SEQ ID NO:228
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039_Ada11mumab_CK(s176k)_Fc_23B3_VH4_VH_CK(s176E)

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		SEQ ID NO:232	SEQ ID NO:233	SEQ ID NO:234
	NA	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGA	GAAATTGTGTTGACG	CAGTCTGTGCTGACG

		GTCTCTGAAGATCTCCTGTAAAGACTTCTGAAATACAGCTTTACCAGCT ACTGGATCGGCTGGGTGCGCCAGATGCCCGGAAAGCCCTGGAGTGG ATGGGATCATCTATCTTGGTACTCAGATACCAGATACAGCCCGTC CTTCCAAGGCCAGGTCACCATCTCAGCCGACAAAGTCCATCAGTACCG CCTACCTGCAGTGGAGCAGCCTGAAGGCCCTCGGACACCGCCATGTAT TACTGTCCGAGAAAGTAACTGGGTCTTGACTACTGCGGCCAGGGAAC CCTGGTCACCGTCTCTAGTCAGCCCCAAGCCAAACCCCACTGTCACTC TGTTCCCGCCCTCCTCTGAGGAGCTCCAAGCCAAACAAGCCACACTA GTGTGTCTGATCAGTGACTTCTACCCGGGAGCTGTGACAGTGGCCTG GAAGGCAGATGGCAGCCCCGTCAAGCGGGAGTGGAGACCACCAAAC CCTCCAAACAGAGCAACAAAGTACGCGGCCAAGAGCTACCTGAGC CTGACGCCCCGAGCAGTGAAGTCCCACAGAAGCTACAGCTGCCAGGT CACGCAAGAAGGAGCACCCGTGGAGAAAGACAGTGGCCCTACAGAAT GTTCAGACAAAACTCACACATGCCCAACCGTGCCCAAGCACCCTGAACTC CTGGGGGACCGTCAGTCTTCCTCTTCCCGCCAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGTGGACG TGAGCCACGAAGACCCTGAGGTCAAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAAATGCCAAGACAAAGCCGTGTGAGGACAGTACGG CAGCACGTACCGTTGTGTCAAGCTCCTCACCGTCTTGCAACCAGGACT GGCTGAATGGCAAGGAGTACAAAGTGCAAGGTCTCCAACAAGCCCTC CCAGCCCCATCGAGAAAACCAATCTCCAAAGCCAAAGGCAGCCCCG AGAAACCACAGGTGTACACCCCTGCCCCCATCCCCGGAGGAGATGACCA AGAAACCAAGTCAAGCTGACCTGACCTGCCCTGGTCAAAGGCTTCTATCCCAGC GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAACAATA CAAGACCAACGCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCT ATAGCAAGCTCACCGTGGACAAAGACAGGTGGCAGCAGGGGAACGTC TTCTCATGTCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCA GAAGAGCCCTCTCCCTGTCTCCGGTGGTGGCGGATCGGAGGTGGCG GATCCCAGGTGCAGTTACAGCAGTCGGGCGCAGGACTGTTGAAGCCCT TCGGAGACCCCTGTCCCTCACCTGCGCTGTCCATGGTGGTCCCTTCAG TGGTTACTACTGGAACCTGGATTGCGCAGCCACAGGAAGGGCTAG AGTGGATTGGGAAATCAATCATGTCTGGAACACCAACTACAACCCG TCCCTCAAGAGTCGAGTCACCATATCATTAGACACGTCCAAGAAACCA GTTCTCCCTGACGTGACCTCTGTGACCGCGCGGACACGGCTGTGT ATTACTGTGCGAGAGGATATTGTAGAAGTACCACCTGCTACTTTGAC TACTGGGGCCAGGGAACCCTAGTCAACCGTCTCCTCAACTGTGGCTGC ACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTG	CAGTCTCCAGGCACC CTGTCTTTGTCTCCA GGGAAAGAGCCACC CTCTCCTGCAGGGCC AGTCAGAGTGTAGA AGCAGTTACTTAGCC TGGTACCAGCAGAAA CCTGGCCAGCTCCC AGGTCCTCATCTAT GGTGCATCCAGCAGG GCCACTGGCATCCCA GACAGGTTCAGTGGC AGTGGTCTGGGACA GACTTCACCTCTACC ATCAGCAGACTGGAG CCTGAAGATTTTGCA GTGATTACTGTCTAG CAGTATGGTAGCTCA CCTACCTTCGGCCAA GGGACACGACTGGAG ATTAAACGAGCCTCC ACCAAGGGCCCATCG GTCTTCCCGCTGGCA CCCTCCTCCAAGAGC ACCTCTGGGGCACA GCGGCCCTGGGCTGC CTGGTCAAGGACTAC TTCCCGAAACCGGTG ACGGTGTCTGTGGAAC TCAGGCGCCCTGACC AGCGCGTGCACACC TTCCCGGCTGTCCCTA CAGTCCCTCAGGACTC TACTCCCTCAAAAGC GTGGTGACCGTGCCC TCCAGCAGCTTGGGC ACCCAGACCTACATC	CAGCCGCCCTCAGTG TCTGGGGCCCCAGGG CAGAGGTACCATC TCCTGCAC TGGGAGC AGTTCAAACATCGGG GCAGGTTATGATGTA CACTGGTACCAGCAG TTTCCAGGAACAGCC CCCAAACTCCTCATC CAAGGTAAACAGCAAT CGGCCCTCAGGGGTC CCTGACCGATTCTCT GGTCCAAAGTCTGGC ACCTCAGCCTCCCTG GCCATCAGTGGGCTC CAGGCTGAGGATGAG GCTGATTATTACTGC CAGTCCATATGACAGC AGCCTGAGTGGTTCTG GTGTTCTGGCGGAGGG ACCAAGCTGACCGTC CTAGGTGCCCTCCACC AAGGCCCATCGGTC TTCCCCCTGGCACCC TCCTCCAAGAGCACC TCTGGGGGCACAGCG GCCCTGGGCTGCCCTG GTCAAGGACTACTTC CCCGAACCGGTGACG GTGTCGTGGAAC TCAGGCGCCCTGACC AGCGCGTGCACACC TTCCCGGCTGTCCCTA CAGTCCCTCAGGACTC TACTCCCTCAAAAGC GTGGTGACCGTGCCC TCCAGCAGCTTGGGC AGCAGCTTGGGCACC
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			GAAC TGCC TCTG TTG TGTG CCGT GCTGA ATAACTTCTATCCAGAGAGGCCAAA GTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCAGGAGAGTGTCACAGAGCAGACAGCAAGGACAGCACCTACAGCCTCGAAAAGCACCCGTGACGCTGAGCAAAGCAGACTACGAGAAAACACAAAGTCTACGCCTGCGAAGTCA CCGCATCAGGCGCTGAGCTCGCCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	TGCAACGTGAATCAC AAGCCAGCAACACC AAGTGACAAAGAAA GTTGAGCCCCAAATCT TGT	CAGACCTACATCTGC AACGTGAATCACAAG CCAGCAACACCAAG GTGACAAGAAAGTT GAGCCCAAATCTTGT
			SEQ ID NO:235	SEQ ID NO:236	SEQ ID NO:237
AA			EVQLVQSGAEVKKPGESLKISKTS EYFTSYWIGVVRQMPGKGLEW MGI IYLGDS DTRYSPSFQGV TISADKSI STAYLQWSSLKASDTAMY YCARSNWGLDYWGQGLVT VSSQPKANPTVTLFPSSSEELQANKATL VCLISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAAKS YLS LTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECSDKTHTCPPCPAPEL LGGPSVFLFPKP KDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMH EALHNHYTQKSLSLSPGGGGSGGSQVQLQSGAGLLKP SETLSLTCAVHGGSFSGYYWNWIRQPPGKGLEWIGEINHAGNTNYP SLKSRVTISLDTSKNQFSLT LTVTAADTA VYYCARGYCRSTTCYFD YWGQGLVTVSS TVAAPSVFIFPPSDEQLKSGTASVVC LLNNFYPRE AKVQWKVDNALQSGNSQESVTEQDSKDS TYSLESTLTLSKADYEKHK VYACEVTHQGLSSPVTKSFNRGEC	EIVLTQSPGTL SLSP GERATLSCRASQSVR SSYLAWYQQKPGQAP RLLIYGASSRATGIP DRFSGSGGTDFTLT ISRLEPEDFAVYCYQ QYGSPTFGQGRLE IKRASTKGPSVFPLA PSSKSTGGTAALGC LVKDYFFPEPVTVSWN SGALTSGVHTFPAVL QSSGLYSLKSVVTVP SSSLGTQTYICNVNH KPSNTKVDKKVEPKS C	QSVLTQPPPSVSGAPG QRVTISCTGSSSNIG AGYDVHWYQQFPGTA PKLLIQGNSNRPSGV PDRFSGSKSGTSASL AITGLQAEDEADYYC QSYDSSLSGSVFGGG TKLTVLGASTKGPSV FPLAPSSKSTSGGTA ALGCLVKDYFFPEPT VSWNSGALTSGVHTF PAVLQSSGLYSLESV VTVPSSSLGTQTYIC NVNHKPSNTKVDKKV EPKSC
			SEQ ID NO:238	SEQ ID NO:239	SEQ ID NO:240
NA	041_3.2 CL(S176K)_Fc_9C8 _VH_CR(S176E)	1PS:376784	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAGCCCGGGA GTCTCTGAAGATCTCCTGTAA GACTTCTGAATACAGCTTTACCAGCT ACTGGATCGGCTGGGTGCGCCAGATGCCCGGAAAGGCTGGAGTGG ATGGGATCATCTATCTTGTGACTCAGATACCAGATACAGCCCGTC CTTCCAAGGCCAGGTCACCATCTCAGCCGACAAAGTCCATCAGTACCG CCTACCTGCAGTGGAGCAGCCTGAAGCCTCGGACACCGCCATGTAT TACTGTCCGAGAGTA ACTGGGTCTTGACTACTGGGCCAGGGAAC CCTGGTCACCGTCTCTAGTCAGCCCAAGGCCAACCCCACTGTCACTC TGTTCCCGCCCTCCTCTGAGGAGCTCCAAGCCAACAAGGCCACACTA GTGTGTCTGATCAGTGACTTCTACCCGGGAGCTGTGACAGTGGCCTG GAAGGCAGATGGCAGCCCGCTCAAGCGGGAGTGGAGACCAACCAAC CCTCCAAACAGAGCAACAACAAGTACGGGGCCAAGAGCTACCTGAGC CTGACGCGCGAGCAGTGGAAAGTCCCACAGAAAGCTACAGCTGCCAGGT CACGCA TGAAAGGGAGCACCCGTGGAGAAAGACAGTGGCCCCCTACAGAA T	GACATCCAGATGACC CAGTCTCCATCCTCC CTGTCTGCATCTGTA GGAGACAGATCACCC ATCACTTGCCGGGCA AGTCAGAGCATTAAC AACTATTAAATTGG TATCAGCAGAGACCA GGGAAAGCCCTAAG CTCCTGATCTATGCT GCATCCAGTTTGCAA AGTGGGTCCCATCA AGGTTCAGTGGCAGT GGATCTGGGACAGAT	CAGTCTGTGCTGACG CAGCCGCCCTCAGTG TCTGGGGCCCCAGGG CAGAGGTCACCATC TCCTGCACTGGGAGC AGTTCCAACATCGGG GCAGGTTATGATGTA CACTGGTACCAGCAG TTTCCAGGAACAGCC CCCAAACCTCCTCATC CAAGGTAACAGCAAT CGGCCCTCAGGGGTC CCTGACCGATTCTCT GGTCCAAAGTCTGGC

		GTTCAGACAAAACCTCACACATGCCACCGTGCCACGACACCTGAACTCCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCCAAAGGACACCTCATGATCTCCGGACCCCTGAGGTACATGCGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAAGTTCAACTGGTACGTGGACGGGTGAGAGGTGCATAATGCCAAGACAAAGCCGTTGTGAGGACGTACGGCAGCACGTACCCGTTGTGTACGGTCTCACCGTCTGTGCACCCAGGACTGGCTGAATGGCAAGGAGTACAAAGTGCAAGGTCTCCAACAAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGCAGCCCCGAGAACCACAGGTGTACACCCCTGCCCCCATCCCCGGAGGAGATGACCAAGAACCAAGTCAGCCTGACCTGCCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGAGTGGGAGAGCAATGGGCAGCCGGAGAAACAATAACAAGCACGCCCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAAGACAGGTGGCAGAGGGGAACGCTTCTCATGTCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAAGAAGCCTCTCCCTGTCTCCGGTGGTGGCGATCGGAGGTGGCGGATCCCCAGGTGCAGGAGTGGGAGTCCGAGCCCAAGACTGGTGAAGCCTTCGGAGACCCCTGTCCCCTCACCTGCACGTGTCTGTGGTCCATCAGTAGTTACTTCTGGAGCTGGATTCCGGCAGCCCCCAGGTAAAGGACTGGAGTGGATTGGCTATATCTATTACAGTGGGCAGACCAAATACAAACCCCTCCCTCAAGAGTCGAGTCACCATATCAATAGACACAGTCCAAGAACCA GTTCTCCCTGAAGCTGAGCTCTGTGACCGCTGCGGACACAGGCCGTGTATTACTGTGCGAGAGAAACTGGGAGCTACTACGGCTTTGACTACTGGGCCAGGGAACCCCTGGTCACCGTCTCCTCAACTGTGGCTGCACCATCTGTCTTCACTTCCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCCTGTTGTGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAA GTACAGTGGAAGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCGAAA GCACCCCTGACGCTGAGCAAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAAGTCACCCATCAGGGCCTGAGCTCGCCCCGTACACAAAGAGCTTCAACACAGGGGAGAGTGT	TTCACTCTCACCATCAGCATCTGCAAACCTGAAGATTTTGCAACTACTACTGTCAACAGAGTTACAGTACCCCTCGGACGTTCGGCCAAGGACCAAGAGCCCTCCACCAAGGCCCATCGGTCTTCCCCCTGGCACCCTCTCCAAGAGCACCTCTGGGGGCACAACCTCTGGGGGCATCTGGTCAAGGACTAC TTCCCCGAACCGGTGACGGTGTCTGTGGAAC TCAGGGCCCCTGACCAGCGCGTGCACACC TTCCCCGGCTGTCCCTA CAGTCCTCAGGACTCTACTCCCTCAAAAGC GTGGTGACCGTGCCCC TCCAGCAGCTTGGGCTCCAGACCTTACATC TGCAACGTGAATCAC AAGCCAGCAACACC AAGGTGACAAAGAAA GTTGAGCCCCAAATCTTGT	ACCTCAGCCTCCCTG GCCATCACTGGGCTC CAGGCTGAGGATGAG GCTGATTATTACTGC CAGTCCTATGACAGC AGCCTGAGTGGTTCC GTGTTCCGGCGGAGGG ACCAAGCTGACCGTC CTAGGTGCCCTCCACC AAGGCCCATCGGTC TTCCCCCTGGCACCC TCCTCCAAGAGCACCC TCTGGGGCACAGCG GCCCTGGGCTGCCCTG GTCAAGGACTACTTC CCCGAACCCGGTGACG GTGTCGTGGAAC TCA GGGCCCTGACCAGC GCGTGCAACCTTC CCGGCTGTCC TACAGGACTCTAC TCCCTCGAAAGCGTG GTGACCGTGCCCTCC AGCAGCTTGGGCACC CAGACCTACATCTGC AACGTGAATCACAAAG CCCAGCAACACCAAAG GTGACAAAGAAAGTT GAGCCCCAAATCTTGT
		SEQ ID NO: 241	SEQ ID NO: 242	SEQ ID NO: 243
AA	EVQLVQSGAEVKKPGESLKISCKTSEYSFTSYWIGWVRQMPGKGLEWMGII YLGDS DTRYSPSFQGQVTISADKSI STAYLQWSSLKASDTAMY YCARSNWGLDYWGQGLVT VSSQPKANPTVTLFPSSSEELQANKATLVCLISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNKNKYAAKSYLS LTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECSDKTHTCPPCPAPEL LGGPSVFLFPKP KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG	DIQMTQSPSSLSASVGDRVITICRASQSIN NYLNWYQQRPGKAPK LLIYAASSLQSGVPS RFSGSGSGTDFTLTISLQPEDFATYYCQQ	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQFPGTAPKLLIQGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYC	

			VEVHNAKTKPEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPVLDSGSEFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGGGGSGGSQVQLQESGPGGLVKP SETLSLTCTVSGGSISSYFWSWIRQPPGKGLEWIGYIYYSGQTKYNP SLKSRVTISIDTSKNQFSKLSSVTAADTAVYYCARETGSYYGFDYW GQGTLVTVSSSTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAK VQWKVDNALQSGNSQESVTEQDSKDSYSTYSLESTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC	SYSTPRTFGQGTKLE IKRASTKGPSVFFPLA PSSKSTSGGTAALGC LVKDYFFPEPVTVSWN SGALTSGVHTFFPAVL QSSGLYSLKSVVTVP SSSLGTQTYICNVNH KPSNTKVDKKVEPKS C	QSYDSSLSGSVFGGG TKLTVLGASTKGPSV FPLAPSSKSTSGGTA ALGCLVKDYFFPEPVT VSWNSGALTSGVHTF PAVLQSSGLYSLESV VTVPSSSLGTQTYIC NVNHHKPSNTKVDKKV EPKSC
			SEQ ID NO:244	SEQ ID NO:245	SEQ ID NO:246
		042_3.2_CL(S176K)_Fc_23B3_VH4_VH_CK(S176E)	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGA GTCTCTGAAGATCTCCTGTAAAGACTTCTGAATACAGCTTTACCAGCT ACTGGATCGGCTGGGTGCGCCAGATGCCGGGAAAGGCTGGAGTGG ATGGGGATCATCTATCTTGGTGACTCAGATACCAGATACAGCCCCGTC CTTCCAAGGCCAGGTCACCATCTCAGCCGACAAAGTCCATCAGTACCG CCTACCTGCAGTGGAGCAGCCTGAAGGCCCTCGGACACCCGCATGTAT TACTGTGCGAGAAATACTGGGGTCTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTCTCTAGTCAGCCCAGGCCAACCCCACTGTCACTC TGTTCCCGCCCTCCTCTGAGGAGCTCCAAGCCAAACAAGGCCACACTA GTGTGTCTGATCAGTGACTTCTACCCGGGAGCTGTGACAGTGGCCTG GAAGGCAGATGGCAGCCCCGTCAAGCGGGAGTGGAGACCAACCAAAC CCTCCAAACAGAGCAACAAAGTACGCGGCCAAGAGCTACCTGAGC CTGACGCCCGAGCAGTGAAGTCCCACAGAAGCTACAGCTGCCAGGT CACGCA TGAAAGGAGCACCGTGGAGAAAGACAGTGGCCCCCTACAGAA GTTCAGACAAAACTCACACATGCCACCGTCCCCAGCACCTGAACTC CTGGGGGACCGTCAGTCTTCCCTCTTCCCCCAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACG TGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGTGAGGAGCAGTACGG CAGCACGTACCGTTGTGTACGCGTCTCACCGTCCCTGCACCCAGGACT GGCTGAATGGCAAGGAGTACAAAGTGCAAGGTCTCCAACAAGCCCTC CCAGCCCCCATCGAGAAAAACCATCTCCAAGGCCAAAGGCGAGCCCCG AGAAACCAAGGTGTACACCTTGCCCCCATCCCGGGAGGAGATGACCA AGAAACCAAGGTACGCTGACCTGCCCTGGTCAAAGGCTTCTATCCCAGC GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAACAATA CAAGACCAAGCTCCCGTGTGACTCCGACGGCTCCTTCTTCTCCTCT ATAGCAAGCTCACCGTGGACAAAGAGCAGGTGGCAGCAGGGGAACGTC	GACATCCAGATGACC CAGTCTCCAAGCTCC CTGTCTGCGTCTGTG GGGATAGGGTCAACC ATCACTTGCAGGTCC AGCCAGAGTGTGTTA TACAGCTCCAACAAT AAGAACTACTTAGTT TGGTACCAGCAGAAA CCAGGAAAAGGTTCCCT AAACTGCTCATTTAC TGGGCATCTACCCGG GAATCCGGGGTCCCT AGTCGATTCAAGTGGC AGCGGTCTGGGACA GATTTCACTCTCACCC ATCAGCAGCCTGCAG CCTGAAGATGTGGCA ACTTATTACTGTGAG CAATATTATAAGACT CCTCTCACTTTCGGC GGAGGACCAAGGTG GAGATCAAACGAGCC TCCACCAAGGGCCCA TCGGTCTTCCCCCTG GCACCCCTCCTCCAAG AGCACCTCTGGGGGC	CAGTCTGTGCTGACG CAGCCGCCCTCAGTG TCTGGGGCCCCCAGG CAGAGGCTCACCATC TCCCTGCACCTGGGAGC AGTTCCAAACATCGGG GCAGGTTATGATGTA CACTGGTACCAGCAG TTTCCAGGAACAGCC CCCAAACCTCCTCATC CAAGGTAAACAGCAAT CGGCCCTCAGGGGTC CCTGACCGATTCTCT GGCTCCAAGTCTTGGC ACCTCAGCCTCCCCTG GCCATCACTGGGCTC CAGGCTGAGGATGAG GCTGATTATTACTGC CAGTCCCTATGACAGC AGCCTGAGTGGTTCG GTGTTCCGGCGGAGGG ACCAAAGCTGACCGTC CTAGGTGCCTCCACC AAGGGCCCATCGGTC TTCCCCCTGGCACCC TCCTCCAAGAGCACCC TCTGGGGGCACAGCG

1PS: 376789

042_3.2_CL(S176K)_Fc_23B3_VH4_VH_CR(S176E)

NA

1PS:376789

		TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCA GAAGAGCCTCTCCCTGTCTCCGGGTGGTGGCGGATCGGAGGTGGCG GATCCCAGGTACAGTTGCAGAGTCAAGTCCAGGACTGTTGAAGCCC TCGGAGACCCCTCTCACTCACCTGTACCATCTCCGGGGACAGTGTCTC TACCAACAGTGTGCTTGAACTGGATTAGGCAGCCCCCAGGGAAG GCCTTGAGTGGATAGGAAGGACATACACAGTCCAAGTGGTATAAT GATTATGCAGTTTCTCTGAAAAAGTCGAGTAACCATCAGCCCAGACAC ATCCAAAGAACCAAGTTCTCCCTGAAGCTGAGCTCTGTGACTGCCGCGG ACACGGCTGTGTATTACTGTGCAAGAGAGGATGGGGATAGCTACTAC CGCTACGGTATGGACGTCTGGGCCAAGGACACCGTCACCGTCTC CTCAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATG AGCAGTTGAAATCTGGAACCTGCCCTCTGTGTGTGCTGCTGAAATAAC TTCTATCCCAGAGAGGCCAAAGTACAGTGAAGGTGGATAAACGCCCT CCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGG ACAGCACCTACAGCCTCGAAAGCACCCCTGACGCTGAGCAAAAGCAGAC TAGGAGAAACACAAAGTCTACGCCCTGCGAAGTCACCCATCAGGGCCT GAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	ACAGCGGCCCTGGGC TGCCCTGGTCAAGGAC TACTTCCCCGAACCG GTGACGGTGTCTGG AACTCAGGCGCCCTG ACCAGCGCGTGCAC ACCTTCCCGGCTGTC CTACAGTCCCTCAGGA CTCTACTCCCTCAAA AGCGTGTGACCGTG CCCTCCAGCAGCTTG GGCACCAGACCTAC ATCTGCAACGTGAAT CACAAGCCCAGCAAC ACCAAGGTGACAAG AAAGTTAGCCCCAAA TCTTGT	GCCCTGGGCTGCCTG GTCAAGGACTACTTC CCCGAACCGGTGACG GTGTCTGTGAACTCA GGCGCCCTGACCAGC GGGTGCACACCTTC CCGGCTGTCTTACAG TCCCTCAGGACTCTAC TCCCTCGAAAGCGTG GTGACCGTGCCCTCC AGCAGCTTGGGCACC CAGACCTACATCTGC AACGTGAATCACAAG CCCAGCAACACCAAG GTGGACAAAGAAAGTT GAGCCCCAAATCTTGT
		SEQ ID NO:247	SEQ ID NO:248	SEQ ID NO:249
AA		EVQLVQSGAEVKKPGESLKISCKTSEYSFTSYWIGVVRQMPKGLEW MGI IYLGDS DTRYSPSFQGV TISADKSI STAYLQWSSLKASDTAMY YCARSNWGLDYWGQGLVTVSSQPKANPTVTLFPPSSSEELQANKATL VCLISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAAKSYLS LTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECSDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMH EALHNHYTQKSLSLSPGGGGSGGSQVQLQESGPGLVKP SETLSLTCTISGDSVSTNSVAWNWIRQPPGKGLEWIGRTYYRSKWYN DYAVSLKSRVTISPDTSKNQFSLKLSVTAADTAVYYCAREDGDSYY RYGMDVWGQGT VTVSS TVAAPSVFI FPPSDEQLKSGTASVVCLLNN FYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLESTLTLSKAD YEKHKVYACEVTHQGLSSPVTKSFNRGEC	DIQMTQSPSSLSASV GDRV TITCRSSQSVL YSSNNKNYLVWYQQK PGKVPKLLIYWASTR ESGVPSRFSGSGSGT DFTLTISSLQPEDVA TYYCQQYYKTPLTFG GGTKVEIKRASTKGP SVFPLAPSSKSTSGG TAALGCLVKDYFPEP VTVSWNSGALTSGVH TFPAVLQSSGLYSLK SVVTVPSSSLGTQTY ICNVNHHKPSNTKVDK KVEPKSC	QSVLTQPPSVSGAPG QRVTISCTGSSSNIG AGYDVHWYQQFPGTA PKLLIQGNSNRPSGV PDRFSGSKSGTSASL AITGLQAEDEADYYC QSYDSSLSGSVFGGG TKLTVLGASTKGPSV FPLAPSSKSTSGGTA ALGCLVKDYFPEPVT VSWNSGALTSGVHTF PAVLQSSGLYSLESV VTVPSSSLGTQYIC NVNHHKPSNTKVDKKV EPKSC
		SEQ ID NO:250	SEQ ID NO:251	SEQ ID NO:252

1PS: 376793	043_3B3v2_CK(S176K)_Fc_Ada1immunab_VH_CK(S176E)	NA	CAGGTGCAGTTACAGCAGTCGGGCGCAGGACTGTTGAAAGCCTTCGGA GACCCGTGTCCTCACCTGCGCTGTCCATGGTGGGTCTCTCAGTGGTT ACTACTGGAACTGGATTGCCAGCCACCAGGGAAGGGCTAGAGTGG ATTGGGAAAATCAATCATGCTGGAACACCAACTACAACCCGTCCCT CAAGAGTCGAGTCACCATATCATTAGACACGTCCAAGAACCAAGTTCT CCCTGACGCTGACCTCTGTGACCGCGCGGACACGGCTGTGTATTAC TGTGCGAGAGGATATTGTAGAAGTACCACCTGCTACTTTGACTACTG GGCCAGGAAACCCTAGTCAACCCTCTCCTCAACGGTGGCTGCACCAT CTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACT GCCCTGTGTGTGCCCTGCTGAATAACTTCTATCCAGAGAGGCCAA AGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAACCTCCCAGG AGAGTGTCAAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAAG AGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTA CGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCAACAAAG GCTTCAACACAGGGAGAGTGTGACAAAACCTCACACATGCCACCCGTGC CCAGCACCTGAACCTCCTGGGGGACCGTCAGTCTTCTCTTCCCCC AAAACCCAAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGGACGTGAGCCAAGAACCCCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAAGCCGTG TGAGGAGCAGTACGGCAGCACGTACCGTTGTGTGTCAGCGTCTCTACCG TCCTGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTC TCCAAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAGC CAAGGGCAGCCCCGAGAAACACAGGTGTACACCCCTGCCCCCATCCC GGGAGGAGATGACCAAGAACCAAGTCAGCCTGACCTGCCCTGGTCAAA GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCA GCCGGAGAAACAATAACAAGACCAAGCCCTCCCGTCTGGACTCCGACG GCTCCTTCTTCTCTATAGCAAAGCTCACCGTGGAACAAGACAGGTGG CAGCAGGGGAAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCA CAACCACTACAGCAGAGAGCCCTCTCCCTGTCTCCGGGTGGTGGCG GATCGGAGGTGGCGGATCCGAGGTACAACCTGGTGGAATCAGGTGGA GGTTTGGTGCAGCCGGGAGATCGCTCAGGCTTAGCTGTGCGGCATC GGGTTTACTTTTCGATGATTATGCGATGCATTTGGGTCCGGCAAGCGC CTGGAAAAGGGCTCGAGTGGGTTTCCGCCATTACGTGGAATAGCGGA CACATCGATTATGCAGACAGTGTGGAGGGCAGATTCACAATCTCACG AGACAAATGCTAAGAACAGCCTGTACCTTCAGATGAACCTCACTTCGCG CGGAAGATACCGCCGTATACTACTGCGCCAAAGTCTCCTACTTGTCT ACAGCTTCGTGCTCGACTATTGGGGTCAAGGAACGTTGGTCACCGT	GATATCCAAATGACA CAATCACCATCGTCG CTTTCAGCGTCTGTT GGCGACCGTGTGACG ATTACCTGTCGCGG TCCCAGGGAATCCGG AATTACCTCGCATGG TATCAGCAAAAACCC GGAATAAGCACCGAAG CTCCTGATCTATGCC GCCTCGACTCTTCAG AGTGGTGTGCCGTCCG AGGTTTAGCGGGTCC GGTCAAGTACGGAC TTTACTCTACAATT TCCAGCCTGCAGCCC GAAGATGTAGCTACC TATTACTGCCAGAGA TACAACCGAGCGCCT TACACATTCGGACAA GGACAAAAGTCGAG ATCAAGCGTGCCCTCC ACCAAGGCCCATCG GTCTTCCCCCTGGCA CCCTCCTCCAAGAGC ACCTCTGGGGCACAA GCGGCCCTGGGCTGC CTGGTCAAGGACTAC TTCCCCGAACCGGTG ACGGTGTCTGTGAAC TCAGGCGCCCTGACC AGCGGCGTGACACCC TTCCCGGCTGTCCCTA CAGTCCTCAGGACTC TACTCCCTCAAAAGC GTGGTGACCGTGCCC TCCAGCAGCTTGGGC	GAAATTGTGTTGACG CAGTCTCCAGGCACC CTGTCTTTGTCTCCA GGGAAAAGAGCCACC CTCTCCTGCAGGGCC AGTCAGAGTGTTAGA AGCAGTTACTTAGCC TGGTACCAGCAGAAA CCTGGCCAGGCTCCC AGGCTCCTCATCTAT GGTGCAATCCAGCAGG GCCACTGGCATCCCA GACAGGTTCAGTGGC AGTGGGTCTGGGACA GACTTCACCTCACC ATCAGCAGACTGGAG CCTGAAGATTTTGCA GTGTATTACTGTCTAG CAGTATGGTAGCTCA CCTACCTTCGGCCAA GGACACGACTGGAG ATTAACCGAGCCTCC ACCAAGGCCCATCG GTCTTCCCCCTGGCA CCCTCCTCCAAGAGC ACCTCTGGGGCACAA GCGGCCCTGGGCTGC CTGGTCAAGGACTAC TTCCCCGAACCGGTG ACGGTGTCTGTGAAC TCAGGCGCCCTGACC AGCGGCGTGACACCC TTCCCGGCTGTCCCTA CAGTCCTCAGGACTC TACTCCCTCGAAAGC GTGGTGACCGTGCCC TCCAGCAGCTTGGGC
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			CTCTAGTACTGTGGCTGCACCATCTGTCTTTCATCTTCCCGCCATCTG ATGAGCAGTTGAAATCTGGAACCTGCTCTGTGTTGTGCTGCTGAAT AACTTCTATCCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACGC CCTCCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCA AGGACAGCACCTACAGCCTCGAAAGCACCCCTGACGCTGAGCAAAAGCA GACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGG CCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	ACCCAGACCTACATC TGCAACGTGAATCAC AAGCCAGCAACACC AAGGTGGACAAAGAAA GTTGAGCCCCAAATCT TGT	ACCCAGACCTACATC TGCAACGTGAATCAC AAGCCAGCAACACC AAGGTGGACAAAGAAA GTTGAGCCCCAAATCT TGT	SEQ ID NO:253	SEQ ID NO:254	SEQ ID NO:255
	AA		QVQLQQSGAGLLKPSETLSLTCAVHGGSFSGYYWNWIRPPGKGLEW IGEINHAGNTNYPNPSLKSRVTISLDTSKNQFSLTLTSVTAADTAVYY CARGYCRSTTCYFDYWGGTLVTVSSTVAAPSVFIFPPSDEQLKSGT ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSLK STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECDKHTCPPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDLNLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGGSGGGSEVQLVESGG GLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVAITWNSG HIDYADSVEGRFTISRDNKNSLYLQMNSLRAEDTAVYYCAKVSYLS TASSLDYWGGTLVTVSSTVAAPSVFIFPPSDEQLKSGTASVVCLLN NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSLESTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC	C C	C C	SEQ ID NO:256	SEQ ID NO:257	SEQ ID NO:258
1ps: 376797	044_3B3v2_CK(s176K)_Fc _3.2_VH_CL(s176E)	NA	CAGGTGCAGTTACAGCAGTCGGGCGCAGGACTGTTGAAGCCTTCGGA GACCCGTGCCCTCACCTGCGCTGTCCATGGTGGTCCCTTCAGTGGTT ACTACTGGAACCTGGATTGCGCAGCCACCAGGGAAGGGCTAGAGTGG ATTGGGAAATCAATCATGTCTGGAACACCAACTACAACCCGTCCCT CAAGAGTCGAGTCACCATATCATTAGACACGTCCAAGAACCAAGTTCT CCCTGACGCTGACCTCTGTGACCGCGCGGACACGGCTGTGTATTAC TGTGCGAGAGGATATTGTAGAAGTACCACCTGCTACTTTGACTACTG GGGCCAGGGAACCCTAGTCACCGTCTCCTCAACGGTGGCTGCACCAT CTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAAATCTGGAAC GCCCTGTGTTGTGCGCTGCTGAATAACTTCTATCCCAGAGAGGCCAA AGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCCAGG AGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAAG AGCACCCCTGACGCTGAGCAAAAGCAGACTACGAGAAACACAAAGTCTA	CAGTCTGTGCTGACG CAGCCGCCCTCAGTG TCTGGGCCCCCAGGG CAGAGGGTCACCATC TCCTGCACTGGGAGC AGTTCCAAACATCGGG GCAGGTTATGATGTA CACTGGTACCAGCAG TTTCCAGGAACAGCC CCCAAACCTCCTCATC CAAGGTAACAGCAAT CGGCCCTCAGGGGTC CCTGACCGATTCTCT	GAAATTGTTGTGACG CAGTCTCCAGGCACC CTGTCTTTGTCTCCA GGGAAAAGAGCCACC CTCTCCTGCAGGGCC AGTCAGAGTGTTAGA AGCAGTTACTTAGCC TGGTACCAGCAGAAA CCTGGCCAGGCTCCC AGGCTCCTCATCTAT GGTGCAATCCAGCAG GCCACTGGCATCCCA GACAGGTTCAGTGCG			

		CGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGA GCTTCAACAGGGGAGAGTGTGACAAAACCTCACACATGCCACCCGTGC CCAGCACTGAACCTCCTGGGGACCGTCAGTCTTCCCTCTTCCCCC AAAACCCAAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCACAT GCGTGTGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAAGCCGTG TGAGGAGCAGTACGGCAGCACGTACCGTTGTGTCAAGCTCCTCACCG TCCTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTC TCCAAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGC CAAAGGCAGCCCCGAGAAACACAGGTGTACACCCTGCCCCCATCCC GGAGGAGATGACCAAGAACCAAGGTACGCCGTGACCTGCCCTGGTCAAA GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCA GCCGGAACAACTACAAGACCACGCCCTCCCGTGCTGGACTCCGACG GCTCCTTCTTCTCTATAGCAAAGCTCACCGTGGACAAGAGCAGGTGG CAGCAGGGAAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCA CAACCACTACACGAGAGAGCCCTCTCCCTGTCTCCGGTGGTGGCG GATCGGAGGTGGCGGATCCGAGGTGCAGCTGGTGCACTCTGGAGCA GAGTGAAAAAGCCCGGAGTCTCTGAAGATCTCCTGTAAAGACTTC TGAATACAGCTTTACCAGCTACTGGATCGGCTGGTGCGCCAGATGC CCGGAAAGGCCTGGAGTGGATGGGATCATCTATCTTGGTGACTCA GATACCAGATACAGCCCGTCTTCCAAGCCAGGTCACCATCTCAGC CGACAAAGTCCATCAGTACCGCCTACCTGCAGTGGAGCAGCCTGAAG CCTCGGACACCGCCATGTATTACTGTGCGAGAAAGTAAGTGGGTCTT GACTACTGGGGCCAGGAAACCTTGTCAACCTCTCTAGTCAGCCCAA GGCCAAACCCCACTGTCACTCTGTTCCTCCGCCCTCCTCTGAGGAGCTCC AAGCCAAACAAGGCCACACTAGTGTGTCTGATCAGTGACTTCTACCCG GGAGCTGTGACAGTGGCCTGGAAGGCAGATGGCAGCCCCCGTCAAGGC GGAGTGGAGACCAACCAACCCCTCCAACACAGAGCAACAACAGTACG CGGCCGAGAGCTACCTGAGCCTGACGCCCGAGCAGTGGAAGTCCCAC AGAAAGCTACAGCTGCCAGGTCAAGCATGAAGGAGCACCGTGGAGAA GACAGTGGCCCTACAGAAATGTTCA	GGCTCCAAGTCTGGC ACCTCAGCCTCCCCTG GCCATCACTGGGCTC CAGGCTGAGGATGAG GCTGATTATTACTGC CAGTCCATATGACAGC AGCCTGAGTGGTTCG GTGTTGCGCGGAGGG ACCAAGCTGACCGTC CTAGGTGCCCTCCACC AAGGCCCATCGGTC TTCCCCCTGGCACCC TCCTCCAAGAGCACCC TCTGGGGGCACAGCG GCCCTGGGCTGCCCTG GTCAAGGACTACTTC CCCGAACCGGTGACG GTGTCGTGGAACCTCA GGCGCCTGACCCAGC GGCGTGACACACCTTC CCGGCTGTCTCTACAG TCCTCAGGACTCTAC TCCCTCAAAAAGCGTG GTGACCGTGCCCTCC AGCAGCTTGGGCACC CAGACCTACATCTGC AACGTGAATCACAAG CCCAGCAACACCCAAG GTGGACAAGAAAAGTT GAGCCCAAATCTTGT	AGTGGGTCTGGGACA GACTTCACCTCTCACC ATCAGCAGACTGGAG CCTGAAAGATTTTGCA GTGTATTACTGTGAG CAGTATGGTAGCTCA CCTACCTTCGGCCAA GGACACGACTGGAG ATTAAACGAGCCTCC ACCAAGGGCCCATCG GTCTTCCCCCTGGCA CCCTCCTCCAAGAGC ACCTCTGGGGCACA GCGGCCCTGGGCTGC CTGGTCAAGGACTAC TTCCCCGAACCGGTG ACGGTGTCTGTGGAAC TCAGGCGCCTGACC AGCGGCGTGCACACC TTCCCCGGCTGTCCTA CAGTCTCAGGACTC TACTCCCTCGAAAGC GTGTGACCGTGCCC TCCAGCAGCTTGGGC ACCCAGACCTACATC TGCAACGTGAATCAC AAGCCCAGCAACACC AAGGTGGACAAAGAA GTTGAGCCCCAAATCT TGT
		SEQ ID NO:259	SEQ ID NO:260	SEQ ID NO:261
AA		QVQLQQSGAGLLKPSSETLSLTCAVHGGSFSGYYWNWIRQPPGKGLEW IGELNHAGNTNYPNPSLKSRTISLDTSKNQFSLTLTSVTAADTAVYY CARGYCRSTTCYFDYWGQGLVTVSSSTVAAPSVFIFFPSDEQLKSGT ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSLK STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECDKTHTCPPC	QSVLTQPPSVSGAPG QRVTISCTGSSSNIG AGYDVHWYQQFPFGTA PKLLIQNSNRPSGV PDRFSGSKSGTSASL	EIVLTQSPGTLSP GERATLSCRASQSVR SSYLAWYQQKPGQAP RLLIYGASSRATGIP DRFSGSGGTDFTLT

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		TCTTCCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG GGAAACGTCTTCTCATGTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAAGAGCCTCTCCCTGTCTCCGGTGGTGCGGATCGG GAGTGCGGATCCGAGGTACAAC TGGTGGAA TCAGGTGGAGGTTTG GTGAGCCGGGAGATCGCTCAGGCTTAGCTGTGCGGCATCGGGGTT TACTTTCGATGATTATGCGATGCATTGGGTCCGGCAAGCGCCTGGAA AAGGGCTCGAGTGGGTTTCCGCCATTACGTGGAATAGCGGACACATC GATTATGCAGACAGTGTGAGGGCAGATTCACAATCTCACGAGACAA TGCTAAGAACAGCCTGTACCTTTCAGATGAAC TCACTTCGCGCGGAAG ATACCGCCGTATACTACTCGGCCAAAGTCTCCTACTTGCTACAGCT TCGTCGCTCGACTATTGGGGTCAAGGAACGTTGGTCAACCGTCTCTAG TACTGTGGCTGCACCATCTGTCTTCACTTCCCGCCATCTGATGAGC AGTTGAAATCTGGAAC TGCCTCTGTTGTGTGCTGCTGAATAACTTC TATCCCAGAGAGGCCAAAGTACAGTGGAAAGTGGATAACGCCCTCCA ATCGGGTAACTCCAGGAGAGTGTCA CAGAGCAGGACAGCAAGGACA GCACCTACAGCCTCGAAAGCACCC TGA CGCTGAGCAAAAGCAGACTAC GAGAAACACAAAGTCTACGCCCTGCGAAGTCACCCATCAGGGCCTGAG CTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT	GCGGCCCTGGGCTGC CTGGTCAAGGACTAC TTCCCGAACC GG TG ACGGTGTCTGTGAAC TCAGGCGCCTGACC AGCGCGTGCACACC TTCCCGGCTGTCCTA CAGTCCTCAGGACTC TACTCCCTCAAAAGC GTGGTACCGTGCCC TCCAGCAGCTTGGGC ACCCAGACCTACATC TGCAACGTGAATCAC AAGCCCAGCAACACC AAGGTGGACAAAGAA GTTGAGCCCCAAATCT TGT	GCGGCCCTGGGCTGC CTGGTCAAGGACTAC TTCCCGAACC GG TG ACGGTGTCTGTGAAC TCAGGCGCCTGACC AGCGCGTGCACACC TTCCCGGCTGTCCTA CAGTCCTCAGGACTC TACTCCCTCAAAAGC GTGGTACCGTGCCC TCCAGCAGCTTGGGC ACCCAGACCTACATC TGCAACGTGAATCAC AAGCCCAGCAACACC AAGGTGGACAAAGAA GTTGAGCCCCAAATCT TGT	SEQ ID NO:265	SEQ ID NO:266	SEQ ID NO:267
	AA	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYFWSWIRQPPGKGLEW IGYIYSGQTKYNPSLKS RVTISIDTSKNQFSLKLSSTVAADTAVYY CARETGSYYGFDYWGGQTLVTVSSTVAAPSVFI FPPSDEQLKSGTAS VVCLLN NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLKST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC DKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCVMHEALHNHYTQKSLSLSPGGGGGGGSEVQLVESGGGL VQPG RSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSAITWNSGHI DYADSV EGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAKVSYLSTA SSLDYWGGQTLVTVSSTVAAPSVFI FPPSDEQLKSGTASVVC LLN NF YPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL ESTLTLSKADY EKHKVYACEVTHQGLSSPVTKSFNRGEC	C C	C C	C		
		SEQ ID NO:268	SEQ ID NO:269	SEQ ID NO:270			

1PS: 376806	046_9C8_CR(S176K)_Fc_3.2_VH_CL(S176E)	NA	CAGGTGCAGCTGCAGGAGTCGGGGCCAGGACTGGTGAAAGCCTTCGGA GACCTGTCCCTCACCTGCACCTGTCTCTGGTGGCTCCATCAGTAGTT ACTTCTGGAGCTGGATTCGGCAGCCCCCAGGTAAGGACTGGAGTGG ATTGGCTATATCTATTACAGTGGCAGACCAATAACAACCCCTCCCT CAAGAGTCGAGTCACCATATCAATAGACACGTCCAAGAACCAGTTCT CCCTGAAGCTGAGCTCTGTGACCGCTGCGGACACGCGCGTGATTAC TGTGCGAGAGAAAAC TGGGAGCTACTACGGCTTTGACTACTGGGGCCA GGGAACCC TGGTCACCGTCTCCTCAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAA TCTGGAAC TGCCTCT GTTGTGTGCTGCTGAATAACTTC TATCCAGAGAGGCCAAAGTACA GTGGAAGGTGGATAACGCCCTCCAA TCGGGTAACTCCCAGGAGAGTG TCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAAGAGCAC CTGACGCTGAGCAAAAGCAGACTACGAGAAAACACAAAGTCTACGCCTG CGAAGTCACCCATCAGGGCTGAGCTCGCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGTGACAAAAC TCAACATGCCACCGTGCCCAAGCA CCTGAACTCCTGGGGACCGTCAGTCTTCTCTTCCCTTCCCTCCAAAAC CAAGGACACCC TCATGATCTCCCGGACCCCTGAGGTCACATGCGTGG TGGTGACGTGAGCCACGAAAGACCCCTGAGGTCAAGTTCAACTGGTAC GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACC GTTGTGTGTCAGCGTCC TCACCGTCTGC ACCAAGACTGGCTGAA TGGCAAAGGAGTACAAGTGCAAGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAAA CCACTCTCCAAAGCCAAAG GCAGCCCCGAGAAACACAGGTGTACACCC TGCCCCATCCCCGGAGG AGATGACCAAGAAC CAGGT CAGCCTGACCTGCC TGGTCAAAGGCTTC TATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGCAGCCGGA GAACAACTACAAGACCA CGCTCCCGTGTGGACTCCGACGGCTCCT TCTTCCCTCTATAGCAA GCTCACCGTGGACAAGACAGGTGGCAGCAG GGGAACGTCTTCTCATGTCTCCGTGATGCATGAGGCTCTGCACAA CCA CTACACGCAGAAAGCCCTCTCCCTGTCTCCGGGTGGTGGCGGATCGG GAGGTGGCGGATCCGAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTG AAAAAGCCCGGGAGTCTCTGAAGATCTCCTGTAA GACTTCTGAATA CAGCTTTAC CAGCTACTGGATCGGCTGGGTGCGCCAGATGCCCGGGA AAGCCCTGGAGTGGATGGGATCATCTATCTTGGTGACTCAGATA CC AGATACAGCCCGTCTCTCC AAGCCAGGTCA CCACTCTCAGCCGACAA GTCCATCAGTACCGCC TACCTG CAGTGGAGCAGCCTGAAGCCCTCGG ACACCGCCATGTATTACTGTGCGGAGAAGTAACTGGGGTCTTGACTAC TGGGGCCAGGGAACCC TGGTCACCGTCTCTAGTCAGCCCCAAGGCCAA	CAGTCTGTGCTGACG CAGCCGCCCTCAGTG TCTGGGCCCCAGGG CAGAGGTCACCATC TCCTGCACTGGAGC AGTTCCAACATCGGG GCAGGTTATGATGA CACTGGTACCAGCAG TTTCCAGGAACAGCC CCCAAACTCCTCATC CAAGGTAACAGCAAT CGCCCTCAGGGGTC CCTGACCGATTCTCT GGCTCCAAGTCTGGC ACCTCAGCCTCCCTG GCCATCACTGGGCTC CAGGCTAGGATGAG GCTGATTATTACTGC CAGTCC TATGACAGC AGCCTGAGTGGTTCG GTGTTGCGCGGAGGG ACCAAGCTGACCGTC CTAGGTGCCCTCCACC AAGGCCCATCGGTC TTCCCCCTGGCACCC TCCTCCAAGAGCAC TCTGGGGGCACAGCG GCCCTGGGCTGCC TG GTCAAGGACTACTTC CCCGAAACCGGTGACG GTGTCGTGGAAC TCA GGCGCCCTGACCAGC GGCGTGACACCTTC CCGGCTGTCTTACAG TCCTCAGGACTCTAC TCCCTCAAAAGCGTG GTGACCGTGCCCTCC	GACATCCAGATGACC CAGTCTCCATCCTCC CTGTCTGCATCTGTA GGAGACAGAGTCACC ATCACTTGCCGGCA AGTCAGAGCATTAAC AACTATTTAAATTGG TATCAGCAGAGACCA GGGAAAGCCCCCTAAG CTCCTGATCTATGCT GCATCCAGTTTGCAA AGTGGGGTCCCATCA AGGTTAGTGGCAGT GGATCTGGGACAGAT TTCAC TCTCACCATC AGCAGTCTGCAACCT GAAGATTTTGCAACT TACTACTGTCAACAG AGTTACAGTACCCCT CGGACGTTCGGCCAA GGGACCAAGCTGGAA ATCAAAACGAGCCTCC ACCAAGGCCCATCG GTCTTCCCCCTGGCA CCCTCCTCCAAGAGC ACCTCTGGGGCACA GCGGCCCTGGGCTGC CTGGTCAAGGACTAC TTCCCCGAACCGGTG ACGGTGTCTGTGAAC TCAGGCGCCCTGACC AGCGCGTGCACACC TTCCCGGCTGTCCTA CAGTCTCAGGACTC TACTCCCTCGAAAGC GTGGTGACCGTGCCC TCCAGCAGCTTGGGC
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			CCCCACTGTCACTCTGTTCCCGCCCTCCTCTGAGGAGCTCCAAGCCA ACAAGGCCACACTAGTGTGTCTGATCAGTGACTTCTACCCGGGAGCT GTGACAGTGGCCTGGAAGGCAGATGGAGCCCGCTCAAGCGGGAGT GGAGACCACCAACCCTCCAAACAGAGCAACAACAAAGTACGCGGCCG AGAGCTACCTGAGCCTGACGCCCGAGCAGTGGAAGTCCACAGAAGC TACAGCTGCCAGGTCACGCATGAAGGGAGCACCGTGGAGAAAGACAGT GGCCCTACAGAAATGTTCA	AGCAGCTTGGGCACC CAGACCTACATCTGC AACGTGAATCACAAG CCCAGCAACACCAAG GTGACAAAGAAAAGTT GAGCCCAAATCTTGT	ACCCAGACCTACATC TGCAACGTGAATCAC AAGCCAGCAACACC AAGTGGACAAAGAAA GTTGAGCCCAAATCT TGT
			SEQ ID NO:271	SEQ ID NO:272	SEQ ID NO:273
AA			QVQLQESGPGGLVKPSETLSLTCTVSGGSISSYFWSWIRPPGKGLEW IGYIYYSGQTKYNPSLKSRTISIDTSKNQFSLKLSVTAADTAVYY CARETGSYYGFDYWGGTLVTVSSSTVAAPSVFI FPPSDEQLKSGTAS VVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLKST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPPVLDSGSFFLYSKLTVDKSRWQQ GNVFSCVMHEALHNHYTQKSLSLSPGSGSGGSEVQLVQSGAEV KKPGESLKISCKTSEYSFTSYWIGWVRQMPGKGLEWMGIIYLGDSDT RYSPSFQGQVTISADKSI STAYLQWSSLKASDTAMYCARSNWGLDY WGQGLTVTVSSQPKANPTVTLFPPSSEELQANKATLVCLISDFYPGA VTVAWKADGSPVKAGVETTKPSKQSNNKYAAESYLSLTPEQWKSHRS YSCQVTHEGSTVEKTVAPTCS	QSVLTQPPSVSGAPG QRVTISCTGSSSNIG AGYDVHWYQQFPGTA PKLLIQNSNRPSGV PDRFSGSKGTSASL AITGLQAEDEADYYC QSYDSSLSGSVFGGG TKLTVLGASTKGPSV FPLAPSSKSTSGGTA ALGCLVKDYFPEPVT VSWNSGALTSGVHTF PAVLQSSGLYSLKSV VTVPSSSLGTQTYIC NVNHNKPSNTKVDKKV EPKSC	DIQMTQSPSSLSASV GDRVITITCRASQIN NYLNWYQQRP GKAPK LLIYAASSLQSGVPS RFGSGSGTDFTLTI SSLQPEDFAITYCQQ SYSTPRRTFGQTKLE IKRASTKGPSVFPLA PSSKSTSGGTAALGC LVKDYFPEPVTVSWN SGALTSGVHTFPAVL QSSGLYSLESVVTVP SSSLGTQTYICNVNH KPSNTKVDKKVEPKS C
			SEQ ID NO:274	SEQ ID NO:275	SEQ ID NO:276
NA	047_23B3_VH4_CK (S176K) Fc_Adalimumab_VH_CK (S176E)		CAGGTACAGTTGCAGGAGTCAGGTCCAGGACTGGTGAAGCCCTCGGA GACCCCTCAGTCACCTGTACCATCTCCGGGGACAGTGCTCTACCA ACAGTGTGCTTGGAAC TGGAATTAGGCAGCCCCCAGGAAAGGCCCTT GAGTGGATAGGAAGGACATACACAGGTCCAAGTGGTATAATGATTA TGCAGTTTCTCTGAAAAGTCGAGTAACCATCAGCCCAGACACATCCA AGAACCCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGCCCGGGACACG GCTGTGATTA TACTGTGCAAGAGAGGATGGGATAGCTACTACCGCTA CGGTATGGACGTC TGGGGCCAAAGGACCAACGGTCACCGTCTCCTCAA CGGTGGCTGCACCATCTGTCTTCA TCTTCCCGCCATCTGATGAGCAG TTGAAAATCTGGAAC TGCCTCTGTGTGTGCTGCTGAATAACTTCTA TCCCAGAGAGGCCAAAGTACAGTGGAAAGTGGAATAACGCCCTCCAAT CGGTAAC TCCCAGGAGAGTGTCA CAGAGCAGGACAGCAAGGACAGC ACCTACAGCCTCAAGAGCAACCTGTACGCTGAGCAAAAGCAGACTACGA	GATATCCAAATGACA CAATCACCATCGTCG CTTTCAGCGTCTGTT GGCGACCGTGTGACG ATTACCTGTCGCGCG TCCCAGGGAATCCGG AATTACCTCGCATGG TATCAGCAAAAACCC GGA AAAAGCACCGAAG CTCCTGATCTATGCC GCCTCGACTCTTCAG AGTGGTGTGCCGTCG AGGTTTAGCGGGTCC	GACATCCAGATGACC CAGTCTCCAAGCTCC CTGTCTGCCGCTGTG GGCGATAGGTCACC ATCACTTGCAGTCC AGCCAGAGTGTGTTA TACAGCTCCAACAAT AAGAACTACTTAGTT TGGTACCAGCAGAAA CCAGGAAAAGGTTCT AAACTGCTCATTTAC TGGGCATCTACCCGG GAATCCGGGTCCT

		GAAACAAAAGTCTACGCCTGCGAAAGTCACCCATCAGGGCCTGAGCTCGCCCCACAAAAGAGCTTCAACAGGGGAGAGTGTGACAAAACTCACACATGCCACCCGTGCCAGCACCTGAACCTCCTGGGGACCGTCAGTCTTCCTCTTCCCCCAAACCCAAAGGACACCCCTCATGATCTCCCGGA CCCCTGAGGTCACATGCGTGGTGGTGACGTGAGCCACGAAGACCCCTGAGTCAAGTTCAACTGGTACGTGGACGGCGTGAGGTGCATAATGCAAGACAAAAGCCGTGTAGGAGCAGTACGGCAGCACGTACCGTTGTGTACAGCTCCTCACCCGTCTGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAGCCCTCCCAGCCCCCATCGAGAA AACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACACACAGGTGTACA CCCTGCCCCCATCCCGGAGGAGATGACCAAGAACACAGTCAGCCCTG ACCTGCCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTG GGAGAGCAATGGCAGCCGGAGAACAACTACAAGACCAACGCTCCCG TGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTG GACAAAGACAGGTGGCAGCAGGGAACGTCTTCTCATGCTCCGTGAT GCATGAGGCTCTGCACAACCACTACACGCAGAAAGAGCCCTCTCCCTGT CTCCGGGTGGTGGCGGATCGGGAGGTGGCGGATCCGAGGTACAAC GTGGAAATCAGGTGGAGGTTTGGTGAGCCGGGAGATCGCTCAGGCT TAGCTGTGCGGCATCGGGGTTTACTTTCGATGATTATGCGATGCATT GGGTCCGGCAAGCGCCTGGAAGGGCTCGAGTGGGTTTCCGCCATT ACGTGGAATAGCGGACACATCGATTATGCAGACAGTGTGGAGGGCAG ATTACAAATCTCACGAGACAAATGCTAAGAACAGCCCTGTACCTTCAGA TGAACTCACTTCGCGGGAAGATACCGCCGTATACTACTGCGCCAAA GTCTCCTACTTGTCTACAGCTTCGTGCTCGACTATTGGGGTCAAGG AACGTTGGTCACCGTCTCTAGTACTGTGGCTGCACCATCTGTCTTCA TCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCCTCTGTT GTGTGCCCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTG GAAAGTGGATAACGCCCTCCAATCGGGTAACTCCAGGAGAGTGTCA CAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCGAAAGCACCCCTG ACGCTGAGCAAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGA AGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACA GGGAGAGTGT	GGGTCAGGTACGGAC TTTACTCTCACAATT TCCAGCCTGCAGCCC GAAGATGTAGCTACC TATTACTGCCAGAGA TACAACCGAGCGCCT TACACATTCCGGACAA GGACAAAAGTCGAG ATCAAGCGTGCCCTCC ACCAAGGGCCCATCG GTCTTCCCCCTGGCA CCCTCCTCCAAGAGC ACCTCTGGGGCACA GCGGCCCTGGGCTGC CTGGTCAAGGACTAC TTCCCCGAACCGGTG ACGGTGTCTGGAAC TCAGGCGCCTGACC AGCGGCGTGCACACC TTCCCGGCTGTCCTA CAGTCTCAGGACTC TACTCCCTCAAAAGC GTGGTGACCGTGCCC TCCAGCAGCTTGGGC ACCCAGACCTACATC TGCAACGTGAATCAC AAGCCCAGCAACACC AAGGTGACAAAGAAA GTTGAGCCCCAAATCT TGT	AGTCGATTCAGTGGC AGCGGGTCTGGGACA GATTTACTCTCACC ATCAGCAGCCTGCAG CCTGAAGATGTGGCA ACTTATTACTGTGAG CAATATTATAAGACT CCTCTCACTTTCGGC GGAGGGACCAAGGTG GAGATCAAACGAGCC TCCACCAAGGGCCCA TCGGTCTTCCCCCTG GCACCCCTCCTCCAAG AGCACCTCTGGGGGC ACAGCGGCCCTGGGC TGCCTGGTCAAAGGAC TACTTCCCCGAACCG GTGACGGTGTCTGTG AACTCAGGCGCCCTG ACCAGCGCGTGCAC ACCTTCCCGGCTGTC CTACAGTCTCTCAGGA CTCTACTCCCTCGAA AGCGTGGTGACCGTG CCCTCCAGCAGCTTG GGCACCCAGACCTAC ATCTGCAACGTGAAT CACAAGCCCAGCAAC ACCAAGGTGGACAA AAAGTTGAGCCCCAA TCTTGT
		SEQ ID NO:277 QVQLQESGPGLVKPSETLSLTCTISGDSVSTNSVAWNWIRQPPGKGL EWIGRTYYRSKWYNDYAVSLKSRVTISPDTSKNQFSLKLSVTAADT AVYYCAREDDGSYYRYGMDVWGQGTTVTVSSTVAAPSVFIFFPPSDEQ LKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS	SEQ ID NO:278 DIQMTQSPSSLSASV GDRVITITCRASQGIR NYLAWYQQKPGKAPK LLIYAASTLQSGVPS	SEQ ID NO:279 DIQMTQSPSSLSASV GDRVITITCRSSQSVL YSSNNKNYLVWYQQK PGKVPKLLIYWASTR

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			TYSLKSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGGSGGGSEVQL VESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSAI TWNSGHIDYADSVVEGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAK VSYLSTASSLDYWGGQGLVTVSVSTVAAPSVFIFPPSDEQLKSGTASV VCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYSLESTL TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	RFSGSGSGTDFTLTI SSLQPEDVATYYCQR YNRAPYTFGQGTKE IKRASTKGPSVFPLA PSSKSTSGTAALGC LVKDYFPEPVTVSWN SGALTSGVHTFFAVL QSSGLYSLKSVVTVP SSSLGTQTYICNVNH KPSNTKVDKKVEPKS C	ESGVPSRFSGSGSGT DFTLTISSLQPEDVA TYYCQQYYKTPLTFG GGTKVEIKRASTKGP SVFPLAPSSKSTSGG TAAALGCLVKDYFPEP VTVSWNSGALTSGVH TFPAVLQSSGLYSLE SVVTVPSSSLGTQTY ICNVNHKPSNTKVDK KVEPKSC
			SEQ ID NO:280	SEQ ID NO:281	SEQ ID NO:282
	048_23B3_VH4_CK(S176K)_Fc_3.2_VH_CL(S176F)	NA	CAGGTACAGTTGCAGGAGTCAGGTCCAGGACTGGTGAAGCCCTCGGA GACCCCTCACTCACTGATACCATCTCCGGGGACAGTGCTCTACCA ACAGTGTGCTTGGAACGTGATTAGGCAGCCCCCAGGGAAAGGCCTT GAGTGGATAGGAAGGACATACTACAGGTCCAAGTGGTATAATGATTA TGCAAGTTTCTTGAAAAAGTCGAGTAACCATCAGCCCCAGACACATCCA AGAACCAAGTTCTCCCTGAAGCTGAGCTCTGTGACTGCCGCGACACG GCTGTGATTACTGTGCAAGAGAGGATGGGGATAGCTACTACCGCTA CGGTATGGACGCTCTGGGGCCAAAGGGACCAACGGTCACCGTCTCCTCAA CGGTGGCTGCACCATCTGTCTTTTCATCTTCCCGCCATCTGATGAGCAG TTGAAAATCTGGAACCTGCCTCTGTTGTGTGCTGCTGAATAACTTCTA TCCCAGAGAGGCCAAAGTACAGTGGAAAGTGGATAACGCCCTCCAAT CGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGC ACCTACAGCCTCAAGAGCACCCCTGACGCTGAGCAAAAGCAGACTACGA GAAACACAAAGTCTACGCCCTGCCAAGTCAACCATCAGGGCCCTGAGCT CGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTGACAAAACTCAC ACATGCCCACCGTGCACACCTGAACCTCCTGGGGGACCGTCAGT CTTCCTCTTCCCCCCCCAAAACCCAAAGACACCCCTCATGATCTCCCCGA CCCCTGAGGTACATGCGTGTGTGTGGTGGACGTGAGCCACGAAGACCCT GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGC CAAGACAAAAGCCGTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTG TCAGCGTCCCTCACCGTCTGTCAACCAAGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGGTCTCCAACAAAAGCCCTCCCAGCCCCCATCGAGAA AACCATCTCAAAGCCAAAGGGCAGCCCCCGAGAAACCAAGGTGTACA CCCTGCCCCCATCCCCGGGAGGAGATGACCAAGAACCCAGGTCAAGCTG ACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTG	CAGTCTGTGCTGACG CAGCCGCCCTCAGTG TCTGGGGCCCCAGGG CAGAGGTCACCATC TCCTGCACTGGGAGC AGTTCCAACATCGGG GCAGGTTATGATGTA CACTGGTACCAGCAG TTTCCAGGAACAGCC CCCAAACCTCCTCATC CAAGGTAACAGCAAT CGGCCCTCAGGGGTC CCTGACCGATTCTCT GGTCCAAGTCTGGC ACCTCAGCCTCCCTG GCCATCACTGGGCTC CAGGCTGAGGATGAG GCTGATTATTACTGC CAGTCCCTATGACAGC AGCCTGAGTGGTTCG GTGTTCCGGCGGAGGG ACCAAGCTGACCGTC CTAGGTGCCCTCCACC AAGGGCCCATCGGTC TTCCCCCTGGCACCC	GACATCCAGATGACC CAGTCTCCAAGCTCC CTGTCTGCGTCTGTG GGCGATAGGTCACC ATCACTTGCAGGTCC AGCCAGAGTGTGTTA TACAGCTCCAACAAT AAGAACTACTTAGTT TGGTACCAGCAGAAA CCAGGAAAAGGTTCC AAACTGCTCATTTAC TGGCATCTACCCGG GAATCCGGGTCCTCT AGTCGATTTCAGTGCG AGCGGTCTGGGACA GATTTCACTCTCACC ATCAGCAGCCTGCAG CCTGAAGATGTGGCA ACTTATTACTGTCTAG CAATATTATAAGACT CCTCTCACTTTCCGGC GGAGGGACCAAGGTG GAGATCAAACGAGCC TCCACCAAAGGCCCA TCGGTCTTCCCCCTG

1PS: 376816

		GGAGAGCAATGGGAGCCGGAGAAACAACACTACAAGACCAACGCCCTCCCG TGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTG GACAAGACAGGTGGCAGCAGGGAACGTCTTCTCATGTCCGTGAT GCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCCTCTCCCTGT CTCCGGGTGGTGGCGGATCGGAGGTGGCGGATCCGAGGTGCAGCTG GTGCAGTCTGGAGCAGAGGTGAAAAAGCCCCGGGAGTCTCTGAAGAT CTCCTGTAAGACTTCTGAATACAGCTTTACCAGCTACTGGATCGGCT GGTGCGCCAGATGCCCGGAAAGCCCTGGAGTGGATGGGATCATC TATCTTGGTGACTCAGATACCAGATACAGCCCGTCTTCCAAGGCCA GGTCACCATCTCAGCCGACAAGTCCATCAGTACCGCTACCTGCAGT GGAGCAGCCTGAAGGCTCGGACACCGCCATGTATTACTGTGCGAGA AGTAACTGGGGTCTTGACTACTGGGGCCAGGGAACCTGGTCACCGT CTCTAGTCAGCCCAAGCCCAACCCCACTGTCACTCTGTTCCCGCCCT CCTCTGAGGAGTCCAAGCCCAACAAGGCCACACTAGTGTCTGATC AGTGACTTCTACCCGGGAGCTGTGACAGTGGCTGGAAGGCAGATGG CAGCCCCGTCAAGCGGGAGTGGAGACCACCAACCCCTCCAAACAGA GCAACAACAAGTACGCGGCCGAGAGCTACCTGAGCCTGACGCCCCGAG CAGTGGAAGTCCACAGAAAGCTACAGCTGCCAGGTACGCAATGAAGG GAGCACCGTGGAGAAACAGACGTGGCCCCCTACAGAAATGTTCA	TCCTCCAAGAGCACCC TCTGGGGGCACAGCG GCCCTGGGCTGCCTG GTCAAGGACTACTTC CCCGAACCGGTGACG GTGTCGTGGAAC TCA GGCGCCCTGACCAGC GGCGTGACACCTTC CCGGCTGTCTACAG TCCTCAGGACTCTAC TCCCTCAAAAAGCGTG GTGACCGTGCCCTCC AGCAGCTTGGGCACC CAGACCTACATCTGC AACGTGAATCACAA CCCAGCAACACCAAG GTGGACAAGAAAATT GAGCCCAAATCTTGT	GCACCCCTCCTCCAAG AGCACCTCTGGGGGC ACAGCGCCCTGGGC TGCCCTGGTCAAAGGAC TACTTCCCCGAACCG GTGACGGTGTCTGTGG AACTCAGGCGCCCTG ACCAGCGCGTGCAC ACCTTCCCCGGCTGTC CTACAGTCTCAGGA CTCTACTCCCTCGAA AGCGTGGTGACCGTG CCCTCCAGCAGCTTG GGACCCAGACCTAC ATCTGCAACGTGAAT CACAAAGCCAGCAAC ACCAAGGTGGACAAG AAAGTTGAGCCCCAAA TCTTGT
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		SEQ ID NO:286	SEQ ID NO:287	SEQ ID NO:288

1PS: 376821	059_Adalimumab_IgG.002_3B3v2_VH_CH1 (S183E) . 001	NA	GATATCCAAATGACA CAATCACCATCGTCG CTTTCAGCGTCTGTT GGCGACCGTGTGACG ATTACCTGTCGCGG TCCCAGGGAATCCGG AATTACCTCGCATGG TATCAGGAAAAACCC GGAAAAGCACCGAAG CTCCTGATCTATGCC GCCTCGACTCTTCAG AGTGGTGTCCTGTCG AGGTTTAGCGGGTCC GGGTACGGTACGGAC TTTACTCTCACAAAT TCCAGCCTGCAGCCC GAAGATGTAGCTACC TATTACTGCCAGAGA TACAACCGAGCGCCT TACACATTGGACAA GGGACAAAAGTCGAG ATCAAGCGTACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGAAC TGCC TCTGTTGTGTGCCTG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCCCAG GAGAGTGTACACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC GAAAGCACCCCTGACG CTGAGCAAAAGCAGAC	GAAATTGTGTTGACG CAGTCTCCAGGCACC CTGTCTTTGTCTCCA GGGAAAAGAGCCACC CTCTCCTGCAGGGCC AGTCAGAGTGTTAGA AGCAGTTACTTAGCC TGGTACCAGAGAAA CCTGGCCAGGCTCCC AGGCTCCTCATCTAT GGTGCA TCCAGCAGG GCCACTGGCATCCCCA GACAGGTTCAGTGGC AGTGGGTCTGGGACA GACTTCACTCTCACC ATCAGCAGACTGGAG CCTGAAAGATTTTGCA GTGTATTACTGT CAG CAGTATGGTAGCTCA CCTACCTTCGGCCAA GGGACACGACTGGAG ATTAAAACGAACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGTACCGCC TCTGTTGTGTGCCTG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCCCAG GAGAGTGTACACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC AAGAGCACCCCTGACG CTGAGCAAAAGCAGAC	GAGGTACAAC TGGTGGAAATCAGGTGGAGGTTTGGTGCA GCCGGGAG ATCGCTCAGGCTTAGCTGTGCGGCATCGGGGTTTACTTTCGATGATT ATCGGATGCAT TGGGTCCGGAAGCGCTGGA AAGGGCTCGAGTGG GTTTCCGCCATTACGTGGAATAGCGGACACATCGATTATGCAGACAG TGTGGAGGCGAGATTACA AATCTCACGAGACAATGCTAAGAACAGCC TGTA CCTTTCAGATGAAC TCACTTTCGCGCGGAAGATACCGCCGTATAC TACTGCGCCAAAGTCTCCTACTTGTCTACAGCTTTCGTGCTCGACTA TTGGGTCAAGGAACGTTGGTCA CCGTCTCTAGTGCC TCCACCAAGG GCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGG GGCACAGCGGCCCTGGGCTGCC TGGTCAAGGACTACTTCCCCGAACC GGTGACGGTGTCTGTGGAAC TCAAGGCGCCTGACCAGCGGCGTGCACA CCTTCCCCGGCTGTCTACAGTCTC CAGGACTCTACTCCCTCAAAAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG CAACGTGAATCACAAGCCCCAGCAACACCAAGGTGGACAAGAAA GTTG AGCCCAAAATCTGTGACAAA AACTCACACATGCCACCGTGCCCCAGCA CCTGAACTCCTGGGGACCGTCA GTCTTCTCTTCCCCCAAACC CAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGG TGGTGACGTGAGCCACGAA GACCCCTGAGGTCAAGTTCAACTGGTAC GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACC GTTGTGT CAGCGTCCCTCACCGTCTG C ACCAGACTGGCTGAATGGCAA GGAGTACAAGTGCAAGTCTCCAAC AAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGG GCAGCCCCGAGAAACCA CAGGTGTACACCCCTGCCCCATCCCCGGAGG AGATGACCAAGAAC CAGGTCA GCCCTGACCTGCC TGGTCAAAGGCTTC TATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA GAACAACTACAAGACCA CGCCTCCC GTGTGGACTCCGACGGCTCCT TCTTCCCTCTATAGCAA GCTCACCGTGGACAAGAGCAGGTGGCAGCAG GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAGAAGACCTCTCCCTGTCTCCGGGTGGTGGCGGATCGG GAGGTGGCGGATCCCAGGTGCAGTTACAGCAGTCGGGCGCAGGACTG TTGAAGCCTTCGGAGACCC TGTCCCTCACCTGCGCTGTCCATGGTGG GTCCCTTCAGTGGTTACTACTGGA ACTGGATTTCGCAAGCCACCAAGGA AGGGCTAGAGTGGATTGGGAAATCAATCATGTGGAAACACCAAC TACAACCCGTCCCTCAAGAGTCGAGTCA CCAATATCATTAGACACGTC CAAGAACCAGTTCTCCCTGACGCTGACCTCTGTGACCGCCGCGGACA CGGCTGTGTATTACTGTGCGGAGAGGATATTGTAGAAGTACCACTGC TACTTTGACTACTGGGGCCAGGGAACCCCTAGTCACCGTCTCCTCAGC
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		TACGAGAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	TACGAGAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	CTCCACCAAGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGA GCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC TTCCCCGAACCGGTGACGGTGTCTGTGAACCTCAGGCGCCCTGACCCAG CGCGTGACACACCTTCCCCGGCTGTCTACAGTCTCAGGACTCTACT CCCTCGAGAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAG ACCTACATCTGCAACGTGAATCACAAAGCCCAGCAACACCAAGGTGGA CAAGAAAGTTGAGCCCCAAAATCTTGT
		SEQ ID NO:289	SEQ ID NO:290	SEQ ID NO:291
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		SEQ ID NO:292	SEQ ID NO:293	SEQ ID NO:294
		GATATCCAAATGACA CAATCACCATCGTCG CTTTCAGCGTCTGTT GGCGACCGTGTGACG ATTACCTGTCGCGCG TCCCAGGGAATCCGG AATTACCTCGCATGG TATCAGGAAAAACCC GGAAAAGCACCCGAAG CTCCTGATCTATGCC GCCTCGACTCTTCAG AGTGGTGTGCCGTCG AGGTTTAGCGGGTCC	GACATCCAGATGACC CAGTCTCCATCCTCC CTGTCTGCATCTGTA GGAGACAGAGTCACC ATCACTTGCCGGGCA AGTCAGAGCATTAAC AACTATTTAAATTGG TATCAGGAGAGACCA GGGAAAAGCCCTAAG CTCCTGATCTATGCT GCATCCAGTTTGCAA AGTGGGTCCCATCA AGGTTCAGTGGCAGT	GAGGTACAACCTGGTGGAAATCAGGTGGAGGTTTGGTGACCCGGGGAG ATCGCTCAGGCTTAGCTGTGCGGCATCGGGGTTTACTTTCGATGATT ATCGGATGCATTGGTCCGGAAAGCGCCTGGAAAAGGGCTCGAGTGG GTTTCCGCCATTACGTGGAATAGCGGACACATCGATTATGCAGACAG TGTGGAGGCGAGATTCACAATCTCACGAGACAAATGCTAAGAACAGCC TGTAACCTTCAGATGAACCTCACTTCGCGCGGAAGATACCGCCGTATAC TACTGCGCCAAAGTCCTCTACTTGTCTACAGCTTCGTGCTCGACTA TTGGGGTCAAGGAAACGTTGGTCAACGTCCTCTAGTGCCCTCCACCAAGG GCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGG GGCACAGCGGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCCGAACC GGTGACGGTGTCTGTGGAACCTCAGGGGCCCTGACCAAGCGGTGCACA CCTTCCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAAAAGC GTGGTGACCGTGCCCTCCAGCAGCCTTGGGCACCCAGACCTACATCTG
!PS: 376826	060 Adalimumab IgG.002 _9C8_VH CH1 (S183E).001	NA		

		GGGTCAAGGTACGGAC TTTACTCTCACAATT TCCAGCCTGCAGCCC GAAGATGTAGCTACC TATTACTGCCAGAGA TACAACCGAGCGCCT TACACATTCCGACAA GGGACAAAAGTCGAG ATCAAGCGTACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGAAC TGCC TCTGTTGTGTGCCCTG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCCAG GAGAGTGCACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC GAAAGCACCCCTGACG CTGAGCAAAGCAGAC TACGAGAAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	GGATCTGGGACAGAT TTCAC TCTCACCATC AGCAGTCTGCAACCT GAAGATTTTGCAACT TACTACTGTCAACAG AGTTACAGTACCCCT CGGACGTTCCGGCCAA GGGACCAAGCTGGAA ATCAAAACGAACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGTACCGCC TCTGTTGTGTGCCCTG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCCAG GAGAGTGCACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC AAGAGCACCCCTGACG CTGAGCAAAGCAGAC TACGAGAAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	CAACGTGAATCACAAAGCCAGCAACACCAAGGTGGACAAAGAAAGTTG AGCCCAAAATCTTGTGACAAAAACTCACACATGCCACCCGTGCCCAGCA CCTGAACTCCTGGGGACCGTCAGTCTTCTCTTCCCCCAAACC CAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGG TGGTGACGTAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTAC GTGGACGGGTGGAGGTGCATAATGCCAAGACAAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTGTCAGCGTCCTCACCGTCCCTGC ACCAAGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAAC AAAGCCCTCCCAGCCCCCATCGAGAAAAACCATCTCCAAGCCAAAGG GCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCCGGAGG AGATGACCAAGAACCAAGGTCAAGCTGACCTGCCCTGGTCAAAGGCTTC TATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA GAACAACTACAAGACCACGCCCTCCCGTGCTGGACTCCGACGGCTCCT TCTTCCCTCTATAGCAAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG GGAAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAAGAGCCCTCTCCCTGTCTCCGGTGGTGGCGGATCGG GAGGTGGCGGATCCCAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTG GTAAAGCCTTCGGAGACCCTGTCCCTCACCTGCAC TGTCTCTGGTGG CTCCATCAGTAGTTACTTCTGGAGCTGGATTTCGGAAGCCCCCAGGTA AGGACTGGAGTGGA TTGGCTATATCTATTACAGTGGGCAGACCAAA TACAACCCCTCCCTCAAGAGTCGAGTCACCATATCAATAGACACGTC CAAGAAACCAAGTTCTCCCTGAAGCTGAGCTCTGTGACCCGTCCGGACA CGCCGTGTATTACTGTGCGAGAGAAA CTGGAGCTACTACGGCTTT GACTACTGGGGCCAGGGAACCCCTGGTCA CCGTCTCCTCAGCCTCCAC CAAGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCT CTGGGGGCACAGCGGCCCTGGGCTGCC TGGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCTGTGGAAC TCAGGCGCCCTGACCAGCGCGT GCACACCTTCCCGGTGTCTCTACAGTCCTCAGGACTCTACTCCCTCG AGAGCGTGGTGACCGTCCCCCTCCAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAAGCCCAAGCAACCAAGGTGGACAAGAA AGTTGAGCCCAAA TCTTGT	SEQ ID NO:295	SEQ ID NO:296	SEQ ID NO:297
	AA	DIQMTQSPSSLSASV GDRVITTCRASQGIR NYLAWYQEKPGKAPK LLIYAASTLQSGVPS RFSGSGSGTDFTLT I	DIQMTQSPSSLSASV GDRVITTCRASQ SIN NYLWYQERPGKAPK LLIYAASSLQSGVPS RFSGSGSGTDFTLTI	EVQLVESGGGLVQPGRSLRLS CAASGFTFDDYAMHWVRKAPGKLEW VSAITWNSGHIDYADSV EGRFTI SRDNAKNSLYLQMNSLRAEDTAVY YCAKVS YLSTASSLDYWGQGT LVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLKS VVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH TCPPCPA			

		TCTGTTGTGTGCCTG CTGAATAACTTCTAT CCCAGAGAGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCCGAG GAGAGTGCACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC GAAAGCACCCTGACG CTGAGCAAAAGCAGAC TACGAGAAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	TTGAAATCTGGTACC GCCTCTGTTGTGTGC CTGCTGAATAACTTC TATCCCAGAGAGGCC AAAGTACAGTGGAAG GTGGATAACGCCCTC CAATCGGGTAACTCC CAGGAGAGTGTACACA GAGCAGGACAGCAAG GACAGCACCTACAGC CTCAAGAGCACCCCTG ACGCTGAGCAAAAGCA GACTACGAGAAAACAC AAAGTCTACGCCCTGC GAAAGTCACCCATCAG GGCCTGAGCTCGCCC GTCACAAAAGAGCTTC AACAGGGGAGAGTGT	TCTTCCCTCTATAGCAAAGCTCACCGTGGACAAAGAGCAGGTGGCAGCAG GGGAAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGCAAGAGAGCCCTCTCCCTGTCTCCGGTGTGGCGGATCGG GAGTGGCGGATCCCAGGTACAGTTGCAGGAGTCAGGTCCAGGACTG GTGAAGCCCTCGGAGACCCTCTCACTCACCTGTACCATCTCCGGGGA CAGTGTCTCTACCAACACAGTGTGCTTGGAAC TGGAATTAGGAAGCCCC CAGGAAAAGGCCTTGAGTGGATAGGAAAGGACATACTACAGGTCCAAG TGGTATAATGATTATGCAGTTTCTCTGAAAAGTCGAGTAACCATCAG CCCAGACACATCCAAGAACCAAGTTTCTCCCTGAAGCTGAGCTCTGTGA CTGCCGCGACACGGCTGTGTATTACTGTGCAAGAGAGGATGGGAT AGCTACTACCGCTACGGTATGGACGTCTGGGGCCAAAGGACCAACGGT CACCGTCTCCTCAGCCTCCACCAAGGCCCATCGGTC TCCCCCTGG CACCTCCTCCAAGAGCACCTCTGGGGCACAGCGGCCCTGGGCTGC CTGGTCAAGGACTACTTCCCCGAAACCGGTGACGGTGTCTGTGGAATC AGCGCCCTGACCAGCGGCGTGCACACCTTCCC GGCTGTCTCTACAGT CCTCAGGACTCTACTCCCTCGAGAGCGTGTGACCCGTGCCCTCCAGC AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCCAG CAACACCAAGGTGACAAAGAAAGTTGAGCCCCAAATCTTGT
		SEQ ID NO: 301	SEQ ID NO: 302	SEQ ID NO: 303
	AA	DIQMTQSPSSLSASV GDRVITICRASQGIR NYLAWYQEKPGKAPK LLIYAASTLQSGVPS RFSGSGGTDFTLTI SSLQPEDVATYYCQR YNRAPYTFGQTKVE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLESTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEK	DIQMTQSPSSLSASV GDRVITICRSSQSVL YSSNNKNYLVWYQEK PGKVPKLLIYWASTR ESGVPSRFSGSGSGT DFTLTISLIQPEDVA TYYCQQYYKTPLTFG GGTKVEIKRTVAAPS VFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGNS QESVTEQDSKDSITYS LKSTLTLSKADYEKH KVYACEVTHQGLSSP VTKSFNRGEC	EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRKAPGKGLEW VSAITWNSGHIDYADSVETRFTISRDNAKNSLYLQMNSLRAEDTAVY YCAKVSYLESTASLDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLKS VVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTPPCPA PELLGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGGGGGGGSQVQLQESGPGL VKPSETLSLTCTISGDSVSTNSVAVNNWIRKPPGKGLEWIGRTYYRSK WYNDYAVSLKSRVITISPDTSKNQFSLKLSSTAAADTAVYYCAREDDG SYRYGMDVWGQGTITVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLVESVTVTPSS SLGTQTYICNVNHKPSNTKVDKKVEPKSC
		SEQ ID NO: 304	SEQ ID NO: 305	SEQ ID NO: 306

1PS : 376834	062_3.2_IgG.002_3B3v2_VH_CH1 (S183E) . 001	NA	CAGTCTGTGCTGACG CAGCCGCCCTCAGTG TCTGGGCCCCAGGG CAGAGGGTCACCATC TCCGTGCACTGGGAGC AGTTCCAAACATCGGG GCAGGTTATGATGTA CAC TGGTACCAGGAG TTTCCAGGAACAGCC CCC AAACTCCTCATC CAAGGTAACAGCAAT CGGCCCTCAGGGGTC CCTGACC GATTCTCT GGCTCCAAAGTCTGGC ACCTCAGCCTCCCTG GCCATCACTGGGCTC CAGGCTGAGGATGAG GCTGATTATTACTGC CAGTCCCTATGACAGC AGCCTGAGTGGTTCCG GTGTTCCGGCGGAGGG ACCAAGCTGACCGTC CTAGGTCAGCCCCAAG GCTGCCCCCTCGGTC ACTCTGTTCCCGCCC TCCTCTGAGGAGCTT CAAGCCAAACAAGGC ACACTGGTGTGTCCTC ATAAGTGACTTCTAC CCGGAGCCCGTGACA GTGGCCTGGAAGGCA GATAGCAGCCCCGTC AAGCGGGAGTGGAG ACCACCAACCCCTCC AAACAAAGCAACAAC AAGTACGGGCGCGAG AGCTATCTGAGCCTG	GAAATTGTGTTGACG CAGTCTCCAGGCACC CTGTCTTTGTCTCCA GGGAAAAGAGCCACC CTCTCCTGCAGGGCC AGTCAGAGTGTTAGA AGCAGTTACTTAGCC TGGTACCAGGAGAAA CCTGGCCAGGCTCCC AGGCTCCTCATCTAT GGTGCAATCCAGCAGG GCCACTGGCATCCCA GACAGGTTCAGTGGC AGTGGGTC TGGGACA GACTTCACTCTCACC ATCAGCAGACTGGAG CCTGAAGATTTTGCA GTGTATTACTGTCAG CAGTATGGTAGCTCA CCTACCTTCGGCCAA GGGACACGACTGGAG ATTAAACGAACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGTACCGCC TCTGTTGTGTGCC TG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAAGTG GATAACGCCCTCCAA TCGGGTAAC TCCCAG GAGAGTGTCA CAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC AAGAGCACCC TGACG CTGAGCAAAAGCAGAC	GAGTGCAGCTGGTGCA GTCTCTGAAGATCTCT ACTGGATCGGCTGGTG ATGGGGATCATCTATCT CTTCCAAGGCCAGGTCA CCTACCTGCAGTGGAG TACTGTGCGAGAAAGTA CCTGGTCACCGTCTCT CCCTGGCAACCCTCCTC GGCTGCC TGGTCAAGGA GAACTCAGGCGCCTGAC TACAGTCCCTCAGGACT TCCAGCAGCTTGGCAC GCCCAGCAACACCAAG ACAAAACTCACACATGC GGACCGTCAGTCTTCT GATCTCCCGGACCCCTG ACGAAGACCCCTGAGGT GTGCATAATGCCAAGAC GTACCCGTTGTGTCAG ATGGCAAGGAGTACAAG CCCATCGAGAAAACCAT ACAGGTGTACACCCCTG AGGTCAGCCCTGACCTG GCCGTGGAGTGGAGAG CACGCCCTCCCGTGTG AGCTCACCCGTGACACA TGCTCCCGTGATGCA CCTCTCCCTGTCTCCGG AGGTGCAGTTACAGCAG ACCCGTGCCCTCACCTG CTACTGGAAC TGGATT TTGGGGAAATCAATCAT AAGAGTCGAGTCACCAT CCTGACGCTGACCTCT GTGCGAGAGGATATTGT GGCCAGGGAAACCTAG
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			ACGCCTGAGCAGTGG AAGTCCCACAGAAAGC TACAGCTGCCAGGTC ACGCATGAAGGGAGC ACCGTGGAAGAGACA GTGGCCCCTACAGAA TGTTCA	TACGAGAAACACAAA GTCTACGCCCTGCCAA GTACCCCATCAGGC CTGAGCTCGCCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	ATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCA CAGCGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCCGAACCCGGTG ACGGTGCTGTGAACCTCAGGCGCCCTGACGCGGCGTGACACACCTT CCCCGCTGTCCACAGTCCCTCAGGACTCTACTCCCTCGAGAGCGGTGG TGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAAC GTGAATCACAAAGCCAGCAACACCAAGGTGGACAAAGAAAGTTGAGCC CAAATCTTGT
			SEQ ID NO:307	SEQ ID NO:308	SEQ ID NO:309
AA			QSVLTQPPSVSGAPG QRVTISCTGSSSNIG AGYDVHWYQEFPGTA PKLLIQGNSNRPSGV PDRFSGSKSGTSASL AITGLQAEDEADYYC QSYDSSLSGSVFGGG TKLTVLGQPKAAPSV TLFPPSSEELQANKA TLVCLISDFYPGAVT VAWKADSSPVKAGVE TTTTPSKQSNNKYAAE SYLSLTPEQWKSHRS YSCQVTHEGSTVEKT VAPTECS	EIVLTQSPGTLSLSP GERATLSCRASQSVR SSYLAWYQEKPGQAP RLLIYGASSRATGIP DRFSGSGSGLTFTLT ISRLEPEDFAVYCYQ QYSSSPTFGQGRLE IKRTVAAPSVFIAPP SDEQLKSGTASVVCL LNNFYPPREAKVQWKV DNALQSGNSQESVTE QDSKDSYSTSLKSTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGE	EVQLVQSGAEVKKPGESLKISCKTSEYSFTSYWIGVVRKMPGKGLEW MGI IYLGDSDTRYSPSFQGQVTISADKSI STAYLQWSSLKASDTAMY YCARSNWGLDYGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLKSVVTVP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGGSGGGSQVQLQSSGAGLLKPSE TSLTCAVHGGSFSGYYWNWIRKPPGKGLEWIGEINHAGNTNYPNPSL KSRVTISLDTSKNQFSLTILTSVTAADTAVYYCARGYCRSTTCYFDYW GQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLESVVTVFPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSC
			SEQ ID NO:310	SEQ ID NO:311	SEQ ID NO:312
			CAGTCTGTGCTGACG CAGCCGCCCTCAGTG TCTGGGGCCCCCAGGG CAGAGGGTCACCATC TCCTGCAC TGGGAGC AGTTCCAAACATCGGG GCAGGTTATGATGTA CACTGGTACCAGGAG TTTCCAGGAACAGCC CCCCAAACTCCTCATC CAAGGTAAACAGCAAT CGGCCCTCAGGGGTC CCTGACCGATTCTCT	GACATCCAGATGACC CAGTCTCCATCCTCC CTGTCTGCATCTGTA GGAGACAGAGTCACC ATCACTTGCCGGGCA AGTCAGAGCATTAAC AACTATTTAAATGG TATCAGGAGAGACCA GGGAAAGCCCCTAAG CTCCTGATCTATGCT GCATCCAGTTTGCAA AGTGGGGTCCCATCA AGGTTCAGTGGCAGT	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCCGGGA GTCTCTGAAGATCTCCTGTAAGACTTCTGAATACAGCTTTACCAGCT ACTGGATCGGCTGGTGCGCAAGATGCCCGGGAAGGCCCTGGAGTGG ATGGGGATCATCTATCTTGGTGACTCAGATACCAGATACAGCCCCGTC CTTCCAAGGCCAGGTCACCATCTCAGCCGACAAAGTCCATCAGTACC CCTACCTGCAGTGGAGCAGCCTGAAGGCCCTCGGACACCCGCCATGTAT TACTGTGCAGAAAGTAAC TGGGCTCTTGACTACTGGGCCAGGGAAC CCTGGTCAACGCTCTAGTGCCCTCCACAAAGGCCCATCGGTCTTCC CCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTG GGCTGCCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTG GAACTCAGGCGCCCTGACCAAGCGGCGTGACACACCTTCCCGGCTGTCC TACAGTCCTCAGGACTCTACTCCCTCAAAAAGCGTGTGACCGTGCCC TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAA
			063_3.2_1g_002_9c8_VH _CH1(S183E).001	NA	
!PS:376838					

		GGCTCCAAGTCTGGC ACCTCAGCCTCCCTG GCCATCACTGGGCTC CAGGCTGAGGATGAG GCTGATTATTACTGC CAGTCCATATGACAGC AGCCTGAGTGGTTCC GTGTTCCGGGAGGG ACCAAGCTGACCGTC CTAGGTCAGCCCAAG GCTGCCCTTCGGTC ACTCTGTTCCCGCCC TCCTCTGAGGAGCTT CAAGCCAAACAAGGC ACACTGGTGTGTCCT ATAAGTGACTTCTAC CCGGGAGCCGTGACA GTGGCCTGGAAGGCA GATAGCAGCCCCGTC AAGCGGGAGTGGAG ACCAACACACCTCC AAACAAAGCAACAAC AAGTACGGGCCCGAG AGCTATCTGAGCCTG ACGCCTGAGCAGTGG AAGTCCCACAGAAGC TACAGCTGCCAGGTC ACGCATGAAGGGAGC ACCGTGAGAAAGACA GTGGCCCCTACAGAA TGTTCA	GGATCTGGGACAGAT TTCACCTCACCATC AGCAGCTGCAACCT GAAGATTTTGCAACT TACTACTGTCAACAG AGTTACAGTACCCCT CGGACGTTCCGGCCAA GGACCAAGCTGGAA ATCAAAACGAACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGTACCGCC TCTGTTGTGTGCTG CTGAATAACTTCTAT CCCAGAGAGCCAAA GTACAGTGGAAGTG GATAACGCCCTCCAA TCGGGTAACTCCCCAG GAGAGTGTACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC AAGAGCACCTGACG CTGAGCAAAAGCAGAC TACGAGAAAACACAAA GTCTACGCCCTGCGAA GTCACCCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	GCCAGCAACCAAGGTGGACAAGAAAGTTGAGCCCCAAATCTTGTG ACAAAACTCACACATGCCCACCCGTGCCCAGCACCTGAACCTCCTGGGG GGACCGTCAGTCTTCCCTCTTCCCCCAAAACCAAGGACACCCCTCAT GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCC ACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGACGGCGTGGAG GTGCATAATGCCAAGACAAAGCCGTGTGAGGAGCAGTACGGCAGCAC GTACCGTTGTGTCAAGCTCCTCACCGTCCCTGCACCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAGCCCTCCCAGCC CCCATCGAGAAAACCATCTCCAAAAGCCAAAAGGCAGCCCCGAGAAACC ACAGGTGTACACCCCTGCCCCCATCCCGGGAGGAGATGACCAAGAAACC AGGTCAGCCTGACCTGCCCTGGTCAAAGGCTTCTATCCCAGGCACATC GCCGTGGAGTGGGAGAGCAATGGGCAGCCCGGAGAAACAACATAAGAC CACGCCCTCCGTGTGTGACTCCGACGGCTCCTTCTTCCCTCTATAGCA AGCTCACCCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAAGAG CCTCTCCCTGTCTCCGGTGGTGGGGATCGGGAGGTGGCGGATCCC AGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGGAG ACCCGTGCCCTCACCTGCACCTGTCTCTGGTGGCTCCATCAGTAGTTA CTTCTGGAGCTGGATTTCGGAAGCCCCCAGGTAAAGGACTGGAGTGGA TTGGCTATATCTATTACAGTGGGCAGACCAATAACAACCCCTCCCTC AAGAGTCGAGTCACCATATCAATAGACACGTCCAAGAACCAAGTTCTC CCTGAAGCTGAGCTCTGTGACCCGTGCGGACACGGCCGTGATTACT GTGCGAGAGAAACTGGGAGCTACTACGGCTTTGACTACTGGGCCAG GGAACCTGGTCACCGTCTCCTCAGCCTCCACCAAGGCCCATCGGT CTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGCACAGCGG CCCTGGGCTGCCGTGGTCAAAGGACTACTTCCCCGAACCGGTGACGGTG TCGTGGAACCTCAGCGCCCTGACCAAGCGCGTGCACACCTTCCCCGC TGTCCTACAGTCCCTCAGGACTCTACTCCCTCGAGAGCGTGTGACCG TGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT CACAAAGCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCCAAATC TTGT
		SEQ ID NO:313	SEQ ID NO:314	SEQ ID NO:315
	AA	QSVLTQPPSVSGAPG QRVTISCTGSSSNI AGYDVHWYQEFPGTA PKLLIQGNSNRPSGV PDRFSGSKSGTSASL	DIQMTQSPSSLSASV GDRVITITCRASQ SYLNWYQERPGKAPK LLIYAASSLQSGVPS RFSGSGSGTDFTLTI	EVQLVQSGAEVKKPGESLKISCKTSEYFTSYWIGWVRKMPGKGLEW MGI IYLGDS DTRYSPSFQGV TISADKSI STAYLQWSSLKASDTAMY YCARSNWGLDYGQGT LVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLKSVVTP SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG

			AITGLQAEDEADYYC QSYDSSLSGSVFGG TKLTVLGQPKAAPSV TLFPPSSEELQANKA TLVCLISDFYPGAVT VAWKADSSPVKAGVE TTTPSKQSNNKYAAE SYLSLTPEQWKSHRS YSCQVTHEGSTVEKT VAPTECS	SSLQPEDFATYYCQ SYSTPRTFGQGTLE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYBREAKVQWKV DNALQSGNSQESVTE QDSKDSYSTSLKSTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RREC	GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGYSTYRCVSLTVLHQDWLNGKEYKCKVSNKALPAP PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTTPVLDSGSEFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGSGSGGSQVQLQESGPGLVKPS TSLTCTVSGGSISSYFSWIRKPPGKLEWIGYIYISGQTKYNPSL KSRVTISIDTSKNQFSLKLSVTAADTAVYYCARETGSYYGFDYWGQ GTLVTVSSASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPTV SWNSGALTSGVHTFPAVLQSSGLYSLESVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSC
			SEQ ID NO:316	SEQ ID NO:317	SEQ ID NO:318
	064_3.2_1gg.002_23B3_VH4_VH_CH1(S183E).001	NA	CAGTCTGTGCTGACG CAGCGCCCTCAGTG TCTGGGCCCCCAGGG CAGAGGGTCACCATC TCCTGCACTGGGAGC AGTTCCAAACATCGGG GCAGGTTATGATGTA CACTGGTACCAGGAG TTTCCAGGAACAGCC CCCAAACCTCCTCATC CAAGGTAACAGCAAT CGGCCCTCAGGGGTC CCTGACCGATTCTCT GGCTCCAAGTCTGGC ACCTCAGCCTCCCCTG GCCATCACTGGGCTC CAGGCTGAGGATGAG GCTGATTATTACTGC CAGTCCATATGACAGC AGCCTGAGTGGTTCC GTGTTCCGGCGGAGGG ACCAAGCTGACCGTC CTAGGTGAGCCCCAAG GCTGCCCCCTCGGTC ACTCTGTTCCCGCCC TCCTCTGAGGAGCTT	GACATCCAGATGACC CAGTCTCCAAGCTCC CTGTCTGCGTCTGTG GGCGATAGGGTCACC ATCACTTGCAGGTCC AGCCAGAGTGTGTTA TACAGCTCCAACAAT AAGAACTACTTAGTT TGGTACCAGGAGAAA CCAGGAAAGGTTCCCT AAACTGCTCATTTAC TGGGCATCTACCCGG GAATCCGGGGTCCCT AGTCGATTCAGTGGC AGCGGCTCTGGGACA GATTTCACTCTCACC ATCAGCAGCCTGCAG CCTGAAGATGTGGCA ACTTATTACTGTGAG CAATATTATAAGACT CCTCTCACTTTCGGC GGAGGACCAAGGTG GAGATCAAACGAACG GTGGCTGCACCATCT GTCTTCATCTTCCCG CCATCTGATGAGCAG	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCCGGGA GTCTCTGAAGATCTCCTGTAAAGACTTCTGAATACAGCTTTACCAGCT ACTGGATCGGCTGGTGGCGCAAGATGCCCGGGAAGGCCCTGGAGTGG ATGGGGATCATCTATCTTGGTGACTCAGATACCAGATACAGCCCCGTC CTTCCAAGGCCAGGTACCATCTCAGCCGACAAAGTCCATCAGTACCG CCTACCTGCAGTGGAGCAGCCTGAAGGCCCTCGGACACCCGCCATGTAT TACTGTGCAGAAAGTAACCTGGGCTTTGACTACTGGGCCAGGGAAC CCTGGTCAACCGTCTTAGTGCTTCCACCAAGGCCCATCGGTCTTCC CCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTG GGCTGCCCTGGTCAAGGACTACTTCCCCGAAACCGGTGACGGTGTCTGTG GAACTCAGGCGCCCTGACCAAGCGGTGCACACCTTCCCCGGCTGTCC TACAGTCCTCAGGACTCTACTCCTCAAAAAGCGTGGTGACCCGTGCC TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAA GCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCAAATCTTGTG ACAAAACTCACACATGCCCACCCGTGCCAGCACCTGAACCTCCTGGGG GGACCGTCAGTCTTCTCTTCCCCCAAAAACCAAGGACACCCCTCAT GATCTCCCGACCCCTGAGGTACATGCGTGGTGGTGACGTGAGCC ACGAAGACCCCTGAGGTCAAAGTTCAACTGTACGTGGACGGCGTGGAG GTGCATAATGCCAAGACAAAGCCGCTGTGAGGAGCAGTACGGCAGCAC GTACCGTTGTGTACGCTCCTCACCGTCTGCACCCAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAGCCCTTCCCAGCC CCCATCGAGAAAACCATCTCCAAGCCAAAAGGCAGCCCCGAGAACC ACAGGTGTACACCCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACC AGGTCAGCCTGACCTGCCCTGGTCAAAGGCTTCTATCCCAGCGACATC GCCGTGGAGTGGGAGAGCAATGGCAGCCGGAGAACAACTACAAGAC CACGCCCTCCCGTGTGTGGACTCCGACGGCTCCTTCTTCTCTATAGCA

		CAAGCCAAACAAGGCC ACACTGGTGTGTCTC ATAAGTGACTTCTAC CCGGAGCCGTGACA GTGGCCTGGAAGGCA GATAGCAGCCCCGTC AAGCGGGAGTGGAG ACCACCACACCCCTCC AAACAAAGCAACAAC AAGTACGGGCCGAG AGCTATCTGAGCCTG ACGCCTGAGCAGTGG AAGTCCACAGAAAGC TACAGCTGCCAGGTC ACGCATGAAGGGAGC ACCGTGAGAAAGACA GTGGCCCCTACAGAA TGTTCA	TTGAAATCTGGTACC GCCTCTGTTGTGTGC CTGCTGAATAACTTC TATCCCAGAGAGGCC AAAGTACAGTGGAAG GTGGATAACGCCCTC CAATCGGGTAACTCC CAGGAGAGTGTACACA GAGCAGGACAGCAAG GACAGCACCTACAGC CTCAAGAGCACCCCTG ACGCTGAGCAAAAGCA GACTACGAGAAACAC AAAGTCTACGCCCTGC GAAAGTCACCCATCAG GGCCTGAGCTCGCCC GTCACAAAGAGCTTC AACAGGGGAGAGTGT	AGTCAACCCTGGACAAGAGCAGAGGTGGCAGAGGGGAACGTCTTCTCA TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAG CCTCTCCCTGTCTCCGGTGGTGGCGATCGGAGGTGGCGATCCC AGGTACAGTTGCAGGAGTCAGGTCCAGGACTGGTGAAGCCCTCGGAG ACCCTCTCACTCACCTGTACCATCTCCGGGACAGGTGTCTCTACCAA CAGTGTGCTTGAACTGGATTAGGAAGCCCCCAGGGAAAGGCCTTG AGTGGATAGGAAGGACATATACTACAGGTCCAAGTGGTATAATGATTAT GCAGTTTCTCTGAAAAGTCGAGTAACCATCAGCCCAGACACATCCAA GAACCAAGTTCTCCCTGAAGCTGAGCTCTGTGACTGCCCGGACACGG CTGTGTATTACTGTGCAAGAGAGGATGGGATAGCTACTACCGCTAC GGTATGAGCGTCTGGGGCCAAAGGACCAAGGTACCGTCTCCTCAGC CTCCACCAAGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGA GCACCTCTGGGGCACAGCGGCCCTGGGCTGCCGTGCTAAGGACTAC TTCCCCGAACCGGTGACGGTGTCTGTGAACTCAGGCGCCCTGACCCAG CGCGTGACACACCTTCCCCGGCTGTCTCTACAGTCTCAGGACTCTACT CCCTCGAGAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAG ACCTACATCTGCAACGTGAATCACAAAGCCCAGCAACACCAAGGTGGA CAAGAAAGTTGAGCCCCAAATCTTGT
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	AA	QSVLTQPPSVSGAPG QRVTISCTGSSSNI AGYDVHWYQEFPGTA PKLLIQGNSNRPSGV PDRFSGSKSGTSASL AITGLQAEDEADYYC QSYDSSLSGSVFGGG TKLTVLGQPKAAPSV TLFPPSSEELQANKA TLVCLISDFYPGAVT VAWKADSSPVKAGVE TTTPSKQSNNKYAAE SYLSLTPEQWKSHRS YSCQVTHEGSTVEKT VAPTECS	DIQMTQSPSSLSASV GDRVITICRSSQSVL YSSNNKNYLVWYQEK PGKVPKLLIYWASTR ESGVPSRFSGSGGT DFTLTISLIQPEDVA TYYCQQYYKTPLTFG GGTKVEIKRTVAAPS VFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGNS QESVTEQDSKDSITYS LKSTLTLSKADYEKH KVYACEVTHQGLSSP VTKSFNRGEC	EVQLVQSGAEVKKPESGSLKISCKTSEYFTSYWIGWVRKMPGKGLEW MGI IYLGDS DTRYSPSFQGV TISADKSI STAYLQWSSLSKASDTAMY YCARSNWGLDYGQGT LVTVSSASTKGPSVFFLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLKSVVTV SSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTI SKAKGPQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGSGSGGSQVQLQESGPGLVKPS TSLTCTISGDSVSTNSVANNWIRKPPGKGLEWIGRTYYRSKWINDY AVSLKSRVTISPDTSKNQFSLKLSVTAADTAAYYCAREDGDSYYRY GMDVWGQGTITVTVSSASTKGPSVFFLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLVESVTVTPSSSLGTQ TYICNVNHKPSNTKVDKKVEPKSC
		SEQ ID NO:322	SEQ ID NO:323	SEQ ID NO:324

1PS: 376846	065_3B3v2_IgG.002_Ada1Imumab_VH_CH1 (S183E) . 001	NA	GAAATTGTGTTGACG CAGTCTCCAGGCACC CTGTCTTTGTCTCCA GGGAAAGAGCCACC CTCTCCTGCAGGGCC AGTCAGAGTGTTAGA AGCAGTTACTTAGCC TGGTACCAGGAGAAA CCTGGCCAGGCTCCC AGGCTCCTCATCTAT GGTGCAATCCAGCAGG GCCACTGGCATCCCA GACAGGTTCAGTGGC AGTGGGTCTGGGACA GACTTCACCTCTCACC ATCAGCAGACTGGAG CCTGAAGATTTTGCA GTGTATTACTGTCTAG CAGTATGGTAGCTCA CCTACCTTCGGCCAA GGGACACGACTGGAG ATTAAACGAACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGTACCGCC TCTGTTGTGTGCCCTG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCCAG GAGAGTGTACACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC GAGAGCACCCCTGACG CTGAGCAAAAGCAGAC	GATATCCAAATGACA CAATCACCATCGTCG CTTTCAGCGTCTGTT GGCGACCGTGTGACG ATTACCTGTCGCGG TCCCAGGGAATCCGG AATTACCTCGCATGG TATCAGGAGAAAACC GGAATAAGCACCGAAG CTCCTGATCTATGCC GCCTCGACTCTTCAG AGTGGTGTGCCGTCG AGGTTTAGCGGGTCC GGTTCAGGTACGGAC TTTACTCTACAATT TCCAGCCTGCAGCCC GAAGATGTAGCTACC TATTACTGCCAGAGA TACAACCGAGCGCCT TACACATTCGGACAA GGGACAAAAGTCGAG ATCAAGCGTACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGAAC TGCC TCTGTTGTGTGCCTG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCCAG GAGAGTGTACACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC AAGAGCACCCCTGACG CTGAGCAAAAGCAGAC	CAGGTGCAGTTACAGCAGTCGGGGCGCAGGACTGTTGAAGCCTTCGGA GACCCGTGTCCTCACCTCGCGCTGTCCAATGGTGGTCCCTTCAGTGGTT ACTACTGGAAC TGGATCCGCAAGCCACACAGGGAAGGGCTAGAGTGG ATTGGGGAAATCAATCATGTCTGGAACACCAACTACAACCCGTCCTT CAAGAGTCGAGTCACCATATCATATTAGACACGTCCAAGAACCAGTTCT CCCTGACGCTGACCTCTGTGACCGCGCGGACACGGCTGTGTATTAC TGTGCGAGAGGATATTGTAGAAAGTACCACCTGCTACTTTGACTACTG GGCCAGGGAACCTTAGTCAACCGTCTCCTCAGCCTCCACCAAGGGCC CATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGC ACAGCGGCCCTGGGCTGCCGTGGTCAAGGACTACTTCCCCGAACCGGT GACGGTGTGTTGGAAC TCAAGGCGCCTGACCAGCGGCGTGCACACCT TCCCCGCTGTCTACAGTCCCTCAGGACTCTACTCCTCAAAAAGCGTG GTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAA CGTGAATCACAAGCCCCAGCAACACCAAGGTGGACAAAGAAAGTTGAGC CCAAATCTTGTGACAAAAC TCAACATGCCACCGTGCCCGACGACCT GAACTCCTGGGGACCGTCAGTCTTCTCTTCCCCCCCCAAAACCCAA GGACACCCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGG TGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTG GACGGCGTGGAGTGCAATAATGCCAAGACAAAGCCCGTGTGAGGAGCA GTACGGCAGCACGTACC GTTGTGTGTCAGCGTCCCTCACCGTCCCTGCACC AGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGTCTCCAACAAA GCCCTCCCAGCCCCCATCGAGAAAAACCATCTCCAAGCCAAAGGGCA GCCCCGAGAACCACAGGTGTACACCCCTGCCCCCATCCCGGAGGAGA TGACCAAGAAACCAGGT CAGCCTGACCTGCCCTGGTCAAAGGCTTCTAT CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAA CAACTACAAGACCA CGCCTCCCGTGTGCTGGACTCCGACGGCTCCTTCT TCCTCTATAGCAAAGCTCACCGTGGACAAGACAGGTTGGCAGCAGGGG AACGTC TTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTA CACGCAGAAGAGCCTCTCCCTGTCTCCGGGTGGTGGCGGATCGGGAG GTGGCGGATCCGAGGTACAAC TGGTGAATCAGGTGGAAGTTTGGTG CAGCCGGGAGATCGCTCAGGCTTAGCTGTGCGGCATCGGGGTTTAC TTTTCGATGATTATCGGATGCATTTGGGTCCGGAAGCGCCTGGAAAAAG GGCTCGAGTGGGTTTCCGCCATTACGTGGAATAGCGGACACATCGAT TATGCAGACAGTGTGGAGGGCAGATTCACAATCTCACGAGACAAATGC TAAGAACAAGCCTGTACCTTCAGATGAAC TCACTCCTACTTGTCTACAGCTTCG CCGCCGTATACTACTGCGCCAAAAGTCTCCTACTTGTCTACAGCTTCG TCGCTCGACTATTGGGGTCAAGGAACGTTGGTCACCGTCCTCTAGTGC
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			TACGAGAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	TACGAGAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	CTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGA GCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCGTCAAGGACTAC TTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGGCGCCCTGACCCAG CGGCGTGACACACCTTCCCCGGCTGTCTACAGTCTCAGGACTCTACT CCCTCGAGAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAG ACCTACATCTGCAACGTTGAATCACAAAGCCCAGCAACACCAAGGTGGA CAAGAAAGTTGAGCCCCAAATCTTGT
			SEQ ID NO:325	SEQ ID NO:326	SEQ ID NO:327
	AA		EIVLTQSPGTLISLSP GERATLSCRASQSVR SSYLAWYQEKPGQAP RLLIYGASSRATGIP DRFSGSGTDFTLT ISRLEPEDFAVYYCQ QYGSPTFGQGTRLE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLESTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEN	DIQMTQSPSSLSASV GDRVITITCRASQGIR NYLAWYQEKPGKAPK LLIYAASTLQSGVPS RFSGSGTDFTLTI SSLQPEDVATYYCQR YNRAPYTFGQGTKVE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLKSTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEN	QVQLQSGAGLLKPSSETLSLTCAVHGGSFSGYYWNWIRKPPGKLEW IGEINHAGNTNYP SLKSRVTI SLDTSKNQFSLT LTSVTAADTAVYY CARGYCRSTTCYFDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSKSV VTVPSSSLGTQTY ICNVN HKPNTKVDKKVEPKSCDKTHTCPPCPAP ELLGPGSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTTPV L DSDGSFFLYSKLTVDKSRWQQG NVFSCSVMH EALHNHYTQKSLSLSPGGSGGGSEVQLVESGGGLV QPGRSLRLSCAASGFTFDDYAMHWVRKAPGKGLEWVSAITWNSGHID YADSV EGRFTI SRD NAKNSLYLQMNSLRAEDTAVYYCAKVSYLSTAS SLDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGTAAIGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLESVTVTPSSSLGTQ TYICNVN HKPNTKVDKKVEPKSC
			SEQ ID NO:328	SEQ ID NO:329	SEQ ID NO:330
	NA	066_3B3v2_1gG.002_3.2_1PS:376850 _VH_CH1(S183E).001_	GAAATTGTGTTGACG CAGTCTCCAGGCACC CTGTCTTTGTCTCCA GGGAAAGAGCCACC CTCTCCTGCAGGGCC AGTCAGAGTGTTAGA AGCAGTTACTTAGCC TGGTACCAGGAGAAA CCTGGCCAGGCTCCC AGGCTCCTCATCTAT GGTGATCCAGCAGG GCCACTGGCATCCCA GACAGGTTCAGTGCC	CAGTCTGTGCTGACG CAGCCGCCCTCAGTG TCTGGGCCCCCAGGG CAGAGGGTCACCATC TCCTGCACTGGGAGC AGTTCCAAACATCGGG GCAGGTTATGATGTA CACTGGTACCAGGAG TTTCCAGGAACAGCC CCCAAAC TCCTCATC CAAGGTAACAGCAAT CGGCCCTCAGGGGTC CCTGACCCGATTCTCT	CAGGTGCAGTTACAGCAGTCGGGGCGCAGGACTGTTGAAGCCTTCGGA GACCCGTCTCCCTCACCTGCGCTGTCCATGGTGGTCCCTTCAGTGGTT ACTACTGGAACTGGATCCGCAAGCCACAGGGAAGGGCTAGAGTGG ATTGGGGAAATCAATCATGTCTGGAACACCAACTACAACCCGTC CCT CAAGAGTCGAGTCACCATATCATTAGACACGTCCAAGAACAGTTCT CCCTGACGCTGACCTCTGTGACCGCCGCGGACACGGCTGTGTATTAC TGTGCGAGAGGATATTGTAGAAGTACCACCTGCTACTTTGACTACTG GGCCAGGGAAACCTAGTCACCGTCTCTCCTCAGCCTCCACCAAGGGCC CATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGC ACAGCGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCGAACCCGGT GACGGTGTCTGTGGAAC T CAGGGGCCCTGACCAGCGGCGTGCACACCT TCCCGGCTGTCTACAGTCTCTCAGGACTCTACTCCCTCAAAAGCGTG GTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAA

		AGTGGGTCTGGGACA GACTTCACTCTCACC ATCAGCAGACTGGAG CCTGAAGATTTTGCA GTGTATTACTGTGTCAG CAGTATGGTAGCTCA CCTACCTTCGGCCAA GGGACACGACTGGAG ATTAAACGAACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGTACCGCC TCTGTTGTGTGCCTG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCCAG GAGAGTGTACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC GAGAGCACCCCTGACG CTGAGCAAAAGCAGAC TACGAGAAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	GGCTCCAAGTCTGGC ACCTCAGCCTCCCCTG GCCATCACTGGGCTC CAGGCTGAGGATGAG GCTGATTATTACTGC CAGTCCCTATGACAGC AGCCTGAGTGGTTCG GTGTTGCGCGGAGGG ACCAAGCTGACCCGTC CTAGGTGAGCCCAAG GCTGCCCCCTCGGTC ACTCTGTTCCCGCCC TCCCTCTGAGGAGCTT CAAGCCAAACAAGGCC ACACTGGTGTGTCCTC ATAAGTGACTTCTAC CCGGGAGCCGTGACA GTGGCCTGGAAGGCA GATAGCAGCCCCGTC AAGCGGGAGTGGAG ACCACCAACCCCTCC AAACAAAAGCAACAAC AAGTACGCGGCCAAG AGCTATCTGAGCCTG ACGCCTGAGCAGTGG AAGTCCCACAGAAGC TACAGCTGCCAGGTC ACGCATGAAGGGAGC ACCGTGGAGAAGACA GTGGCCCTTACAGAA TGTTCA	CGTGAAATCACAAGCCAGCAACACCAAGGTGGACAAGAAAGTTGAGC CCAAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCCAGCACCT GAACTCCTGGGGACCGTCAGTCTTCTCTTCCCCC AAAACCCAA GGACACCTCATGATCTCCCGGACCCCTGAGGTCACATGCCGTGGTGG TGGAACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTG GACGGCTGGAGGTGCATAATGCCAAGACAAAGCCGTGTGAGGAGCA GTACGGCAGCACGTACCGTTGTGTGTCAGCGTCCTCACCGTCCCTGCACC AGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAA GCCCTCCCAGCCCCCATCGAGAAAAACCATCTCCAAGCCAAAGGGCA GCCCCGAGAACCACAGGTGTACACCCCTGCCCCCATCCCGGGAGGAGA TGACCAAGAAACAGGTGAGCCTGACCTGCCCTGGTCAAAAGCTTCTAT CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAA CAACTACAAGACCAACGCCCTCCCGTGTGCTGGACTCCGACGCTCCTTCT TCCTCTATAGCAAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG AACGTCTTCTCATGCTCCGTGATGTCATGAGGCTCTGCACAACCACTA CACGCAAGAGCCCTCTCCCTGTCTCCGGTGTGCGGATCGGGAG GTGGCGGATCCGAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAA AAGCCCGGGAGTCTCTGAAGATCTCCTGTAAGACTTCTGAATACAG CTTTACCAGCTACTGGATCGGCTGGTGCGCAAGATGCCCGGGAAG GCCTGAGTGGATGGGATCATCTATCTTGGTGACTCAGATACCAGA TACAGCCCGTCTTCCAAGGCCAGGTCAACATCTCAGCCGACAAGTC CATCAGTACCGCCTACCTGCAGTGGAGCAGCCTGAAGGCCCTCGGACA CCGCCATGTATTACTGTGCGAGAAGTAAGTGGGTCTTGACTACTGG GGCCAGGGAACCTGGTCACCGTCTCTAGTGCTTCCACCAAGGCCCC ATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGCA CAGCGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCCGAACCCGTG ACGGTGTCTGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGCACACCTT CCCGCTGTCCCTACAGTCCCTCAGGACTCTACTCCCTCGAGAGCGTGG TGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAAC GTGAATCACAAGCCCGACCAACACCAAGGTGGACAAGAAAGTTGAGCC CAAATCTTGT
		SEQ ID NO: 331	SEQ ID NO: 332	SEQ ID NO: 333
	AA	EIVLTQSPGTLISLP GERATLSCRASQSVR SSYLAWYQEKPGQAP RLLIYGASSRATGIP DRFSGSGSGTDFTLT	QSVLTQPPSVSGAPG QRVTISCTGSSSNIG AGYDVHWYQEFPGTA PKLLIQNSNRPSGV PDRFSGSKSGTSASL	QVQLQSGAGLLKPSSETLSLTCAVHGGSFSGYYWNWIRKPPGKLEW IGEINHAGNTNYPNPSLKSRTVTSIDTSKNQFSLTTLTSVTAADTAVYY CARGYCRSTTCYFDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLKSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTHTCPPAP

			ISRLEPEDFAVYYCQ QYGSSTFFGQTRLE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLESTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEN	AITGLQAEDEADYYC QSYDSSLSGSVFGGG TKLTVLGQPKAAPSV TLFPPSSEELQANKA TLVCLISDFYPGAVT VAWKADSSPVKAGVE TTTPSKQSNNKYAAK SYLSLTPEQWKSHRS YSCQVTHEGSTVEKT VAPTECS	ELGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTTPVLDSGSEFFLYSKLTVDKSRWQQG NVFSCSVMEALHNHYTQKSLSLSPGGGGGGSEVQLVQSGAEVK KPGESLKISCKTSEYSFYSYWIWVRKMPGKGLEWMGIYYLGDSDTR YSPSFQGGVTISADKSIISTAYLQWSSSLKASDTAMYYCARSNWGLDYW GQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSQVHTFPAVLQSSGLYSLESVVTVFPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSC
			SEQ ID NO: 334	SEQ ID NO: 335	SEQ ID NO: 336
	067_9c8_1Ig.002_Ada1Imumab_VH_CH1 (S183E) . 001	NA	GACATCCAGATGACC CAGTCTCCATCCTCC CTGTCTGCATCTGTA GGAGACAGAGTCACC ATCACTTGCCGGCA AGTCAGAGCATTAAAC AACTATTAAATTGG TATCAGGAGAGACCA GGGAAAAGCCCCTAAG CTCCTGATCTATGCT GCATCCAGTTTGCAA AGTGGGTCCCATCA AGGTTCAGTGGCAGT GGATCTGGGACAGAT TTCACTCTCACCATC AGCAGCTGCAACCT GAAGATTTTGCAACT TACTACTGTCAACAG AGTTACAGTACCCCT CGGACGTTCGGCCAA GGGACCAAGCTGGAA ATCAAAACGAACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGTACCGCC	GATATCCAAATGACA CAATCACCATCGTCG CTTTCAGCGTCTGTT GGCGACCGTGTGACG ATTACCTGTCGCGG TCCCAGGGAATCCGG AATTACCTCGCATGG TATCAGGAGAAAACC GGAAAAGCACCGAAG CTCCTGATCTATGCC GCCTCGACTCTTCAG AGTGGTGTGCCGTCG AGGTTTAGCGGGTCC GGGTCAGGTACGGAC TTTACTCTCACAATT TCCAGCCTGCAGCCC GAAGATGTAGCTACC TATTACTGCCAGAGA TACAACCGAGCGCCT TACACATTCCGACAA GGGACAAAAGTCGAG ATCAAGCGTACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGAACTGCC	CAGGTGCAGCTGCAGGAGTCGGGGCCCAGGACTGGTGAAGCCTTCGGA GACCCGTGCCCTCACCTGCACGTGCTCTGTGTGGCTCCATCAGTAGTT ACTTCTGGAGCTGATCCGGAAAGCCCCAGGTAAGGACTGGAGTGG ATTGGCTATATCTATTACAGTGGCAGACCAAAATACAACCCCTCCCT CAAGAGTCAGTCAACCATATCAATAGACACGTCCAAGAACCAAGTTCT CCCTGAAGCTGAGCTCTGTGACCGCTGCGGACACGCGCGTGATTAC TGTCGAGAGAAACTGGGAGCTACTACGGCTTTGACTACTGGGCCA GGGAAACCTGGTCACCGTCTCCTCAGCCTCCACCAAGGCCCATCGG TCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG GCCCTGGGTGCCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGT GTCGTGGAACCTCAGGCGCCCTGACCAGCGCGGTGCACACCTTCCCCG CTGTCTACAGTCTCTCAGGACTCTACTCCTCAAAAGCGTGGTGACC GTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAA TCACAAGCCCCAGCAACACCAAGGTGGACAAGAAAAGTTGAGCCCCAAAT CTTGTGACAAAACCTCACACATGCCACCCGTGCCAGCACCTGAACCTC CTGGGGGACCGTCAGTCTTCTCTTCCCCCCCCAAACCCAAAGGACAC CCTCATGATCTCCCGACCCCTGAGGTCACATGCGTGGTGGTGACG TGAGCCACGAAACCCCTGAGGTCAAGTTCAACTGCTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGTGAGGAGCAGTACGG CAGCACGTACCGTTGTGTACGCGTCCTCACCGTCCCTGCACCAAGACT GGCTGAATGGCAAGGAGTACAAAGTGCAAGGTCTCCAAACAAAGCCCTC CCAGCCCCCATCGAGAAAACCATCTCCAAAAGCCAAAGGCGAGCCCCG AGAACACAGGTGTACACCCCTGCCCCCATCCCGGGAGGAGATGACCA AGAACCCAGGTCAGCCTGACCTGCCCTGGTCAAAGGCTTCTATCCCAGC GACATCGCCGTGGAGTGGGAGAGCAATGGCAGCCCGGAGAACAACTA CAAGACCAACGCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTCT

		TCTGTTGTGTGCCTG CTGAATAACTTCTAT CCCAGAGGCCAAA GTACAGTGGAAGTG GATAACGCCCTCCAA TCGGGTAACTCCCAG GAGAGTGCACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC GAGAGCACCTGACG CTGAGCAAAAGCAGAC TACGAGAAAACAAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	TCTGTTGTGTGCCTG CTGAATAACTTCTAT CCCAGAGGCCAAA GTACAGTGGAAGTG GATAACGCCCTCCAA TCGGGTAACTCCCAG GAGAGTGCACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC AAGAGCACCTGACG CTGAGCAAAAGCAGAC TACGAGAAAACAAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	ATAGCAAGCTCACCGTGGACAAAGAGCAGGTTGGCAGCAGGGGAAACGTC TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAACCACCTACACGCA GAAAGACCTCTCCCTGTCTCCGGTGGTGGCGGATCGGAGGTGGCG GATCCGAGGTACAACTGGTGGAATCAGGTGGAGGTTTGGTGCAGCCG GGGAGATCGCTCAGGCTTAGCTGTGCGGCATCGGGGTTTACTTTCGA TGATTATGCGATGCATTGGGTCCGGAAGCGCCTGGAAGGGCTCG AGTGGGTTTCCGCCATTACGTGGAATAGCGGACACATCGATTATGCA GACAGTGTGAGGGCAGATTCACAATCTCACGAGACAAATGCTAAGAA CAGCCTGTACCTTCAGATGAATCACTTCGCGCGGAAGATACCGCCG TATACTACTGCGCCAAAAGTCTCCTACTTGTCTACAGCTTCGTCGCTC GACTATTGGGGTCAAGGAAACGTTGGTCACCGTCTCTAGTGCCCTCCAC CAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCT CTGGGGCACAGCGGCCCTGGGCTGCCGTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCTGTGGAACCTCAGGGGCCCTGACCAGCGCGT GCACACCTTCCCGCTGTCTACAGTCTCAGGACTCTACTCCCTCG AGAGCGTGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAAGCCCGACCAACACCAAGGTGGACAAGAA AGTTGAGCCCAAATCTTGT
		SEQ ID NO:337	SEQ ID NO:338	SEQ ID NO:339
AA		DIQMTQSPSSLSASV GDRVITTCRASQIN NYLNWYQERP GKAPK LLIYAASSLQSGVPS RFSGSGGTDFTLTI SSLQPEDFATYYCQQ SYSTPRTFGQGTKLE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLESTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEN	DIQMTQSPSSLSASV GDRVITTCRASQIR NYLAWYQEKP GKAPK LLIYAASTLQSGVPS RFSGSGGTDFTLTI SSLQPEDVATYYCQR YNRAPYTFGQGTKVE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLKSTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEN	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYFWSWIRKPPGKGLEW IGYIYSGQTKYNPSLKSRTVISIDTSKNQFSLKLSVTAADTAVYY CARETGSYYGFDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLKSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHREALHNHYTQKSLSLSPGSGGGGGSEVQLVESGGGLVQP GRSLRLSCAASGFTFDDYAMHWVRKAPKGLEWVSAITWNSGHIDYA DSVEGRFTISRDNAKNSLYLQMNSLRAEDTAVYCAKVSYLESTASSL DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLVESVVTVPSSSLGTQTY ICNVNHKPSNTKVDKKVEPKSC
		SEQ ID NO:340	SEQ ID NO:341	SEQ ID NO:342

			GACATCCAGATGACC CAGTCTCCATCCTCC CTGTCTGCATCTGTA GGAGACAGAGTCACC ATCACTTGCCGGCA AGTCAGAGCATTAAC AACTATTTAAATTGG TATCAGGAGAGACCA GGGAAAGCCCCTAAG CTCCTGATCTATGCT GCATCCAGTTTGCAA AGTGGGTCCCCATCA AGGTTCAGTGGCAGT GGATCTGGGACAGAT TTCACCTCACCATC AGCAGTCTGCAACCT GAAGATTTTGCAACT TACTACTGTCAACAG AGTTACAGTACCCCT CGGACGTTCGGCCAA GGGACCAAGCTGGAA ATCAAAACGAACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGTACCGCC TCTGTTGTGTGCCCTG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCCCAG GAGAGTGTACACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC GAGAGCACCCCTGACG CTGAGCAAAAGCAGAC	068_9C8_IgG.002_3.2_VH_CH1(S183E).001	NA	CAGTCTGTGCTGACG CAGCCGCCCTCAGTG TCTGGGCCCCAGGG CAGAGGGTCACCATC TCCTGCACTGGGAGC AGTTCCAACATCGGG GCAGGTTATGATGTA CACTGGTACCAGGAG TTTCCAGGAACAGCC CCCAAACTCCTCATC CAAGGTAACAGCAAT CGGCCCTCAGGGGTC CCTGACCGATTCTCT GGCTCCAAGTCTGGC ACCTCAGCCTCCCTG GCCATCACTGGGCTC CAGGCTGAGGATGAG GCTGATTATTACTGC CAGTCCCTATGACAGC AGCCTGAGTGGTTCG GTGTTCGCGGAGGG ACCAAGCTGACCGTC CTAGGTCAGCCCCAAG GCTGCCCCCTCGGTC ACTCTGTTCCCGCCC TCCTCTGAGGAGCTT CAAGCCAAACAAGGCC ACACTGGTGTGTC ATAAGTGACTTCTAC CCGGGAGCCGTGACA GTGGCCTGGAAGGCA GATAGCAGCCCCGTC AAGCGGAGTGGAG ACCACCAACCCCTCC AAACAAAAGCAACAAC AAGTACGCGGCCAAG AGCTATCTGAGCCTG	CAGGTGCAGCTGCAGGAGTCGGGCCCCAGGACTGGTGAAAGCCTTCGGA GACCCCTGTCCCTCACCTGCACCTGTCTCTGTGTGGCTCCATCAGTAGTT ACTTCTGGAGCTGGATCCGGAAAGCCCCCAGGTAAGGACTGGAGTGG ATTGGCTATATCTATTACAGTGGGCAGACCAAAATACAACCCCTCCCT CAAGAGTCGAGTCACCATATCAATAGACACGTCCAAGAACACAGTTCT CCCTGAAGCTGAGCTCTGTGACCGCTGCGGACACGGCCGTGTATTAC TGTGCGAGAGAAACTGGGAGCTACTACGGCTTTGACTACTGGGGCCA GGGAACCCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGCCCATCGG TCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGTGGGGCACAGCG GCCCTGGGCTGCCGTGTCAGGACTACTTCCCCGAACCGGTGACGGT GTCGTGGAACTCAGGGCCCTGACCAGCGGCGTGCACACCTTCCCGG CTGTCCCTACAGTCCCTCAGGACTCTACTCCCTCAAAAGCGTGTGACC GTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAA TCACAAGCCCCAGCAACACCAAGGTGGACAAAGAAAGTTGAGCCCCAAAT CTTGTGACAAAACTCACACATGCCACCGTGCCCGACGACCTGAACCTC CTGGGGGACCGTCAGTCTTCTCTCTTCCCCCAAAACCCAAAGGACAC CCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGACG TGAGCCACGAAGACCCCTGAGGTCAAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAATGCCAAGACAAAGCCGTGTGAGGAGCAGTACGG CAGCACGTACCCTGTGTGTCAGCGTCTCACCGTCTGACCCAGGACT GGCTGAATGGCAAGGAGTACAAAGTGCAAGTCTCCAACAAAGCCCTC CCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCG AGAACACAGGTGTACACCCCTGCCCCATCCGGGAGGAGATGACCA AGAACCCAGTCAAGCTGACCTGCCCTGGTCAAAGGCTTCTATCCCAGC GACATCGCCGTGGAGTGGAGAGCAATGGGCAGCCGGAGAACAACATA CAAGACCAAGCCTCCCGTGTGACTCCGACGGCTCCTTCTTCTCTCT ATAGCAAGCTCACCGTGGACAAGACAGCAGGTGGCAGCAGGGAAACGTC TTCTCATGTCCGTGATGCATGAGGCTCTGCACAAACCACTACACGCA GAAAGCCCTCTCCCTGTCTCCGGGTGGTGGCGGATCGGGAGGTGGCG GATCCGAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCC GGGAGTCTCTGAAGATCTCCTGTAAAGACTTCTGAATACAGCTTTAC CAGCTACTGGATCGGCTGGGTGCGCAAGATGCCCGGGAAGGCCCTGG AGTGGATGGGATCATCTATCTTGGTGACTCAGATACCAGATACAGC CCGTCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAAGTCCATCAG TACCGCCTACCTGCAGTGGAGCAGCCTGAAGGCCCTCGGACACCGCCA TGTATTACTGTGCGAGAAAGTAACTGGGCTCTTGACTACTGCGGCCAG GGAACCCCTGGTCACCGTCTCTAGTGCCCTCCACCAAGGGCCCATCGGT
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		TACGAGAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	ACGCCTGAGCAGTGG AAGTCCCACAGAAGC TACAGCTGCCAGGTC ACGCATGAAGGGAGC ACCGTGAGAGAACAA GTGGCCCCCTACAGAA TGTTCA	CTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG CCCTGGGCTGCCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTG TCGTGAACTCAGCGCCCTGACCAAGCGGCTGCACACCTTCCCCGGC TGTCCTACAGTCCCTCAGGACTCTACTCCCTCGAGAGCGTGTGTGACCG TGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT CACAAAGCCAGCAACACCAAGGTGGACAAAGAAAGTTGAGCCCCAAATC TTGT
		SEQ ID NO: 343	SEQ ID NO: 344	SEQ ID NO: 345
AA		DIQMTQSPSSLSASV GDRVITITCRASQIN NYLNWYQERPGKAPK LLIYAASSLQSGVPS RFGSGSGTDFTLTI SSLQPEDFATYYCQQ SYSTPRTFGQGTKLE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLESTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGE	QSVLTQPPSVSGAPG QRVTISCTGSSSNIG AGYDVHWYQEFPGTA PKLLIQNSNRPSGV PDRFSGSKGTSASL AITGLQAEDEADYYC QSYDSSLSGSVFGGG TKLTVLGQPKAAPSV TLFPPSSEELQANKA TLVCLISDFYPGAVT VAWKADSSPVKAGVE TTTTPSKQSNNKYAAK SYLSLTPEQWKSHRS YSCQVTHEGSTVEKT VAPTECS	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYFWSWIRKPPGKGLEW IGYIYYSGQTKYNP SLKSRVTISIDTSKNQFSLKLSVTAADTAVYY CARETGSYYGFDYWGQGLVTVSSASTKGPSVFPLAPSSKSTSGGTA ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLKSVVT VPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDNLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMEALHNHYTQKSLSLSPGSGSGGGSEVQLVQSGAEVKKP GESLKISCKTSEYSFYSYWIGWVRKMPGKGLEWMGIIYLGDSDTSYS PSFQGQVTISADKSI STAYLQWSSLKASDTAMYCARSNWGLDYWGQ GTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV SWNSGALTSGVHTFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVN HKPSNTKVDKKVEPKSC
		SEQ ID NO: 346	SEQ ID NO: 347	SEQ ID NO: 348
		GACATCCAGATGACC CAGTCTCCAAGCTCC CTGTCTGCGTCTGTG GGCGATAGGGTCACC ATCACTTGCAGGTCC AGCCAGAGTGTGTTA TACAGCTCCAACAAT AAGAACTACTTAGTT TGGTACCAGGAGAAA CCAGGAAAGGTTCCCT AAACTGCTCATTAC TGGGCATCTACCCGG GAATCCGGGGTCCCT	GATATCCAAATGACA CAATCACCATCGTCG CTTTCAGCGTCTGTT GGCGACCGTGTGACG ATTACCTGTCGCGCG TCCCAGGGAATCCGG AATTACCTCGCATGG TATCAGGAGAAAACCC GGAATAAGCACCGAAG CTCCTGATCTATGCC GCCTCGACTCTTCAG AGTGGTGTGCCGTCG AGGTTTAGCGGGTCC	CAGGTACAGTTGCAGGAGTCAGGTCCAGGACTGGTGAAAGCCCTCGGA GACCCCTCACTACCTGTACCATCTCCGGGGACAGTGTCTCTACCA ACAGTGTGCTTGAACTGGATCAGGAAGCCCCCAGGAAAGGCCCTT GAGTGGATAGGAAGGACATACACAGGTCCAAGTGGTATAATGATTA TGCAGTTTCTGTGAAAAGTCGAGTAACCATCAGCCAGACACATCCA AGAACCCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGCCCGGACACG GCTGTGTAATTA CTGTGCAAGAGAGAGATGGGGATAGCTACTACCGCTA CGGTA TGGA CGTCTGGGGCCAAAGGACACAGGTACCCGTCCTCCTCAG CCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAG AGCACCTCTGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCTGTGGAAC TCAGGCGCCCTGACCA GCGGCGTGCAACACCTTCCCGGCTGTCTCTACAGTCCCTCAGGACTCTAC TCCCTCAAAAGCGTGGTGACCCGTGCCCTCCAGCAGCTTGGGCACCCA
		069_23B3_VH4_IgG.002_A dal ¹ Imuab ¹ _VH ¹ _CH1(S183E)).001	NA	

		AGTCGATTTCAGTGGC AGCGGGTCTGGGACA GATTTCACTCTCACC ATCAGCAGCCTGCAG CCTGAAGATGTGGCA ACTTATTACTGTCTAG CAATATTATAAGACT CCTCTCACTTTCGGC GGAGGGACCAAGGTG GAGATCAAAACGAACG GTGGCTGCACCATCT GTC TTCATCTTCCCG CCATCTGATGAGCAG TTGAAAATCTGGTACC GCCTCTGTTGTGTGC CTGCTGAATAACTTC TATCCCAGAGAGGCC AAAGTACAGTGGGAAG GTGGATAACGCCCTC CAATCGGGTAACCTC CAGGAGAGTGTCAACA GAGCAGGACAGCAAG GACAGCACCTACAGC CTCGAGAGCACCCCTG ACGCTGAGCAAAAGCA GACTACGAGAAAACAC AAAGTCTACGCCCTGC GAAGTCACCCATCAG GGCCTGAGCTCGCCC GTCACAAAAGAGCTTC AACAGGGGAGAGTGT	GGGTCAGGTACGGAC TTTACTCTCACAAATT TCCAGCCTGCAGCCC GAAGATGTAGCTACC TATTACTGCCAGAGA TACAACCGAGCGCCT TACACATTTCGGACAA GGACAAAAGTCGAG ATCAAGCGTACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGAAC TGCC TCTGTTGTGTGCC TG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGAAGGTG GATAACGCCCTCCAA TCGGGTAAC TCCCGAG GAGAGTGTACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC AAGAGCACCTTGACG CTGAGCAAAAGCAGAC TACGAGAAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAAGAGCTTCAAC AGGGGAGAGTGT	GACCTACATCTGCAACGTGAATCACAAAGCCCAGCAACACCAAGGTGG ACAAGAAAAGTTGAGCCCCAAAATCTTTGTGACAAAAACTCACACATGCCCCA CCGTGCCAGCACCTGAAC TCTCGGGGACCGTCA GTCTTCCCTCTT CCCCCAAACCAAGGACACCCCTCATGATCTCCCCGACCCCTGAGG TCACATGCGTGGTGGTGACGTGAGCCACGAAGACCC TGAGGTCAAG TTCAA CTGTTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAA GCCGTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTGT CAGCGTCC TCACCGTCTGTCA CCAGGACTGGCTGAATGGCAAGGAGTACAAAGTGC AAGGTCTCCAAACAAAGCCCTCC CAGCCCCCATCGAGAAAACCATCTC CAAAGCCAAAGGCGAGCCCCCGAGAACCA CACAGGTGTACACCCCTGCCCC CATCCCGGAGGAGATGACCAAAGAACCAAGT CAGCTGACCTGACCTGCCTG GTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAA TGGCAGCCGGAGAACAACTACAAGAC CACGCCCTCCCGTGTGGACT CCGACGGCTCCTTCTTCTCTCTATAGCAAGCTCACCCGTGGACAAAGAGC AGGTGGCAGCAGGGGAACGTCTTCTCATGTCTCCGTGATGCATGAGGC TCTGCACAA CCACTACACGCAAGAGACCTCTCCCTGTCTCCGGGTG GTGGCGGATCGGGAGGTGGCGGATCCGAGGTACAACTGGTGGAATCA GGTGGAGGTTTGGTGACGCCGGGAGATCGCTCAGGCTTAGCTGTGC GGCATCGGGGTTTACTTTTCGATGATTATGCGATGCATTGGGTCCGGA AAGCGCCTGAAAAGGGCTCGAGTGGGTTTCCGCCATTACGTGGAAT AGCGGACACATCGATTATG CAGACAGTGTGGAGGCGAGATTCACAAT CTCACGAGACAAATGCTAAGAAACAGCCTGTACCTTCAGATGAAC TCAC TTCGCGCGGAAGATACCGCCGTATACTACTGCGCCAAAAGTCTCCTAC TTGTCTACAGCTTCGTGCTCGACTATTGGGGTCAAGGAACGTTGGT CACCGTCTCTAGTGCC TCCACCAAGGCCCATCGGTC TTTCCCCCTGG CACCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGC CTGGTCAAAGGACTACTTCCCCGAA CCGGTGACGGTGTCTGTGGAAC TC AGCGCCCTGACCA CGCGCGTGCACACCTTCCCGCTGTCTCTACAGT CCTCAGGACTCTACTCCCTCGAGAGCGTGGTGACCCGTGCCCTCCAGC AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCCAG CAACACCAAGGTGGACAAAGAAAGTTGAGCCCCAAAATCTTGT
		SEQ ID NO: 349	SEQ ID NO: 350	SEQ ID NO: 351
AA	DIQMTQSPSSLSASV GDRVITTCRSSQSVL YSSNNKNYLVWYQEK PGKVPKLLIYWASTR ESGVPSRFSGSGSGT	DIQMTQSPSSLSASV GDRVITTCRASQGIR NYLAWYQEKPGKAPK LLIYAASTLQSGVPS RFSGSGSGTDFTLTI	QVQLQESGPGLVKPSETLSLTCTISGDSVSTNSVAWNWIRKPPGKGL EWIGRTYYRSKWINDYAVSLKSRVTISPDTSKNQFSLKLSVTAADT AVYYCAREDGDSYYRYGMDVWGQGT TTVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLY SLKSVVTVPPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKSCDKHTHTCP	

			DFTLTISLQPEDVA TYYCQQYYKTPLTFG GGTKVEIKRTVAAPS VFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGNS QESVTEQDSKDSSTYS LESTLTLSKADYEKH KVYACEVTHQGLSSP VTKSFNRGEC	SSLQPEDVATYYCQR YNRAPYTFGQGTKVE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYBREAKVQWKV DNALQSGNSQESVTE QDSKDSYSTLSKSTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEN	PCPAPELLGGPSVFLFPPKPKD TLMISRTP EVT CVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGS TYRCVSVLTVLHQDWLNGKEYKCK KVSNAKALPAIEKTIKAKGQPREPQ VYTLPPSREEMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKT TPPVLDSGSEFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKS LSLSPGGGGGGGSEVQLVES GGGLVQPGRSLRLSCAASGFTFDDY AMHWVRKAPGKGLEWVSAITWN SGHIDYADSVETRFTISRDNAKNSL YLQMNSLRAEDTAVYYCAKVS YLS TASSLDYWGGQTLVTVSSASTKGPS VFPLAPSSKSTSGGTAALGC LVKDYFPEPVTVSWNSGALTS GVHTFPAVLQSSGLYSLESV VTVPPSS SLGTQTYICNVNHNKPSNTKVDK KVEPKSC
			SEQ ID NO: 352	SEQ ID NO: 353	SEQ ID NO: 354
			GACATCCAGATGACC CAGTCTCCAAGCTCC CTGTCTGCGTCTGTG GGCGATAGGGTCACC ATCACTTGCAGGTCC AGCCAGAGTGTGTTA TACAGCTCCAACAAT AAGAACTACTTAGTT TGGTACCAGGAGAAA CCAGGAAAGGTTCCCT AAACTGCTCATTAC TGGGCATCTACCCGG GAATCCGGGGTCCCT AGTCGATTCAGTGGC AGCGGGTCTGGGACA GATTTCACCTCACC ATCAGCAGCCTGCAG CCTGAAAGATGTGGCA ACTTATTACTGTCAG CAATATATAAGACT CCTCTCACTTTCGGC GGAGGGACCAAGGTG GAGATCAAAACGAACG GTGGCTGCACCATCT GTCTTCATCTTCCCG CCATCTGATGAGCAG	CAGTCTGTGCTGACG CAGCCGCCCTCAGTG TCTGGGGCCCCAGGG CAGAGGGTCACCATC TCCTGCACTGGGAGC AGTTCCAAACATCGGG GCAGGTTATGATGTA CACTGGTACCAGGAG TTTCCAGGAACAGCC CCCAAACCTCCTCATC CAAGGTAACAGCAAT CGGCCCTCAGGGGTC CCTGACCGATTCTCT GGCTCCAAGTCTGGC ACCTCAGCCTCCCTG GCCATCACTGGGCTC CAGGCTGAGGATGAG GCTGATTATTACTGC CAGTCCCTATGACAGC AGCCTGAGTGGTTCCG GTGTTCCGGCGGAGGG ACCAAGCTGACCGTC CTAGGTCAGCCCCAAG GCTGCCCCCTCGGTC ACTCTGTTCCCGCCC TCCTCTGAGGAGCTT	CAGGTACAGTTGCAGGAGTCAGGTCCAGGACTGGTGAAAGCCCTCGGA GACCCCTCACTACCTGTACCATCTCCGGGGACAGTGTCTCTACCA ACAGTGTGCTTGAACTGGATCAGGAAGCCCCCAGGGAAGGCCCTT GAGTGGATAGGAAGGACATAC TACAGGTCCAAGTGGTATAATGATTA TGCAGTTTCTCGAAAAGTCGAGTAACCATCAGCCCAGACACATCCA AGAAC CAGTTCTCCCTGAAGCTGAGCTCTGTGACTGCCCGGGACACG GCTGTGTA TTACTGTGCAAGAGAGGATGGGGATAGCTACTACCGCTA CGGTA TGGACGTCTGGGGCCAAAGGACACAGGTCA CCGTCTCCCTCAG CCTCCACCAAGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAG AGCACCTCTGGGGCACAGCGGCCCTGGCTGCCTGGTCAAGGACTA CTTCCCCGAACCGGTGACGGTGTCTGTGGAACTCAGGCGCCCTGACCA GCGGCGTGACACACCTTCCCGGCTGTCTCTACAGTCCCTCAGGACTCTAC TCCCTCAAAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCA GACCTACATCTGCAACGTGAATCA CAAAGCCCAGCAACCAAGGTGG ACAAAGAAAGTTGAGCCC AAATCTTGTGACAAA ACTCACATGCCCA CCGTGCCCCAGCACCTGA ACTCTCTGGGGGACCGTCA GTCTTCCCTTT CCCCCAA AACCCACCCCTCATGATCTCCCGGACCCCTGAGG TCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTC AAG TTCAACTGGTACGTGGACGGCGGTGGAGGTGCATAATGCCAAGACAAA GCCGTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTGT CAGCGTCC TCACCGTCTCTGCAC CAGGACTGGCTGAATGGCAAGGAGTACAAAGTGC AAGGTCTCCAA CAAAAGCCCTCC CAGCCCCCATCGAGAAA ACCATCTC CAAAGCCAAAGGCGAGCCCGGAGAACCA CAGGTGTACACCCCTGCCCC CATCCCCGGGAGGAGATGACCAAGAA CCAGGT CAGCCTGACCTG CCCTG GTCAAAGGCTTCTATCC CAGCGACATCGCCGTGGAGTGGAGAGCAA TGGGCAGCCGGAGAACTACAA GACACGCTTCCCCTGCTGGACT

		TTGAAATCTGGTACC GCTCTGTTGTGTGC CTGCTGAATAACTTC TATCCCAGAGAGGCC AAAGTACAGTGAAG GTGGATAACGCCCTC CAATCGGGTAACTCC CAGGAGAGTGTACA GAGCAGGACAGCAAG GACAGCACCTACAGC CTCGAGAGCACCCCTG ACGCTGAGCAAAAGCA GACTACGAGAAACAC AAAGTCTACGCCCTGC GAAGTACCCCATCAG GGCCTGAGCTCGCCC GTCACAAAAGAGCTTC AACAGGGGAGAGTGT	CAAGCCAAACAAGGCC ACACTGGTGTTCTC ATAAGTGACTTCTAC CCGGAGCCGTGACA GTGGCCTGGAAGGCA GATAGCAGCCCCGTC AAGCGGGAGTGGAG ACCACCAACCCCTCC AAACAAAAGCAACAAC AAGTACGCGCCAAG AGCTATCTGAGCCTG ACGCCTGAGCAGTGG AAGTCCCACAGAAGC TACAGCTGCCAGGTC ACGCATGAAGGGAGC ACCGTGAGAGAAGACA GTGGCCCCCTACAGAA TGTTCA	CCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCCGTGGACAAAGAGC AGGTGGCAGCAGGGGAACGTCTTCTCATGTCTCCGTGATGCATGAGGC TCTGCACAACCACTACACGCAGAAAGACCTCTCCTGTCTCCGGGTG GTGGCGGATCGGGAGGTGGCGGATCCGAGGTGCAGTGTGCAGTCT GGAGCAGAGGTGAAAAAGCCCCGGGAGTCTCTGAAGATCTCCTGTAA GACTTCTGAATACAGCTTTACCAGCTACTGGATCGGCTGGGTGCGCA AGATGCCCCGGAAGGCCCTGGAGTGGATGGGGATCATCTATCTTGGT GACTCAGATACCAGATACAGCCCGTCCCTTCCAAGGCCAGGTCACCAT CTCAGCCGACAAAGTCCATCAGTACCGCCTACCTGCAGTGGAGCAGCC TGAAGGCCCTCGGACACCGCCATGTATTACTGTGCGAGAAGTAACTGG GGTCTTGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCTAGTGC CTCCACCAAGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGA GCACCTCTGGGGCACAGCGGCCCTGGGCTGCCGTGCTAAGGACTAC TTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCCTGACCCAG CGCGTGCACACCTTCCCCGGCTGTCTCTACAGTCTCAGGACTCTACT CCCTCGAGAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAG ACCTACATCTGCAACGTGAATCACAAAGCCCAGCAACACCAAGGTGGA CAAGAAAGTTGAGCCCCAAATCTTGT
		SEQ ID NO:355	SEQ ID NO:356	SEQ ID NO:357
	AA	DIQMTQSPSSLSASV GDRVITITCRSSQSVL YSSNNKNYLVWYQEK PGKVPKLLIYWASTR ESGVPSRFSGSGSGT DFTLTISLQPEDVA TYYCQQYYKTPLTFG GGTKVEIKRTVAAPS VFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGNS QESVTEQDSKDSSTYS LESTLTLSKADYEKH KVYACEVTHQGLSSP VTKSFNRGEC	QSVLTQPPSVSGAPG QRVTISCTGSSSNIG AGYDVHWYQEFFGTA PKLLIQGNSNRPSGV PDRFSGSKSGTSASL AITGLQAEDEADYYC QSYDSSLSGSVFGGG TKLTLVLGQPKAAPSV TLFPPSSEELQANKA TLVCLISDFYPGAVT VAWKADSSPVKAGVE TTTPSKQSNNKYAAK SYLSLTPEQWKSHRS YSCQVTHEGSTVEKT VAPTECS	QVQLQESGPGLVKPSSETLSLTCTISGDSVSTNSVANNWIRKPPGKGL EWIGRTYRYSKWYNDYAVSLKSRVTISPDTSKNQFSLKLSVTAADT AVYYCAREDDGDSYYRYGMDVWGQGTTVTVSSASTKGPSVFPLAPSSK STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY SLKSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTHCP PCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK FNWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKC KVSNAKALPAPIEKTIISKAKGQPREPQVYITLPPSRREMTKNQVSLTCL VKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGSGSGGGSEVQLVQS GAEVKKPGEISLKISCKTSEYSFTSYWIGWVRKMPGKGLEWMGI IYLG DSDTRYSPSFQGGQVTISADKSI STAYLQWSSSLKASDTAMYICARSNW GLDYGWQGGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLESVTVTPSSSLGTQ TYICNVNHKPSNTKVDKKVEPKSC
		SEQ ID NO:358	SEQ ID NO:359	SEQ ID NO:360

1PS: 376872	071_Ada1Imuab_CK(S176K)_Fc.001_3B3v2_VH_CH1(S183E).001	NA	GAAATTGTGTTGACG CAGTCTCCAGGCACC CTGTCTTTGTCTCCA GGGAAAGAGCCACC CTCTCCTGCAGGGCC AGTCAGAGTGTTAGA AGCAGTTACTTAGCC TGGTACCAGGAGAAA CCTGGCCAGGCTCCC AGGCTCCTCATCTAT GGTGCAATCCAGCAGG GCCACTGGCATCCCA GACAGGTTCAGTGGC AGTGGGTCTGGGACA GACTTCACCTCACC ATCAGCAGACTGGAG CCTGAAGATTTTGCA GTGTATTACTGTGTCAG CAGTATGGTAGCTCA CCTACCTTCGGCCAA GGGACACGACTGGAG ATTAAACGAACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGTACCGCC TCTGTTGTGTGCCCTG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCCCAG GAGAGTGTACACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC AAGAGCACCCCTGACG CTGAGCAAAAGCAGAC	GAGGTACAACTGGTGGAATCAGGTGGAGGTTTGGTGCAGCCGGGGAG ATCGCTCAGGCTTAGCTGTGCGGCATCGGGGTTTACTTTCGATGATT ATGCGATGCAATGGGTCCGGAAGCGCCTGGAAGAGGGCTCGAGTGG GTTTCCGCCATTACGTGGAATAGCGGACACATCGATTATGCAGACAG TGTGGAGGGCAGATTCACAATCTCACGAGACAATGCTAAGAACAGCC TGTAACCTTCAGATGAACCTCACTTCGCGCGGAAGATACCGCCGTATAC TACTGCGCCAAAAGTCTCCTACTTGTCTACAGCTTCGTCGCTCGACTA TTGGGTCAAAGGAACGTTGGTCACCGTCTCTAGTACGGTGGCTGCAC CATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAAATCTGGA ACTGCCCTCTGTTGTGTGCCCTGCTGAATAACTTCTATCCAGAGAGGC CAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCC AGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC AAGAGCACCCCTGACGCTGAGCAAAAGCAGACTACGAGAAAACACAAAGT CTACGCCCTGCCAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAA AGAGCTTCAACAGGGGAGAGTGTGACAAAACCTCACACATGCCCACCG TGCCCAGCACCTGAACTCCTGGGGGACCGTCAGTCTTTCCTCTTCCC CCCAAAACCCAAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCA CATGCGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAAGTTC AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAAGCC GTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTGTGTCAGCGTCCCTCA CCGTCTTGCAACCAGACTGGCTGAAATGGCAAAGGAGTACAAGTGCAAG GTCTCCAACAAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAA AGCCAAAGGCAGCCCCGAGAACCAAGGTGTACACCCCTGCCCCCAT CCCGGGAGGAGATGACCAAGAACCAAGTCAAGCTGACCTGACCTGGTGC AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGG GCAGCCGGAGAAACAACTACAAGACCAACGCTCCCGTGTGGACTCCG ACGGCTCCTTCTTCCCTCTATAGCAAAGCTCACCGTGGACAAGAGCAGG TGGCAGCAGGGGAACGTCTTCTCATGTCTCCGTGATGCATGAGGCTCT GCACAAACCACTACACGCAGAAAGACCTCTCCCTGTCTCCGGGTGGTG GCGGATCGGAGGTGGCGGATCCCAAGTCCAGGTGCAGTTACAGCAGTCGGGC GCAGGACTGTTGAAGCCTTCGGAGACCCGTGTCCCTCACCTGCGCTGT CCATGGTGGGTCCCTTCAGTGGTTACTACTGGAACCTGGATTTCGCAAGC CACCAGGAAAGGGCTAGAGTGGATTGGGAAATCAATCATGCTGGA AACACCAACTACAACCCGTCCCTCAAGAGTCGAGTCACCATATCATTT AGACACGTCCAAGAACCAAGTTCTCCCTGACGCTGACCTCTGTGACCG CCGGGACACGGCTGTGTATTACTGTGCGAGAGGATATTGTAGAAGT ACCACCTGCTACTTTGACTACTGGGGCCAGGGAACCCCTAGTCACCGT	GATATCCAAATGACA CAATCACCATCGTCG CTTTCAGCGTCTGTT GGGACCGTGTGACG ATTACCTGTGCGCG TCCCAGGGAATCCGG AATTACCTCGCATGG TATCAGGAAAAACCC GGAAAAAGCACCGAAG CTCCTGATCTATGCC GCCTCGACTCTTCAG AGTGGTGTGCCGTGG AGGTTAGCGGTCC GGTCAGGTACGGAC TTTACTCTCACAATT TCCAGCCTGCAGCCC GAGTTAGCGGTCC GGTCAGGTACGGAC TATTAATTCGAGAGA TACAAACCGAGCGCCT TACACATTCGGACAA GGGACAAAAGTCGAG ATCAAAGCGTGCCCTCC ACCAAGGCCCATCG GTCTTCCCCCTGGCA CCCTCCTCCAAGAGC ACCTCTGGGGCACA GCGGCCCTGGGCTGC CTGGTCAAGGACTAC TTCCCCGAACCGGTG ACGGTGTCTGGAAC TCAGGCGCCCTGACC AGCGGCGTGACACACC TTCCCCGGCTGTCCCTA CAGTCCTCAGGACTC TACTCCCTCGAAAGC GTGGTGACCGTGCCC TCCAGCAGCTTGGGC
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		TACGAGAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	CTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCT CCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCCTGGTC AAGGACTACTTCCCCGAACCGGTGACGGTGTGCGTGAACCTCAGGCGC CCTGACCAGCGGTGCACACCTTCCCCGGCTGTCTACAGTCTCTCAG GACTCTACTCCCTCGAGAGCGTGTGACCGTGCCCTCCAGCAGCTTG GGCACCAGACCTACATCTGCAACGTGAATCACAAAGCCCAGCAACAC CAAGGTGGACAAAGAAAGTTGAGCCCCAAAATCTTGT	ACCCAGACCTACATC TGCAACGTGAATCAC AAGCCAGCAACACC AAGGTGGACAAAGAA GTTGAGCCCCAAATCT TGT
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AA		EIVLTQSPGTLISLP GERATLSCRASQSVR SSYLAWYQEKPGQAP RLLIYGASSRATGIP DRFSGSGTDFTLT ISRLEPEDFAVYYCQ QYGSSTFFGQGRLE IKRTVAAPSVFIIPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLKSTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEC	EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRKAPGKGLEW VSAITWNSGHIDYADSVEGRFTISRDNAKNSLYLQMNSLRAEDTAVY YCAKVSYLSTASSLDYWGGTLVTVSSSTAAPSVEIFPPSDEQLKSG TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSL KSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECDKTHTCPP CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGGSGSGGSQVQLQQSG AGLLKPSSETLSLTCAVHGGSFSGYYWNWIRKPPGKGLEWIGEINHAG NTNYPNPSLKSRVTISLDTSKNQFSLTLTSVTAADTAVYYCARGYCRS TTCYFDYWGGQTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLESVVTVPSSSL GTQTYICNVNHKPSNTKVDKKVEPKSC	DIQMTQSPSSLSASV GDRVITITCRASQGIR NYLAWYQEKPGKAPK LLIYAASTLQSGVPS RFGSGSGTDFTLTI SSLQPEDVATYYCQR YNRAPYTFGQGTKVE IKRASTKGPSVFPLA PSSKSTSGGTAALGC LVKDYFFPEPVTVSWN SGALTSGVHTFPAVL QSSGLYSLESVVTVP SSSLGTQTYICNVNH KPSNTKVDKKVEPKS C
		SEQ ID NO:364	SEQ ID NO:365	SEQ ID NO:366
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		NA		
!PS: 376879	072 Adalimumab_CK (S176 R)_Fc.001_9C8_VH_CH1 (S 183E).001			

		GGATCTGGGACAGAT TTCACTCTCACCATC AGCAGTCTGCAACCT GAAGATTTTGCAACT TACTACTGTCAACAG AGTTACAGTACCCCT CGGACGTTCGGCCAA GGGACCAAGCTGGAA ATCAAAACGAACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGTACCGCC TCTGTTGTGTGCCTG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCCGAG GAGAGTGCACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC AAGAGCACCCCTGACG CTGAGCAAAAGCAGAC TACGAGAAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	CTACGCCCTGCGAAGTCA AGAGCTTCAACAGGGAGAG TGCCCAGCACCTGA CCCAAAACCCAAAGGAC CATGCGTGGTGGACG AACTGGTACGTGGACG GTGTGAGGAGCAGTAC CCGTCCTGCAACCAAG GTCTCCAACAAAAGCC AGCCAAAAGGCAGCC CCCGGAGGAGATGAC AAAGGCTTCTATCCC GCAGCCGGAGAAACAA ACGGCTCCTTCTTCC TGGCAGCAGGGAAAC GCACAAACCACTACAC GCGGATCGGGAGGTG CCAGGACTGGTGAGCC CTCTGGTGGCTCCATC CCCCAGGTAAGGACTG CAGACCAAATACAAAC AGACACGTCCAAAGAAC CTGCGGACACGGCCGT TACGGCTTTGACTACT AGCCTCCACCAAGGCC AGAGCACCTCTGCGGG TACTTCCCCGAAACCG CAGCGCGTGCACACCT ACTCCCTCGAGAGCGT CAGACCTACATCTGCA GGACAAAGAAAGTTGAG	GGTCAAGGTACGGAC TTTACTCTCACAATT TCCAGCCTGCAGCCC GAAGATGTAGCTACC TATTAATGCCAGAGA TACAAACGAGCGCCT TACACATTCGGACAA GGGACAAAAGTCGAG ATCAAAGCGTGCCCTC ACCAAAGGCCCATCG GTCTTCCCCCTGGCA CCCTCCTCCAAAGAGC ACCTCTGGGGCACA GCGGCCCTGGGCTGC CTGGTCAAAGGACTAC TTCCCCGAACCCGGTG ACGGTGTCTGTGGAAC TCAGGCGCCCTGACC AGCGGCGTGACACACC TTCCCCGGCTGTCCTA CAGTCCCTCAGGACTC TACTCCCTCGAAAAGC GTGGTGACCGTGCCC TCCAGCAGCTTGGGC ACCCAGACCTACATC TGCAACGTGAATCAC AAGCCCAGCAACACC AAGGTGGACAAAGAAA GTTGAGCCCCAAATCT TGT
		SEQ ID NO:367	SEQ ID NO:368	SEQ ID NO:369
AA	DIQMTQSPSSLSASV GDRVITTCRASQIN NYLNWYQERPGKAPK LLIYAASSLQSGVPS RFSGSGSGTDFTLTI	EVQLVESGGGLVQPGRSLRLS VSAITWNSGHIDYADSV YCAKVSYLSTASSLDYWG TASVVCLLNNFYPREAKV KSTLTLSKADYEKHKVYA	FDDYAMHWVRKAPKGLEW LSRDNKNSLYLQMNSLRAEDTAVY FPPSDEQLKSG QESVTEQDSKDSYSL SSPVTKSFNRGECDKTHTCPP	DIQMTQSPSSLSASV GDRVITTCRASQIR NYLAWYQEKPGKAPK LLIYAASTLQSGVPS RFSGSGSGTDFTLTI

			SSLQPEDFATYYCQQ SYSTPRTFGQTKLE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLKSTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEN	CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGGSGGGSQVQLQESG PGLVKPSETLSLTCTVSGGSISSYFWSWIRKPPGKGLEWIGIYIYSG QTKYNPSLKSrvTISIDTSKNQFSLKLSsvTAADTAVYYCARETGSY YGFdYWQGTlVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKD YFPEPVTvSWNSGALTSgvHTFFPAVLQSSGLYSLESvVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC	SSLQPEDVATYYCQR YNRAPYTFGQGTKVE IKRASTKGPSVFPLA PSSKSTSGGTAALGC LVKDYFFPEPVTVSWN SGALTSGVHTFFPAVL QSSGLYSLESvVTVP SSSLGTQTYICNVNH KPSNTKVDKKVEPKS C
			SEQ ID NO: 370	SEQ ID NO: 371	SEQ ID NO: 372
	073 Adalimumab_CK (S176K)_Fc.001_23B3_VH4_VH_CH1 (S183E).001	NA	GACATCCAGATGACC CAGTCTCCAAGCTCC CTGTCTGCCGTCTGTG GGCGATAGGGTCACC ATCACTTGCAGGTCC AGCCAGAGTGTGTTA TACAGCTCCAACAAT AAGAACTACTTAGTT TGGTACCAGGAGAAA CCAGGAAAGGTTCCCT AAACTGCTCATTAC TGGGCATCTACCCGG GAATCCGGGGTCCCT AGTCGATTCA GTGGC AGCGGGTCTGGGACA GATTTCAC TCTCACC ATCAGCAGCCTGCAG CCTGAAGATGTGGCA ACTTATTACTGT CAG CAATATATAAGACT CCTCTC ACTTTCCGGC GGAGGACCAAGGTG GAGATCAAAACGAACG GTGGCTGCACCATCT GTCTTCATCTTCCCG CCATCTGATGAGCAG	GAGGTACAACTGGTGGAATCAGGTGGAGGTTTGGTGCAGCCCGGGGAG ATCGCTCAGGCTTAGCTGTGCGGCATCGGGGTTTACTTTCGATGATT ATGCCGATGCATTGGTCCGGAAAGCGCCTGGAAAAGGGCTCGAGTGG GTTTCCGCCATTACGTGGAATAGCGGACACATCGATTATGCAGACAG TGTGGAGGCAGATTCACAATCTCACGAGACAAATGCTAAGAACAGCC TGTA CCTTCAGATGA ACTCACTTCGCGCGGAAGATACCGCCGTATAC TACTGCGCCAAAAGTCTCCTACTTGTCTACAGCTTCGTCGCTCGACTA TTGGGGTCAAGGAACGTTGGTCA CCGTCTCTAGTACGGTGGCTGCAC CATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAA TCTGGA ACTGCCCTCTGTTGTGTGCCCTGCTGAATAACTTCTATCCAGAGAGGC CAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAACTCCC AGGAGAGTGTCA CAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC AAGAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAAGT CTACGCCCTGCGAAGTCA CCCCATCAGGGCCTGAGCTCGCCCGTCACAA AGAGCTTCAACAGGGGAGAGTGTGACAAAAC TCAACATGCCCACCG TGCC CAGCACCTGAACTCCTGGGGGACCGTCAGTCTTCTCTTTCCC CCCAAAACCCAAAGGACAC C C C T C A T G A T C T C C G G A C C C T G A G G T C A CATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAA GTTC AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAAGCC GTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTGTGTCAGCGTCCCTCA CCGTCCCTGCAC C CAGGACTGGCTGAA TGGCAAGGAGTACAAAGTGCAAG GTCTCCAACAAAAGCCCTCC CAGCC C C C C A T C G A G A A A A C C A T C T C C A A AGCCAAAAGG CAGCC C C C G A G A A C C A C A G G T G T A C A C C C T G C C C C C A T C C C G G G A G G A G A T G A C C A A G A A C C A G G T C A G C C T G A C C T G C C T G G T C AAAGGCTTCTATCC CAGCGACATCGCCGTGGAGTGGAGAGCAATGG GCAGCCGGAGAAACAACTACAAGACCACGCTCCCGTGGTGGACTCCG	GATATCCAAATGACA CAATCACCATCGTCG CTTTCAGCGTCTGTT GGCACC GTGACG ATTACCTGTCGCG TCCCAGGGAATCCGG AATTACCTCGCATGG TATCAGGAAAAACCC GGA AAA GCACCGAAG CTCCTGATCTATGCC GCCTCGACTCTTCAG AGTGGTGTCCGTCG AGGTTAGCGGTCC GGTCAGGTACGGAC TTTACTCTACAATT TCCAGCCTGCAGCCC GAAGATGTAGCTACC TATTACTGCCAGAGA TACAACCGAGCGCCT TACACATTCCGACAA GGGACAAAAGTCGAG ATCAAGCGTGCCTCC ACCAAGGCCCATCG GTCTTCCCCCTGGCA CCCTCCTCCAAGAGC ACCTCTGGGGGCACA

		TTGAAATCTGGTACC GCTCTGTTGTGTGC CTGCTGAATAAATTCT TATCCCAGAGAGGCC AAAGTACAGTGAAG GTGGATAACGCCCTC CAATCGGGTAACTCC CAGGAGAGTGTACACA GAGCAGGACAGCAAG GACAGCACCTACAGC CTCAAGAGCACCCCTG ACGCTGAGCAAAAGCA GACTACGAGAAACAC AAAGTCTACGCCCTGC GAAGTACCCCATCAG GGCCTGAGCTCGCCC GTCACAAAAGAGCTTC AACAGGGAGAGTGT	ACGGCTCCTTCTTCCCTCTATAGCAAAGCTCACCGTGGACAAGAGCAGG TGGCAGCAGGGGAACGTCTTCTCATGTCTCCGTGATGCATGAGGCTCT GCACAACCACTACACGAGAGAGCCCTCTCCCTGTCTCCGGTGGTG GCGGATCGGAGGTGGCGGATCCCAGGTACAGTTGCAGGAGTCAGGT CCAGGACTGTTAAGCCCTCGGAGACCCCTCTCACTACCTGTACCAT CTCCGGGACAGTGTCTCTACCAACAGTGTGCTTGGAACCTGGATTA GGAAGCCCCCAGGGAAGGCCCTTGAGTGGATAGGAAGGACATACTAC AGGTCCAAGTGGTATAATGATTATGCAGTTTCTCTGAAAAGTCGAGT AACCATCAGCCCCAGACACATCCAAGAACAGTTTCTCCCTGAAGCTGA GCTCTGTGACTGCCCGGACACGGCTGTGTATTACTGTGCAAGAGAG GATGGGATAGCTACTACCGCTACGGTATGGACGTCTGGGGCCAAGG GACCACGGTCACCGTCTCTCAGCCTCCACCAGGGCCCATCGGTCT TCCCCCTGGACCCCTCCTCCAAGAGCACCTCTGGGGCACAGCGGCC CTGGGCTGCCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTC GTGGAACCTCAGCGCCCTGACCAGCGGCTGCACACCTTCCC GGCTG TCCTACAGTCCTCAGGACTCTACTCCCTCAGAGCGGTGGTGACCCGTG CCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCA CAAGCCCAGCAACACCAAGGTGGACAAGAAAAGTTGAGCCCCAAATCTT GT	GCGGCCCTGGGCTGC CTGGTCAAGGACTAC TTCCCCGAACCGGTG ACGGTGTCTGTGAAC TCAGGCGCCCTGACC AGCGCGTGCACACC TTCCCCGGCTGTCCTA CAGTCCCTCAGGACTC TACTCCCTCGAAAGC GTGGTGACCGTGCCC TCCAGCAGCTTGGGC ACCCAGACCTACATC TGCAACGTGAATCAC AAGCCCAGCAACACC AAGGTGGACAAAGAAA GTTGAGCCCCAAATCT TGT
		SEQ ID NO: 373	SEQ ID NO: 374	SEQ ID NO: 375
AA		DIQMTQSPSSLSASV GDRVTTITCRSSQSVL YSSNNKNYLVWYQEK PGKVPKLLIYWASTR ESGVPSRFSGSGGT DFTLTISSLQPEDVA TYYCQQYYKTPLTFG GGTKVEIKRTVAAPS VFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGNS QESVTEQDSKDSSTYS LKSTLTLSKADYEKH KVYACEVTHQGLSSP VTKSFNRGEC	EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRKAPKGLEW VSAITWNSGHIDYADSVVEGRFTISRDNAKNSLYLQMNSLRAEDTAVY YCAKVSYLSTASSLDYWGGQGLVTVSSSTAAPSVFIFPPSDEQLKSG TASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSL KSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECDKTHTCPP CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPCEEQYGSYRCVSVLTVLHQDWLNGKEYKCK VSNKALPAPIEKTIISKAGQPREPQVYTLPPSREEMTKNQVSLTCLV KGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR WQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGSQVQLQESG PGLVKPSETLSLTCTISGDSVSTNSVAWNWI RKP PPKGLEWIGRTYY RSKWYNDYAVSLKSRVTISPDTSKNQFSLKLSVTAADTAVYYCARE DGDSYYRYRGMVDWGQGT VTVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLESVTV PSSSLGTQTYICNVNHKPSNTKVKDKKVEPKSC	DIQMTQSPSSLSASV GDRVTTITCRASQGIR NYLAWYQEKPKGKAPK LLIYAASTLQSGVPS RFSGSGSGTDFTLTIT SSLQPEDVATYYCQR YNRAPYTFGQGTKVE IKRASTKGPSVFPLA PSSKSTSGGTAALGC LVKDYFPEPVT VSWN SGALTSGVHTFPAVL QSSGLYSLESVTVTP SSSLGTQTYICNVNH KPSNTKVDKKVEPKS C
		SEQ ID NO: 376	SEQ ID NO: 377	SEQ ID NO: 378
1	1	GAAATTGTGTTGACG	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCCGGGA	CAGTCTGTGCTGACG

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GCCACTGGCATCCCA	CCTCCAAACAGACAAACAAGTACGGGCCAAAGAGCTACCTGAGC	CGGCCCTCAGGGGTC
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GCTGCACCATCTGTC	AGAAACCACAGGTGTACACCCCTGCCCCCATCCCGGGAGGAGATGACCA	CTAGGTGCCCTCCACC
TTCAATCTTCCCGCCA	AGAAACCAGGTCAAGCTGACCTGCCTGGTCAAAGGCTTCTATCCCCAGC	AAGGCCCATCGGTC
TCTGATGAGCAGTTG	GACATCGCCGTGGAGTGGGAGAGCAAATGGGCAGCCGGAGAAACAACTA	TTCCCCCTGGCACCC
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TCTGTTGTGTGCCTG	ATAGCAAAGCTCACCGTGGACAAAGAGCAGGTGGCAGCAGGGGAACGTC	TCTGGGGGCACAGCG
CTGAAATAACTTCTAT	TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAACCACTACACGCA	GCCCTGGGCTGCCCTG
CCCAGAGAGGCCAAA	GAAGAGCCTCTCCCTGTCTCCGGGTGGTGGCGATCGGAGGTGGCG	GTCAAGGACTACTTC
GTACAGTGGAAGGTG	GATCCCAGGTGCAGTTACAGCAGTCGGGCGCAGGACTGTTGAAGCCT	CCCGAACCCGGTGACG
GATAACGCCCTCCAA	TCGGAGACCCCTGTCCCTCACCTGCGCTGTCCATGGTGGTCTTTCAG	GTGTCGTGGAACCTCA
TCGGGTAACTCCCCAG	TGGTTACTACTGGAACTGGATTTCGCAAGCCACCAAGGGAAGGGGCTAG	GGCGCCCTGACCAGC
GAGAGTGTACAGAG	AGTGGAATTGGGGAATCAATCATGCTGGAACAACCAACTACAACCCG	GGCGTGCAACCTTC
CAGGACAGCAAGGAC	TCCCTCAAGAGTCGAGTCACCATATCATTAGACACGTCCAAGAAACCA	CCGGCTGTCCCTACAG
AGCACCTACAGCCTC	GTTCCTCCCTGACGCTGACCTCTGTGACCGCCGCGGACACAGGCTGTGT	TCCTCAGGACTCTAC
AAGAGCACCCCTGACG	ATTACTGTGCGAGAGGATATTGTAGAAGTACCACCTGCTACTTTTGAC	TCCCTCGAAAGCGTG
CTGAGCAAAAGCAGAC	TACTGGGGCCAGGGAACCCCTAGTCAACCGTCTCCTCAGCCTCCACCAA	GTGACCGTGCCCTCC
TACGAGAAAACACAAA	GGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTG	AGCAGCTTGGGCACC

			GTCTACGCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGAGAGTGTT	GGGGCACAGCGGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCCGAA CCGGTGACGGTGTCGTGGAACCTCAGGCGCCCTGACCAGCGCGGTGCA CACCTTCCCGGCTGTCCACAGTCCCTCAGGACTCTACTCCCTCGAGA GCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATC TGCAACGTGAATCACAAAGCCAGCAACACCAAGGTGGACAAGAAAGT TGAGCCCCAAATCTTGT	CAGACCTACATCTGC AACGTGAATCACAAAG CCCAGCAACACCAAG GTGGACAAAGAAAGTT GAGCCCCAAATCTTGT
			SEQ ID NO:379	SEQ ID NO:380	SEQ ID NO:381
AA			EIVLTQSPGTLISLSP GERATLSCRASQSVR SSYLAWYQEKPGQAP RLLIYGASSRATGIP DRFSGSGGTDFTLT ISRLEPEDFAVYYCQ QYGSPTFGQGRLE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSYSLKSTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEN	EVQLVQSGAEVKKPGESLKI SCKTSEY SFTSYWIGWVRKMPGKGLEW MGI IYLGDS DTRYSPSFQGGVTI SADKSI STAYLQWSSLKASDTAMY YCARSNWGLDYWGQGTI LVTVSSQPKANPTVTLFPPSSEELQANKATL VCLISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAAKS YLS LTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECSDKTHTCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPI EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMH EALHNHYTQKSLSLSPGGGGSGGSQVQLQQSGAGLLKP SETLSLTCAVHGGSFGSYYNWIRKPPGKGLEWIGE INHAGNTNYP SLKSRVTISLDTSKNQFSLT LTVTAADTAVYYCARGYCRSTTTCYFD YWQQGT LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSGLYSLESVVTVTPSSSLGTQTYI CNVNHKPSNTKVDKKVEPKSC	QSVLTQPPPSVSGAPG QRVTISCTGSSSNIG AGYDVHWYQEFPGTA PKLLIQGNSNRPSGV PDRFSGSKSGTSASL AITGLQAEDEADYYC QSYDSSLSGSVFGGG TKLTVLGASTKGPSV FPLAPSSKSTSGGTA ALGCLVKDYFPEPVT VSWNSGALTSGVHTF PAVLQSSGLYSLESV VTVPSSSLGTQTYIC NVNHKPSNTKVDKKV EPKSC
			SEQ ID NO:382	SEQ ID NO:383	SEQ ID NO:384
			GACATCCAGATGACC CAGTCTCCATCCTCC CTGTCTGCATCTGTA GGAGACAGAGTCACC ATCACTTGCCGGGCA AGTCAGAGCATTAAC AACTATTTAAATTGG TATCAGGAGAGACCA GGGAAAGCCCCCTAAG CTCCTGATCTATGCT GCATCCAGTTTGCAA AGTGGGTCCCCATCA AGGTTCAGTGGCAGT GGATCTGGGACAGAT	GAGGTGCAGCTGGTG CAGTCTGGAGCAGAGGTGAAAAGCCCCGGGA GTCTCTGAAGATCTCCTGTAA GACTTCTGAATACAGCTTTACCAGCT ACTGGATCGGCTGGGTGCGCAAGATGCCGGGAAAGGCTGGAGTGG ATGGGGATCATCTATCTTGGTGACTCAGATACCAGATACAGCCCCGTC CTTCCAAAGGCCAGGTCACCATCTCAGCCGACAAAGTCCATCAGTACCG CCTACCTGCAGTGGAGCAGCCTGAAGGCCCTCGGACACCGCCATGTAT TACTGTGCGAGAGTA AACTGGGTCTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTCTCTAGT CAGCCCCAAGGCCAACCCCACTGTCACTC TGTTCCCCCCTCCTCTGAGGAGCTCCAAGCCAAACAAGGCCACACTA GTGTGTCTGATCAGTGACTTCTACCCGGGAGCTGTGACAGTGGCCTG GAAGGCAGATGGCAGCCCCGTC AAGCGGGAGTGGAGACCACCAAAC CCTCCAAACAGAGCAACAACAAGTACGCGGCCAAGAGCTACCTGAGC CTGACGCCCCGAGCAGTGAAAGTCCCACAGAAAGCTACAGCTGCCAGGT CACGCA TGAAGGGAGCACCGGTGGAGAAAGACAGTGGCCCCCTACAGAA T	CAGTCTGTGCTGACG CAGCCGCCCTCAGTG TCTGGGGCCCCAGGG CAGAGGTCACCATC TCCTGCACTGGGAGC AGTTCCAACATCGGG GCAGGTTATGATGTA CACTGGTACCAGGAG TTTCCAGGAACAGCC CCCAAACTCCTCATC CAAGGTAACAGCAAT CGGCCCTCAGGGGTC CCTGACCGATTCTCT GGTCCAAAGTCTTGGC
			075_3.2_CL(S176K)_Fc.001 _9C8_VH_CH1(S183E)_001		
1PS:376896					

	TTCAC TCTC ACCATC AGCAG TCTG CAACTT GAAGAT TTTG CAACT TACTACT GTCAACAG AGTTACAG TACCCCT CGGACG TTCGGCCAA GGGACCA AGCTGGAA ATCAAA CGAACGGTG GCTGCAC CATCTGTC TTCAATCT TCCCGCCA TCTGATG AGCAGTTG AAATCTG GTACCGCC TCTGTTG TGTGCCCTG CTGAA TAACTTCTAT CCGAGAG AGGCCAAA GTACAGT GGAAGGTG GATAAC GCGCTCCAA TCGGGTAA CTCCCAG GAGAGTGC ACAGAG CAGGACAG CAAGGAC AGCACCTAC AGCCTC AAGAGCACC CTGACG CTGAGCAAA AGCAGAC GTCACCCATCAGGGC CTGAGCTCG CCGCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	GTTCAGACAAA AACTCACACATGCCCA CTGGGGGACCGTCAGTCTTCCCTCTTCC CCTCATGATCTCCCGACCCCTGAGTCA TGAGCCACGAAGACCCCTGAGGTCAA GTGGAGTGCATAAATGCCAAGACAAAG CAGCACGTACCGTTGTGTGTCAGCGT GGCTGAATGGCAAGGAGTACAAAGT CCAGCCCCATCGAGAAAACCATCTC AGAAACCAAGGTGTACACCCCTGCC AGAAACCAAGTCAAGCTGACCTGAC GACATCGCCGTGGAGTGGAGAGCA CAAGACCAAGCTTCCCGTGTGCTG ATAGCAAGCTCACCGTGGACAAGAG TTCTCATGCTCCGTGATGCATGAGG GAAAGACCTCTCCCTGTCTCCGGT GATCCCAGGTGCAGCTGCAGGAGT TCGGAGACCCCTGTCCCTCACCTG TAGTTACTTCTGGAGCTGGATTTC AGTGGATTGGCTATATCTATTACAG TCCCTCAAGAGTCGAGTCACCATAT GTTCTCCCTGAAAGCTGAGCTCTGT ATTACTGTGCGAGAGAAAACCTGG GGCCAGGAAACCCTGTTACCGTCTC ATCGGTCTTCCCCCTGGCACCCCTC CAGCGGCCCTGGCGTGCCTGTTCA ACGGTGTGCTGGAACTCAGGCGCC CCCCGGCTGTCTCTACAGTCTCAG TGACCGTGCCCTCCAGCAGCTTGG GTGAATCACAAAGCCCAGCAACAC CAAAATCTTGT	ACCTCAGCCTCCCTG GCCATCACTGGGCTC CAGGCTGAGGATGAG GCTGATTATTACTGC CAGTCCTATGACAGC AGCCTGAGTGGTTCG GTGTTCCGGCGGAGG ACCAAGCTGACCGTC CTAGGTGCCCTCCACC AAGGCCCATCGGTC TTCCCCCTGGCACCC TCCTCCAAAGACACC TCTGGGGCACAGCG GCCCTGGGCTGCCCTG GTCAAAGACTACTTC CCCGAACCCGGTGACG GTGTCGTGGAAC TCA GGCGCCCTGACCAGC GGGTGCACACCTTC CCGGCTGTCC TACAG TCCCTCAGGACTCTAC TCCCTCGAAAAGCGTG GTGACCGTGCCCTCC AGCAGCTTGGGCACC CAGACCTACATCTGC AACGTGAATCACAAAG CCCAGCAACACCAAG GTGGACAAAGAAAGTT GAGCCCCAAATCTTGT
	SEQ ID NO: 385	SEQ ID NO: 386	SEQ ID NO: 387
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			SYSTPRTFGQGTKLE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSYSLKSTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEN	VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTTLPSSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCVMHEALHNHYTQKSLSLSPGGGGSGGSQVQLQESGPGLVKP SETLSLTCTVSGGSISSYFWSWIRKPPGKLEWIGYIYYSGQTKYNP SLKSRVTISIDTSKNQFSCLKLSLVTAADTAVYYCARETGSYYGFDYW GQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLESVVTVTPSSSLGTQTYICN VNHKPSNTKVDKKVEPKSC	QSYDSSLSGSVFGGG TKLTVLGASTKGPSV FPLAPSSKSTSGGTA ALGCLVKDYFPEPVT VSWNSGALTSGVHTF PAVLQSSGLYSLESV VTVPSSSLGTQTYIC NVNHHKPSNTKVDKKV EPKSC
			SEQ ID NO:388	SEQ ID NO:389	SEQ ID NO:390
	076_3.2_CL(S176K)_Fc.001_23B3_VH4_VH_CH1(S183E).01	1PS:376901	GACATCCAGATGACC CAGTCTCCAAGCTCC CTGTCTGCGTCTGTG GGCGATAGGGTCACC ATCACTTGCAGGTCC AGCCAGAGTGTGTTA TACAGCTCCAACAAT AAGAATACTTAGTT TGGTACCAGGAGAAA CCAGGAAAGGTTCCCT AAACTGCTCATTTAC TGGGCATCTACCCGG GAATCCGGGGTCCCT AGTCGATTCAGTGGC AGCGGGTCTGGGACA GATTTCACCTCACC ATCAGCAGCCTGCAG CCTGAAGATGTGGCA ACTTATTACTGTCAG CAATATTATAAGACT CCTCTCACTTTCGGC GGAGGGACCAAGGTG GAGATCAAAACGAACG GTGGCTGCACCATCT GTC TTCATCTTCCCG CCATCTGATGAGCAG TTGAAAATCTGGTACC	GAGGTGCAGCTGGTG CAGTCTGGAGCAGAGGTGAAAAAGCCCCGGGA GTCTCTGAAGATCTCCTGTAA GACTTCTGAATACAGCTTTACCAGCT ACTGGATCGGCTGGGTGCGCAAGATGCCGGGAAAGGCCTGGAGTGG ATGGGGATCATCTATCTTGGTGACTCAGATACCAGATACAGCCCCGTC CTTCCAAAGGCCAGGTCACCATCTCAGCCGACAAAGTCCATCAGTACCCG CCTACCTGCAGTGGAGCAGCCTGAAGGCCCTCGGACACCGCCATGTAT TACTGTGCGAGAAGTAACTGGGTCTTGACTACTGGGGCCAGGGAAC CCTGGTCACCGTCTCTAGTCA GCCCAAGGCCAACCCCACTGTCACTC TGTTCCCGCCCTCCTCTGAGGAGCTCCAAGCCAAACAAGGCCACACTA GTGTGTCTGATCAGTGACTTCTACCCGGGAGCTGTGACAGTGGCCTG GAAGGCAGATGGCAGCCCCGTCAAGCGGGAGTGGAGACCACCAAAC CCTCCAAACAGAGCAACAACAAGTACGGGGCCAAAGAGCTACCTGAGC CTGACGCCCGAGCAGTGAAAGTCCCA CAGAAAGCTACAGCTGCCAGGT CACGCA TGAAGGGAGCACCGTGGAGAGACAGTGGCCCCCTACAGAAAT GTTCAGACAAAACTCACACATGCCCA CCGTGCCAGCACCTGAACTC CTGGGGGACCGTCAGTCTTCCCTCTTCCCCCAAACCCAAAGGACAC CCTCATGATCTCCGGACCCCTGAGGTCA CATGCGTGGTGGGACG TGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGC GTGGAGGTGCATAA TGCCAAAGACAAAGCCGTGTGAGGAGCAGTACGG CAGCACGTACCGTTGTGTCA GCGTCTCACCGTCTCTGCACCGGACT GGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAGCCCTC CCAGCCCCCATCGAGAAAAACCATCTCCAAGCCAAAGGCAGCCCCCG AGAAACCACAGGTGTACACCC TGCCCCCATCCCGGAGGAGATGACCA AGAAACCAGGTCA GCCTGACCTGCCCTGGTCAAAGGCTTCTATCCCAGC GACATCGCCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAACAATA CAAGACACG CCTCCCGTGTGCTGGACTCCGACGGCTCCTTCTTCCCTCT ATAGCAAAGCTCACCGTGGACA AAGAGCAGGTGGCAGCAGGGGAACGTC	CAGTCTGTGCTGACG CAGCCGCCCTCAGTG TCTGGGGCCCCAGGG CAGAGGTCACCATC TCCTGCAC TGGGAGC AGTTCCAAACATCGGG GCAGGTTATGATGTA CACTGGTACCAGGAG TTTCCAGGAACAGCC CCCAAAC TCTCATC CAAGGTAA CAGCAAT CGGCCCTCAGGGGTC CCTGACCCGATTCTCT GGCTCCAAGTCTGGC ACCTCAGCCTCCCCTG GCCATCACTGGGCTC CAGGCTGAGGATGAG GCTGATTATTACTGC CAGTCCCTATGACAGC AGCCTGAGTGGTTCG GTGTTCCGGCGGAGGG ACCAAAGCTGACCGTC CTAGGTGCCTCCACC AAGGCCCATCGGTC TTCCCCCTGGCACCC TCCTCCAAGAGCACCC TCTGGGGGCACAGCG

		GCC TCTGTTGTGTGC CTGCTGAATAACTTC TATCCCAGAGAGGCC AAAGTACAGTGGAAG GTGGATAACGCCCTC CAATCGGGTAACTCC CAGGAGAGTGCACA GAGCAGACAGCAAG GACAGCCTACAGC CTCAAGAGCACCCCTG ACGCTGAGCAAAAGCA GACTACGAGAAACAC AAAGTCTACGCCTGC GAAGTCACCCATCAG GGCCTGAGCTCGCCC GTCACAAAGAGCTTC AACAGGGGAGAGTGT	TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAACCACTACACGCA GAAGAGCCTCTCCCTGTCTCCGGGTGGTGGCGGATCGGGAGGTGGCG GATCCCAGGTACAGTTGCAGGAGTCAGGTCCAGGACTGGTGAAGCCC TCGGAGACCCCTCTCACTCACCTGTACCATCTCCGGGGACAGTGTCTC TACCAACAGTGTGCTTGGAAC TGGATTAGGAAGCCCCCAGGGAAG GCCTTGAGTGGATAGGAAGGACATACTACAGGTCCAAGTGGTATAAT GATTATGCAGTTTCTCTGAAAAAGTCGAGTAACCATCAGCCCCAGACAC ATCCAAGAACCAAGTTCTCCCTGAAGCTGAGCTCTGTGACTGCCGCGG ACACGGCTGTGTATTACTGTGCAAGAGAGGATGGGGATAGCTACTAC CGCTACGGTATGACGTCTGGGCCAAGGACCAACGCTACCGTCTC CTCAGCCTCCACAAAGGCCCATCGGTCTTCCCCCTGGCACCCCTCCT CCAAAGAGCACCTCTGGGGGCACACGGGCCCTGGGCTGCCCTGGTCAAG GACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAAC TCAAGCGCCCT GACCAGCGGCTGCACACCTTCCCGGCTGTCTACAGTCTCAGGAC TCTACTCCCTCGAGAGCGTGTGACCGTGCCCTCCAGCAGCTTGGGC ACCCAGACCTACATCTGCAACGTGAATCACAAGCCCCAGCAACACCAA GGTGGACAAAGAAAGTTGAGCCCCAAA TCTTGT	GCCCTGGGCTGCCTG GTCAAGGACTACTTC CCCGAACCGGTGACG GTGTCGTGGA ACTCA GGCGCCCTGACCAGC GGCTGCACACCTTC CCGGCTGTCTTACAG TCCCTCAGGACTCTAC TCCCTCGAAAGCGTG GTGACCGTGCCCTCC AGCAGCTTGGGCACC CAGACCTACATCTGC AACGTGAATCACAAG CCCAGCAACACCAAG GTGGACAAAGAAAGTT GAGCCCCAAATCTTGT
		SEQ ID NO: 391	SEQ ID NO: 392	SEQ ID NO: 393
	AA	DIQMTQSPSSLSASV GDRVITITCRSSQSVL YSSNNKNYLVWYQEK PGKVPKLLIYWASTR ESGVPSRFSGSGSGT DFTLTISSLQPEDVA TYYCQQYYKTPLTFG GGTKVEIKRTVAAPS VFIFPPSDEQLKSGT ASVVCLLNNFYPREA KVQWKVDNALQSGNS QESVTEQDSKDS TYS LKSTLTLSKADYEKH KVYACEVTHQGLSSP VTKSFNRGEC	EVQLVQSGAEVKKPGESLKISCKTSEYSF TSYWIGVRKMPGKGLEW MGI IYLGDS DTRYSPSFQGQVTI SADKSI STAYLQWSSLKASDTAMY YCARSNWGLDYWGQGLVTIVSSQPKANPTVTLFPPSSEELQANKATL VCLISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAAKS YLS LTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECSDKTH TCPPCPAPEL LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG VEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKAL PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGGGGSGGSQVQLQESGPGLVKP SETLSLTCTISGDSVSTNSVAWNWIRKPPGKGLEWIGRTYYRSKWYN DYAVSLKSRVTISPDTSKNQFSLKLSVTAADTAVYYCARE DGD SY Y RYGMDVWGQGT TTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK DYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLESVVTVPSSSLG TQTYICNVNHKPSNTKVDKKVEPKSC	QSVLTQPPPSVSGAPG QRVTISCTGSSSNIG AGYDVHWYQEFPGTA PKLLIQGNSNRPSGV PDRFSGSKSGTSASL AITGLQAEDEADYYC QSYDSSLSGSVFGGG TKLTVLGASTKGPSV FPLAPSSKSTSGGTA ALGCLVKDYFPEPVT VSWNSGALTSGVHTF PAVLQSSGLYSLESV VTVPSSSLGTQTYIC NVNHKPSNTKVDKKV EPKSC
		SEQ ID NO: 394	SEQ ID NO: 395	SEQ ID NO: 396

1PS: 376906	077_3B3v2_CK(S176K)_Fc.001_Ada1immunab_VH_CH1(S183E).001	NA	GATATCCAAATGACA CAATCACCATCGTCG CTTTCAGCGTCTGTT GGCGACCGTGTGACG ATTACCTGTCGCGG TCCCAGGGAATCCGG AATTACCTCGCATGG TATCAGGAGAAACCC GGAAAAGCACCGAAG CTCCTGATCTATGCC GCCTCGACTCTTCAG AGTGGTGTCCTGTCG AGGTTTAGCGGTCC GGGTCAAGTACGGAC TTTACTCTCACAAAT TCCAGCCTGCAGCCC GAAGATGTAGCTACC TATTACTGCCAGAGA TACAACCGAGCCCT TACACATTGGACAA GGGACAAAAGTCGAG ATCAAGCGTACGGTG GCTGCACCATCTGTC TTCATCTTCCCCGCA TCTGATGAGCAGTTG AAATCTGGAAC TGCC TCTGTTGTGTGCC TG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCCCAG GAGAGTGTACACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC AAGAGCACCCCTGACG CTGAGCAAAAGCAGAC	CAGGTGCAGTTACAGCAGTCGGGCGCAGGACTGTTGAAGCCTTTCGGA GACCCCTGTCCCTCACCTGCGCTGTCCATGGTGGTCTCTCAGTGGTT ACTACTGGAAC TGGATTTCGAAAGCCACCCAGGAAAGGGCTAGAGTGG ATTGGGGAAATCAATCATGCTGGAAACACCAACTACAACCCGTCCCT CAAGAGTCGAGTCACCATATCATTAGACACGTC CAAGAACCAGTTCT CCCTGACGCTGACCTCTGTGACCGCGCGGACACGGCTGTGTATTAC TGTGCGAGAGGATATTGTAGAAAGTACCACCTGCTACTTTGACTACTG GGCCAGGGAACCCTAGTCACCGTCTCCTCAACGGTGGCTGCACCAT CTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAAATCTGGAACT GCC TCTGTTGTGCTGCTGCTGAATAACTTC TATCCAGAGAGGCCAA AGTACAGTGGAAGGTGGATAACGCCCTCCAAATCGGGTAACTCCCAGG AGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAAG AGCACCC TGACGCTGAGCAAAAGCAGACTACGAGAAACACAAAAGTCTA CGCCTGCGAAAGTCACCCATCAGGGCTGAGCTCGCCCGTCACAAAGA GCTTCAACAGGGGAGAGTGTGACAAAAC TCACACATGCCCACCGTGC CCAGCACCTGAACTCTGGGGGACCGTCAGTCTTCTCTTCCCCC AAAACCCCAAGGACACCC TCATGATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGGTGACGTGAGCCACGAAACCC TGAGGTCAAGTTCAAC TGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAAGCCGTG TGAGGAGCAGTACGGCAGCACGTACC GTTGTGTGTCAGCGTCC TCACCG TCCTGCACCAAGACTGGCTGAA TGGCAAAGGAGTACAAAGTGCAAAGTC TCCAACAAAAGCCCTCCCAGCCCCCATCGAGAAAAACCATCTCCAAAGC CAAAGGCAGCCCCGAGAACCAACAGGTGTACACCTGCCCCCATCCC GGGAGGAGATGACCAAGAACCAAGTCAAGCTGACCTGACCTGCTGTCAAA GGCTTC TATCCAGCGACATCGCCGTGGAGTGGAGAGCAATGGGCA GCCGGAGAACTACAAGACCAACGCCCTCCCGTGTGGACTCCGACG GCTCCTTCTTCC TCTATAGCAAAGCTCACCGTGGACAAAGCAGGTGG CAGCAGGGGAACGCTTCTCATGTCTCCGTGATGCATGAGGCTCTGCA CAACCACTACACGCAGAAAGCCCTCTCCCTGTCTCCGGGTGGTGGCG GATCGGAGGTGGCGGATCCGAGGTACAAC TGGTGAATCAGGTGGA GGTTTGGTGACGCCGGGAGATCGCTCAGGCTTAGCTGTGCGGCATC GGGGTTTACTTTTCGATGATTATGCGATGCAT TGGGTCCGGAAGCGC CTGGAAAAGGCTCGAGTGGGTTTCCGCCATTACGTGGAATAGCGGA CACATCGATTATGCAGACAGTGTGGAGGGCAGATTCACAATCTCACG AGACAA TGCTAAGAACAGCCCTGTACCTTCAGATGAAC TCACTTCGCG CGGAAGATAACGCCGTATACTACTGCGCCAAAGTCTCCTACTTGTCT ACAGCTTCGTCGCTCGACTATTGGGGTCAAGGAACGTTGGTCACCGT	GAAATTGTGTTGACG CAGTCTCCAGGCACC CTGTCTTTGTCTCCA GGGAAAAGAGCCACC CTCTCCTGCAGGGCC AGTCAGAGTGTTAGA AGCAGTTACTTAGCC TGGTACCAGGAGAAA CCTGGCCAGGCTCCC AGGCTCCTCATCTAT GGTGCA TCCAGCAGG GCCACTGGCATCCCA GACAGGTTCAGTGGC AGTGGGTCTGGGACA GACTTCAC TCTCACC ATCAGCAGACTGGAG CCTGAAGATTTTGCA GTGATTACTGT CAG CAGTATGGTAGCTCA CCTACCTTCGGCCAA GGGACACGACTGGAG ATTAAAACGAGCCTCC ACCAAGGCCCATCG GTCTTCCCCCTGGCA CCCTCCTCCAAGAGC ACCTCTGGGGCACA GCGGCCCTGGGCTGC CTGGTCAAGGACTAC TTCCCCGAACCCGTG ACGGTGTCTGTGAAC TCAGGCGCCCTGACC AGCGGCGTGCA CACC TTCCCCGGCTGTCC TA CAGTCTCAGGACTC TACTCCCTCGAAAGC GTGGTGACCGTGCCC TCCAGCAGCTTGGGC
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		TACGAGAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGAGAGTGT	CTCTAGTGCCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCT CCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCCTGGTC AAGGACTACTTCCCCGAACCGGTGACGGTGTGCGTGAACCTCAGGCGC CCTGACCAGCGGTGCACACCTTCCCCGGCTGTCTACAGTCCTCAG GACTCTACTCCCTCGAGAGCGTGTGACCGTGCCCTCCAGCAGCTTG GGCACCAGACCTACATCTGCAACGTGAATCACAAAGCCCAGCAACAC CAAGGTGGACAAAGAAAGTTGAGCCCCAAAATCTTGT	ACCCAGACCTACATC TGCAACGTGAATCAC AAGCCAGCAACACC AAGGTGGACAAGAAA GTTGAGCCCCAAATCT TGT
		SEQ ID NO:397	SEQ ID NO:398	SEQ ID NO:399
AA		DIQMTQSPSSLSASV GDRVITITCRASQGIR NYLAWYQEKPGKAPK LLIYAASTLQSGVPS RFSGSGGTDFTLTI SSLQPEDVATYYCQR YNRAPYTFGQGTKVE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLKSTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEN	QVQLQQSGAGLLKPSSETLSLTCAVHGGSFSGYYWNWIRKPPGKGLEW IGEINHAGNTNYPNPSLKSRVTISLDTSKNQFSLTLTSVTAADTAVYY CARGYCRSTTCYFDYWGGQLVTVSSSTVAAPSVFIFPPSDEQLKSGT ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLK STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECDKHTCPCPC PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGGSGGGSEVQLVESGG GLVQPGRSRLRLSCAASGFTFDDYAMHWVRKAPGKGLEWVAITWNSG HIDYADSVETRFTISRDNAKNSLYIQMNSLRAEDTAVYYCAKVSYLS TASSLDYWGGQLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLESVVTVPSSSL GTQTYICNVNHPKPSNTKVDKKVEPKSC	EIVLTQSPGTLSLSP GERATLSCRASQSVR SSYLAWYQEKPGQAP RLLIYGASSRATGIP DRFSGSGGTDFTLT ISRLEPEDFAVYYCQ QYGSSTFFGQGRLE IKRASTKGPSVFPLA PSSKSTSGGTAALGC LVKDYFPEPVTVSWN SGALTSGVHTFPAVL QSSGLYSLESVVTVP SSSLGTQTYICNVNH KPSNTKVDKKVEPKS C
		SEQ ID NO:400	SEQ ID NO:401	SEQ ID NO:402
		CAGTCTGTGCTGACG CAGCCGCCCTCAGTG TCTGGGGCCCCAGGG CAGAGGGTCACCATC TCCTGCAC TGGGAGC AGTTCCAAACATCGGG GCAGGTTATGATGTA CACTGGTACCAGGAG TTTCCAGGAACAGCC CCCCAAACTCCTCATC CAAGGTAAACAGCAAT CGGCCCTCAGGGGTC CCTGACCGATTCTCT	CAGGTGCAGTTACAGCAGTCGGGGCGCAGGACTGTTGAAGCCTTCGGA GACCCCTGTCCCTCACCTGCGCTGTCCATGGTGGTCTCTCAGTGTT ACTACTGGAAC TGGATTGCGAAGCCACCCAGGAAGGGCTAGAGTGG ATTGGGGAAATCAATCATGCTGGAACACCAACTACAACCCGTCCCT CAAGAGTCGAGTCACCATATCATTAGACACGTCCAAGAACCAAGTTCT CCCTGACGCTGACCTCTGTGACCGCGCGGACACGGCTGTGTATTAC TGTGCGAGAGGATATTGTAGAAGTACCACCTGCTACTTTGACTACTG GGCCAGGGAACCTAGTCACCGTCTCCTCAACGGTGGCTGCACCCAT CTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAAATCTGGAAC T GCCCTCTGTTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAA AGTACAGTGGAAGGTGGATAACGCCCTCCAAATCGGGTAACTCCCCAGG AGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAAG AGCACCCCTGACGCTGAGCAAAAGCAGACTACGAGAAACACAAAAGTCTA	GAAATTGTGTTGACG CAGTCTCCAGGCACC CTGTCTTTGTCTCCA GGGAAAAGAGCCACC CTCTCCTGCAGGGCC AGTCAGAGTGTTAGA AGCAGTTACTTAGCC TGGTACCAGGAGAAA CCTGGCCAGGCTCCC AGGCTCCTCATCTAT GGTGCA TCCAGCAGG GCCACTGGCATCCCA GACAGGTTCAGTGGC
		NA		

		GGCTCCAAGTCTGGC ACCTCAGCCTCCCCTG GCCATCACTGGGCTC CAGGCTGAGGATGAG GCTGATTATTACTGC CAGTCCATATGACAGC AGCCTGAGTGGTTCCG GTGTTCCGGCGAGGG ACCAAGCTGACCGTCT CTAGGTCAGCCCAAG GCTGCCCTTCGGTCT ACTCTGTTCCCGCCC TCCTCTGAGGAGCTT CAAGCCAAACAAGGCC ACACTGGTGTCTCTC ATAAGTGACTTCTAC CCGGGAGCCGTGACA GTGGCCTGGAAGGCA GATAGCAGCCCCGTC AAGCGGAGTGGAG ACCAACACACCCCTCC AAACAAAGCAACAAC AAGTACGGGCCAAG AGCTATCTGAGCCCTG ACGCCTGAGCAGTGG AAGTCCCACAGAAGC TACAGCTGCCAGGTC ACGCATGAAGGGAGC ACCGTGAGAAAGACA GTGGCCCCTACAGAA TGTTCA	CGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGA GCTTCAACAGGGGAGAGTGTGACAAAACCTCACACATGCCCCACCGTGC CCAGCACCTGAACCTCCTGGGGACCGCTCAGTCTTCTCTTCCCCCCC AAAACCCAAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCACAT GCGTGGTGAGACGTGAGCCACGAAGACCCCTGAGGTCAAAGTTCAAC TGGTACGTGGACGGCGTGAGGTTGCATAAATGCCAAGAGACAAAGCCGTG TGAGGAGCAGTACGGCAGCACGTACCGTTGTGTGTCAGCGTCTCTACCG TCCTGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTC TCCAAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGC CAAAAGGCAGCCCCGAGAACCCACAGGTGTACACCCCTGCCCCCATCCC GGAGAGATGACCAAGAACCAAGTCAAGCTGACCTGCCCTGGTCAAA GGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCA GCCGGAGAACAACTACAAAGACCAACGCTCCCGTGTGCTGGACTCCGACG GCTCCTTCTTCCCTCTATAGCAAGCTCACCGTGGACAAGCAGCAGGTGG CAGCAGGGGAACGTCTTCTCATGTCTCCGTGATGCATGAGGCTCTGCA CAACCACTACACGCAAGAGCCCTCTCCCTGTCTCCGGGTGGTGGCG GATCGGGAGGTGGCGGATCCGAGGTGCAGCTGGTGCAGTCTGGAGCA GAGGTGAAAAAGCCCCGGGAGTCTCTGAAGATCTCCTGTAAGACTTC TGAATACAGCTTTACCAGCTACTGGATCGGCTGGGTGCGCAAGATGC CCGGGAAAGCCTGGAGTGGATGGGATCATCTATCTTGGTGACTCA GATACCAGATACAGCCCGTCTTCCAAGCCAGGTACCATCTCAGC CGACAAAGTCCATCAGTACCGCTACCTGCAGTGGAGCAGCCTGAAGG CCTCGGACACCGCCATGTATTACTGTGCGAGAAGTAAC TGGGTCTT GACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCTAGTCCCTCCAC CAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCT CTGGGGGCACAGCGGCCCTGGGCTGCCGTGCTCAAGGACTACTTCCCC GAACCGGTGACGGTGTCTGTGGAAC TCAAGCGCCCTGACCAGCGGCGT GCACACCTTCCCCGGCTGTCTCTACAGTCCCTCAGGACTCTACTCCCTCG AGAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTAC ATCTGCAACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAA AGTTGAGCCCCAAATCTTGT	SEQ ID NO:403	SEQ ID NO:404	SEQ ID NO:405
AA	QSVLTQPPSVSGAPG QRVTISCTGSSSNIG AGYDVHWYQEFPGTA PKLLIQGNSNRPSGV PDRFSGSKSGTSASL	QVQLQQSGAGLLKPS ETLSLTCAVHGGSFSGY YWNWIRKPPKGLEW IGEINHAGNTNYP SLKSRVTISLDT SKNQFSLTLTSV TAADTAVYY CARGYCRSTTCY FDYWGQGLTV TVSSSTVAAPSVFI FPPSDEQLKSGT ASVVCLLN NFYPREAKVQ WKVDNALQSGNSQ ESVTEQDSKDS TYSLKSTLTLSKADY EKHKVYACEV THQGLSSPVT KSFNRGECDK THTCPPC	EIVLTQSPGTL SLSPGERATL SCRASQSVR SSYLAWYQEK PGQAPRLLIY GASSRATGIP DRFSGSGS GTDFTLT			

			AITGLQAEDEADYYC QSYDSSLSGSVFGG TKLTVLGQPKAAPSV TLFPPSSEELQANKA TLVCLISDFYPGAVT VAWKADSSPVKAGVE TTTPSKQSNNKYAAK SYLSLTPEQWKSHRS YSCQVTHEGSTVEKT VAPTECS	PAPELLGGPSVFLFPPKPKD ¹ TLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKV SNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVK GFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRW QÖGNVFSCSVMHEALHNHYTQKSLSLSPGGSGGGSEVQLVQSGA EVKKPGESLKI ² ISCKTSEYSFTSYWIGWVRKMPGKGLEWMGI ³ IYLGDS DTRYSPSFÖGQVTI ⁴ SADKSI ⁵ STAYLQWSSLKASDTAMY ⁶ YCARSNWGL DYWGÖGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP EPVTVSWNSGALTS ⁷ GVHTFFPAVLQSSGLYSLESVVTVPSSSLGTQTY ICNVN ⁸ HKPSNTKVDKKVEPKSC	ISRLEPEDFAVYYCQ QYGSSTFFGQGRLE IKRASTKGPSVFPLA PSSKSTSGGTAALGC LVKDYFFPEPVTVSWN SGALTSGVHTFFPAVL QSSGLYSLESVVTVP SSSLGTQTYICNVNH KPSNTKVDKKVEPKS C
			SEQ ID NO: 406	SEQ ID NO: 407	SEQ ID NO: 408
		079_9C8_CK(S176K)_Fc.001_Ada11mumab_VH_CH1(S183) (E).001	GATATCCAAATGACA CAATCACCATCGTCG CTTTCAGCGTCTGTT GGCGACCGTGTGACG ATTACCTGTCGCGCG TCCCAGGGAATCCGG AATTACCTCGCATGG TATCAGGAGAAACCC GGAAAAGCACCCGAAG CTCCTGATCTATGCC GCCTCGACTCTTCAG AGTGGTGTGCCGTGG AGGTTTAGCGGGTCC GGGTACGGTACGGAC TTTACTCTCACAAATT TCCAGCCTGCAGCCC GAAGATGTAGCTACC TATTACTGCCAGAGA TACAAACCGAGCGCCT TACACATTCCGGACAA GGGACAAAAGTCGAG ATCAAGCGTACGGTG GCTGCACCATCTGTC TTCATCTTCCCCGCCA TCTGATGAGCAGTTG AAATCTGGAACTGCC	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTTCGGA GACCCCTGTCCCTCACCTGCACCTGCTCTCTGGTGGCTCCATCAGTAGTT ACTTCTGGAGCTGGATTTCGGAAGCCCCCAGGTAAGGACTGGAGTGG ATTGGCTATATCTATTACAGTGGGAGACCAAAATACAAACCCCTCCCT CAAGAGTCGAGTCACCATATCAATAGACACGTC ⁹ CAAGAACCA ¹⁰ AGTTCT CCCTGAAGCTGAGCTCTGTGACCGCTGCGGACACGGCCGTGTATTAC TGTCGAGAGAAACTGGGAGCTACTACGGCTTTGACTACTGGGGCCA GGGAACCCTGGTCACCGTCTCCTCAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCCTCT GTTGTGTGCCGTGCTGAATAA ¹¹ ACTTCTATCCAGAGAGGCCAAAGTACA GTGGAAGGTGGATAACGCCCTTCCAA ¹² TCGGGTAACTCCCAGGAGAGTG TCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAAGAGCACCC CTGACGCTGAGCAAAAGCAGACTACGAGAAACACAAAGTCTACGCCTG CGAAGTCACCCATCAGGGCCTGAGCTCGCCCCGTACAAAGAGCTTCA ACAGGGGAGAGTGTGACAA ¹³ AAC ¹⁴ TCA ¹⁵ CACATGCCACCGTGCCACAGCA CCTGA ¹⁶ ACTCCTGGGGGACCGTCAGTCTTCTCTTCCCCCCAAAACC CAAGGACACCC ¹⁷ TCATGATCTCCCGACCCCTGAGGTCA ¹⁸ CATGCGTGG TGGTGGACGTGAGCCACGAAGACCC ¹⁹ TGAGGTCAAGTTCAACTGGTAC GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCA ²⁰ GCCTCACCGTCCCTGC ACCAGGACTGGCTGAATGGCAAGGATACAAAGTGC ²¹ AAAGTCTCCCAAC AAAGCCCTCCCAGCCCCCATCGAGAA ²² AAACCATCTCCAAAGCCAAAGG GCAGCCCCGAGAACCA ²³ CAGGTGTACACCC ²⁴ TGCCCCCATCCCGGAGG AGATGACCAAGAACCA ²⁵ GGTCAGCCTGACCTGCC ²⁶ TGGTCAAAGGCTTC TATCCCAGCGACATCGCCGTGGAGTGGAGAGCAATGGCAGCCGGA GAACAACTACAAGACCA ²⁷ CGCCTCCCGTGTGGACTCCGACGGCTCCT	GACATCCAGATGACC CAGTCTCCATCCTCC CTGTCTGCATCTGTA GGAGACAGAGTCACC ATCAC ²⁸ TTGCCGGCA AGTCAGAGCATTAAC AACTATTTAAATTGG TATCAGGAGAGACCA GGGAAAAGCCCCTAAG CTCCTGATCTATGCT GCATCCAGTTTGCAA AGTGGGTCCCATCA AGGTTCAGTGGCAGT GGATCTGGGACAGAT TTCAC ²⁹ TCTCACCATC AGCAGTCTGCAACCT GAAGATTTTGCAACT TACTACTGTCAACAG AGTTACAGTACCCCT CGGACGTTCGGCCAA GGGACCAAGCTGGAA ATCAAAACGAGCCTCC ACCAAGGCCCATCG GTCTTCCCCCTGGCA CCCTCCTCCAAGAGC ACCTCTGGGGGCACA

		TCTGTTGTGTGCCTG CTGAATAACTTCTAT CCCAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCAG GAGAGTGCACAGAG CAGACAGCAAGGAC AGCACCTACAGCCTC AAGAGCACCTGACG CTGAGCAAAAGCAGAC TACGAGAAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	TCTTCCTCTATAGCAAGCTCACCGTGGACAAAGAGCAGGTGGCAGCAG GGGAACGTCTTCTCATGTCTCCGTGATGCATGAGGCTCTGCACAACCA CTACACGAGAACAGCCTCTCCCTGTCTCCGGTGGTGGCGGATCGG GAGTGCGGATCCGAGGTACAACCTGGTGAATCAGGTGAGGTTTG GTGAGCCGGGAGATCGCTCAGGCTTAGCTGTGCGGCATCGGGTT TACTTTCGATGATTATGCGATGCATTGGTCCGGAAGCGCCTGGAA AAGGCTCGAGTGGTTTCCGCCATTACGTGGAATAGCGGACACATC GATTATGCAGACAGTGTGAGGGCAGATTCACAATCTCACGAGACAA TGCTAAGAAACAGCCTGTACCTTCAGATGAACCTCACTTCGCGCGGAAG ATACCGCGTATACTACTGCGCCAAAAGTCTCCTACTTGTCTACAGCT TCGTGCTCGACTATTGGGGTCAAGGAACTTGTTCAACCGTCTCTAG TGCCCTCACCAAGGCCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCA AGAGCACCTCTGGGGCACAGCGGCCCTGGCTGCCCTGGTCAAGGAC TACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCCTGAC CAGCGCGTGCACACCTTCCCGCTGTCTACAGTCTCCTCAGGACTCT ACTCCCTCGAGAGCGTGTGACCGTGCCCTCCAGCAGCTTGGGCACC CAGACCTACATCTGCAACGTGAATCACAAAGCCAGCAACACCAAGGT GGACAAGAAAGTTGAGCCCAAATCTTGT	GGGGCCCTGGGCTGC CTGGTCAAGGACTAC TTCCCGAACCGGTG ACGGTGTCTGGAAC TCAGGCGCCTGACC AGCGCGTGCACACC TTCCCGGCTGTCCTA CAGTCTCAGGACTC TACTCCCTCGAAAGC GTGGTGACCGTGCCC TCCAGCAGCTTGGGC ACCCAGACCTACATC TGCAACGTGAATCAC AAGCCCAGCAACACC AAGGTGGACAAAGAA GTTGAGCCCCAAATCT TGT
		SEQ ID NO:409	SEQ ID NO:410	SEQ ID NO:411
	AA	DIQMTQSPSSLSASV GDRVITICRASQGIR NYLAWYQEKPGKAPK LLIYAASTLQSGVPS RFSGSGGTDFTLTI SSLQPEDVATYYCQR YNRAPYTFGQTKVE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLKSTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEC	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYFWSWIRKPPKGLEW IGYIYSGQTKYNPSLKSRTVISIDTSKNQFSCLKSSVTAADTAVYY CARETGSYYGFDYWGGQTLTVVSSTVAAPSVFIFPPSDEQLKSGTAS VVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLKST LTLISKADYEKHKVYACEVTHQGLSSPVTKSFNRGECDKHTTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGSGGGGSEVQLVESGGGL VQPGRSLRLSCAASGFTFDDYAMHWVRKAPGKGLEWVSAITWNSGHI DYADSVGEGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAKVSYLESTA SSLDYWGGQTLTVVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLESVVTVPSSSLGT QTYICNVNHKPSNTKVDKKVEPKSC	DIQMTQSPSSLSASV GDRVITICRASQIN NYLNWYQERPGKAPK LLIYAASSLQSGVPS RFSGSGGTDFTLTI SSLQPEDFATYYCQQ SYSTPRTFGQTKLE IKRASTKGPSVFFPLA PSSKSTSGGTAALGC LVKDYFPEPVTVSWN SGALTSGVHTFFPAVL QSSGLYSLESVVTVP SSSLGTQTYICNVNH KPSNTKVDKKVEPKS C
		SEQ ID NO:412	SEQ ID NO:413	SEQ ID NO:414

1PS: 376925	080_9C8_CR(S176K)_Fc.001_3.2_VH_CH1(S183E).001	NA	CAGTCTGTGCTGACG CAGCCGCCCTCAGTG TCTGGGCCCCAGGG CAGAGGTCACCATC TCCTGCAC TGGGAGC AGTTCCAAACATCGGG GCAGGTTATGATGTA CACTGGTACCAGGAG TTTCCAGGAACAGCC CCCAAAC TCC TCATC CAAGGTAACAGCAAT CGGCCCTCAGGGGTC CCTGACCGATTCTCT GGCTCCAAGTCTGGC ACCTCAGCCTCCCTG GCCATCACTGGGCTC CAGGCTGAGGATGAG GCTGATTA TTA CTGC CAGTCCTATGACAGC AGCCTGAGTGGTTCG GTGTTGGCGGAGGG ACCAAGCTGACCGTC CTAGGTCAGCCC AAG GCTGCCCCCTCGGTC ACTCTGTTCCCGCCC TCCTCTGAGGAGCTT CAAGCCAA CAAGGCC ACACTGGTG TGTCTC ATAAGTGACTTCTAC CCGGAGCCG TGACA GTGGCC TGGAAGGCA GATAGCAGCCCCGTC AAGCGGGAGTGGAG ACCACCA CACCCTCC AAACAAAGCAACAAC AAGTACGGGCCAAG AGCTATCTGAGCCTG	CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGTTGAAGCCTTTCGGA GACCC TGTCCCTCACCTGCACTGTCTCTGGTGGCTCCATCAGTAGTT ACTTCTGGAGCTGGATTTCGGAAGCCCCCAGGTAAGGACTGGAGTGG ATTGGCTATA TCTATTACAGTGGGCAGACCAAATACAA CCCC TCCCT CAAGAGTCGAGTCACCATATCAATAGACACGTC CAAGAACCAGTTCT CCCTGAAAGCTGAGCTCTGTGACCGCTGCGGACACGCGCTGTATTAC TGTGCGAGAGAAACTGGGAGCTACTACGGCTTTGACTACTGGGGCCA GGGAACCTGGTCACCGTCTCCTCAACGGTGGCTGCACCATCTGTCT TCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCCTCT GTTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACA GTGGAAGGTGGATAACGCCCTCCAA TCGGGTAACTCCCAGGAGAGTG TCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAAGAGCACCC CTGACGCTGAGCAAAAGCAGACTACGAGAAACACAAAGTCTACGCCTG CGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGTGACAAAACTCACACATGCCACCGTGCC CAGCA CCTGAACTCCTG GGGGACCGTCA GTCTTCTCTTCCCCCAA AACC CAAGGACACCC TCA TGATCTCCCGGACCCCTGAGGTCACATGCGTGG TGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAAGTTCAA CTGGTAC GTGGACGGCGTGAGGTGCATAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTCA GCGTCTCACC GTCC TGC ACCAGGACTGGCTGAATGGCAAAGGAGTACAAAGTCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGG GCAGCCCCGAGAACCA CAGGTGTACACCCCTGCCCATCCCGGAGG AGATGACCAAGAAC CAGGT CAGCCTGACCTG CCTGGTCAAAGGCTTC TATCCCAGCGACATCGCCGTGGAGTGGAGTGGAGAGCAATGGCAGCCGGA GAACAACTACAAGACCA CGCCTCCGTGCTGGACTCCGACGGCTCCT TCTTCCCTCTATAGCAAGCTCACCGTGGACAAAGACAGGTGGCAGCAG GGGAACGTCTTCTCATGTCTCCGTGATGCATGAGGCTCTGCACAA CCA CTACACGCAGAAAGCCCTCTCCCTGTCTCCGGTGGTGGCGGATCGG GAGGTGGCGGATCCGAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTG AAAAAGCCCCGGAGTCTCTGAAGATCTCCTGTGAAGACTTCTGAATA CAGCTTTAC CAGCTACTGGATCGGCTGGGTGCGCAAGATGCCCGGGA AAGCCCTGGAGTGGATGGGATCATCTATCTTGGTGACTCAGATA CC AGATACAGCCCGTCC TTTCCAAGGCCAGGTCA CCA TCTCAGCCGACAA GTCCATCAGTACCGCCTACCTGCAGTGGAGCAGCCTGAAGGCC TCGG ACACCGCCATGTATTACTGTGCGGAGAAGTAACTGGG GTCTTGACTAC TGGGGCCAGGGAACCC TGGTCACCGTCTCTAGTGCC TCCACCAAGGG	GACATCCAGATGACC CAGTCTCCATCCTCC CTGTCTGCATCTGTA GGAGACAGAGTCACC ATCACTTGCCGGCA AGTCAGAGCATTAAC AACTATTTAAATTGG TATCAGGAGAGACCA GGGAAAGCCCCTAAG CTCCTGATCTATGCT GCATCCAGTTTGCAA AGTGGGGTCCCATCA AGGTTAGTGGCAGT GGATCTGGGACAGAT TTCAC TCTCACCATC AGCAGTCTGCAACCT GAAGATTTTGCAACT TACTACTGTCAACAG AGTTACAGTACCCCT CGGACGTTCCGCCAA GGGACCAA GCTGGAA ATCAAACGAGCCTCC ACCAAGGCCCATCG GTCTTCCCCCTGGCA CCCTCCTCCAAGAGC ACCTCTGGGGCACA GCGGCCCTGGGCTGC CTGGTCAAGGACTAC TTCCCCGAACCCGTG ACGGTGTCTGTGAAC TCAGGCGCCCTGACC AGCGGCTGCACACC TTCCCGGCTGTCCTA CAGTCTCAGGACTC TACTCCCTCGAAAGC GTG GTACCGTGCCC TCCAGCAGCTTGGGC
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		ACGCTGAGCAGTGG AAGTCCCACAGAAAGC TACAGCTGCCAGGTC ACGCATGAAGGGAGC ACCGTGGAAGAAGACA GTGGCCCTACAGAA TGTTCA	CCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGG GCACAGCGGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCCGAACCG GTGACGGTGTCTGTGAACCTCAGCGCCCTGACCAAGCGGTGCACAC CTTCCCCGGCTGTCTACAGTCCCTCAGGACTCTACTCCCTCGAGAGCG TGGTGACCGTGCCCTCCAGCAGCTTGGCACCCAGACCTACATCTGC AACGTGAATCACAAAGCCAGCAACACCAAGGTGGACAAAGAAAGTTGA GCCCCAAATCTTGT	ACCCAGACCTACATC TGCAACGTGAATCAC AAGCCAGCAACACC AAGTGGACAAAGAAA GTTGAGCCCCAAATCT TGT
		SEQ ID NO:415	SEQ ID NO:416	SEQ ID NO:417
AA		QSVLTQPPSVSGAPG QRVTISCTGSSSNIG AGYDVHWYQEFFPGTA PKLLIQGNSNRPSGV PDRFSGSKSGTSASL AITGLQAEDEADYYC QSYDSSLSGSVFGGG TKLTVLGQPKAAPSV TLFPPSSEELQANKA TLVCLISDFYPGAVT VAWKADSSPVKAGVE TTTTPSKQSNNKYAAK SYLSLTPEQWKSHRS YSCQVTHEGSTVEKT VAPTECS	QVQLQESGPGLVKPSSETLSLTCTVSGGSISSYFWSWIRKPPGKGLEW IGYIYYSGQTKYNPSLKS RVTISIDTSKNQFSLKLS SVTAADTAVYY CARETGSYYGFDYWGGTLTVSSTVAAPS VFIFPPSDEQLKSGTAS VVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLKST LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPV L DSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMEALHNHYTQKSLSLSPGGSGGGSEVQLVQSGAEV KKPGESLKISCKTSEYSFTSYWIGWVRKMPGKGLEWMGI IYLGDSDT RYSPSFQGGVTISADKSI STAYLQWSSLKASDTAMY YCARSNWGLDY WGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP VTVSWNSGALTSGVHTFP AVLQSSGLYSLESVVTVPSSSLGTQTYIC NVNHKPSNTKVDKKVEPKSC	DIQMTQSPSSLSASV GDRVITITCRASQ SIN NYLNWYQERPGKAPK LLIYAASSLQSGVPS RFGSGSGTDFTLTI SSLQPEDFAITYCQQ SYSTPRRTFGG TKLE IKRASTKGPSVFPLA PSSKSTSGGTAALGC LVKDYFFPEPVTVSWN SGALTSGVHTFP AVL QSSGLYSLESVVTVP SSSLGTQTYICNVNH KPSNTKVDKKVEPKS C
		SEQ ID NO:418	SEQ ID NO:419	SEQ ID NO:420
		GATATCCAAATGACA CAATCACCATCGTCG CTTTCAGCGTCTGTT GGCGACCGTGTGACG ATTACCTGTCGCGCG TCCCAGGGAATCCGG AATTACCTCGCATGG TATCAGGAGAAAACCC GGA AAAGCACCCGAAG CTCCTGATCTATGCC GCCTCGACTCTTCAG AGTGGTGTGCCGTCG AGGTTTAGCGGGTCC	CAGGTACAGTTGCAGGAGT CAGGTCCAGGACTGGTGAAGCCCCTCGGA GACCCCTCTCACTCACCTGTACCATCTCCGGGACAGTGTCTCTACCA ACAGTGTGCTTGGA ACTGGATTAGGAAGCCCCCAGGAAAGGCCTT GAGTGGATAGGAAGGACAT ACTACAGGTCCAAGTGGTATAATGATTA TGCAGTTTCTCTGAAAAGTCGAGTAACCATCAGCC CAGACACATCCA AGAAACCA GTTCTCCCTGAAGCTGAGCTCTGTGACTGCCCGGACACG GCTGTGTATTACTGTGCAAGAGAGGATGGG GATAGCTACTACCGCTA CGGTATGGACGTCTGGGGCCAAAGGACCACGGTCA CCGTCTCCTCAA CGGTGGCTGCACCATCTGTCTTTCATCTTCCCGCCATCTGATGAGCAG TTGAAATCTGGA ACTGCCCTCTGTGTGTGCTGCTGTAATAACTTCTA TCCCAGAGAGGCCAAAGTACAGTGGAAAGTGGA TAACGCCCTCCCAAT CGGGTAACTCCCAGGAGAGTGT CACAGAGCAGGACAGCAAGGACAGC ACCTACAGCCTCAAGAGCACCCCTGACGCTGAGCAAAAGCAGACTACGA	GACATCCAGATGACC CAGTCTCCAAGCTCC CTGTCTGCCGTCTGTG GGCGATAGG GTCACC ATCACTTCAGGTCC AGCCAGAGTGTGTTA TACAGCTCCAACAAT AAGAACTACTTAGTT TGGTACCAGGAGAAA CCAGGAAAGGTTCTCT AAACTGCTCATTTAC TGGGCATCTACCCGG GAATCCGGGTCCT
		081_23B3_VH4_CK(S176K) Fc_001_Ada1_Imuab_VH CH1(S183E)_001		
!PS: 376930		NA		

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AA	QVQLQESGPGLVKPSSETLSLTCTISGDSVSTNSVAWNWIRKPPGKGL EWIGRTYYRSKWINDYAVSLKSRVTISPDTSKNQFSLKLSVTAADT AVYYCAREDGDSYYRYGMDVWGQGTVTVSSITVAAPSVFIFPPSDEQ LLIYAASTLQSGVPS	DIQMTQSPSSLSASV GDRVITITCRASQGIR NYLAWYQEKPGKAPK	DIQMTQSPSSLSASV GDRVITITCRSSQSVL YSSNNKNYLVWYQEK	PGKVPKLLIYWASTR

			RFSGSGGTDFTLTI SSLQPEDVATYYCQR YNRAPYTFGQTKVE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLKSTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEN	TYSLKSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECDKTH TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDP EVKFNWYVDGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKE YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSL TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV DKSRWQQGNVFSCSVMHEALHNYTQKSLSLSPGSGSGGGSEVQL VESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRKAPGKGLEWVSAI TWNSGHIDYADSVETRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAK VSYLSTASSLDYWGQGTLLVTVSSASTKGPSVFPLAPSSKSTSGGTAA LGCLVKDYFFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLESVVTV PSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSC	ESGVPSRFSGSGGT DFTLTISSLQPEDVA TYYCQQYYKTPLTFG GGTKVEIKRASTKGP SVFPLAPSSKSTSGG TAALGCLVKDYFPEP VTVSWNSGALTSGVH TFPAVLQSSGLYSLE SVVTVPSSSLGTQTY ICNVNHHKPSNTKVDK KVEPKSC
			SEQ ID NO:424	SEQ ID NO:425	SEQ ID NO:426
		082_23B3_VH4_CK(S176K)_Fc.001_3.2_VH_CH1(S183) E).001	NA	CAGGTACAGTTGCAGGAGTCAGGTCCAGGACTGGTGAAGCCCTCGGA GACCTCTCACTACCTGTACCATCTCCGGGACAGTGTCTCTACCA ACAGTGTTCCTTGGAACTGGATTAGGAAGCCCCCAGGGAAAAGCCCTT GAGTGGATAGGAAGACATACTACAGGTCCAAGTGGTATAATGATTA TGCAGTTTCTCTGAAAAGTCGAGTAAACCATCAGCCCCAGACACATCCA AGAACCAAGTTCTCCCTGAAGCTGAGCTCTGTGACTGCCGCGGACACG GCTGTGATTACTGTGCAAGAGAGGATGGGATAGCTACTACCGCTA CGGTATGGACGTCCTGGGGCCAAAGGACCACGGTCACCGTCTCCTCAA CGGTGGCTGCACCATCTGTCTTTCATCTTCCCGCCATCTGATGAGCAG TTGAAAATCTGGAACTGCCCTCTGTGTGTGCCCTGCTGAATAACTTCTA TCCCAGAGAGGCCAAAGTACAGTGGAAGTGGATAACGCCCTCCAAT CGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGACACAGC ACCTACAGCCTCAAGAGCACCCCTGACGCTGAGCAAAAGCAGACTACGA GAAACACAAAGTCTACGCCCTGCCAAGTCAACCATCAGGGCCTGAGCT CGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTGACAAAACCTCAC ACATGCCCACCGTGCCCAGCACCTGAACCTCCTGGGGGACCGTCAGT CTTCCTCTTCCCCCAAACCCAAAGACACCCCTCATGATCTCCCCGA CCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCT GAGGTCAAGTTCAACTGTTACGTGGACGGCGTGGAGGTGCATAATGC CAAGACAAAAGCCGTGTGAGGAGCAGTACGGCAGCACGTACCGTTGTG TCAGCGTCCTCACCGTCCCTGCACCAGGACTGGCTGAATGGCAAGGAG TACAAGTGCAAGTCTCCAAACAAAGCCCTCCAGCCCCCATCGAGAA AACCATCTCCAAAGCCAAAGGGCAGCCCCCGAGAAACACAGGTGTACA CCCTGCCCCCATCCCCGGGAGGAGATGACCAAGAACCAAGTCAGCCTG ACCTGCCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTG	GACATCCAGATGACC CAGTCTCCAAGCTCC CTGTCTGCGTCTGTG GGCGATAGGTCACC ATCACTTGCAGGTCC AGCCAGAGTGTGTTA TACAGCTCCAACAAT AAGAACTACTTAGTT TGGTACCAGGAGAAA CCAGGAAAAGTTCCT AAACTGCTCATTTAC TGGCATCTACCCGG GAATCCGGGTCCCT AGTCGATTCAGTGGC AGCGGTCTGGGACA GATTTCACTCTCACC ATCAGCAGCCTGCAG CCTGAAGATGTGGCA ACTTATTACTGTGAG CAATATTATAAGACT CCTCTCACTTTCGGC GGAGGACCAAAGGTG GAGATCAAACGAGCC TCCACCAAGGCCCA TCGGTCTTCCCCCTG

			T CCTCTGAGGAGCTT CAAGCCAAACAAGGC ACACTGGTGTCTC ATAAGTGACTTCTAC CCGGAGCCGTGACA GTGGCCTGGAAGGCA GATAGCAGCCCCGTC AAGCGGAGTGGAG ACCACCACCCCTCC AAACAAAGCAACAAC AAGTACGGGCCAAG AGCTATCTGAGCCTG ACGCCTGAGCAGTGG AAGTCCCACAGAAGC TACAGCTGCCAGGTC ACGCATGAAGGGAGC ACCGTGAGAAAGACA GTGGCCCCTACAGAA TGTTCA	GGAGAGCAATGGGCAGCCGGAGAAACAATAAGACCAAGCCTCCCG TGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTG GACAAGACAGGTGGCAGCAGGGAAACGTCTTCTCATGCTCCGTGAT GCATGAGGCTCTGCACAAACCACATACACGCAGAAAGAGCCTCTCCCTGT CTCCGGGTGTCGGGATCGGGAGGTGGCGGATCCGAGGTGCAGCTG GTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGAGTCTCTGAAAGAT CTCCTGTAAGACTTCTGAATACAGCTTTACCAGCTACTGGATCGGCT GGTGCGCAAGATGCCCGGGAAGGCCCTGGAGTGGATGGGATCATC TATCTTGGTGACTCAGATACCAGATACAGCCCGTCCTTCCAAGGCCA GGTCACCATCTAGCCGACAAGTCCATCAGTACCGCTACCTGCAGT GGAGCAGCCTGAAGCCTCGGACACCGCCATGATTACTGTGCGAGA AGTAACTGGGCTCTTGACTACTGGGGCCAGGAACCCCTGTCACCGT CTCTAGTGCTCCACCAAGGCCCATCGGTCTTCCCCCTGGCACCCCT CCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTC AAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGC CCTGACCAGCGGTGCACACCTTCCCGGCTGTCTACAGTCCCTCAG GACTCTACTCCCTCGAGAGCGTGTGTGACCGTGCCCTCCAGCAGCTTG GGCACCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAC CAAGGTGGACAAAGAAAGTTGAGCCCCAAAATCTTGT	GCACCTCTCTCCAAG AGCACCTCTGGGGGC ACAGCGCCCTGGGC TGCTTGGTCAAGGAC TACTTCCCCGAACCG GTGACGGTGTCTGG AACTCAGGCGCCCTG ACCAGCGCGTGCAC ACCTTCCCCGGCTGC CTACAGTCTCAGGA CTCTACTCCCTCGAA AGCGTGTGACCGTG CCCTCAGCAGCTTG GGACCCAGACCTAC ATCTGCAACGTGAAT CACAAAGCCAGCAAC ACCAAGGTGGACAA AAAGTTGAGCCCCAAA TCTTGT
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		CAATCACCATCGTCG CTTTCAGCGTCTGTT GGGACCGTGTGACG ATTACCTGTCGGCG TCCCAGGGAATCCGG AATTACCTCGCATGG TATCAGGAAAAACCC GGAAAAGCACCGAAG CTCCTGATCTATGCC GCCTCGACTCTTCAG AGTGGTGTCGCCGTCG AGGTTTAGCGGGTCC GGGTCAGGTACGGAC TTTTACTCTACAAATT TCCAGCCTGCAGCCC GAAGATGTAGCTACC TATTACTGCCAGAGA TACAACCGAGCGCCT TACACATTGGGACAA GGGACAAAAGTCGAG ATCAAGCGTACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGAAC TGCC TCTGTTGTGTGCCCTG CTGAAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCCCAG GAGAGTGTACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC GAAAGCACCCCTGACG CTGAGCAAAAGCAGAC TACGAGAAAACACAAA	ATCGCTCAGGCTTAGCTGTGCGGCATCGGGGTTTACTTTCGATGATT ATGCCATGCATTGGGTCCGGAAGAGCGCCTGGAAGAGGGCTCGAGTGG GTTTCCGCCATTACGTGGAATAGCGGACACATCGATTATGCAGACAG TGTGGAGGGCAGATTCACAATCTCACGAGACAA TGCTAAGAACAGCC TGTAACCTTCAGATGAAC TCACTTCGCGGGAAGATACCGCCGTATAC TACTGCGCCAAAAGTCTCCTACTTGTCTACAGCTTCGTGCTCGACTA TTGGGGTCAAGGAACGTTGGTCACCGTCTCTAGTGCCCTCCACCAAGG GCCCATCGGTCTTCCCCCTGGCACCCCTCCTCAAAGACACCTCTGGG GGCACAGCGGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCCGAACC GGTGACGGTGTCGTGGAAC TCAAGCTCAGGCGCCCTGACCAGCGCGTGCACA CCTTCCCGGCTGTCTACAGTCTCTCAGGACTCTACTCCCTCAAAAAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG CAACGTGAATCAAAAGCCAGCAACACCAAGGTGGACAAAGAAAGTTG AGCCCCAAATCTTGTGACAAAAC TCAACATGCCCCACCGTGCCCCAGCA CCTGAAC TCTCTGGGGACCGTCAGTCTTCCTCTTCCCGCCAAAACC CAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGG TGGTGGACGTGAGCCACGAAGACCC TGAGGTCAAAGTTCAACTGGTAC GTGGACGGGTGGAGGTGCATAAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCGTTGTGTGTCAGCGTCTCTACCGTCCCTGC ACCAGGACTGGCTGAATGGCAAGGAGTACAAAGTCAAGGTC TCCAAC AAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAAGG GCAGCCCCGAGAACCAACAGGTGTACACCCCTGCCCCCATCCCCGGAGG AGATGACCAAAGAACCAAGTCAAGCTGACCTGACCTGGTCAAAGGCTTC TATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCCGGA GAACAAC TACAAGACCAACGCTCCCGTGTGACTCCGACGCTCCT TCTTCCCTCTATAGCAAGCTCACCGTGGACAAAGACAGGTTGGCAGCAG GGGAACGTC TTTCTCATGTCTCCGTGATGCATGAGGCTCTGCACAAACCA CTACACGCAGAAAGCCCTCTCCCTGTCTCCGGTGGTGGCGGATCGG GAGGTGGCGGATCCCAGGTGCAGTTACAGCAGTCGGGCGCAGGACTG TTGAAGCCTTCGGAGACCCCTGTCCCTCACCTGCGCTGTCCATGGTGG GTCCCTTCAGTGGTTACTACTGGAACTGGATTTCGCAAGCCACAGGGA AGGGGCTAGAGTGGATTGGGGAATCAATCATGTCTGGAACACACCAAC TACAACCGTCCCTCAAGAGTCGAGTCACCATATCATTAGACACGTC CAAGAAC CAGTTCTCCCTGACGCTGACCTCTGTGACCGCCGGGACA CGGCTGTGTATTACTGTGCGAGAGGATATTGTAGAAGTACCACTGC TACTTTGACTACTGGGGCCAGGGAACCC TAGTCAACCGTCTCCTCAAC TGTGGCTGCACCATCTGTCTTTCATCTTCCCGCCATCTGATGAGCAGT	CAGTCTCCAGGCACC CTGTCTTTTGTCTCCA GGGAAAGAGCCACC CTCTCCTGCAGGGCC AGTCAGAGTGTAGA AGCAGTTACTTAGCC TGGTACCAGGAGAAA CCTGGCCAGGCTCCC AGGCTCCTCATCTAT GGTGCA TC CAGCAGG GCCACTGGCATCCCA GACAGGTTCAGTGGC AGTGGTCTGGGACA GACTTCACTCTCACC ATCAGCAGACTGGAG CCTGAAAGATTTTGCA GTGTATTACTGTCTAG CAGTATGGTAGCTCA CCTACCTTCGGCCAA GGGACACGACTGGAG ATTAACAGAGCCTCC ACCAAGGGCCCATCG GTCTTCCCGCTGGCA CCCTCCTCCAAGAGC ACCTCTGGGGCACA GCGGCCCTGGGCTGC CTGGTCAAGGACTAC TTCCCGGAACCGGTG ACGGTGTCTGTGAAC TCAGGCGCCCTGACC AGCGCGTGCACACC TTCCCGGCTGTCCTA CAGTCCTCAGGACTC TACTCCCTCAAAAGC GTGGTGACCGTGCCC TCCAGCAGCTTGGGC ACCCAGACCTACATC
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			GTCTACGCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGAGAGTGTT	TGAAATCTGGAACTGCCTCTGTTGTGTGCTGCTGAATAACTTCTAT CCCAGAGAGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC GGGTAACTCCAGGAGAGTGTACAGAGCAGACAGCAAGGACAGCA CCTACAGCCTCGAAAAGCACCCTGACGCTGAGCAAAGCAGACTACGAG AAACACAAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTC GCCCCACAAAAGAGCTTCAACAGGGGAGAGTGT	TGCAACGTGAATCAC AAGCCAGCAACACC AAGGTGACAAAGAAA GTTGAGCCCCAAATCT TGT
		SEQ ID NO:433	SEQ ID NO:434	SEQ ID NO:435	
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		GDRVITITCRASQGIR	VSAITWNSGHIDYADSVEGRFTISRDNAKNSLYLQMNSLRAEDTAVY	GERATLSCRASQSVR	
		NYLAWYQEKPGKAPK	YCAKVSYLSTASSLDYWGGQTLVTVSSASTKGPSVFFPLAPSSKSTSG	SSYLAWYQEKPGQAP	
		LLIYAASTLQSGVPS	GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLKS	RLLIYGASSRATGIP	
		RFSGSGGTDFTLTI	VVTVPPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSCDKTHTCTPPCPA	DRFSGSGGTDFTLT	
		SSLQPEDVATYYCQR	PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY	ISRLEPEDFAVYYCQ	
		YNRAPYTFGQGTKVE	VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN	QYGSSTFGQGRLE	
		IKRTVAAPSVFIFPP	KALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGF	IKRASTKGPSVFPLA	
		SDEQLKSGTASVVCL	YPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQQ	PSSKSTSGGTAALGC	
		LNNFYPREAKVQWKV	GNVFSCSVMHREALHNHYTQKSLSLSPGGGGSGGSQVQLQQSGAGL	LVKDYFPEPVTVSWN	
NA		DNALQSGNSQESVTE	LKPSETLSLTCAVHGGSFSGYYWNWIRKPPGKLEWIGEINHAGNTN	SGALTSGVHTFFPAVL	
		QDSKDSITYSLESTLT	YNPSLKSrvTISLDTSKNQFSLTTLTSVTAADTAVYYCARGYCRSTTC	QSSGLYSLKSVVTVP	
		LSKADYEKHKVYACE	YFDYWGQGTLVTVSSITVAAPSVFIFPPSDEQLKSGTASVVCLLNNFY	SSSLGTQTYICNVNH	
		VTHQGLSSPVTKSFN	PREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLESTLTLSKADYE	KPSNTKVDKKVEPKS	
		RGEC	KHKVYACEVTHQGLSSPVTKSFNRGEC	C	
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		GATATCCAAATGACA	GAGGTACAACTGGTGGAAATCAGGTGGAGGTTTGGTGCAGCCCGGGAG	GACATCCAGATGACC	
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		CTTTCAGCGTCTGTT	ATGCGATGCATTGGGTCCGGAAGCGCCTGGAAGGAGGGCTCGAGTGG	CTGTCTGCATCTGTA	
		GGCGACCGTGTGACG	GTTTCCGCCATTACGTGGAATAGCGGACACATCGATTATGCAGACAG	GGAGACAGAGTCACC	
		ATTACCTGTCGCGCG	TGTGGAGGGCAGATTCACAATCTCACGAGACAAATGCTAAGAACAGCC	ATCACTTGCCCGGCA	
		TCCCAGGGAATCCGG	TGTACCTTCAGATGAACCTCACTTCGCGCGAAGATACCGCCGTATAC	AGTCAGAGCATTAAC	
		AATTACCTCGCATGG	TACTGCGCCCAAAGTCTCCTACTTGTCTACAGCTTCGTCGCTCGACTA	AACTATTTAAATTGG	
		TATCAGGAAAAACCC	TTGGGGTCAAGGAACGTTGGTCACCGTCTCTAGTGCCTCCACCAAGG	TATCAGGAGAGACCA	
		GGAAAAGCACCCGAAG	GCCCATCGGTCTTCCCCCTGGCACCCCTCTCCAAGAGCACCTCTGGG	GGGAAAGCCCCCTAAG	
		CTCCTGATCTATGCC	GGCACAGCGGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCCGAACC	CTCCTGATCTATGCT	
		GCCTCGACTCTTCAG	GGTGACGGTGTCTGTGGAACCTCAGGCGCCCTGACCAGCGCGTGCACA	GCATCCAGTTTGCAA	
		AGTGGTGTGCGGTCG	CCTTCCCCGGCTGTCCCTACAGTCCCTCAGGACTCTACTCCCTCAAAAGC	AGTGGGTCCCCATCA	
		AGGTTTAGCGGGTCC	GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG	AGGTTCAGTGGCAGT	
		GGGTACGGTACGGAC	CAACGTGAATCACAAAGCCCGACCAACCAAGGTGGACAAAGAAAGTTG	GGATCTGGGACAGAT	

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C8_VH_CK(S176E).001

		TTTACTCTCACAAATT TCCAGCCTGCAGCCC GAAGATGTAGCTACC TATTACTGCCAGAGA TACAACCGAGCGCCT TACACATTGGACAA GGACAAAAAGTCGAG ATCAAGCGTACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGAAC TGCC TCTGTTGTGTGCC TG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAAGTG GATAACGCCCTCCAA TCGGGTAAC TCCAG GAGAGTGCACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC GAAAGCACCC TGACG CTGAGCAAAGCAGAC TACGAGAAAACACAAA GTCTACGCC TCGGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	AGCCCAAATCTTGTGACAAAAC TCA CCTGAAC TCTGGGGGACCGT CAGTCTT CAAGGACACCC TCA TGATCTCCCGGAC TGGTGGACGTGAGCCACGAAGACCC TG GTGGACGGCTGAGGTGCATAATGCCAAG GCAGTACGGCAGCACGTACCGTTGTGTCA ACCAGGACTGGCTGAATGGCAAGGATCA AAAGCCCTCCAGCCCCCATCGAGAAAAC GCAGCCCCGAGAACCAAGGTGTACACCC AGATGACCAAGAACCAAGTCAAGCTGAC TATCCAGCGACATCGCCGTGGAGTGGAG GAAACAACTACAAAGACCAAGCTCCCGT TCTTCC TCTATAGCAAGCTCACCGTGGA GGAAACGTCTTCTCATGTCTCCGTGATGC CTACACGCAGAAAGACCTCTCCCTGTCTC GAGTGCGGATCCAGGTGCAGCTCGGAGTC GTGAAGCCTTCGGAGACCC TGTCCCTCA CTCCATCAGTAGTTACTTCTGGAGCTGGA AGGGACTGGAGTGGATTGGCTATATCTAT TACAACCCCTCCCTCAAGAGTCGAGTCA CAAGAACCAAGTTCTCCCTGAAGCTGTGA CGGCCGTGTATTACTGTGCGAGAGAAAC GACTACTGGGCCAGGGAACCC TGGTCA TGACACCATCTGTCTTCA TCTTCCGCCCA CTGGAAC TGCCTCTGTTGTGTGCTGCTG GAGGCCAAAAGTACAGTGGAAAGTGGA CTCCCAGGAGAGTGTCA CAGAGCAGGACA GCC TCGAAAGCACCC TGA CCGCTGAGCA AAAGTCTACGCCCTGCGAAGTCA CCCC CACAAAGAGCTTCAACAGGGGAGAGTGT	SEQ ID NO: 439	SEQ ID NO: 440	SEQ ID NO: 441
AA	DIQMTQSPSSLSASV GDRVITTCRASQIR NYLAWYQEKPGKAPK LLIYAASTLQSGVPS RFSGSGGTDFLTIT SSLQPEDVATYYCQR	EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRKAPGKLEW VSAITWNSGHIDYADSV EGRFTISRDNAKNSLYLQMNSLRAEDTAVY YCAKVS YLSTASSLDYWGGQTLTVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLKS VVTVPSSSLGTQYIICNVN HKPSNTKVDKKVEPKSCDKTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY	DIQMTQSPSSLSASV GDRVITTCRASQIN NYLWNWYQERP GKAPK LLIYAASSLQSGVPS RFSGSGGTDFLTIT SSLQPEDFATYYCQQ			

			YNRAPYTFGQGTKVE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSYTSLESTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEN	SEQ ID NO:442	SEQ ID NO:443	VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGSQVQLQESGPGL VKPSETLSLTCTVSGGSISSYFWSWIRKPPGKGLEWIGYIYYSGQTK YNPSLKSRVTISIDTSKNQFSKLSSVTAADTAVYYCARETGSYYGF DYWGQGTLLVTVSSSTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR EAKVQWKVDNALQSGNSQESVTEQDSKDSYTSLESTLTLSKADYEKH KVYACEVTHQGLSSPVTKSFNRGEC	SEQ ID NO:444	SYSTPRTFGQGTKLE IKRASTKGPSVFPLA PSSKSTSGGTAALGC LVKDYFFPEPVTVSWN SGALTSGVHTFFPAVL QSSGLYSLKSVVTVP SSSLGTQTYICNVNH KPSNTKVDKKVEPKS C
	085_Adalimumab_IgG.002_23B3_VH4_VH_CK(S176E).001	NA	GATATCCAAATGACA CAATCACCATCGTCG CTTTCAGCGTCTGTT GGCGACCGTGTGACG ATTACCTGTCGCGCG TCCAGGGAATCCGG AATTACCTCGCATGG TATCAGGAAAAACCC GGAAGAAGCACCGAAG CTCCTGATCTATGCC GCCTCGACTCTTCAG AGTGGTGTCCTGTCG AGGTTTAGCGGGTCC GGGTCAGGTACGGAC TTTACTCTACAAT TCCAGCCTGCAGCCC GAAGATGTAGCTACC TATTACTGCCAGAGA TACAACCGAGCGCCT TACACATTCCGACAA GGGACAAAAGTCGAG ATCAAGCGTACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGAACCTGCC TCTGTTGTGTGCTG	SEQ ID NO:442	SEQ ID NO:443	GAGGTACAACTGGTGGAATCAGGTGGAGGTTTGGTGCAGCCGGGGAG ATCGCTCAGGCTTAGCTGTGCGGCATCGGGGTTTACTTTCGATGATT ATGCGATGCATTTGGTCCGGAAGCGCCTGGAAGGAGGCTCGAGTGG GTTTCCGCCATTACGTGGAATAGCGGACACATCGATTATGCAGACAG TGTGGAGGGCAGATTACAATCTCACGAGACAAATGCTAAGAACAGCC TGTAACCTTCAGATGAACCTCACTTCGCGCGGAAGATACCGCCGTATAC TACTGCGCCAAAAGTCTCCTACTTGTCTACAGCTTCGTCTCGCTCGACTA TTGGGTCGAAGGAACGTTGGTCACCGTCTCTAGTGCCTCCACCAAGG GCCATCGGTCTTCCCCCTGGCACCCCTCTCCAAAGACACCTCTGCGG GGCACAGCGGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCCGAACC GGTGACGGTGTCTGTGGAACCTCAGGCGCCCTGACCAGCGCGTGCACA CCTTCCCCGGCTGTCTACAGTCTCTCAGGACTCTACTCCCTCAAAAAGC GTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG CAACGTGAATCACAAAGCCAGCAACACCAAGGTGGACAAAGAAAGTTG AGCCCCAAATCTTGTGACAAAACCTCACACATGCCACCCGTGCCAGCA CCTGAACCTCCTGGGGGACCGTCACTTCTCTCTTCCCCCCTCAAAACC CAAGGACACCCCTCATGATCTCCCCGACCCCTGAGGTCACATGCGTGG TGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTAC GTGGACGGCGTGAGGTGCATAAATGCCAAGACAAAGCCGTGTGAGGA GCAGTACGGCAGCACGTACCCTTGTGTCTCAGCGTCTCTACCGTCTCTGC ACCAGGACTGGCTGAATGGCAAGGAGTACAAAGTCAAGGTCTCCAAC AAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGG GCAGCCCCGAGAACCAAGGTGTACACCTGCCCCCATCCCCGGGAGG AGATGACCAAGAACCAAGGTACGCTGACCTGACCTGGTCAAAGGCTTC TATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGA GAACAACTACAAGACCAAGCTTCCCGTGTGCTGGACTCCGACGGCTCCT TCTTCCCTCTATAGCAAGCTCACCGTGGACAAAGACGAGTGGCAGCAG	SEQ ID NO:444	GACATCCAGATGACC CAGTCTCCAAGCTCC CTGTCTGCGTCTGTG GGCGATAGGTCACC ATCACATTGCAGGTCC AGCCAGAGTGTGTTA TACAGCTCCAACAAT AAGAACTACTTAGTT TGGTACCAGGAGAAA CCAGGAAAAGTTCCT AAACTGCTCATTTAC TGGGCATCTACCCGG GAATCCGGGTCCCT AGTCGATTCAGTGGC AGCGGGTCTGGGACA GATTTCACTCTCACC ATCAGCAGCCTGCAG CCTGAAGATGTGGCA ACTTATTACTGTCTAG CAATATTATAAGACT CCTCTCACTTTCGGC GGAGGGACCAAGGTG GAGATCAAACGAGCC TCCACCAAGGGCCCA TCGGTCTTCCCCCTG GCACCTCTCCTCCAAG AGCACCTCTGGGGC GCACCTCTGGGGC

IPS: 376955

1PS: 376955

		CTGAATAACTTCTAT CCCAGAGAGCCAAA GTACAGTGGAAGGTG GATAAGCCCTCCAA TCGGGTAACTCCCAG GAGAGTGCACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCTC GAAAGCACCCCTGACG CTGAGCAAAAGCAGAC TACGAGAAAACACAAA GTCACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGGAGAGTGT	GGGAACGTCTTCTCATGTCTCCGTGATGCATGAGGCTCTGCACAAACCA CTACACGCAGAAAGAGCCTCTCCCTGTCTCCGGGTGGTGCGGATCGG GAGTGCGGATCCCAGGTACAGTTGCAGAGTCAGGTCCAGGACTG GTGAAGCCCTCGGAGACCCTCTCACTCACTCACTGTACCATCTCCGGGA CAGTGTCTTACCAACAGTGTCTTGAACTGGATTAGGAAGCCCC CAGGAAAAGCCTTGAGTGGATAGGAAGGACATACACAGGTCCAAG TGGTATAATGATTATGCAGTTTCTCTGAAAAAGTCGAGTAACCATCAG CCCAGACACATCCAAAGAACCCAGTTCTCCCTGAAGCTGAGCTCTGTGA CTGCCGGGACACGGCTGTGTATTACTGTGCAAGAGAGGATGGGGAT AGCTACTACCGCTACGGTATGGACGTCTGGGGCCAAAGGACCACGGT CACCGTCTCTCAACTGTGGCTGCACCATCTGTCTTCACTCTCCCGC CATCTGATGAGCAGTTGAAATCTGGAACTGCCCTCTGTTGTGTGCCCTG CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGA TAACGCCCTCCAATCGGGTAACCTCCAGGAGAGTGTCAACAGAGCAGG ACAGCAAGGACAGACCTACAGCCTCGAAAGCACCCCTGACGCTGAGC AAAGCAGACTACGAGAAAACACAAAGTCTACGCCCTGCGAAAGTCACCCA TCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGT GT	ACAGCGGCCCTGGGC TGCCTTGGTCAAGGAC TACTTCCCGAACC GTACGGTGTCTGTG AACTCAGCGCCCTG ACACGGCGGTGCAC ACCTTCCCGGCTGTC CTACAGTCCCTCAGGA CTCTACTCCCTCAAA AGCGTGGTGACCGTG CCCTCCAGCAGCTTG GGCACCCAGACCTAC ATCTGCAACGTGAAT CACAAAGCCAGCAAC ACCAAGGTGGACAAAG AAAGTTGAGCCCCAAA TCTTGT
		SEQ ID NO:445	SEQ ID NO:446	SEQ ID NO:447
	AA	DIQMTQSPSSLSASV GDRVITITCRASQGIR NYLAWYQEKPGKAPK LLIYAASTLQSGVPS RFSGSGGTDFTLTI SSLQPEDVATYYCQR YNRAPYTFGQTKVE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLESTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEN	EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRKAPGKGLEW VSAITWNSGHIDYADSVVEGRFTISRDNAKNSLYLQMNSLRAEDTAVY YCAKVSYLEASTSLDYWGQGLVTVVSSASTKGPSVFPLAPSSKSTSG GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLKS VVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTHTCPPCPA PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSN KALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGF YPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQ GNVFSCSVMHEALHNHYTQKSLSLSPGSGGSGGSQVQLQESGPGL VKPSETLSLTCTISGDSVSTNSVAWNRIKPPGKGLEWIGRTYYRSK WYNDYAVSLKSRVTISPDTSKNQFSLKLSSTAAADTAVYYCAREDDGD SYRYRGMDVWGQGTITVTVSSITVAAPSVFIFPPSDEQLKSGTASVVCL LNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLESTLTLS KADYEKHKVYACEVTHQGLSSPVTKSFNRGEC	DIQMTQSPSSLSASV GDRVITITCRSSQSVL YSSNNKNYLVWYQEK PGKVPKLLIYWASTR ESGVPSRFSGSGSGT DFTLTISLQPEDVA TYYCQQYYKTPLTFG GGTKVEIKRASTKGP SVFPLAPSSKSTSGG TAALGCLVKDYFPEP VTVSWNSGALTSGVH TFP AVLQSSGLYSLK SVVTVPSSSLGTQTY ICNVNHKPSNTKVDK KVEPKSC
37	38	SEQ ID NO:448	SEQ ID NO:449	SEQ ID NO:450
39	39	CAGTCTGTGCTGACG	GAGGTGCAGCTGGTGCACTCTGGAGCAGAGGTGAAAAAGCCCGGGA	GAAATTGTGTTGACG
40	40	CAGCCGCCCTCAGTG	GTCTCTGAAGATCTCCTGTAGACTTCTGAATACAGCTTTACCAGCT	CAGTCTCCAGGCACC

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TCTGGGGCCCCAGGG CAGAGGGTCACCATC TCCTGCACTGGGAGC AGTTCCAAACATCGGG GCAGGTTATGATGTA CACTGGTACCAGGAG TTTCCAGGAACAGCC CCCAAACTCCTCATC CAAGGTAACAGCAAT CGGCCCTCAGGGGTC CCTGACC GATTCTCT GGCTCCAAGTCTGGC ACCTCAGCCTCCCTG GCCATCACTGGGCTC CAGGCTGAGGATGAG GCTGATTATTACTGC CAGTCCTATGACAGC AGCCTGAGTGGTTCG GTGTTCCGGCGGAGGG ACCAAGCTGACCGTC CTAGGTGAGCCCAAG GCTGCCCCCTCGGTC ACTCTGTTCCCGCCC TCCTCTGAGGAGCTT CAAGCCAAACAAGGCC ACACTGGTGTGTCTC ATAAGTGACTTCTAC CCGGAGCCCGTGACA GTGGCCTGGAAGGCA GATAGCAGCCCGTC AAGCGGGAGTGGAG ACCACCACACCCCTCC AAACAAAGCAACAAC AAGTACGCGGCGGAG AGCTATCTGAGCCTG ACGCCTGAGCAGTGG AAGTCCCACAGAAGC	ACTGGATCGGCTGGGTGCGCAAGATGCCCGGGAAGGCCCTGGAGTGG ATGGGGATCATCTATCTTGGTGACTCAGATACCAGATACAGCCCCGTC CTTCCAAGGCCAGGTCAACATCTCAGCCGACAAAGTCCATCAGTACCG CCTACCTGCAGTGGAGCAGCCTGAAGGCTCGGACACCGCCATGTAT TACTGTGCGAGAAGTAAC TGGGTCTTGACTACTGGGCCAGGGAAC CCTGGTCACCGTCTCTAGTGCCCTCCACC AAGGCCCATCGGTCTTCC CCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTG GGCTGCC TGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTG GAACTCAGGGGCCCTGACCAGCGGCGTGCACACCTTCCCCGGCTGTCC TACAGTCTCTCAGGACTCTACTCCCTCAAAAGCGTGGTGACCGTGCCC TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAA GCCCAGCAACACCAAGGTGGACAAAGAAAGTTGAGCCCCAAATCTTGTG ACAAAACTCACACATGCCACACCGTGCCAGCACCTGAAC TCTGGGG GGACCGTCAGTCTTCTCTTCCCCCCCCAAACCC AAGACACCCCTCAT GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCC ACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAG GTGCATAATGCCAAGACAAAGCCGTTGAGGAGCAGTACGGCAGCAC GTACCGTTGTGT CAGCGTCCCTCACCGTCTCTGCAC CAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGTCTCCAACAAAGCCCTCCCAGCC CCCATCGAGAAAACCATCTCCAAGCCAAAGGCAGCCCCCGAGAACC ACAGGTGTACACCCCTGCCCCCATCCCGGAGGAGATGACCAAGAACC AGGTCAGCCCTGACCTGCC TGGTCAAAGGCTTCTATCCCAGCGACATC GCCGTGAGTGGGAGAGCAATGGGCAGCCGGAGAAACAAC TACAAGAC CAGCCTCCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCA AGCTCACCGTGACAAGAGCAGGTGCGACGAGGGAACGTC TTTCTCA TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAAGAG CCTCTCCCTGTCTCCGGGTGGTGGCGGATCGGGAGGTGGCGGATCCC AGGTGCAGTTACAGCAGTCCGGCGCAGGACTGTTGAAGCCTTCGGAG ACCCTG TCCCTCACCTGCGCTGTCCATGGTGGTCCCTTCAGTGGTTA CTACTGGAAC TGGATTCCGAAGCCACCAGGGAAGGGCTAGAGTGGA TTGGGGAATCAATCATGTCTGGAAACACCAACTACAACCCGTCCCTC AAGAGTCGAGTCACCATATCATTAGACACGTCCAAGAAACCA GTTCTC CCTGACGCTGACCTCTGTGACCGCCCGGACACGGCTGTGTA TTACT GTCCGAGAGGATATTGTAGAAGTACCACCTGCTACTTTGACTACTGG GGCCAGGGAACCCTAGTCACCGTCTCCTCAACTGTGGCTGCACCATC TGCTTTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTG CCTCTGTTGTGTGCTGCTGAATAACTTCTATCCCAGAGAGGCCAAA	CTGTCTTTTGTCTCCA GGGAAAAGAGCCACC CTCTCCTGCAGGGCC AGTCAGAGTGTTAGA AGCAGTTACTTAGCC TGGTACCAGGAGAAA CCTGGCCAGGCTCCC AGGCTCCTCATCTAT GGTGCA TCCAGCAGG GCCACTGGCATCCCA GACAGTTCAGTGGC AGTGGGTCTGGGACA GACTTCACTCTCAC ATCAGCAGACTGGAG CCTGAAGATTTTGCA GTGTATTACTGT CAG CAGTATGGTAGCTCA CCTACCTTCGGCCAA GGGACACGACTGGAG ATTAACGAGCCTCC ACCAAGGCCCATCG GTCTTCCCCCTGGCA CCCTCCTCCAAGAGC ACCTCTGGGGGCACA GCGGCCCTGGGCTGC CTGGTCAAGGACTAC TTCCCCGAACCGGTG ACGGTGTCTGTGAAC TCAGGCGCCCTGACC AGCGGCGTGCA CACC TTCCCGGCTGTCCTA CAGTCCCTCAGGACTC TACTCCCTCAAAAGC GTGGTGACCGTGCCC TCCAGCAGCTTGGGC ACCCAGACCTACATC TGCAACGTGAATCAC
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			TACAGCTGCCAGGTC ACGCATGAAGGGAGC ACCGTGAGAAAGACA GTGGCCCCTACAGAA TGTTCA	GTACAGTGGAAGGTGGATAACGCCCTCCAA ¹ TCGGGTAAC ² TCC ³ CAGGA GAGTGTACAGACAGCAGCAGCAAGACAGCACCTACAGCCTCGAAA GCACCC ⁴ TGACGCTGAGCAAAAGCAGACTACGAGAAACACAAAGTCTAC GCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCCGT ⁵ CACAAAGAG CTTCAACAGGGGAGAGTGT	AAGCCCAGCAACACC AAGGTGGACAAAGAAA GTTGAGCCCAATCT TGT
			SEQ ID NO: 451	SEQ ID NO: 452	SEQ ID NO: 453
AA			QSVLTQPPSVSGAPG QRVTISCTGSSSNIG AGYDVHWYQEFPGTA PKLLIQGNSNRPSGV PDRFSGSKSGTSASL AITGLQAEDEADYYC QSYDSSLSGSVFGGG TKLTVLGQPKAAPSV TLFPPSSEELQANKA TLVCLISDFYPGAVT VAWKADSSPVKAGVE TTTTPSKQSNNKYAAE SYLSLTPEQWKSHRS YSCQVTHEGSTVEKT VAPTECS	EVQLVQSGAEVKKPGESLKISCKTSEYFTSYWIGVVRKMPGKGLEW MGI ⁶ IYLGDS ⁷ DTRYSPSFQGGQVTISADKSI ⁸ STAYLQWSSLKASDTAMY YCARSNWGLDYWGQGT ⁹ LVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLKSVVTV ¹⁰ P SSSLGTQTYICNVN ¹¹ HKPSNTKVDKKVEPKSCDK ¹² TH ¹³ TCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGS ¹⁴ TYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEK ¹⁵ TI ¹⁶ SKAKGQPREPQVY ¹⁷ TLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYK ¹⁸ TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGGSGGGSQVQLQQSGAGLLK ¹⁹ PSE TLSLTCAVHGGSFSGYYWNWIRKPPGKLEWIGEIN ²⁰ HAGNTNYP ²¹ SL KSRVTISLDTSKNQFSLT ²² LSVTAADTA ²³ VYYCARGYCRSTTCYFDYW GQGT ²⁴ LVTVSSTVAAPSVFI ²⁵ FPSPDEQLKSGTASVVCLLNNFY ²⁶ PREAK VQWKVDNALQSGNSQESVTEQDSKDS ²⁷ STYSLESTLTLSKADYEKHKVY ACEVTHQGLSSPVTKSFNRGEC	EIVLTQSPGTLSLSP GERATLSCRASQSVR SSYLAWYQEKPGQAP RLLIYGASSRATGIP DRFSGSGGTDF ²⁸ TLT ISRLEPEDFAVYYCQ QYGS ²⁹ SPTFFGQ ³⁰ TRLE IKRASTKGPSVFPLA PSSKSTSGGTAALGC LVKDYFPEPVTVSWN SGALTSGVHTFPAVL QSSGLYSLKSVVTV ³¹ P SSSLGTQTYICNVN ³² H KPSNTKVDKKVEPKS C
			SEQ ID NO: 454	SEQ ID NO: 455	SEQ ID NO: 456
			CAGTCTGTGCTGACG CAGCCGCCCTCAGTG TCTGGGCCCCCAGGG CAGAGGTCACCATC TCCTGCACTGGGAGC AGTTCCAAACATCGGG GCAGGTTATGATGTA CACTGGTACCAGGAG TTTCCAGGAACAGCC CCCAAACTCCTCATC CAAGGTAACAGCAAT CGGCCCTCAGGGGTC CCTGACCGATTCTCT GGCTCCAAGTCTGGC ACCTCAGCCTCCCTG	GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCCGGGA GTCTCTGAAGATCTCCTGTAA ³³ GACTTCTGAATACAGCTTTACCAGCT ACTGGA ³⁴ TCGGCTGGGTGCGCAAGATGCCCGGGAAGGCCCTGGAGTGG ATGGGATCATCTATCTTGGTGA ³⁵ CTCAGATACCA ³⁶ GATACAGCCCCGTC CTTCCAAGGCCAGGTCA ³⁷ CCATCTCAGCCGACAAGTCCATCAGTACCG CCTACCTGCAGTGGAGCAGCCCTGAAGGCCCTCGGACACCGCCATGTAT TACTGTGCGAGAAGTA ³⁸ ACTGGGTCTTGA ³⁹ CTACTGGGCCAGGGAAC CCTGGTCACCGTCTCTAGTGCCTCCACCAAGGCCCATCGGTCTTCC CCCTGGCACCC ⁴⁰ TCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTG GGCTGCC ⁴¹ TGTC ⁴² AAGGACTACTTCCC ⁴³ CGAACCGGTGACGGTGTCTGTG GAACTCAGGCGCCCTGACCA ⁴⁴ GCGCGGTGCACACCTTCCC ⁴⁵ GGCTGTCC TACAGTCTCAGGACTCTACTCCCTCAA ⁴⁶ AAGCGTGGTGACCGTGCCCC TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACA ⁴⁷ AA GCCCAGCAACACCAAGGTGGACAAGAAA ⁴⁸ GTGAGCCCAAATCTTGTG ACAA ⁴⁹ AACTCACACATGCCCA ⁵⁰ CCGTGCCACCTGAAC ⁵¹ TCTCTGGGG	GACATCCAGATGACC CAGTCTCCATCCTCC CTGTCTGCATCTGTA GGAGACAGAGTCACC ATCACTTGCCGGGA AGTCAGAGCATTAAC AACTATTTAAATTGG TATCAGGAGAGACCA GGGAAAGCCCCCTAAG CTCCTGATCTATGCT GCATCCAGTTTGCAA AGTGGGTCCCATCA AGGTTCAGTGGCAGT GGATCTGGGACAGAT TTCAC ⁵² TCTCACCATC
			087_3.2_1g ⁵³ .002_9c8_VH_CK(⁵⁴ s176E).001		
			1ps: 376967		

		GCCATCACTGGGCTC CAGGCTGAGGATGAG GCTGATTATTACTGC CAGTCCATATGACAGC AGCCTGAGTGGTTCCG GTGTTCCGGCGGAGGG ACCAAGCTGACCGTC CTAGGTCAGCCCCAAG GCTGCCCCCTCGGTC ACTCTGTTCCCGCCC TCCTCTGAGGAGCTT CAAGCCAAACAAGGCC ACACTGGTGTGTCCTC ATAAGTGACTTCTAC CCGGAGCCGTGACA GTGGCCTGGAAGGCA GATAGCAGCCCCGTC AAGCGGGAGTGGAG ACCAACACACCCCTCC AAACAAAGCAACAAC AAGTACGGCGCCGAG AGCTATCTGAGCCTG ACGCCTGAGCAGTGG AAGTCCCACAGAAGC TACAGCTGCCAGGTC ACGCATGAAGGGAGC ACCGTGAGAAAGACA GTGGCCCCTACAGAA TGTTCA	GGACCGTCAGTCTTCCCTCTTCCCCCCCCAAACCCAAAGGACACCCCTCAT GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGACGTGAGCC ACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGAGAG GTGCATAATGCCAAGACAAAGCCGTGTGAGGAGCAGTACGGCAGCAC GTACCGTTGTGTGAGCGTCCCTCACCGTCTCTGCACCCAGGACTGGCTGA ATGGCAAGGAGTACAAAGTGCAAGGTCTCCAAACAAAGCCCTCCAGCC CCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCCGAGAACC ACAGGTGTACACCCCTGCCCCCATCCCGGAGGAGATGACCAAGAACC AGGTCAGCCCTGACCTGCCCTGGTCAAAAGGCTTCTATCCCAGCGACATC GCCGTGAGTGGGAGAGCAATGGGCAGCCGGAGAACTACAAAGAC CACGCCCTCCCGTGGACTCCGACGGCTCCTTCTTCTCTATAGCA AGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCCTTCTCA TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAAGAG CCTCTCCCTGTCTCCGGTGGTGGCGGATCGGGAGGTGGCGGATCCC AGGTGCAGCTGCAGGAGTCGGGCCACGGACTGGTGAAGCCTTCGGAG ACCCGTGCCCTCACCTGCACCTGTCTCTGTGGCTCCATCAGTAGTTA CTTCTGGAGCTGGATTTCGGAAGCCCCCAGGTAAGGACTGGAGTGGGA TTGGCTATATCTATTACAGTGGGCAGACCAAATACAAACCCCTCCCCTC AAGAGTCGAGTCACCATATCAATAGACACGTCCAAGAACCACTTCTC CCTGAAGCTGAGCTCTGTGACCGCTCGGCACACGGCCGTGTATTACT GTGCGAGAGAAAACCTGGGAGCTACTACGGCTTTGACTACTGGGGCCAG GGAACCCCTGGTCAACCGTCTCCTCAACTGTGGCTGCACCATCTGTCTT CATCTTCCCGCCATCTGATAGCAGTTGAAATCTGGAACCTGCCTCTG TTGTGTCCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAG TGGAAGGTGATAACGCCCTCCAATCGGTAACCTCCAGGAGAGTGT CACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCGAAAGCACCC TGACGCTGAGCAAAAGCAGACTACGAGAAACACAAAGTCTACGCCCTGC GAAGTCACCCCATCAGGGCCTGAGCTCGCCCGTCAACAAAGAGCTTCAA CAGGGGAGAGTGT	AGCAGTCTGCAACCT GAAGATTTTGCAACT TACTACTGTCAACAG AGTTACAGTACCCCT CGGACGTTTCGGCCAA GGGACCAAGCTGGAA ATCAAAACGAGCCTCC ACCAAGGCCCATCG GTCTTCCCCCTGGCA CCCTCCTCCAAGAGC ACCTCTGGGGCACA GCGGCCCTGGGCTGC CTGGTCAAGGACTAC TTCCCCGAACCGGTG ACGGTGTCTGTGAAC TCAGGGCCCTGACC AGCGGCGTGACACACC TTCCCGGCTGTCCTA CAGTCTCAGGACTC TACTCCCTCAAAAGC GTGGTGACCGTGCCC TCCAGCAGCTTGGGC ACCCAGACCTACATC TGCAACGTGAATCAC AAGCCAGCAACACC AAGGTGGACAAAGAA GTTGAGCCCCAAATCT TGT
		SEQ ID NO: 457	SEQ ID NO: 458	SEQ ID NO: 459
	AA	QSVLTQPPSVSGAPG QRVTISCTGSSSNIG AGYDVHWYQEFFP PKLLIQGNSNRPSGV PDRFSGSKSGTSASL AITGLQAEDEADYYC QSYDSSLSGSVF	EVQLVQSGAEVKKPGESLKISKCTSEYSFYSYWI MGI IYLGDS DTRYSPFQGV YCARSNWGLDYWGQGLV GCLVKDYFPEPVTVSWN SSSLGTQTY I CNVNHKPS GPSVFLFPKPKD TLMIS VHNAKTKPCEEQYGS	DIQMTQSPSSLSASV GDRVITTCRASQ NYLNWYQERPGKAPK LLIYAASSLSQGVPS RFSGSGSGTDFTLTI SSLQPEDFATYCYCQ SYSTPRTFGQGT

			TKLTVLGQPKAAPSV TLFPPSSEELQANKA TLVCLISDFYPGAVT VAWKADSSPVKAGVE TTTTPSKQSNNKYAAE SYLSLTPEQWKSHRS YSCQVTHEGSTVEKT VAPTECS	PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNYHTQKSLSLSLSPGGSGGGSQVQLQESGPGLVKPSSE TSLTCTVSGGSISSYFWSWIRKPPGKLEWIGYIYSGQTKYNPSL KSRVTISIDTSKNQFSKLSSVTAADTAVYYCARETGSYYGFDYWGQ GTLVTVSSTVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPREAKVQ WKVDNALQSGNSQESVTEQDSKDSTYSLESTLTLSKADYEKHKVYAC EVTHQGLSSPVTKSFNRGEC	IKRASTKGPSVFPLA PSSKSTSGGTAALGC LVKDYFPEPVTVSWN SGALTSGVHTFPAVL QSSGLYSLKSVVTVP SSSLGTQTYICNVNH KPSNTKVDKKVEPKS C
			SEQ ID NO:460	SEQ ID NO:461	SEQ ID NO:462
		088_3.2_1g.002_23B3_VH4_VH_CK(S176F).001	CAGTCTGTGCTGACG CAGCCGCCCTCAGTG TCTGGGCCCCCAGGG CAGAGGTCACCATC TCCTGCACTGGGAGC AGTTCCAAACATCGGG GCAGGTTATGATGTA CACTGGTACCAGGAG TTTCCAGGAACAGCC CCCAAACTCCTCATC CAAGGTAACAGCAAT CGGCCCTCAGGGGTC CCTGACCGATTCTCT GGCTCCAAGTC TGCG ACCTCAGCCTCCCTG GCCATCACTGGGCTC CAGGCTGAGGATGAG GCTGATTATTACTGC CAGTCCTATGACAGC AGCCTGAGTGGTTCG GTGTTCGGCGGAGGG ACCAAGCTGACCGTC CTAGGTCAGCCCCAAG GCTGCCCCCTCGGTC ACTCTGTTCCCGCCC TCCTCTGAGGAGCTT CAAGCCAACAAGGCC ACACTGGTGTGTCTC	GAGGTGCAGCTGGTGCACTCTGGAGCAGAGGTGAAAAAGCCCCGGGA GTCTCTGAAGATCTCCTGTAAAGACTTCTGAATACAGCTTTACCAGCT ACTGGATCGGCTGGGTGCGCAAGATCCCCGGGAAAGGCCCTGGAGTGG ATGGGGATCATCTATCTTGGTGACTCAGATACCAGATACAGCCCCGTC CTTCCAAGGCCAGGTCACCATCTCAGCCGACAAAGTCCATCAGTACCG CCTACCTGCAGTGGAGCAGCCCTGAAGGCCCTCGGACACCCGCCATGTAT TACTGTGCGAGAAGTAAC TGGGTCTTGACTACTGGGCCAGGGAAC CCTGGTCACCGTCTCTAGTGCCCTCCACCAAGGCCCATCGGTCTTCC CCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTG GGCTGCCGTGTC AAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTG GAACTCAGGCGCCCTGACCAAGCGGCGTGCAACACTTCCCCGGCTGTCC TACAGTCTCAGGACTCTACTCCCTCAAAGCGTGGTGACCGTGCCCC TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAA TCACAA GCCCAGCAACACCAAGGTGGACAAAGAAAGTTGAGCCCAAATCTTGTG ACAAAACTCACACATGCCCACCCGTGCCAGCACCTGAAC TCTCTGGGG GGACCGTCAGTCTTCTCTTCCCCCAAACCCAAAGGACACCCCTCAT GATCTCCCGACCCCTGAGGTCACATGCCGTGGTGGTGACGTGAGCC ACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAG GTGCATAATGCCAAGACAAAGCCGTTGAGGAGCAGTACGGCAGCAC GTACCGTTGTGTCAAGCTCCTCACCGTCTGTGCAACCAAGGACTGGCTGA ATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCC CCCATCGAGAAACCATCTCCAAGCCAAGGCAGCCCCCGAGAAACC ACAGGTGTACACCCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACC AGGTCAGCCTGACCTGCCCTGGTCAAAGGCTTCTATCCAGCGACATC GCCGTGGAGTGGAGAGCAATGGGCAGCCGGAGAACAACTACAAAGAC CACGCCCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTATAGCA AGCTCACCGTGGACAAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA TGCTCCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAAGAG	GACATCCAGATGACC CAGTCTCCAAGCTCC CTGTCTGCCGTCTGTG GGCGATAGGTCACC ATCACTTGCAGGTCC AGCCAGAGTGTGTTA TACAGCTCCAACAAT AAGAACTACTTAGTT TGGTACCAGGAGAAA CCAGGAAAAGGTTCTT AAACTGCTCATTTAC TGGGCATCTACCCGG GAATCCGGGGTCCCT AGTCGATTCAGTGGC AGCGGTCTGGGACA GATTTCACTCTCACC ATCAGCAGCCTGCAG CCTGAAGATGTGGCA ACTTATTACTGTCTAG CAATATTATAAGACT CCTCTCACTTTCGGC GGAGGACCAAAGGTG GAGATCAAACGAGCC TCCACCAAAGGCCCA TCGGTCTTCCCCCTG GCACCCCTCCTCCAAG AGCACCTCTGGGGC ACAGCGCCCTGGGC

		ATAAGTGACTTCTAC CCGGAGCCGTGACA GTGGCCTGGAAGGCA GATAGAGCCCCGTC AAGCGGGAGTGGAG ACCAACACACCTCC AAACAAAGCAACAAC AAGTACGGGCCGAG AGCTATCTGAGCCTG ACGCCTGAGCAGTGG AAGTCCACAGAAAGC TACAGCTGCCAGGTC ACGCATGAAGGGAGC ACCGTGAGAAAGACA GTGGCCCCTACAGAA TGTTCA	CCTCTCCCTGTCTCCGGGTGGTGGCGGATCGGGAGGTGGCGGATCCC AGGTACAGTTGCAGGAGTCAGGTCAGGACTGGTGAAGCCCTCGGAG ACCCCTCACTACCTGTACCATCTCCGGGACAGTGTCTCTACCAA CAGTGTGCTTGAACTGGATTAGGAAGCCCCCAGGAAAGCCCTTG AGTGGATAGAAAGGACATACTACAGTCCAAGTGGTATAATGATTAT GCAGTTTCTCTGAAAAGTCGAGTAACCATCAGCCCAGACACATCCAA GAACCAGTTCTCCCTGAAGCTGAGCTCTGTGACTGCCCGGGACACGG CTGTGTAATTACTGTGCAAGAGAGGATGGGATAGCTACTACCGCTAC GGTATGGACGTCTGGGGCCAAAGGACCACCGTCACCGTCTCCTCAAC TGTGGCTGCACCATCTGTCTTCACTCTCCCGCCATCTGATGAGCAGT TGAAATCTGAAACTGCCTCTGTTGTGTGCTGCTGAATAACTTCTAT CCCAGAGAGGCCAAAAGTACAGTGAAGGTGGATAACGCCCTCCAATC GGGTAACCTCCAGGAGAGTGTACAGAGCAGAGCAAGCAAGCACAGCA CCTACAGCCTCGAAAGCACCCCTGACGCTGAGCAAAGCAGACTACGAG AAACACAAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTC GCCCCTCACAAAAGAGCTTCAACAGGGGAGAGTGT	TGCCTGGTCAAGGAC TACTTCCCCGAACCG GTACGGTGTCTGTG AACTCAGGGCCCTG ACCAGCGCGTGCAC ACCTTCCCGGTGTC CTACAGTCCCTCAGGA CTCTACTCCCTCAAA AGCGTGGTGACCGTG CCCTCAGCAGCTTG GGACCCAGACCTAC ATCTGCAACGTGAAT CACAAAGCCAGCAAC ACCAAGGTGGACAA AAAAGTTGAGCCCCAA TCTTGT
		SEQ ID NO:463 QSVLTQPPSVSGAPG QRVTISCTGSSSNIG AGYDVHWYQEFFGTA PKLLIQGNSNRPSGV PDRFSGSKGTSASL AITGLQAEDEADYYC QSYDSSLGSVFGGG TKLTVLGQPKAAPSV TLFPPSSEELQANKA TLVCLISDFYPGAVT VAWKADSSPVKAGVE TTTPSKQSNKNKYAAE SYLSLTPEQWKSHRS YSCQVTHEGSTVEKT VAPTECS	SEQ ID NO:464 EVQLVQSGAEVKKPGESLKISCKTSEYFTSYWIGVVRKMPKGLEW MGI IYLGDSDTRYSPSFQGGVTISADKSI STAYLQWSSLKASDTAMY YCARSNWGLDYWGQGTILVTVSSASTKGPSVFPLAPSSKSTSGGTAAL GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLKSVVTVP SSSLGTQTYICNVN HKPSENTKVDKKVEPKSCDKTHTCPPCPAPELLG GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPCEEQYGSTYRCVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTI SKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDI AVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGGGGGGGSQVQLQESGPGLVKPSSE TSLTCTISGDSVSTNSVAWNWIRKPPGKGLEWIGRTYYRSKWYNDY AVSLKSRVTISPDTSKNQFSLKLSVTAADTAVYVCAREDGDSYYRY GMDVWGQGTIVTVSS TVAAPSVFI FPPSDEQLKSGTASVVCLLNIFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYLESTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC	SEQ ID NO:465 DIQMTQSPSSLSASV GDRVITITCRSSQSVL YSSNNKNYLVWYQEK PGKVPKLLIYWASTR ESGVPSPRFSGSGSGT DFTLTISSLQPEDVA TYYCQQYYKTPLTFG GGTKVEIKRASTKGP SVFPLAPSSKSTSGG TAALGCLVKDYFPEP VTVSWNSGALTSGVH TFPAVLQSSGLYSLK SVVTVPSSSLGTQTY ICNVN HKPSENTKVDK KVEPKSC
	AA	SEQ ID NO:466	SEQ ID NO:467	SEQ ID NO:468

1PS: 376976	089_3B3v2_IgG.002_Ada1Imumab_VH_CK(S176E).001	NA	GAAATTGTGTTGACG CAGTCTCCAGGCACC CTGTCTTTGTCTCCA GGGAAAGAGCCACC CTCTCCTGCAGGGCC AGTCAGAGTGTTAGA AGCAGTTACTTAGCC TGGTACCAGGAGAAA CCTGGCCAGGCTCCC AGGCTCCTCATCTAT GGTGCAATCCAGCAGG GCCACTGGCATCCCA GACAGGTTCAGTGGC AGTGGGTCTGGGACA GACTTCACCTCTCACC ATCAGCAGACTGGAG CCTGAAGATTTTGCA GTGTATTACTGTCTAG CAGTATGGTAGCTCA CCTACCTTCGGCCAA GGGACACGACTGGAG ATTAAACGAACGGTG GCTGCACCATCTGTC TTCATCTTCCCGCCA TCTGATGAGCAGTTG AAATCTGGTACCGCC TCTGTTGTGTGCCCTG CTGAATAACTTCTAT CCCAGAGAGGCCAAA GTACAGTGGAAGGTG GATAACGCCCTCCAA TCGGGTAACTCCCCAG GAGAGTGTACACAGAG CAGGACAGCAAGGAC AGCACCTACAGCCCTC GAGAGCACCCCTGACG CTGAGCAAAAGCAGAC	CAGGTGCAGTTACAGCAGTCGGGCGCAGGACTGTTGAAGCCTTTCGGA GACCCCTGTCCCTCACCTGCGCTGTCTCATGGTGGTCTCTCAGTG GTT ACTACTGGAAC TGGATCCGCAAGCCACCCAGGAAAGGGCTAGAGTGG ATTGGGGAAATCAATCATGCTGGAACACCAACTACAACCCGTCCCT CAAGAGTCGAGTCACCATATCATTAGACACGTCCAAGAACCAGTTCT CCCTGACGCTGACCTCTGTGACCGCGCGGACACGGCTGTGTATTAC TGTGCGAGAGGATATTGTAGAAAGTACCACCTGCTACTTTGACTACTG GGCCAGGGAACCCTAGTCACCGTCTCCTCAGCCTCCACCAAGGGCC CATCGGTCTTCCCCCTGGCACCCCTCTCTCAAAGACACCTCTTGGGGC ACAGCGCCCTGGCTGCCCTGGTCAAGGACTACTTCCCCGAACCGGT GACGGTGTCTGGAACTCAGGCGCCCTGACCAAGCGGTGCACACCT TCCCCGGCTGTCTACAGTCCCTCAGGACTCTACTCCCTCAAAAAGCGTG GTGACCGTGCCCTCCAGCAGCTTGGCACCCAGACCTACATCTGCAA CGTGAA TCACAAAGCCAGCAACACCAAGTGGAACAAGAAAGTTGAGC CCAAATCTTGTGACAAAAC TCAACATGCCACCGTGCCCAGCACCT GAACTCCTGGGGACCGTCTAGTCTTCTCTTCCCCC AAAACCCAA GGACACCCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGG TGGACGTGAGCCACGAAGACCCCTGAGGTCAAAGTTCAACTGGTACGTG GACGGCGTGAGGTGCATAATGCCAAGACAAAGCCGTGTGAGGAGCA GTACGGCAGCACGTACCGTTGTGTCTCAGCTCCTCACCGTCTTGCAAC AGGACTGGCTGAATGGCAAGGAGTACAAAGTGCAAAGTCTCCAACAAA GCCCTCCAGCCCCCATCGAGAAAA CCACTCCAAGGCCAAAGGGCA GCCCGAGAACCAAGGTGTACACCTGCCCCCATCCCGGAGGAGA TGACCAAGAACCAAGGTACGCTGACCTGACCTGGTCAAAGCTTCTAT CCCAGCGACATCGCCGTGGAGTGGAGAGCAATGGCAGCCCGGAGAA CAACTACAAGACCAACGCTCCCGTGTGACTCCGACGGCTCCTTCT TCCCTCTATAGCAAGCTCACCGTGGACAAAGACAGGTGGCAGCAGGGG AACGTCTTCTCATGTCTCCGTGATGCATGAGGCTCTGCACAACCACTA CACGCAGAAAGACCTCTCCCTGTCTCCGGGTGGTGGCGGATCGGGAG GTGGCGGATCCGAGGTACAAC TGGTGGATCAGGTGGAGGTTTGGTG CAGCCGGGAGATCGCTCAGGCTTAGCTGTGCGGCATCGGGGTTTAC TTTTCGATGATTATGCGATGCATTTGGTCCGGAAGCGCCTGGA AAAAG GGCTCGAGTGGGTTTCCGCCATTACGTGGAATAGCGGACACATCGAT TATGCAGACAGTGTGGAGGGCAGATTCACAATCTCACGAGACAAATGC TAAGAAACAGCCTGTACCTTCAGATGAAC TCACTTCGCGCGGAAGATA CCGCCGTATACTACTGCGCCAAAAGTCTCCTACTTGTCTACAGCTTCG TCGCTCGACTATTGGGGTCAAGGAACGTTGGTCAACCGTCTCTAGTAC	GATATCCAAATGACA CAATCACCATCGTCG CTTTCAGCGTCTGTT GGGACCGTGTGACG ATTACCTGTCGCGG TCCCAGGGAATCCGG AATTACCTCGCATGG TATCAGGAAAAACCC GGAAAAAGCACCGAAG CTCCTGATCTATGCC GCCTCGACTCTTCAG AGTGGTGTGCCGTGG AGGTTAGCGGTCC GGTCAGGTACGGAC TTTACTCTCACAATT TCCAGCCTGCAGCCC GAAGATGTAGCTACC TATTACTGCCAGAGA TACAAACGAGCGCCT TACACATTCCGACAA GGGACAAAAGTCGAG ATCAAAGCGTGCCTCC ACCAAGGCCCATCG GTCTTCCCCCTGGCA CCCTCCTCCAAGAGC ACCTCTGGGGCACA GCGGCCCTGGGCTGC CTGGTCAAGGACTAC TTCCCCGAACCGGTG ACGGTGTCTGTGAAC TCAGGCGCCCTGACC AGCGGCGTGCACACC TTCCCCGGCTGTCCTA CAGTCTCAGGACTC TACTCCCTCAAAAGC GTGGTGACCGTGCCC TCCAGCAGCTTGGGC
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		TACGAGAAACACAAA GTCTACGCCCTGCGAA GTCACCCATCAGGGC CTGAGCTCGCCCGTC ACAAAGAGCTTCAAC AGGGAGAGTGT	TGTGGCTGCACCATCTGTCTTCAATCTTCCCGCCATCTGATGAGCAGT TGAATCTGGAACCTGCCCTCTGTTGTGTGCCCTGCTGAATAACTTCTAT CCCAGAGAGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATC GGTAACTCCAGGAGAGTGTCAAGAGCAGGACAGCAAGGACAGCA CCTACAGCCTCGAAAAGCACCCCTGACGCTGAGCAAAGCAGACTACGAG AAACACAAAGTCTACGCCCTGCGAAGTCACCCATCAGGGCCTGAGCTC GCCCCGCACAAAAGAGCTTCAACAGGGGAGAGTGT	ACCCAGACCTACATC TGCAACGTGAATCAC AAGCCAGCAACACC AAGTGGACAAGAAA GTTGAGCCCAAATCT TGT
		SEQ ID NO: 469	SEQ ID NO: 470	SEQ ID NO: 471
AA		EIVLTQSPGTLISLSP GERATLSCRASQSVR SSYLAWYQEKPGQAP RLLIYGASSRATGIP DRFSGSGTDFTLT ISRLEPEDFAVYYCQ QYGSSPTFGQGRLE IKRTVAAPSVFIFPP SDEQLKSGTASVVCL LNNFYPREAKVQWKV DNALQSGNSQESVTE QDSKDSITYSLESTLT LSKADYEKHKVYACE VTHQGLSSPVTKSFN RGEN	QVQLQQSGAGLLKPSSETLSLTCAVHGGSFSGYYWNWIRKPPGKGLEW IGEINHAGNTNYPNPSLKSRVTISLDTSKNQFSLTLTSVTAADTAVYY CARGYCRSTTCYFDYWGGQLVTVSSASTKGPSVFPLAPSSKSTSGG TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLKSV VTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP ELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPCEEQYGYSTYRCVSVLTVLHQDWLNGKEYKCKVSNK ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY PSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQG NVFSCSVMH EALHNHYTQKSLSLSPGGSGGGSEVQLVESGGGLV QPGRSLRLSCAASGFTFDDYAMHWVRKAPGKGLEWVSAITWNSGHID YADSV EGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAKVSYLSTAS SLDYWGQGLVTVSSITVAAPSVFIFPPSDEQLKSGTASVVCLLNIFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLESTLTLSKADYE KHKVYACEVTHQGLSSPVTKSFNRGEC	DIQMTQSPSSLSASV GDRVITITCRASQGIR NYLAWYQEKPGKAPK LLIYAASTLQSGVPS RFSGSGSGTDFTLTI SSLQPEDVATYYCQR YNRAPYTFGQGTKVE IKRASTKGPSVFPLA PSSKSTSGGTAALGC LVKDYFPEPVTVSWN SGALTSGVHTFPAVL QSSGLYSLKSVVTVP SSSLGTQTYICNVNH KPSNTKVDKKVEPKS C
		SEQ ID NO: 472	SEQ ID NO: 473	SEQ ID NO: 474
		GAAATTGTTGACG CAGTCTCCAGGCACC CTGTCTTTGTCTCCA GGGAAAGAGCCACC CTCTCCTGCAGGGCC AGTCAGAGTGTTAGA AGCAGTTACTTAGCC TGGTACCAGGAGAAA CCTGGCCAGGCTCCC AGGCTCCTCATCTAT GGTGATCCAGCAGG GCCACTGGCATCCCA GACAGGTTCAGTGGC	CAGGTGCAGTTACAGCAGTCGGGCGCAGGACTGTTGAAGCCTTCGGA GACCCGTGTCCTCACCTGCGCTGTCCATGGTGGTCTCTCAGTGTT ACTACTGGAACCTGGATCCGCAAGCCACCCAGGAAGGGCTAGAGTGG ATTGGGGAAATCAATCATGCTGGAACACCAACTACAACCCGTCCCT CAAGAGTCGAGTCACCATATCATTAGACACGTCCAAGAACCAATTCT CCCTGACGCTGACCTCTGTGACCGCGCGGACACGGCTGTGTATTAC TGTGCGAGAGGATATTGTAGAAGTACCACCTGCTACTTTGACTACTG GGCCAGGGAACCTAGTCACCGTCTCCTCAGCCTCCACCAAGGGCC CATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGC ACAGCGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCCGAACCGGT GACGGTGTCTGGAACTCAGGCGCCCTGACCAAGCGGCTGCACACCT TCCCGGCTGTCTACAGTCCCTCAGGACTCTACTCCCTCAAAAAGCGTG GTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAA	CAGTCTGTGCTGACG CAGCCGCCCTCAGTG TCTGGGGCCCCAGGG CAGAGGGTCACCATC TCCTGCACTGGGAGC AGTCCAAACATCGGG GCAGGTTATGATGTA CACTGTACCAGGAG TTTCCAGGAACAGCC CCCAAACTCCTCATC CAAGGTAACAGCAAT CGGCCCTCAGGGGTC CCTGACCGATTCTCT
!PS: 376983	090 3B3v2 1gG.002 3.2 - VH CL(S176E) .001 -	NA		

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LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET COMPREND PLUS D'UN TOME.

CECI EST LE TOME 1 DE 2
CONTENANT LES PAGES 1 À 201

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JUMBO APPLICATIONS/PATENTS

THIS SECTION OF THE APPLICATION/PATENT CONTAINS MORE THAN ONE VOLUME

THIS IS VOLUME 1 OF 2
CONTAINING PAGES 1 TO 201

NOTE: For additional volumes, please contact the Canadian Patent Office

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NOTE POUR LE TOME / VOLUME NOTE:

CLAIMS

What is claimed is:

1. A bispecific, tetravalent antigen binding protein, comprising:

a) a first polypeptide comprising a first heavy chain of a first antibody comprising a first heavy chain variable region (VH1) and a first CH1 domain, wherein the first antibody specifically binds to a first antigen, and wherein the first heavy chain is fused through its C-terminus to the N-terminus of a polypeptide comprising a second heavy chain variable region of a second antibody (VH2), wherein the VH2 is fused through its C-terminus to the N-terminus of a second CH1 domain, and wherein the second antibody specifically binds to a second antigen; wherein

i) the VH1 or first CH1 domain comprises at least one amino acid substitution to introduce a positively charged amino acid at a residue selected from the group consisting of positions 39, 44, and 183 using EU numbering; and

ii) the VH2 or second CH1 domain comprises at least one amino acid substitution to introduce a negatively charged amino acid at a residue selected from the group consisting of a residue that corresponds to positions 39, 44, and 183 using EU numbering; and

b) a second polypeptide comprising a first light chain of the first antibody of a), wherein the first light chain comprises a first light chain variable region (VL1) and a first CL region; and wherein the VL1 or first CL domain comprises at least one amino acid substitution to introduce a negatively charged amino acid at a residue selected from the group consisting of positions 38, 100, and 176 using EU numbering; and

c) a third polypeptide comprising a second light chain of the second antibody of a), wherein the second light chain comprises a second light chain variable region (VL2) and a second CL region; and wherein the VL2 or second CL domain comprises at least one amino acid substitution to introduce a positively charged amino acid at a residue selected from the group consisting of positions 38, 100, and 176 using EU numbering.

2. The antigen binding protein according to claim 1, wherein the first heavy chain is fused to the VH2 via a peptide linker.

3. The antigen binding protein according to claim 2, wherein the peptide linker comprises a sequence selected from the group consisting of (Gly₃Ser)₂, (Gly₄Ser)₂, (Gly₃Ser)₃, (Gly₄Ser)₃, (Gly₃Ser)₄, (Gly₄Ser)₄, (Gly₃Ser)₅, (Gly₄Ser)₅, (Gly₃Ser)₆, and (Gly₄Ser)₆.
4. The antigen binding protein according to claim 1, wherein
- a) the VH1 or first CH1 domain comprises a mutation selected from the group consisting of Q39K, G44K, and S183K using EU numbering;
 - b) the VH2 or second CH1 domain comprises a mutation selected from the group consisting of Q39E, G44E, and S183E using EU numbering;
 - c) the VL1 or first CL domain comprises a mutation selected from the group consisting of Q38E, G100E, and S176E using EU numbering; and
 - d) the VL2 or second CL domain comprises a mutation selected from the group consisting of Q38K, G100K, and S176K using EU numbering.
5. The antigen binding protein according to claim 4, wherein
- a) the first CH1 domain comprises a S183K mutation using EU numbering;
 - b) the second CH1 domain comprises a S183E mutation using EU numbering;
 - c) the first CL domain comprises a S176E mutation using EU numbering; and
 - d) the second CL domain comprises a S176K mutation using EU numbering.
6. The antigen binding protein according to claim 4, wherein
- a) the VH1 comprises a Q39K mutation and the first CH1 domain comprises a S183K mutation using EU numbering;
 - b) the VH2 comprises a Q39E mutation and the second CH1 domain comprises a S183E mutation using EU numbering;
 - c) the VL1 comprises a Q38E mutation and the first CL domain comprises a S176E mutation using EU numbering; and
 - d) the VL2 comprises a Q38K mutation and the second CL domain comprises a S176K mutation using EU numbering.
7. The antigen binding protein according to claim 4, wherein
- a) the first CH1 domain comprises G44K and S183K mutations using EU numbering;
 - b) the second CH1 domain comprises G44E and S183E mutations using EU numbering;

- c) the first CL domain comprises G100E and S176E mutations using EU numbering; and
- d) the second CL domain comprises G100K and S176K mutations using EU numbering.

8. A bispecific, tetravalent antigen binding protein, comprising:

a) a first polypeptide comprising a first heavy chain of a first antibody comprising a first heavy chain variable region (VH1) and a first CH1 domain, wherein the first antibody specifically binds to a first antigen, and wherein the first heavy chain is fused through its C-terminus to the N-terminus of a polypeptide comprising a second heavy chain variable region of a second antibody (VH2), wherein the VH2 is fused through its C-terminus to the N-terminus of a second CH1 domain, and wherein the second antibody specifically binds to a second antigen; wherein

i) the VH1 or first CH1 domain comprises at least one amino acid substitution to introduce a negatively charged amino acid at a residue selected from the group consisting of positions 39, 44, and 183 using EU numbering; and

ii) the VH2 or second CH1 domain comprises at least one amino acid substitution to introduce a positively charged amino acid at a residue selected from the group consisting of a residue that corresponds to positions 39, 44, and 183 using EU numbering; and

b) a second polypeptide comprising a first light chain of the first antibody of a), wherein the first light chain comprises a first light chain variable region (VL1) and a first CL region; and wherein the VL1 or first CL domain comprises at least one amino acid substitution to introduce a positively charged amino acid at a residue selected from the group consisting of positions 38, 100, and 176 using EU numbering; and

c) a third polypeptide comprising a second light chain of the second antibody of a), wherein the second light chain comprises a second light chain variable region (VL2) and a second CL region; and wherein the VL1 or first CL domain comprises at least one amino acid substitution to introduce a negatively charged amino acid at a residue selected from the group consisting of positions 38, 100, and 176 using EU numbering.

9. The antigen binding protein according to claim 8, wherein the first heavy chain is fused to the VH2 via a peptide linker.

10. The antigen binding protein according to claim 9, wherein the peptide linker comprises a sequence selected from the group consisting of (Gly₃Ser)₂, (Gly₄Ser)₂, (Gly₃Ser)₃, (Gly₄Ser)₃, (Gly₃Ser)₄, (Gly₄Ser)₄, (Gly₃Ser)₅, (Gly₄Ser)₅, (Gly₃Ser)₆, and (Gly₄Ser)₆..

11. The antigen binding protein according to claim 8, wherein

- a) the VH1 or first CH1 domain comprises a mutation selected from the group consisting of Q39E, G44E, and S183E using EU numbering;
- b) the VH2 or second CH1 domain comprises a mutation selected from the group consisting of Q39K, G44K, and S183K using EU numbering;
- c) the VL1 or first CL domain comprises a mutation selected from the group consisting of Q38K, G100K, and S176K using EU numbering; and
- d) the VL2 or second CL domain comprises a mutation selected from the group consisting of Q38E, G100E, and S176E using EU numbering.

12. The antigen binding protein according to claim 11, wherein

- a) the first CH1 domain comprises a S183E mutation using EU numbering;
- b) the second CH1 domain comprises a S183K mutation using EU numbering;
- c) the first CL domain comprises a S176K mutation using EU numbering; and
- d) the second CL domain comprises a S176E mutation using EU numbering.

13. The antigen binding protein according to claim 11, wherein

- a) the VH1 comprises a Q39E mutation and the first CH1 domain comprises a S183E mutation using EU numbering;
- b) the VH2 comprises a Q39K mutation and the second CH1 domain comprises a S183K mutation using EU numbering;
- c) the VL1 comprises a Q38K mutation and the first CL domain comprises a S176K mutation using EU numbering; and
- d) the VL2 comprises a Q38E mutation and the second CL domain comprises a S176E mutation using EU numbering.

14. The antigen binding protein according to claim 11, wherein

- a) the first CH1 domain comprises G44E and S183E mutations using EU numbering;
- b) the second CH1 domain comprises G44K and S183K mutations using EU numbering;

- c) the first CL domain comprises G100K and S176K mutations using EU numbering; and
- d) the second CL domain comprises G100E and S176E mutations using EU numbering.

15. A bispecific, tetravalent antigen binding protein, comprising:

a) a first polypeptide comprising a first heavy chain of a first antibody comprising a first heavy chain variable region (VH1) and a first CH1 domain, wherein the first antibody specifically binds to a first antigen, and wherein the first heavy chain is fused through its C-terminus to the N-terminus of a polypeptide comprising a second heavy chain variable region of a second antibody (VH2), wherein the VH2 is fused through its C-terminus to the N-terminus of a second CH1 domain, and wherein the second antibody specifically binds to a second antigen; wherein

i) the VH1 or first CH1 domain comprises at least one amino acid substitution to introduce a charged amino acid at a residue selected from the group consisting of positions 39, 44, and 183 using EU numbering; and

ii) the VH2 or second CH1 domain comprises at least one amino acid substitution to introduce a charged amino acid at a residue selected from the group consisting of a residue that corresponds to positions 39, 44, and 183 using EU numbering, wherein the charge is the opposite of the substituted residue of the VH1 or first CH1 of the first heavy chain; and

b) a second polypeptide comprising a first light chain of the first antibody of a), wherein the first light chain comprises a first light chain variable region (VL1) and a first CL region; and wherein the VL1 or first CL domain comprises at least one amino acid substitution to introduce a charged amino acid at a residue selected from the group consisting of positions 38, 100, and 176 using EU numbering, wherein

the charge at position 38 is the opposite of the substituted residue of the VH1 or first CH1 of the first heavy chain at position 39; the charge at position 100 is the opposite of the substituted residue of the VH1 or first CH1 of the first heavy chain at position 44; the charge at position 176 is the opposite of the substituted residue of the VH1 or first CH1 of the first heavy chain at position 183; and

c) a third polypeptide comprising a second light chain of the second antibody of a), wherein the second light chain comprises a second light chain variable region (VL2) and a second CL region; and wherein the VL2 or second CL domain comprises at least one amino

acid substitution to introduce a charged amino acid at a residue selected from the group consisting of positions 38, 100, and 176 using EU numbering, wherein

the charge at position 38 is the opposite of the substituted residue of the VH2 or second CH1 of the second heavy chain at position 39; the charge at position 100 is the opposite of the substituted residue of the VH2 or second CH1 of the second heavy chain at position 44; the charge at position 176 is the opposite of the substituted residue of the VH2 or second CH1 of the second heavy chain at position 183.

16. The antigen binding protein according to claim 15, wherein the first heavy chain is fused to the VH2 via a peptide linker.

17. The antigen binding protein according to claim 16, wherein the peptide linker comprises a sequence selected from the group consisting of (Gly₃Ser)₂, (Gly₄Ser)₂, (Gly₃Ser)₃, (Gly₄Ser)₃, (Gly₃Ser)₄, (Gly₄Ser)₄, (Gly₃Ser)₅, (Gly₄Ser)₅, (Gly₃Ser)₆, and (Gly₄Ser)₆.

18. The antigen binding protein according to claim 15, wherein

- a) the VH1 comprises a Q39E mutation and the first CH1 domain comprises a S183K mutation using EU numbering;
- b) the VH2 comprises a Q39K mutation and the second CH1 domain comprises a S183E mutation using EU numbering;
- c) the VL1 comprises a Q38K mutation and the first CL domain comprises a S176E mutation using EU numbering; and
- d) the VL2 comprises a Q38E mutation and the second CL domain comprises a S176K mutation using EU numbering.

19. The antigen binding protein according to claim 16, wherein

- a) the first CH1 domain comprises G44E and S183K mutations using EU numbering;
- b) the second CH1 domain comprises G44K and S183E mutations using EU numbering;
- c) the first CL domain comprises G100K and S176E mutations using EU numbering; and
- d) the second CL domain comprises G100E and S176K mutations using EU numbering.

20. The antigen binding protein according to claim 16, wherein
- a) the VH1 comprises a Q39K mutation and the first CH1 domain comprises a S183E mutation using EU numbering;
 - b) the VH2 comprises a Q39E mutation and the second CH1 domain comprises a S183K mutation using EU numbering;
 - c) the VL1 comprises a Q38E mutation and the first CL domain comprises a S176K mutation using EU numbering; and
 - d) the VL2 comprises a Q38K mutation and the second CL domain comprises a S176E mutation using EU numbering.
21. The antigen binding protein according to claim 16, wherein
- a) the first CH1 domain comprises G44K and S183E mutations using EU numbering;
 - b) the second CH1 domain comprises G44E and S183K mutations using EU numbering;
 - c) the first CL domain comprises G100E and S176K mutations using EU numbering; and
 - d) the second CL domain comprises G100K and S176E mutations using EU numbering.
22. A method for preparing a bispecific, tetravalent antigen binding protein, comprising:
- 1) co-expressing in a host cell:
 - a) a first polynucleotide wherein the first polynucleotide encodes a first polypeptide comprising a first heavy chain of a first antibody comprising a first heavy chain variable region (VH1) and a first CH1 domain, wherein the first antibody specifically binds to a first antigen, and wherein the first heavy chain is fused through its C-terminus to the N-terminus of a polypeptide comprising a second heavy chain variable region of a second antibody (VH2), wherein the VH2 is fused through its C-terminus to the N-terminus of a second CH1 domain, and wherein the second antibody specifically binds to a second antigen; wherein
 - i) the VH1 or first CH1 domain comprises at least one amino acid substitution to introduce a positively charged amino acid at a residue selected from the group consisting of positions 39, 44, and 183 using EU numbering; and

- ii) the VH2 or second CH1 domain comprises at least one amino acid substitution to introduce a negatively charged amino acid at a residue selected from the group consisting of a residue that corresponds to positions 39, 44, and 183 using EU numbering; and
 - b) a second polynucleotide wherein the second polynucleotide encodes a second polypeptide comprising a light chain of the first antibody of a), wherein the light chain comprises a first light chain variable region (VL1) and a first CL region; and wherein the VL1 or first CL domain comprises at least one amino acid substitution to introduce a negatively charged amino acid at a residue selected from the group consisting of positions 38, 100, and 176 using EU numbering;
 - c) a third polynucleotide wherein the third polynucleotide encodes a third polypeptide comprising a light chain of the second antibody of a), wherein the light chain comprises a second light chain variable region (VL2) and a second CL region; and wherein the VL2 or second CL domain comprises at least one amino acid substitution to introduce a positively charged amino acid at a residue selected from the group consisting of positions 38, 100, and 176 using EU numbering;
- 2) cultivating the host cell under conditions such that the polypeptides are produced; and
- 3) recovering from the host cell the antigen binding protein.

23. The method according to claim 22, wherein the first polynucleotide comprises nucleic acid sequence encoding for a peptide linker inserted between the nucleic acid sequences encoding for the first heavy chain and the VH2.

24. The method according to claim 23, wherein the peptide linker comprises a sequence selected from the group consisting of (Gly₃Ser)₂, (Gly₄Ser)₂, (Gly₃Ser)₃, (Gly₄Ser)₃, (Gly₃Ser)₄, (Gly₄Ser)₄, (Gly₃Ser)₅, (Gly₄Ser)₅, (Gly₃Ser)₆, and (Gly₄Ser)₆.

25. The method according to claim 22, wherein

- a) the VH1 or first CH1 domain comprises a mutation selected from the group consisting of Q39K, G44K, and S183K using EU numbering;
- b) the VH2 or second CH1 domain comprises a mutation selected from the group consisting of Q39E, G44E, and S183E using EU numbering;

- c) the VL1 or first CL domain comprises a mutation selected from the group consisting of Q38E, G100E, and S176E using EU numbering; and
- d) the VL2 or second CL domain comprises a mutation selected from the group consisting of Q38K, G100K, and S176K using EU numbering.

26. The method according to claim 22, wherein

- a) the first CH1 domain comprises a S183K mutation using EU numbering;
- b) the second CH1 domain comprises a S183E mutation using EU numbering;
- c) the first CL domain comprises a S176E mutation using EU numbering; and
- d) the second CL domain comprises a S176K mutation using EU numbering.

27. The method according to claim 22, wherein

- a) the VH1 comprises a Q39K mutation and the first CH1 domain comprises a S183K mutation using EU numbering;
- b) the VH2 comprises a Q39E mutation and the second CH1 domain comprises a S183E mutation using EU numbering;
- c) the VL1 comprises a Q38E mutation and the first CL domain comprises a S176E mutation using EU numbering; and
- d) the VL2 comprises a Q38K mutation and the second CL domain comprises a S176K mutation using EU numbering.

28. The method according to claim 22, wherein

- a) the first CH1 domain comprises G44K and S183K mutations using EU numbering;
- b) the second CH1 domain comprises G44E and S183E mutations using EU numbering;
- c) the first CL domain comprises G100E and S176E mutations using EU numbering; and
- d) the second CL domain comprises G100K and S176K mutations using EU numbering.

29. A method for preparing a bispecific, tetravalent antigen binding protein, comprising:

- 1) co-expressing in a host cell:
 - a) a first polynucleotide wherein the first polynucleotide encodes a first polypeptide comprising a first heavy chain of a first antibody comprising a first heavy

chain variable region (VH1) and a first CH1 domain, wherein the first antibody specifically binds to a first antigen, and wherein the first heavy chain is fused through its C-terminus to the N-terminus of a polypeptide comprising a second heavy chain variable region of a second antibody (VH2), wherein the VH2 is fused through its C-terminus to the N-terminus of a second CH1 domain, and wherein the second antibody specifically binds to a second antigen; wherein

i) the VH1 or first CH1 domain comprises at least one amino acid substitution to introduce a negatively charged amino acid at a residue selected from the group consisting of positions 39, 44, and 183 using EU numbering; and

ii) the VH2 or second CH1 domain comprises at least one amino acid substitution to introduce a positively charged amino acid at a residue selected from the group consisting of a residue that corresponds to positions 39, 44, and 183 using EU numbering; and

b) a second polynucleotide wherein the second polynucleotide encodes a second polypeptide comprising a first light chain of the first antibody of a), wherein the first light chain comprises a first light chain variable region (VL1) and a first CL region; and wherein the VL1 or first CL domain comprises at least one amino acid substitution to introduce a positively charged amino acid at a residue selected from the group consisting of positions 38, 100, and 176 using EU numbering; and

c) a third polynucleotide wherein the third polynucleotide encodes a third polypeptide comprising a second light chain of the second antibody of a), wherein the second light chain comprises a second light chain variable region (VL2) and a second CL region; and wherein the VL2 or second CL domain comprises at least one amino acid substitution to introduce a negatively charged amino acid at a residue selected from the group consisting of positions 38, 100, and 176 using EU numbering;

2) cultivating the host cell under conditions such that the polypeptides are produced;

and

3) recovering from the host cell the antigen binding protein.

30. The method according to claim 29, wherein the first heavy chain is fused to the VH2 via a peptide linker.

31. The method according to claim 30, wherein the peptide linker comprises a sequence selected from the group consisting of (Gly₃Ser)₂, (Gly₄Ser)₂, (Gly₃Ser)₃, (Gly₄Ser)₃, (Gly₃Ser)₄, (Gly₄Ser)₄, (Gly₃Ser)₅, (Gly₄Ser)₅, (Gly₃Ser)₆, and (Gly₄Ser)₆.

32. The method according to claim 29, wherein

- a) the VH1 or first CH1 domain comprises a mutation selected from the group consisting of Q39E, G44E, and S183E using EU numbering;
- b) the VH2 or second CH1 domain comprises a mutation selected from the group consisting of Q39K, G44K, and S183K using EU numbering;
- c) the VL1 or first CL domain comprises a mutation selected from the group consisting of Q38K, G100K, and S176K using EU numbering; and
- d) the VL2 or second CL domain comprises a mutation selected from the group consisting of Q38E, G100E, and S176E using EU numbering.

33. The method according to claim 32, wherein

- a) the first CH1 domain comprises a S183E mutation using EU numbering;
- b) the second CH1 domain comprises a S183K mutation using EU numbering;
- c) the first CL domain comprises a S176K mutation using EU numbering; and
- d) the second CL domain comprises a S176E mutation using EU numbering.

34. The method according to claim 32, wherein

- a) the VH1 comprises a Q39E mutation and the first CH1 domain comprises a S183E mutation using EU numbering;
- b) the VH2 comprises a Q39K mutation and the second CH1 domain comprises a S183K mutation using EU numbering;
- c) the VL1 comprises a Q38K mutation and the first CL domain comprises a S176K mutation using EU numbering; and
- d) the VL2 comprises a Q38E mutation and the second CL domain comprises a S176E mutation using EU numbering.

35. The method according to claim 32, wherein

- a) the first CH1 domain comprises G44E and S183E mutations using EU numbering;
- b) the second CH1 domain comprises G44K and S183K mutations using EU numbering;

- c) the first CL domain comprises G100K and S176K mutations using EU numbering; and
- d) the second CL domain comprises G100E and S176E mutations using EU numbering.

36. A method for preparing a bispecific, tetravalent antigen binding protein, comprising:

1) co-expressing in a host cell:

a) a first polynucleotide wherein the first polynucleotide encodes a first polypeptide comprising a first heavy chain of a first antibody comprising a first heavy chain variable region (VH1) and a first CH1 domain, wherein the first antibody specifically binds to a first antigen, and wherein the first heavy chain is fused through its C-terminus to the N-terminus of a polypeptide comprising a second heavy chain variable region of a second antibody (VH2), wherein the VH2 is fused through its C-terminus to the N-terminus of a second CH1 domain, and wherein the second antibody specifically binds to a second antigen; wherein

i) the VH1 or first CH1 domain comprises at least one amino acid substitution to introduce a charged amino acid at a residue selected from the group consisting of positions 39, 44, and 183 using EU numbering; and

ii) the VH2 or second CH1 domain comprises at least one amino acid substitution to introduce a charged amino acid at a residue selected from the group consisting of a residue that corresponds to positions 39, 44, and 183 using EU numbering, wherein the charge is the opposite of the substituted residue of the VH1 or first CH1 of the first heavy chain; and

b) a second polynucleotide wherein the second polynucleotide encodes a second polypeptide comprising a light chain of the first antibody of a), wherein the light chain comprises a first light chain variable region (VL1) and a first CL region; and wherein the VL1 or first CL domain comprises at least one amino acid substitution to introduce a charged amino acid at a residue selected from the group consisting of positions 38, 100, and 176 using EU numbering, wherein

the charge at position 38 is the opposite of the substituted residue of the VH1 or first CH1 of the first heavy chain at position 39; the charge at position 100 is the opposite of the substituted residue of the VH1 or first CH1 of the first heavy chain at position 44; the charge at position 176 is the opposite of the substituted residue of the VH1 or first CH1 of the first heavy chain at position 183; and

c) a third polynucleotide wherein the third polynucleotide encodes a third polypeptide comprising a light chain of the second antibody of a), wherein the light chain comprises a second light chain variable region (VL2) and a second CL region; and wherein the VL1 or first CL domain comprises at least one amino acid substitution to introduce a positively charged amino acid at a residue selected from the group consisting of positions 38, 100, and 176 using EU numbering, wherein

the charge at position 38 is the opposite of the substituted residue of the VH2 or second CH1 of the second heavy chain at position 39; the charge at position 100 is the opposite of the substituted residue of the VH2 or second CH1 of the second heavy chain at position 44; the charge at position 176 is the opposite of the substituted residue of the VH2 or second CH1 of the second heavy chain at position 183;

2) cultivating the host cell under conditions such that the polypeptides are produced;

and

3) recovering from the host cell the antigen binding protein.

37. The method according to claim 36, wherein the first heavy chain is fused to the VH2 via a peptide linker.

38. The method according to claim 37, wherein the peptide linker comprises a sequence selected from the group consisting of (Gly₃Ser)₂, (Gly₄Ser)₂, (Gly₃Ser)₃, (Gly₄Ser)₃, (Gly₃Ser)₄, (Gly₄Ser)₄, (Gly₃Ser)₅, (Gly₄Ser)₅, (Gly₃Ser)₆, and (Gly₄Ser)₆.

39. The method according to claim 36, wherein

a) the VH1 comprises a Q39E mutation and the first CH1 domain comprises a S183K mutation using EU numbering;

b) the VH2 comprises a Q39K mutation and the second CH1 domain comprises a S183E mutation using EU numbering;

c) the VL1 comprises a Q38K mutation and the first CL domain comprises a S176E mutation using EU numbering; and

d) the VL2 comprises a Q38E mutation and the second CL domain comprises a S176K mutation using EU numbering.

40. The method according to claim 39, wherein

a) the first CH1 domain comprises G44E and S183K mutations using EU numbering;

- b) the second CH1 domain comprises G44K and S183E mutations using EU numbering;
- c) the first CL domain comprises G100K and S176E mutations using EU numbering; and
- d) the second CL domain comprises G100E and S176K mutations using EU numbering.

41. The method according to claim 39, wherein

- a) the VH1 comprises a Q39K mutation and the first CH1 domain comprises a S183E mutation using EU numbering;
- b) the VH2 comprises a Q39E mutation and the second CH1 domain comprises a S183K mutation using EU numbering;
- c) the VL1 comprises a Q38E mutation and the first CL domain comprises a S176K mutation using EU numbering; and
- d) the VL2 comprises a Q38K mutation and the second CL domain comprises a S176E mutation using EU numbering.

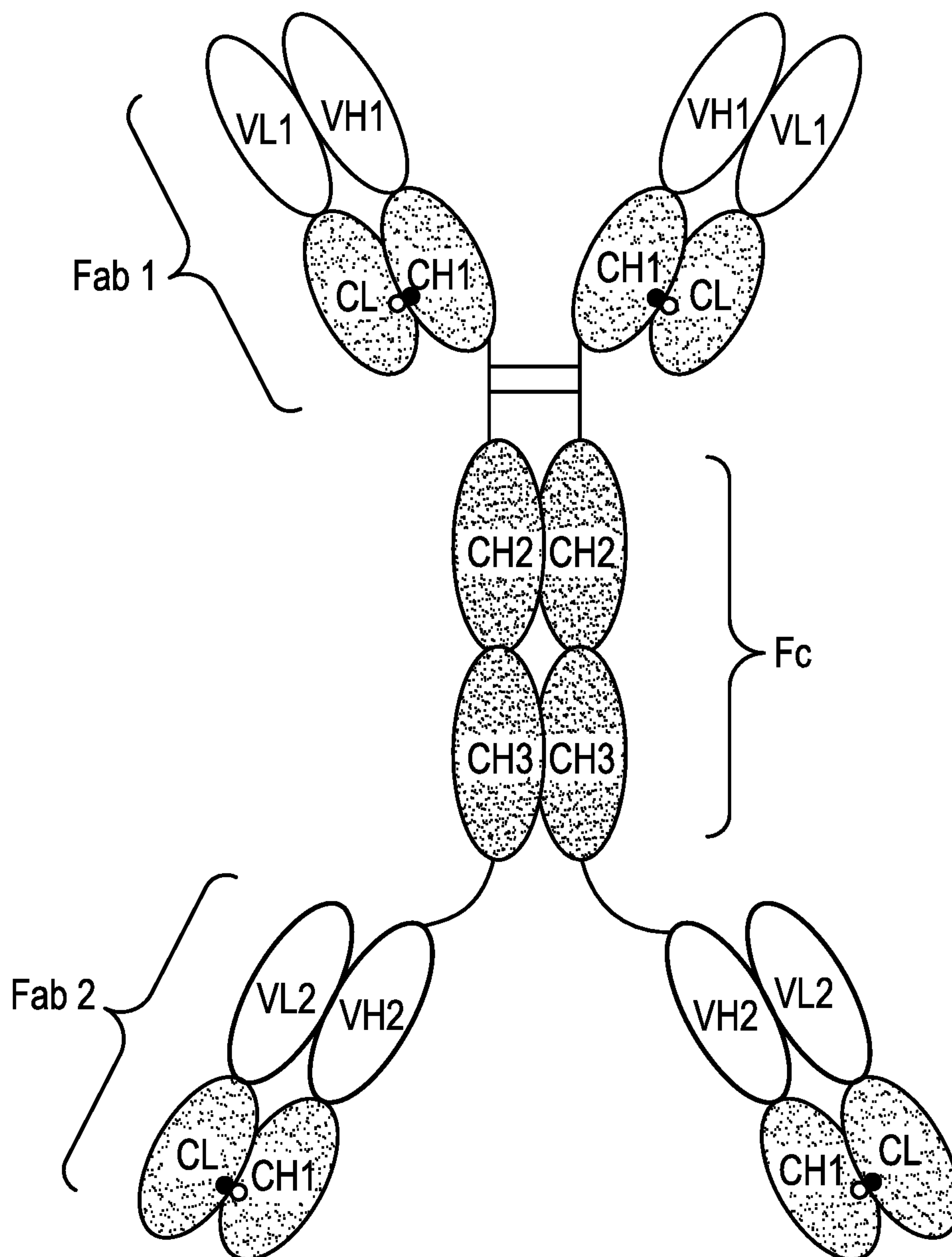
42. The method according to claim 39, wherein

- a) the first CH1 domain comprises G44K and S183E mutations using EU numbering;
- b) the second CH1 domain comprises G44E and S183K mutations using EU numbering;
- c) the first CL domain comprises G100E and S176K mutations using EU numbering; and
- d) the second CL domain comprises G100K and S176E mutations using EU numbering.

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FIG. 1

Bispecific IgG-Fab



⌋ = Ig hinge

⌋ = peptide linker

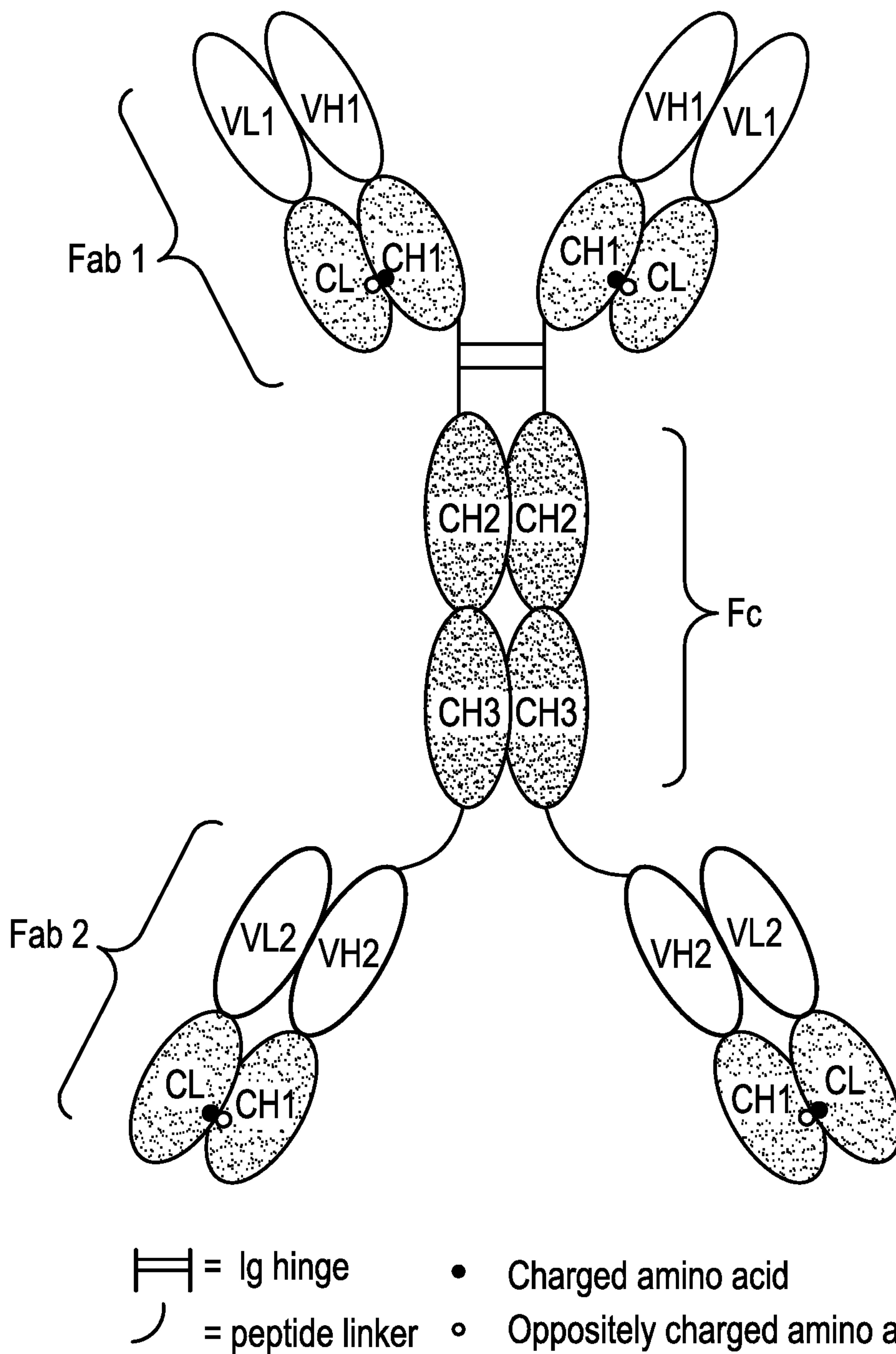
• Charged amino acid

◦ Oppositely charged amino acid

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FIG. 2

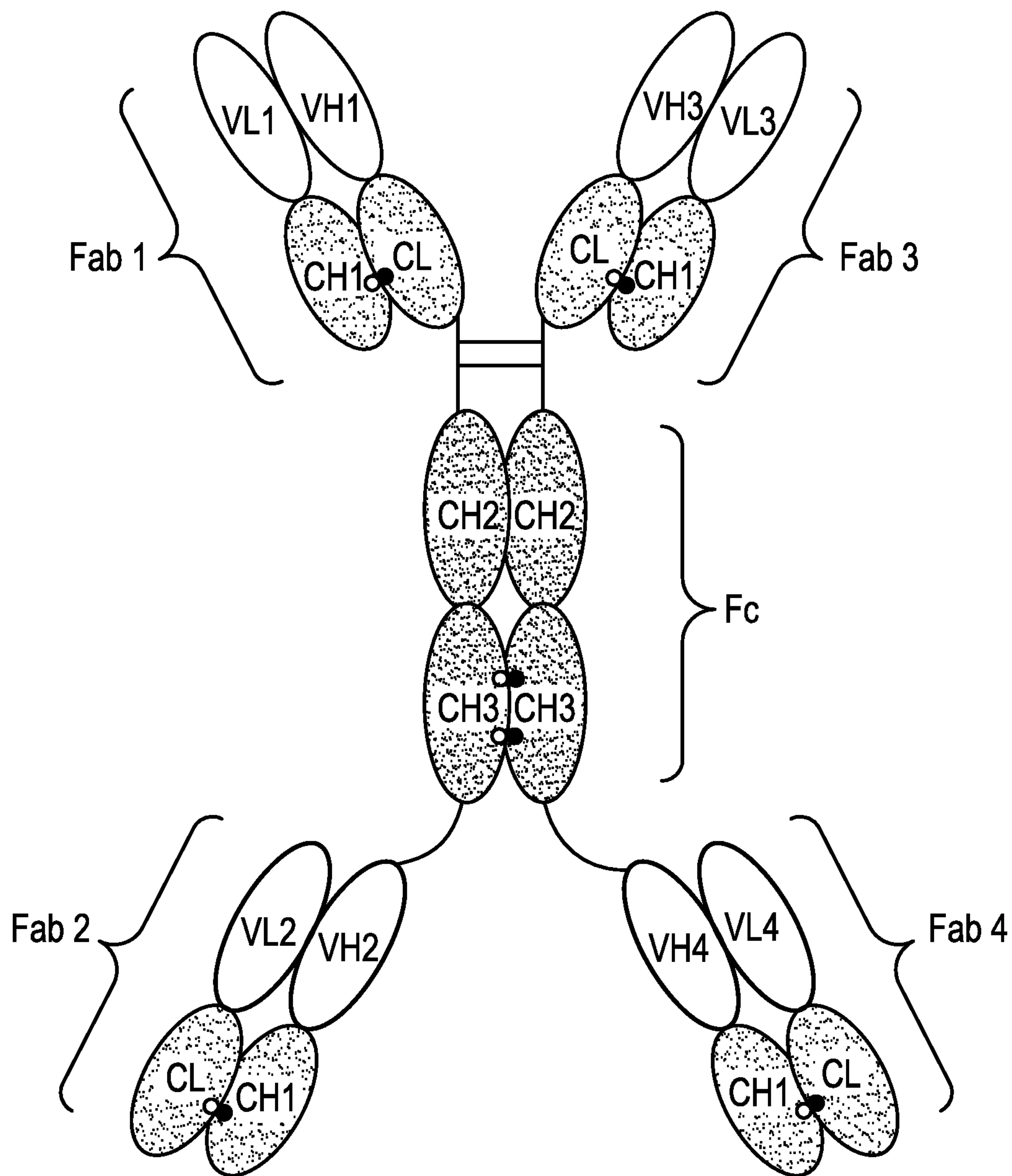
Bispecific IgG-Fab



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FIG. 3

Tetra-specific IgG-Fab variant



= Ig hinge

= peptide linker

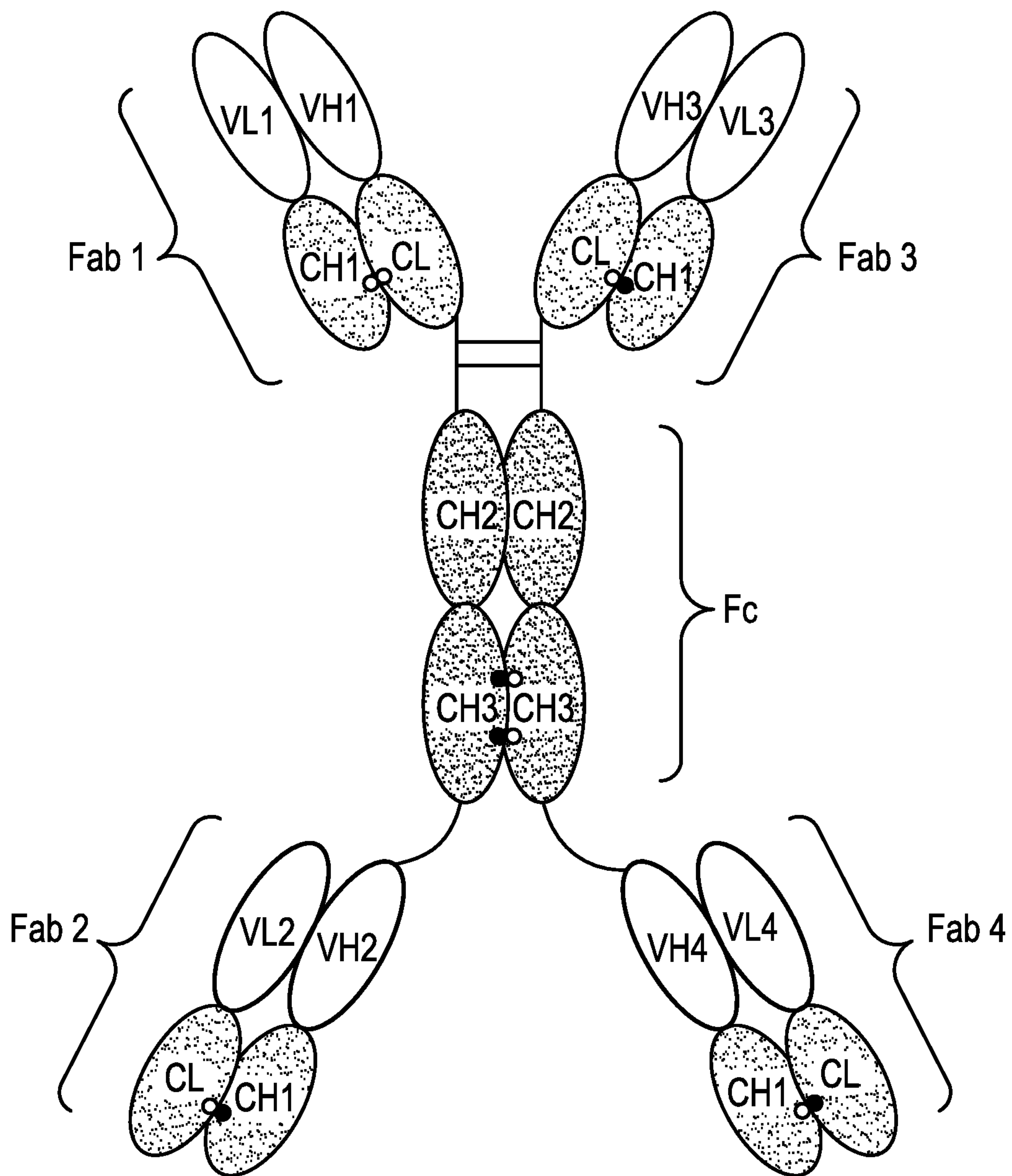
• Charged amino acid

◦ Oppositely charged amino acid

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FIG. 4

Tetraspecific IgG-Fab variant



= Ig hinge

= peptide linker

• Charged amino acid

◦ Oppositely charged amino acid

FIG. 5

[illegible]

FIG. 6

IgG-Fab CPMv1 N-term CH/CL swap

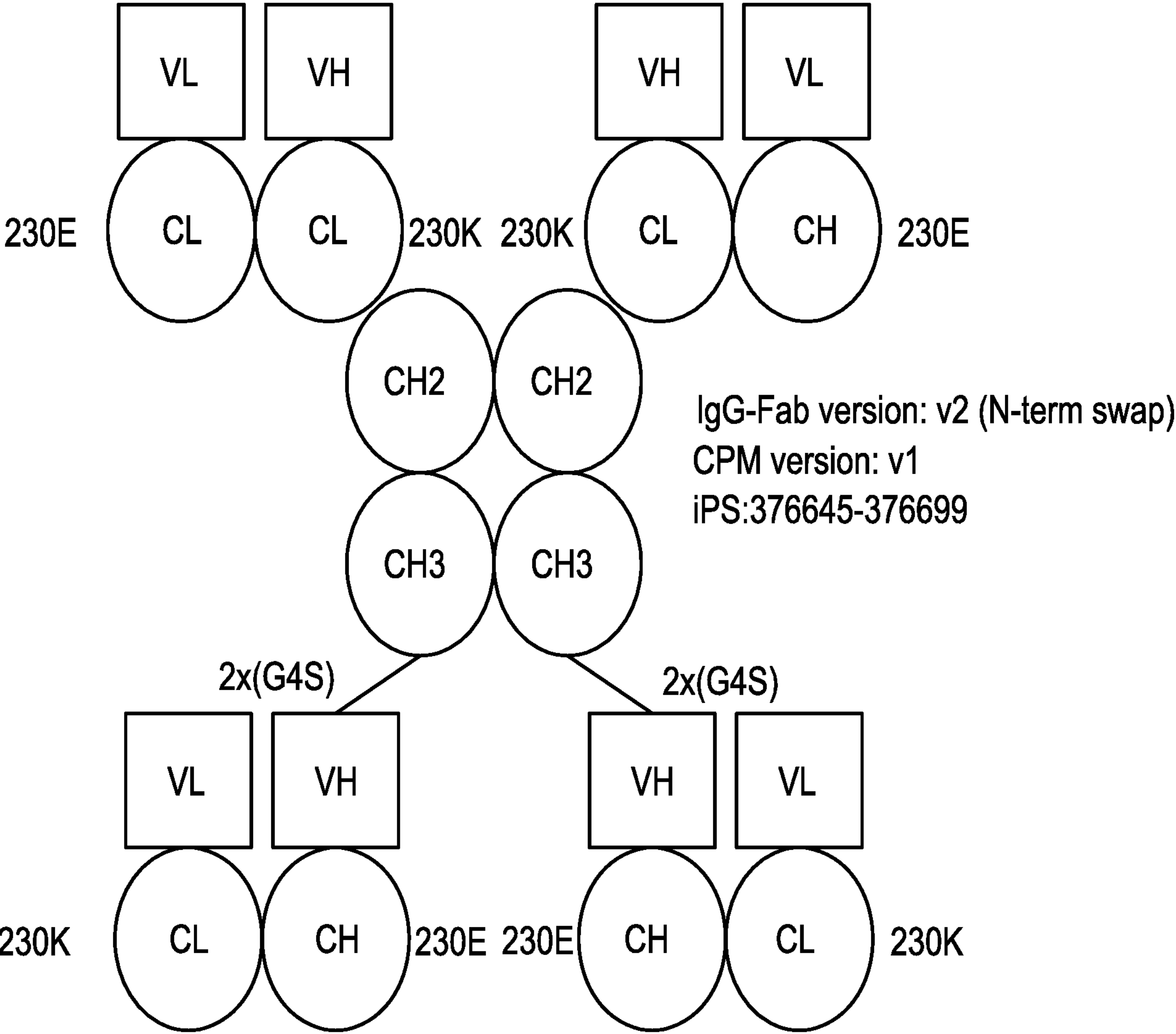


FIG. 7

IgG-Fab CPMv1 C-term CH/CL swap

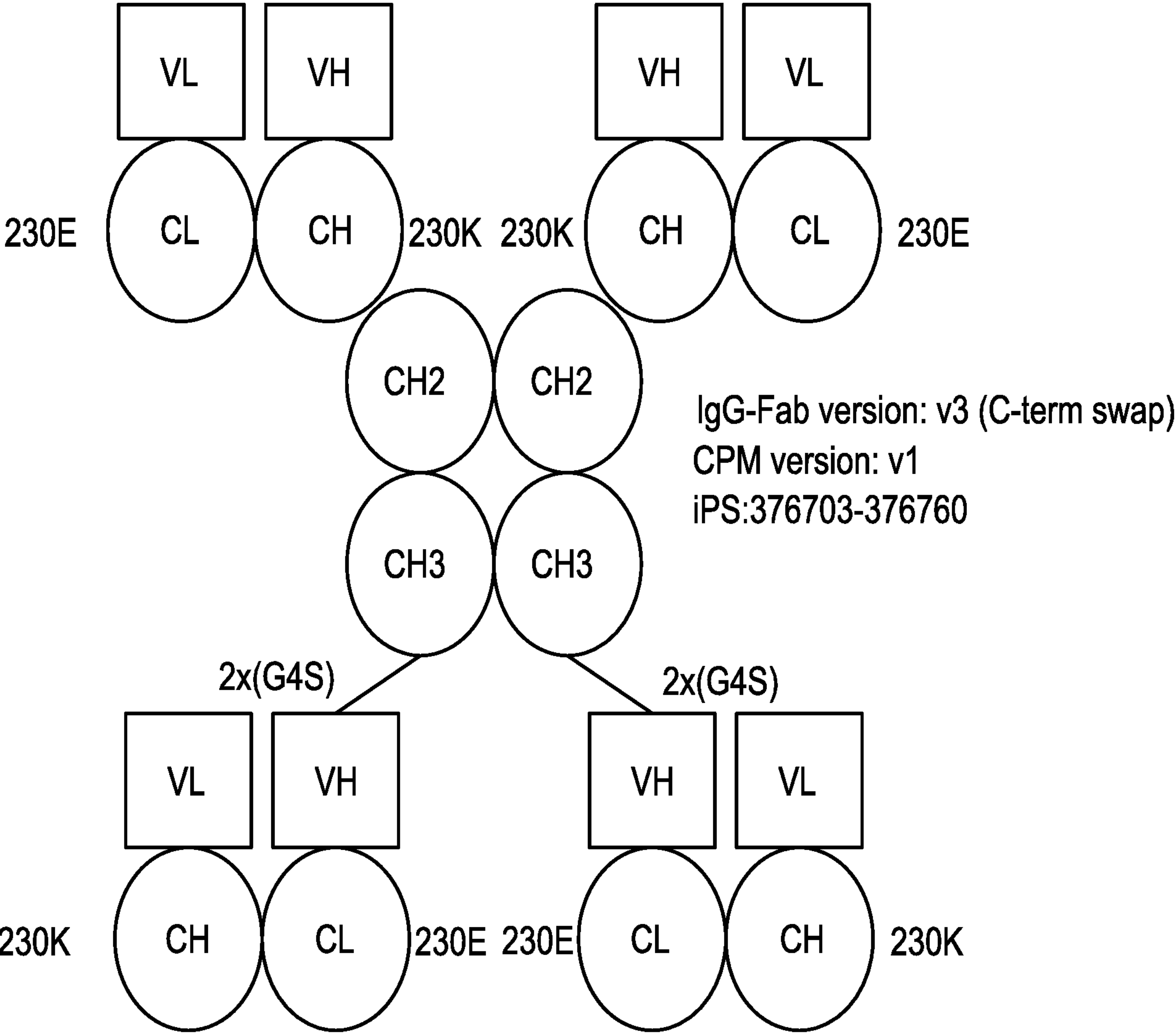


FIG. 8

IgG-Fab CPMv1 CH/CL both swap

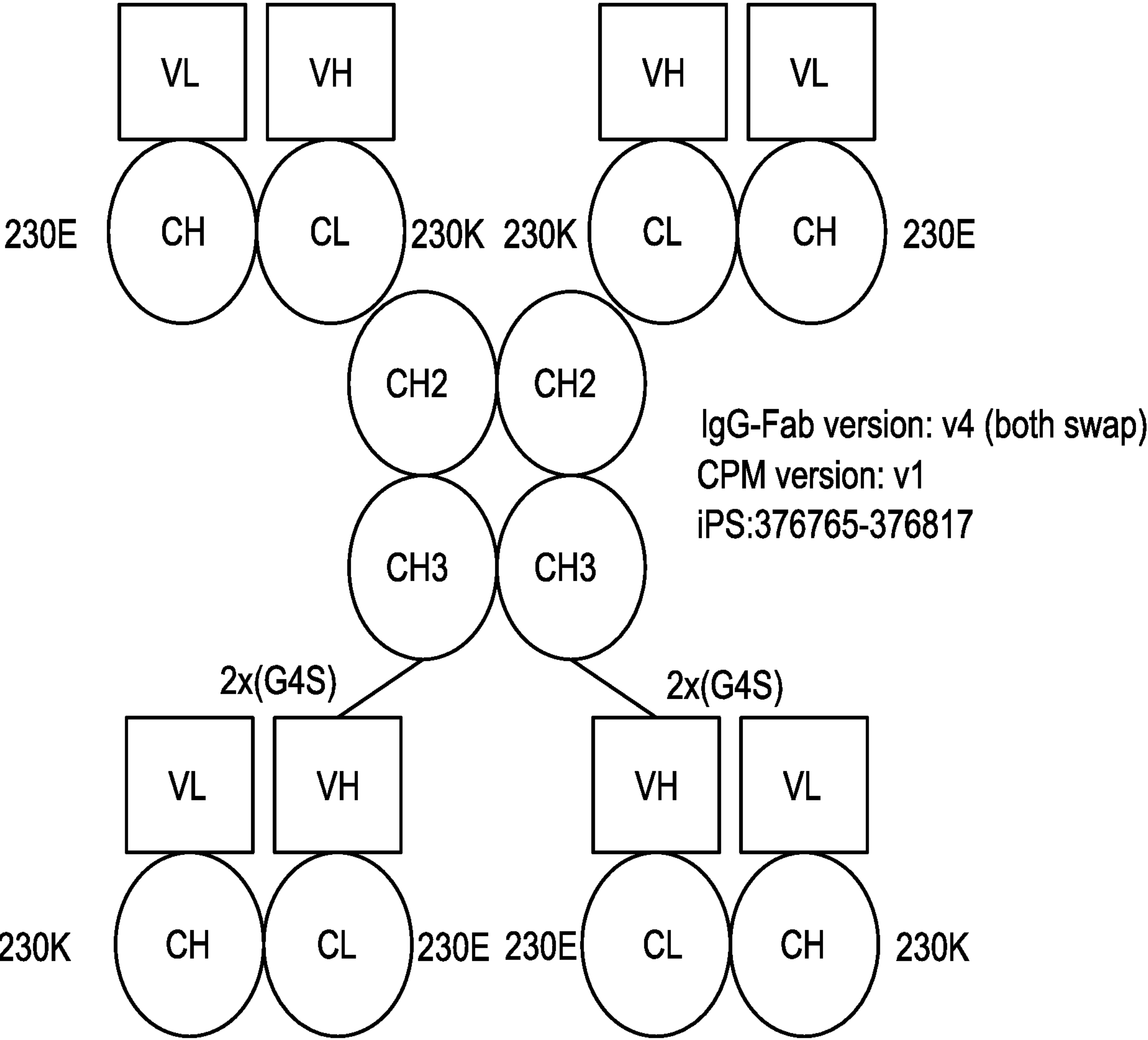
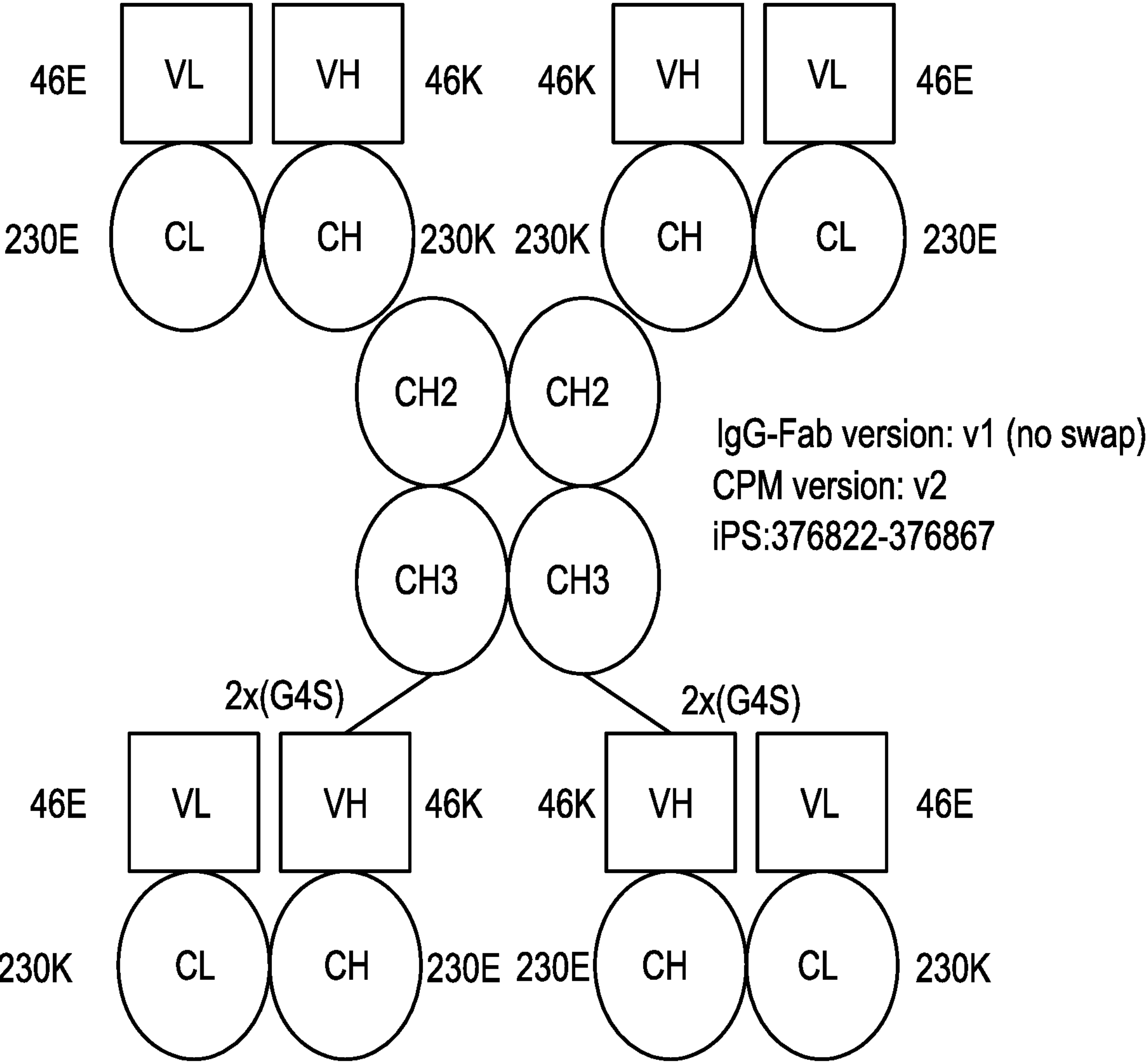


FIG. 9

IgG-Fab CPMv2



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FIG. 10

IgG-Fab CPMv2 N-term CH/CL swap

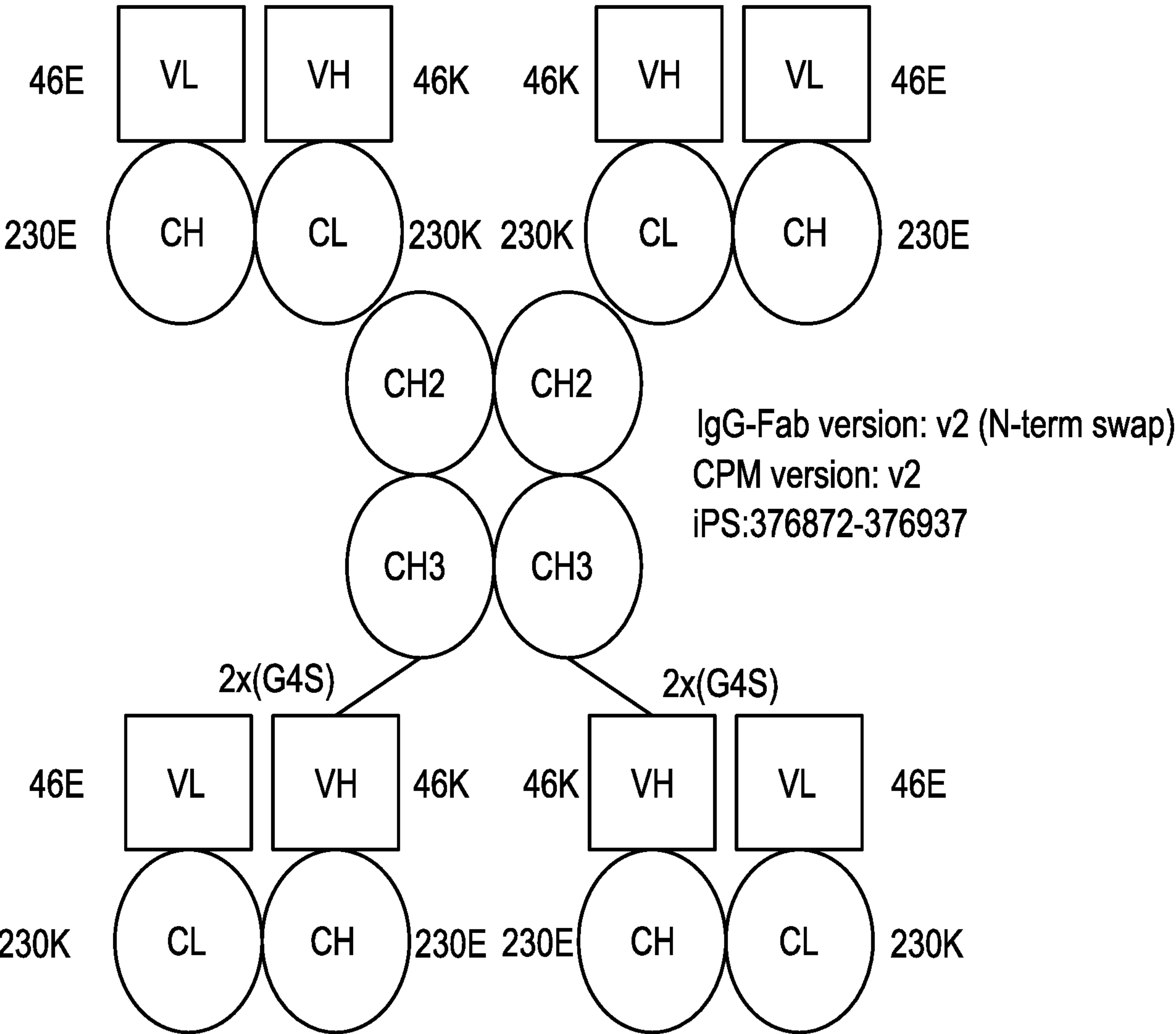


FIG. 11

IgG-Fab CPMv2 C-term CH/CL swap

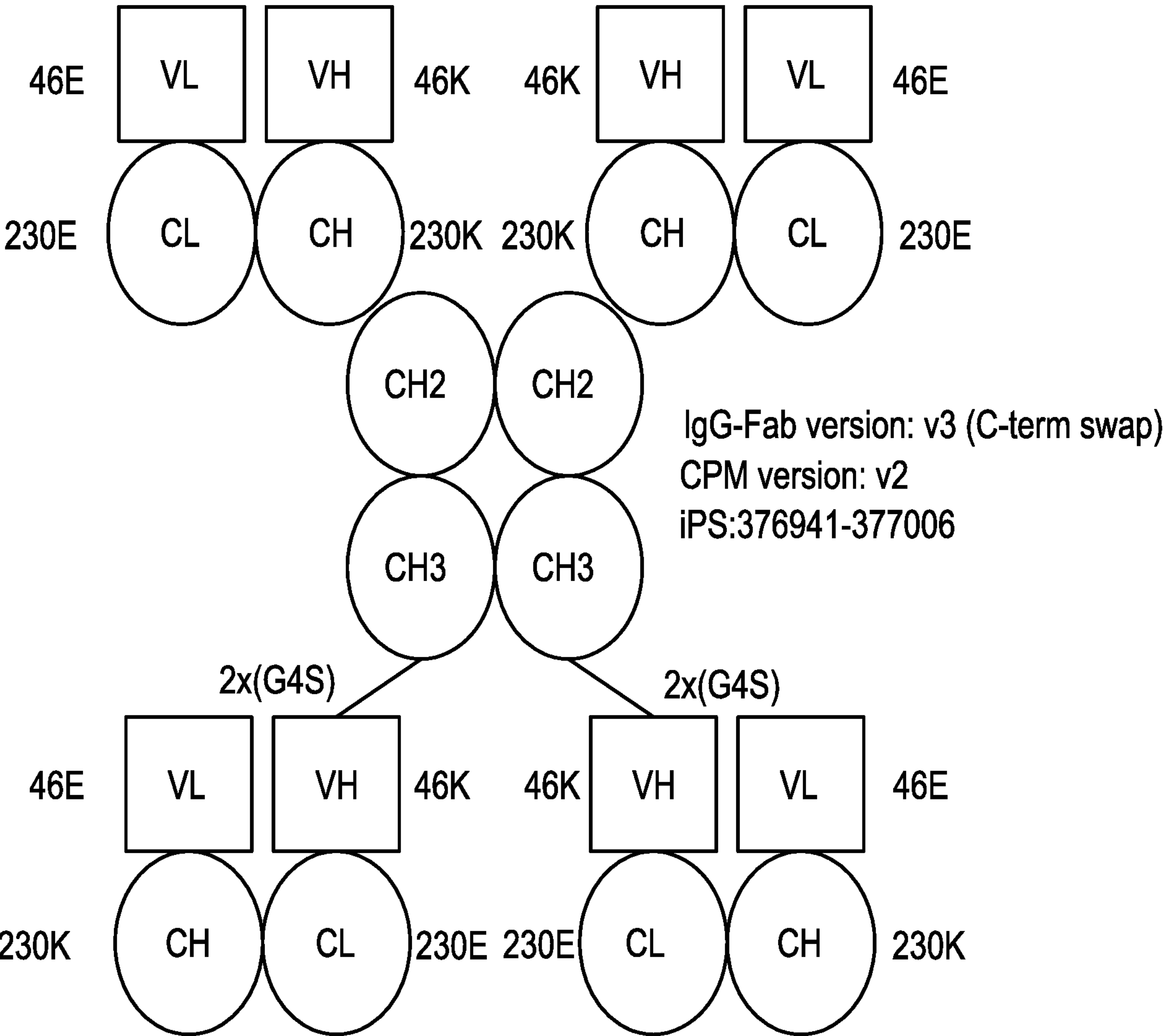


FIG. 12

IgG-Fab CPMv2 CH/CL both swap

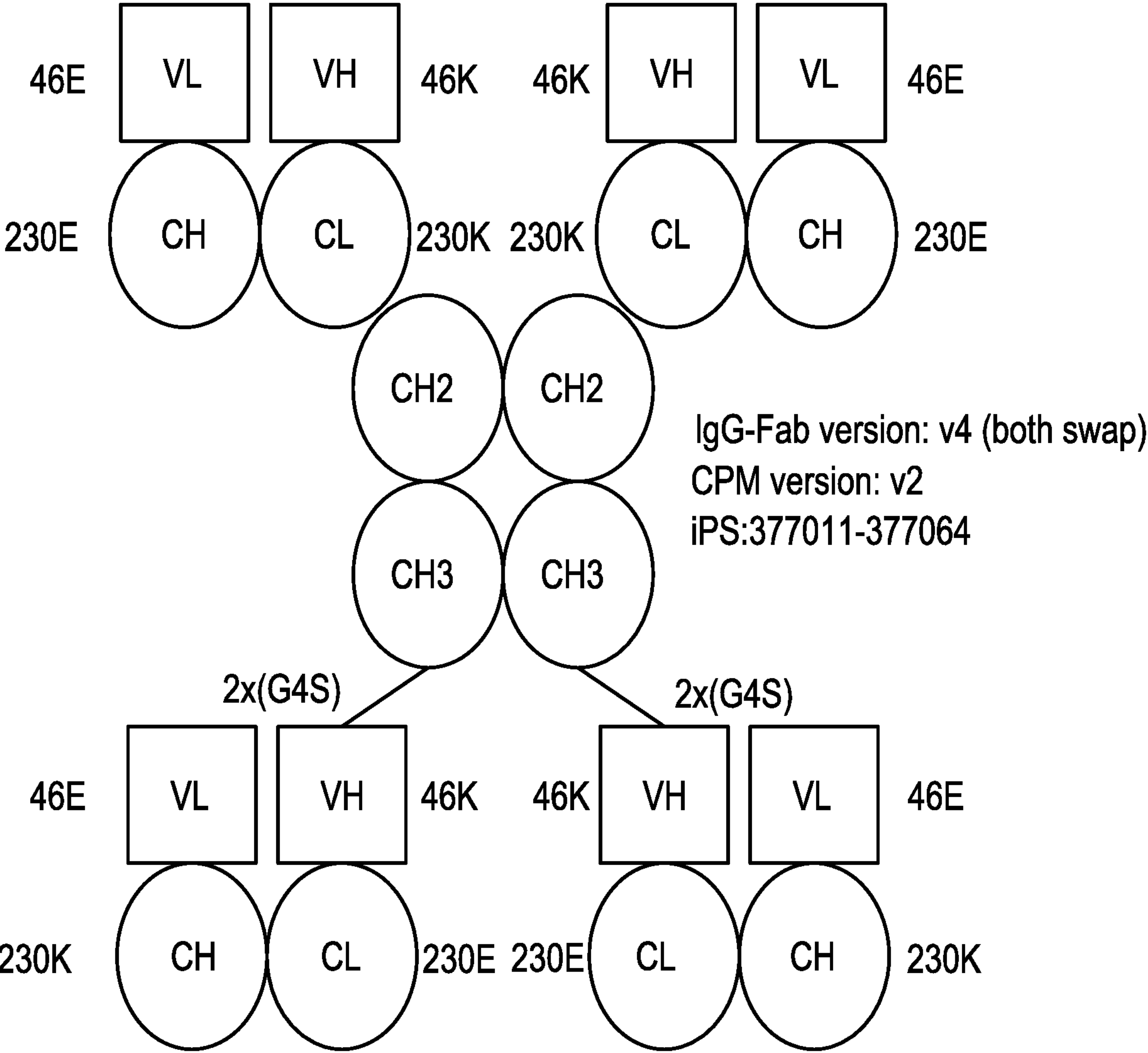


FIG. 13

IgG-Fab CPMv3

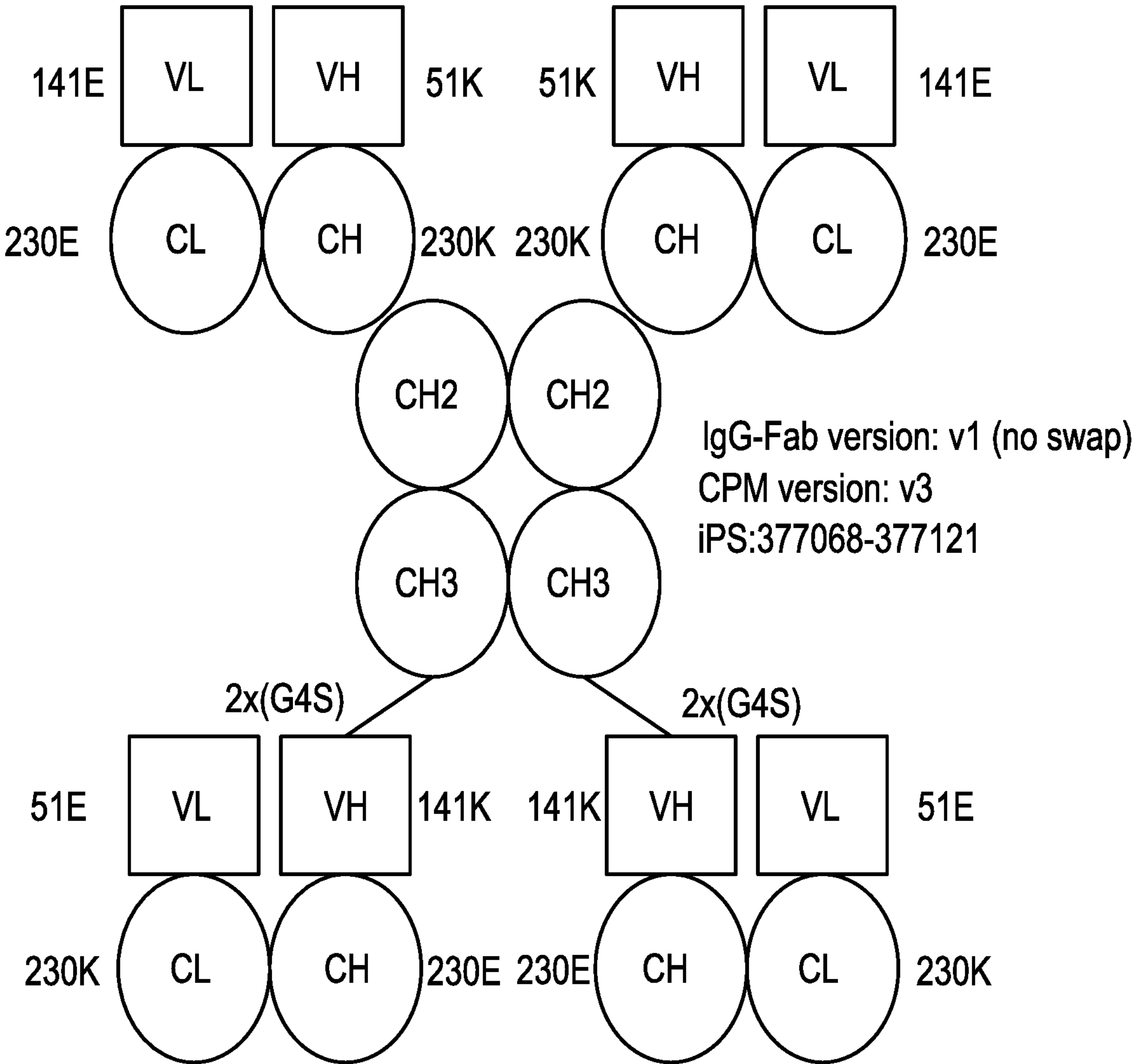


FIG. 14

IgG-Fab CPMv3 N-term CH/CL swap

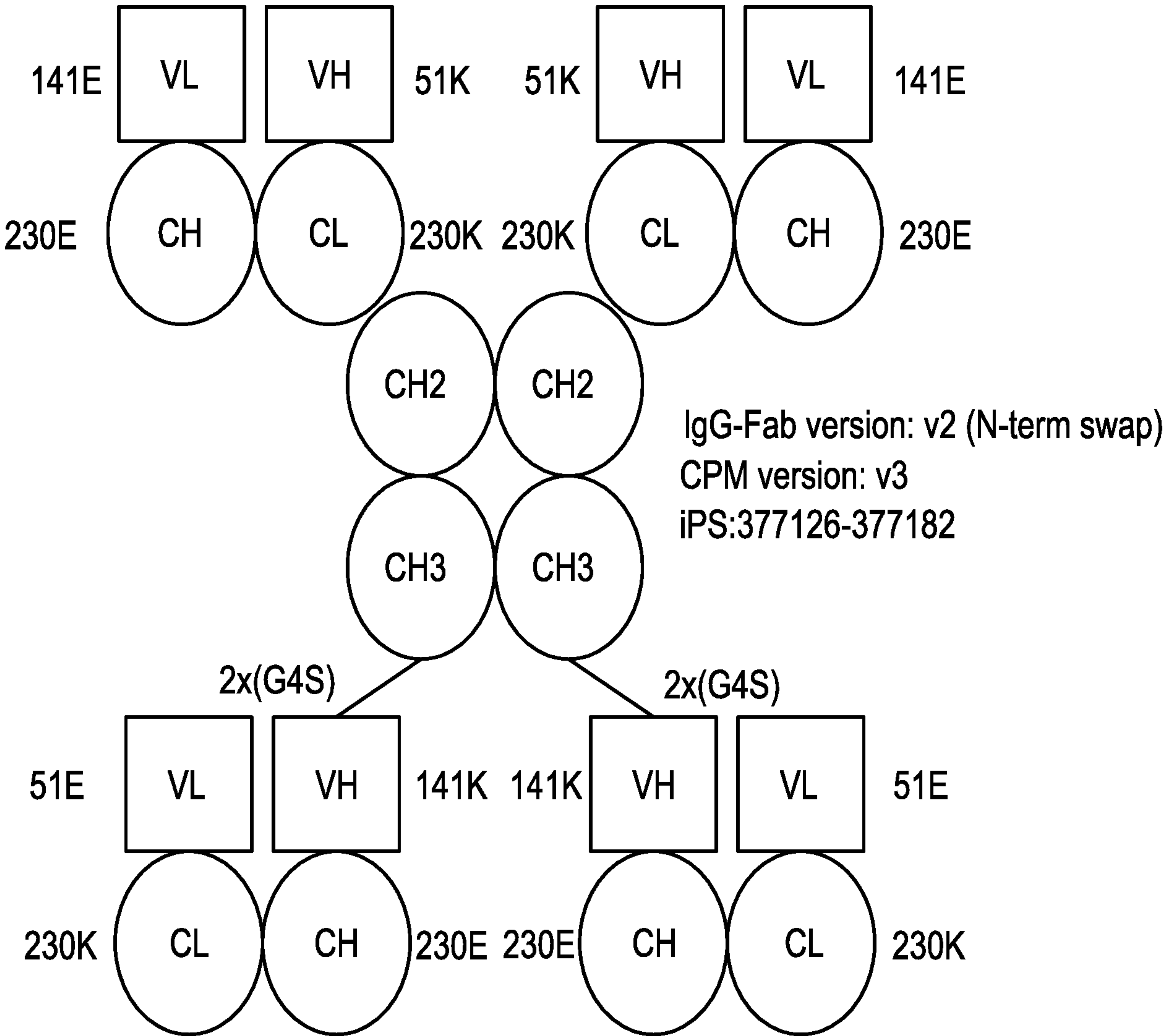


FIG. 15

IgG-Fab CPMv3 C-term CH/CL swap

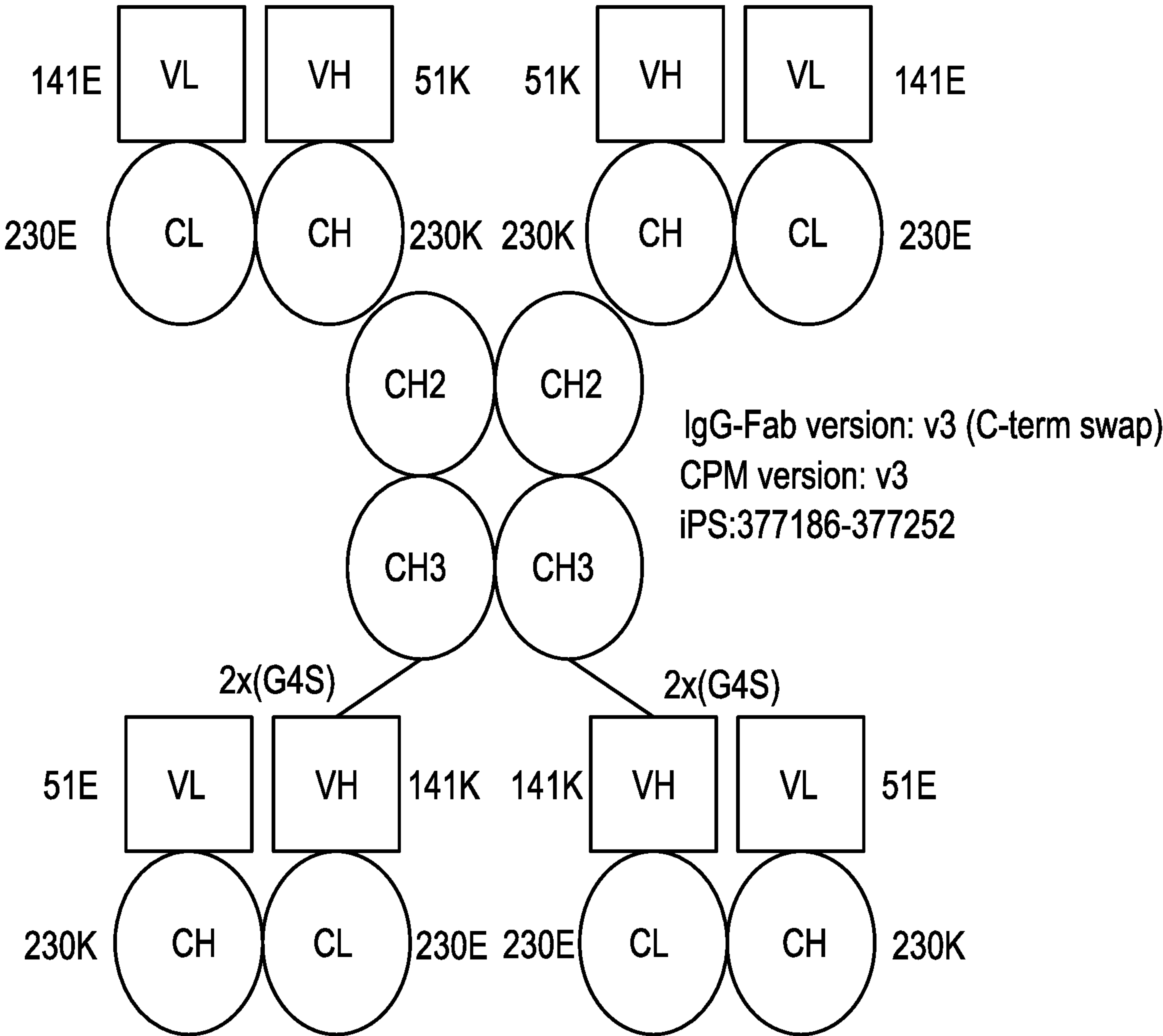


FIG. 16

IgG-Fab CPMv3 CH/CL both swap

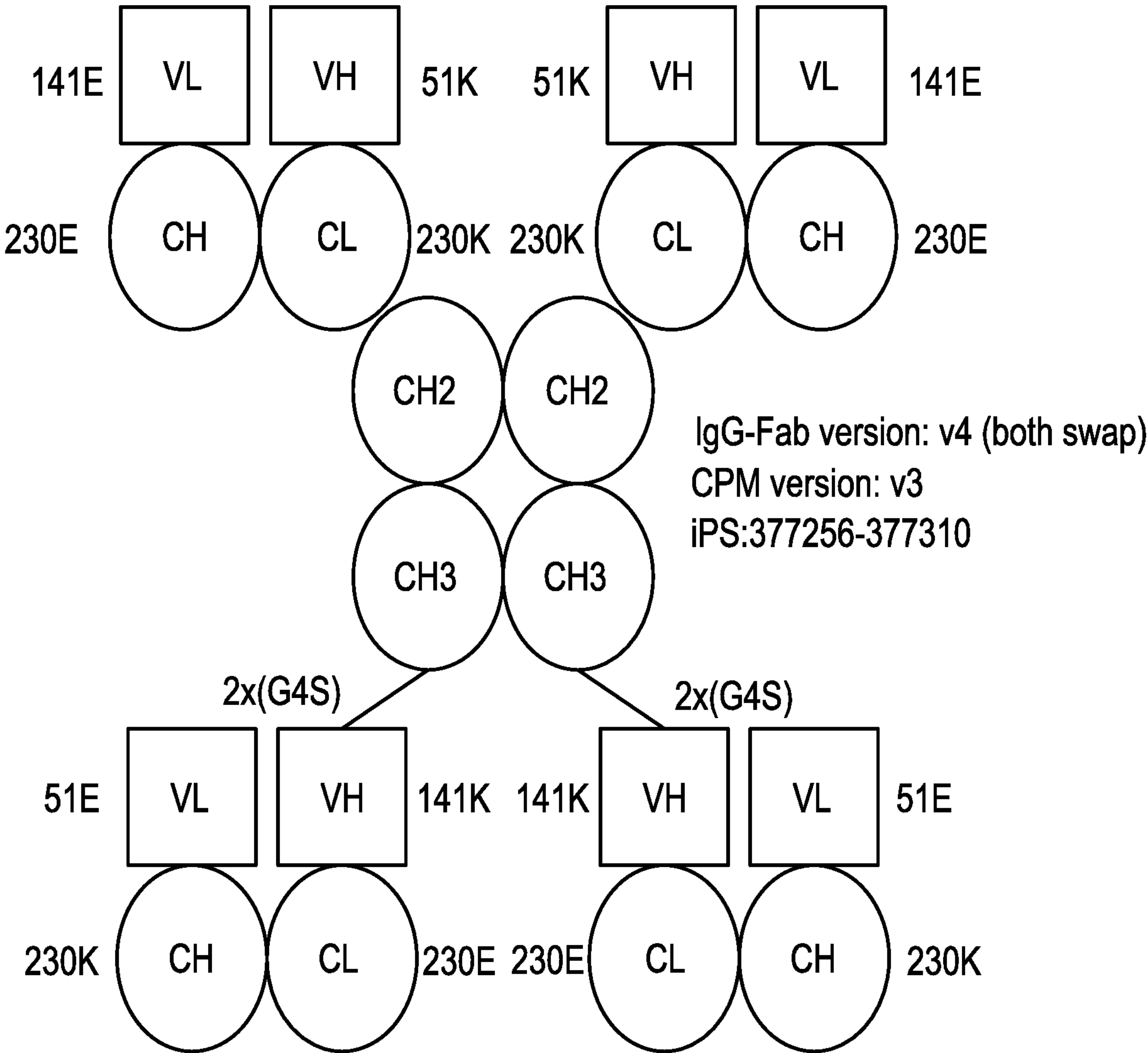


FIG. 17

IgG-Fab Titer: Chain Swapping

Expression Titer (293-6E) & Chain Swapping

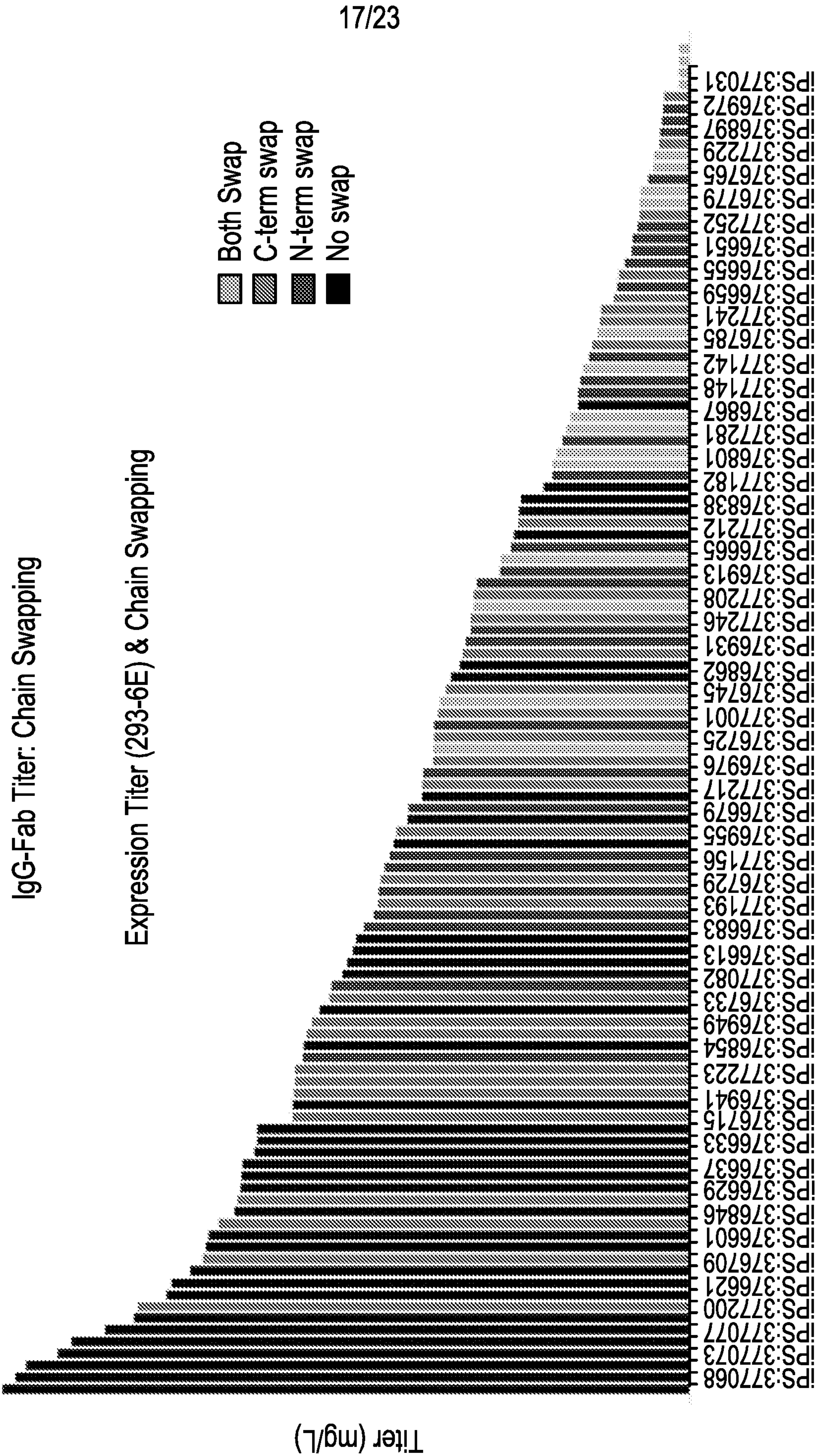


FIG. 18

IgG-Fab Titer: Charge Pair Mutations
Expression Titer (293-6E) & CPM

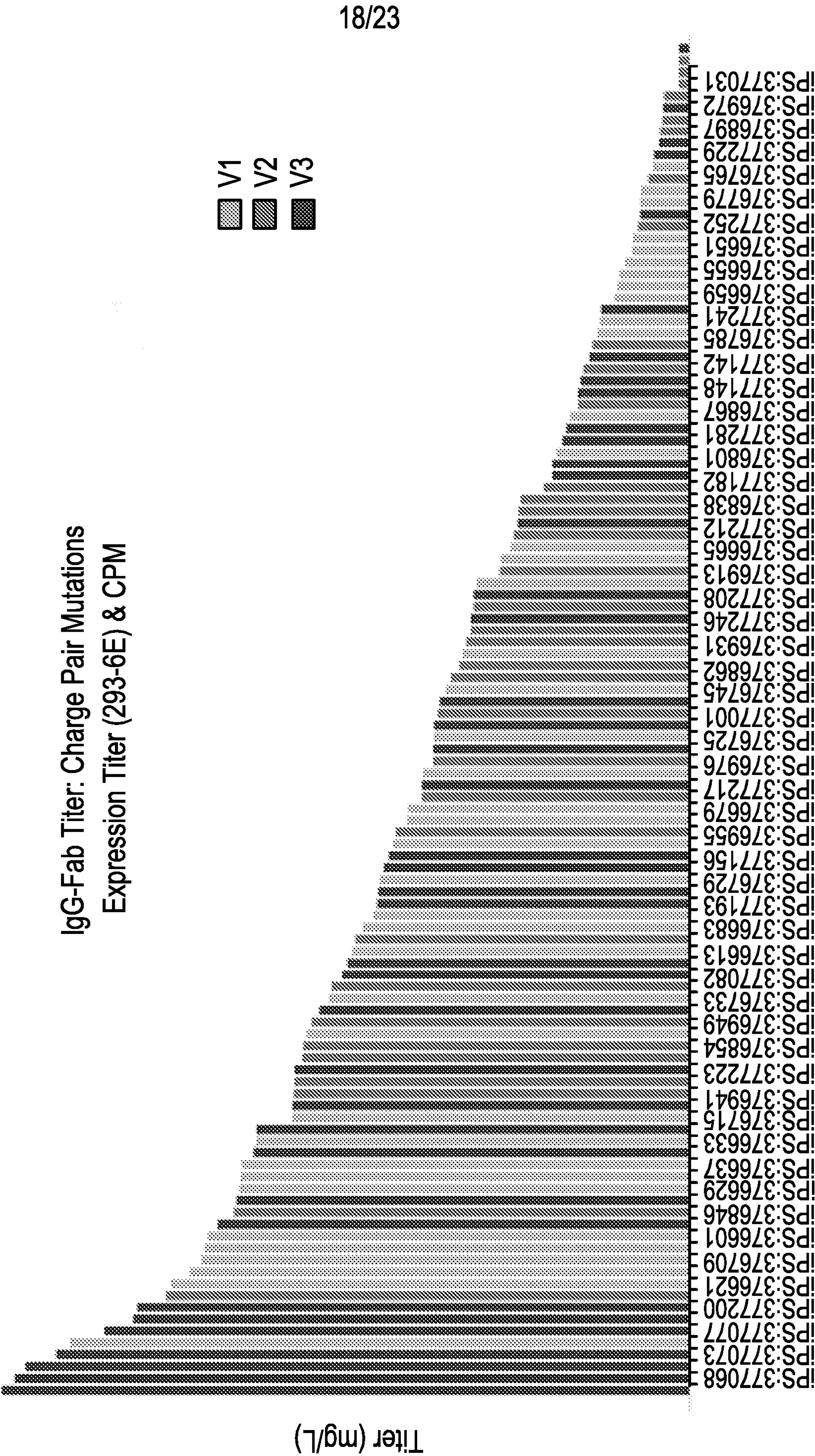


FIG. 19

IgG-Fab Purity: Chain Swaps & CPMs

Effect of Chain Swapping and CPM on HMW

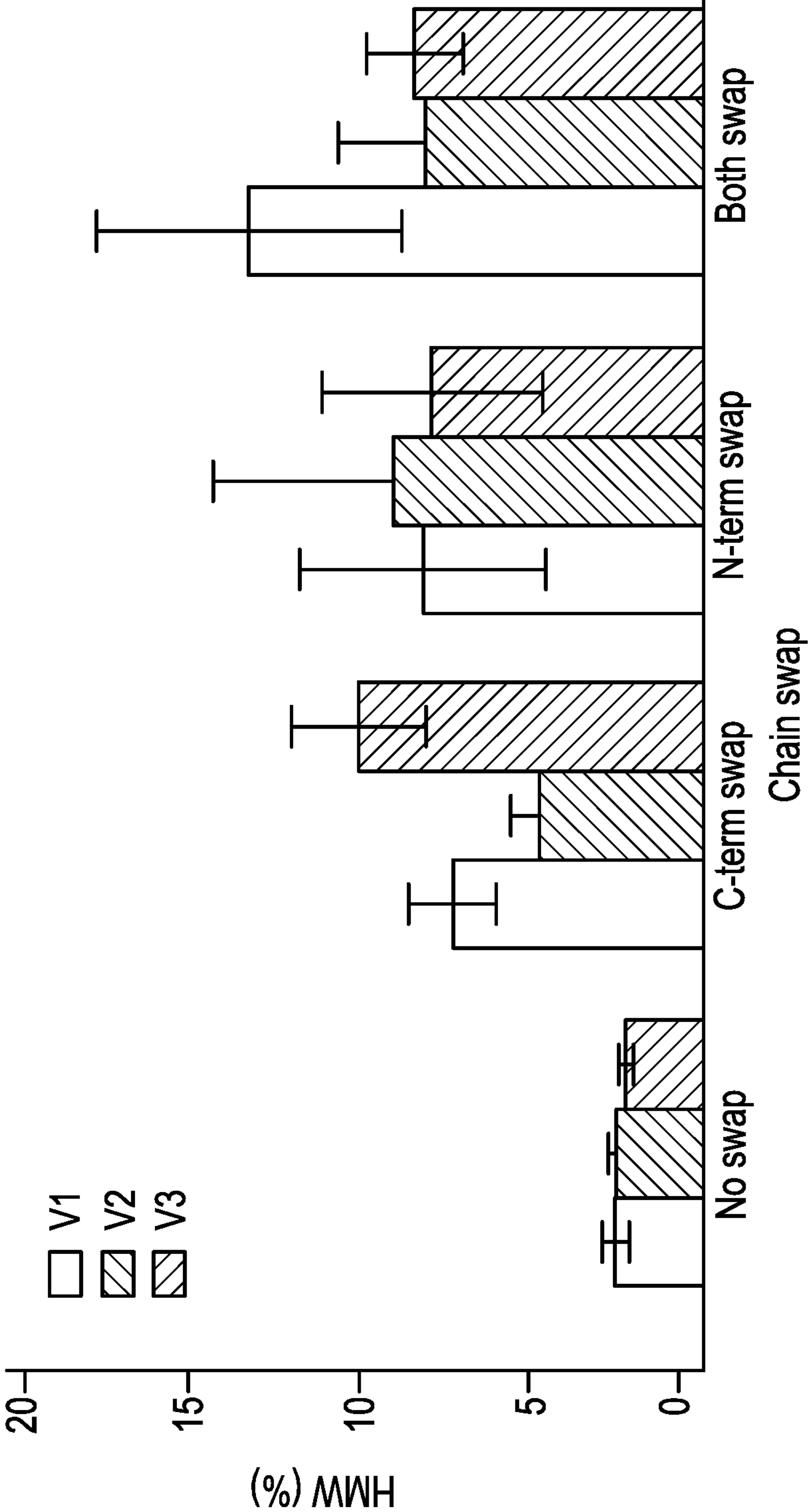


FIG. 20

IgG-Fab TL1A Potency: Chain Swaps

TL1A

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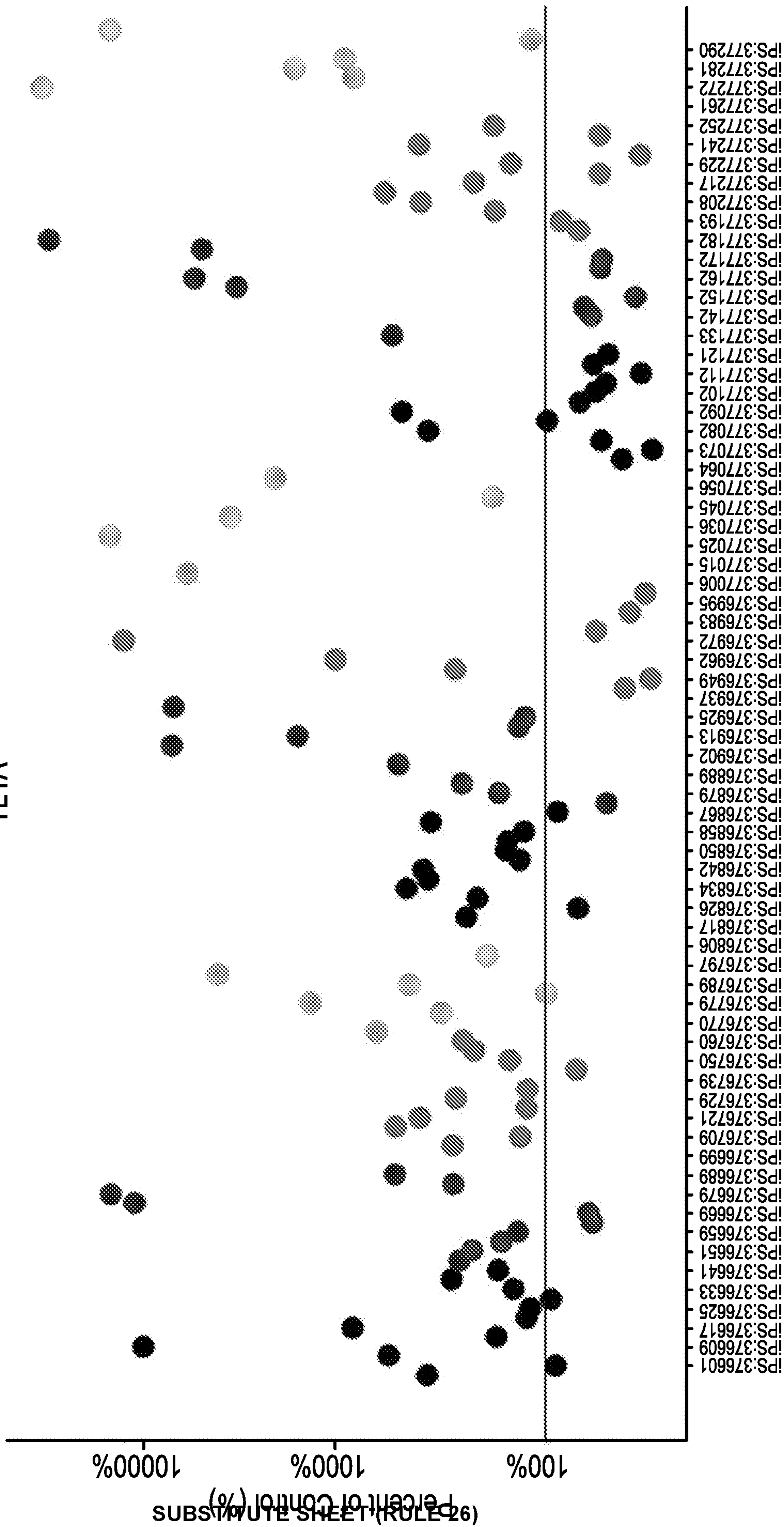


FIG. 21
IgG-Fab TNF α Potency: Chain Swaps
TNF α

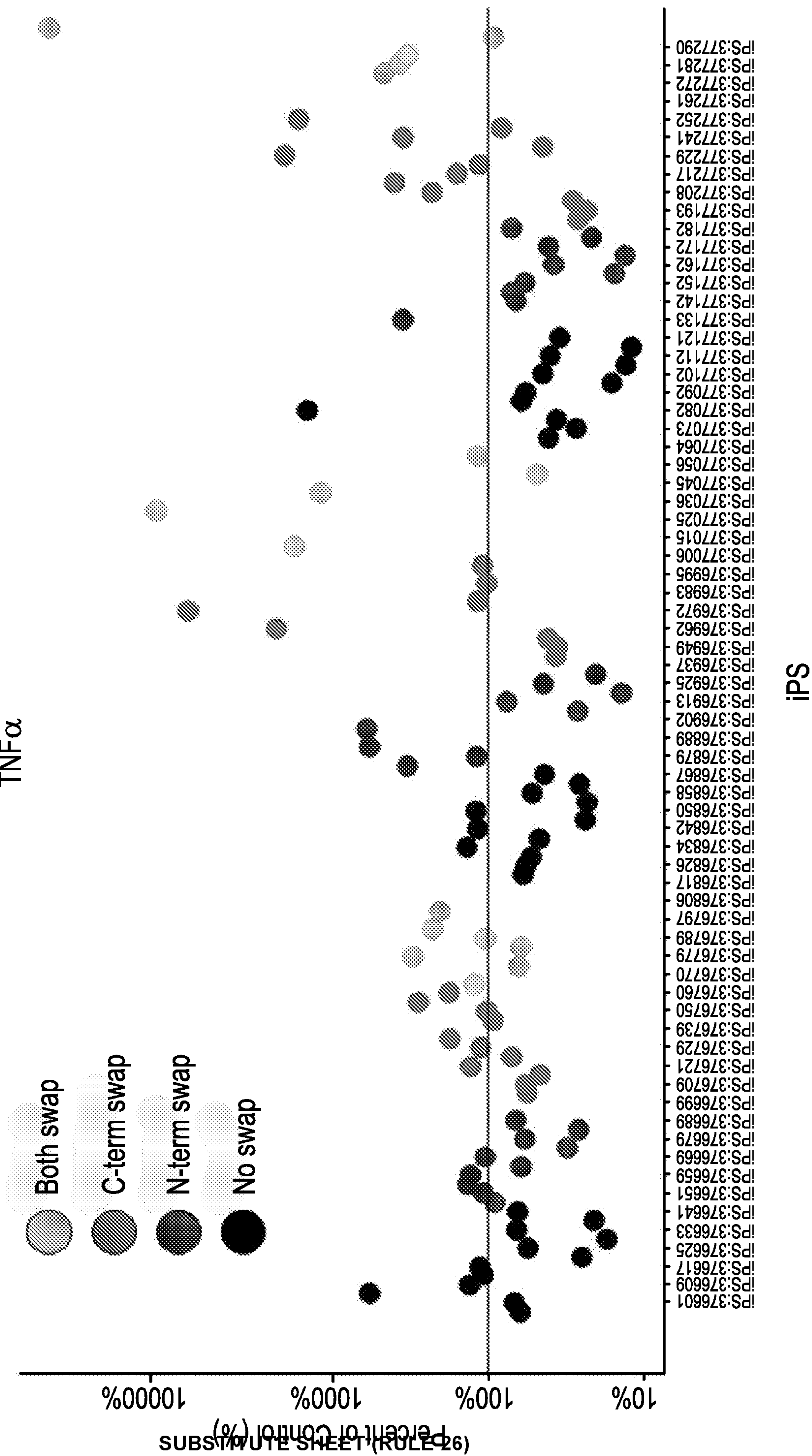
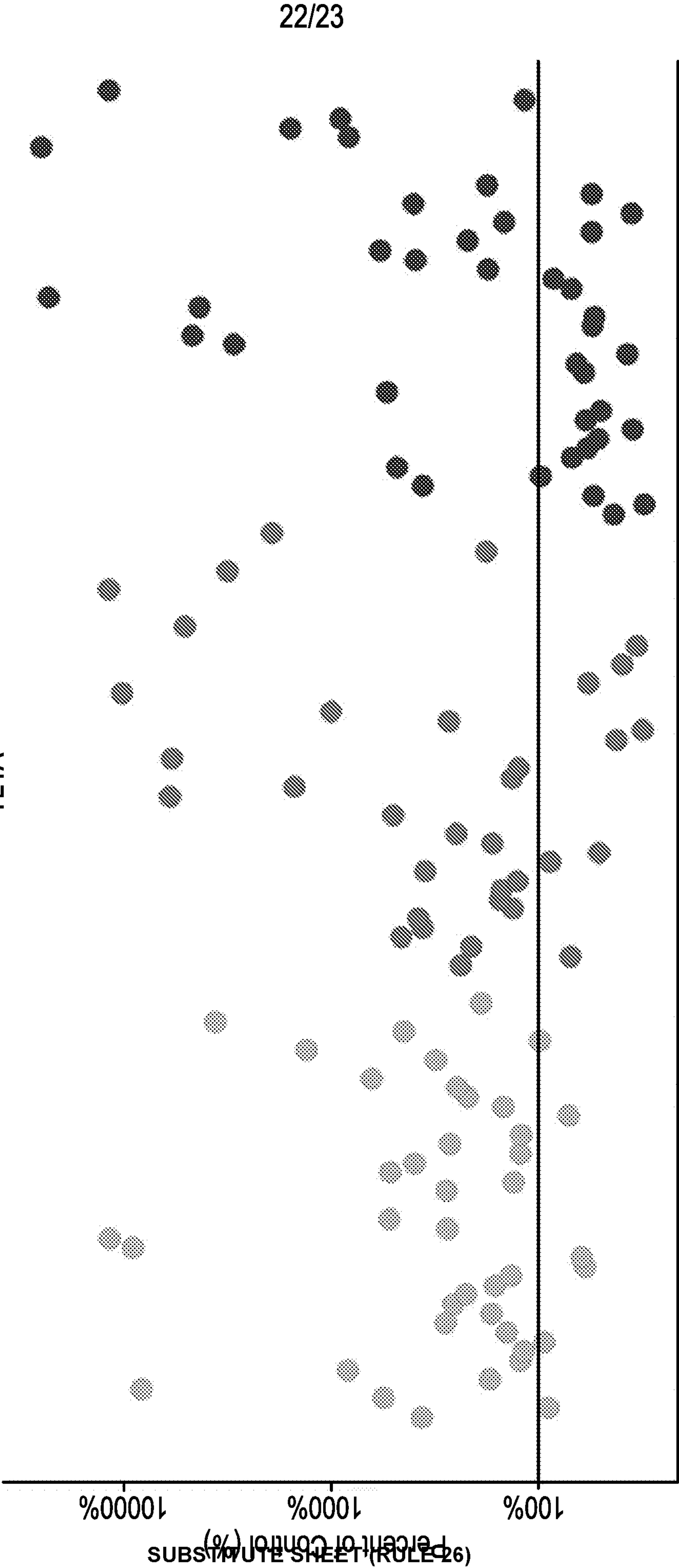


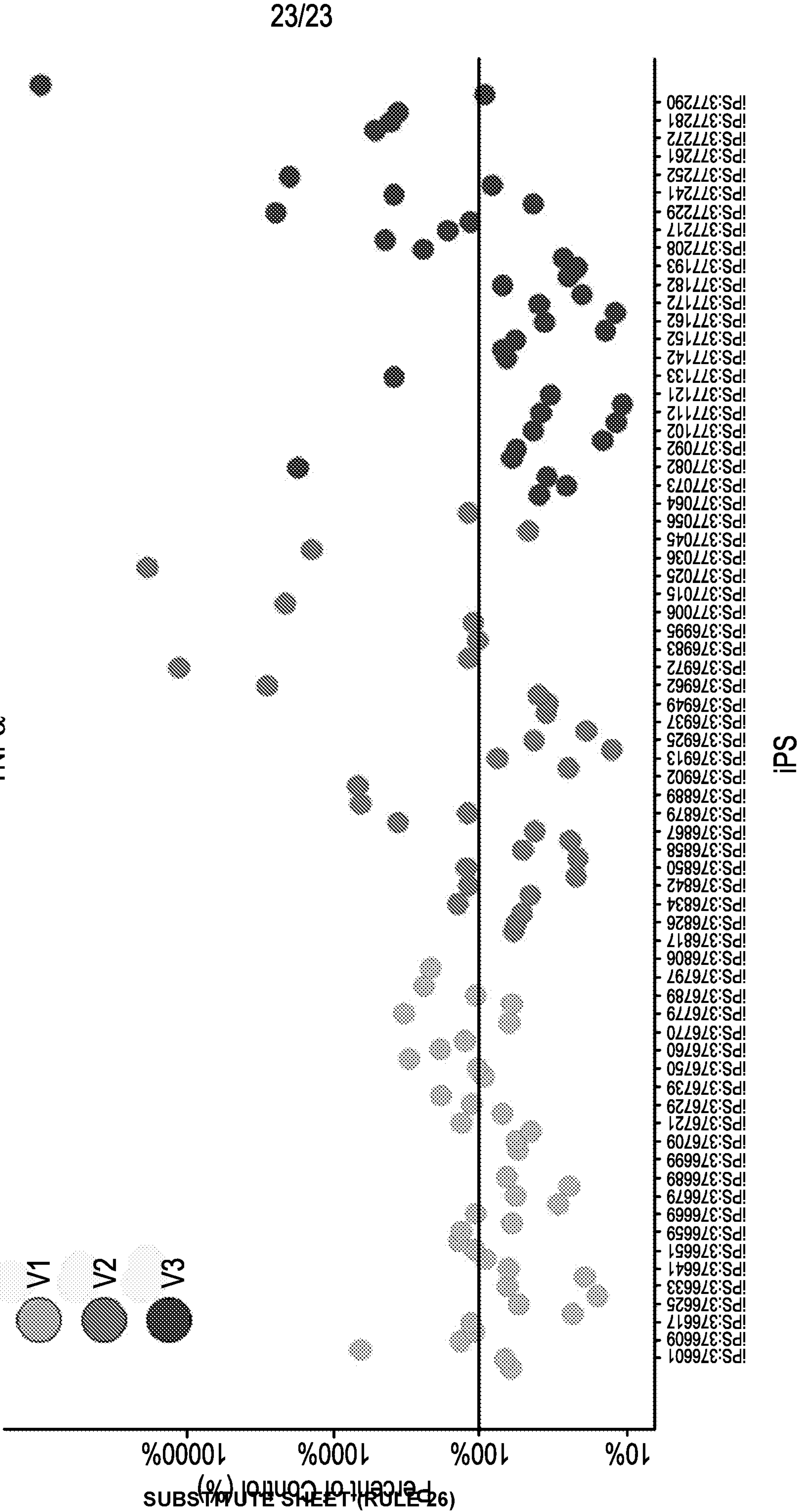
FIG. 22
IgG-Fab TL1A Potency: CPMs
TL1A



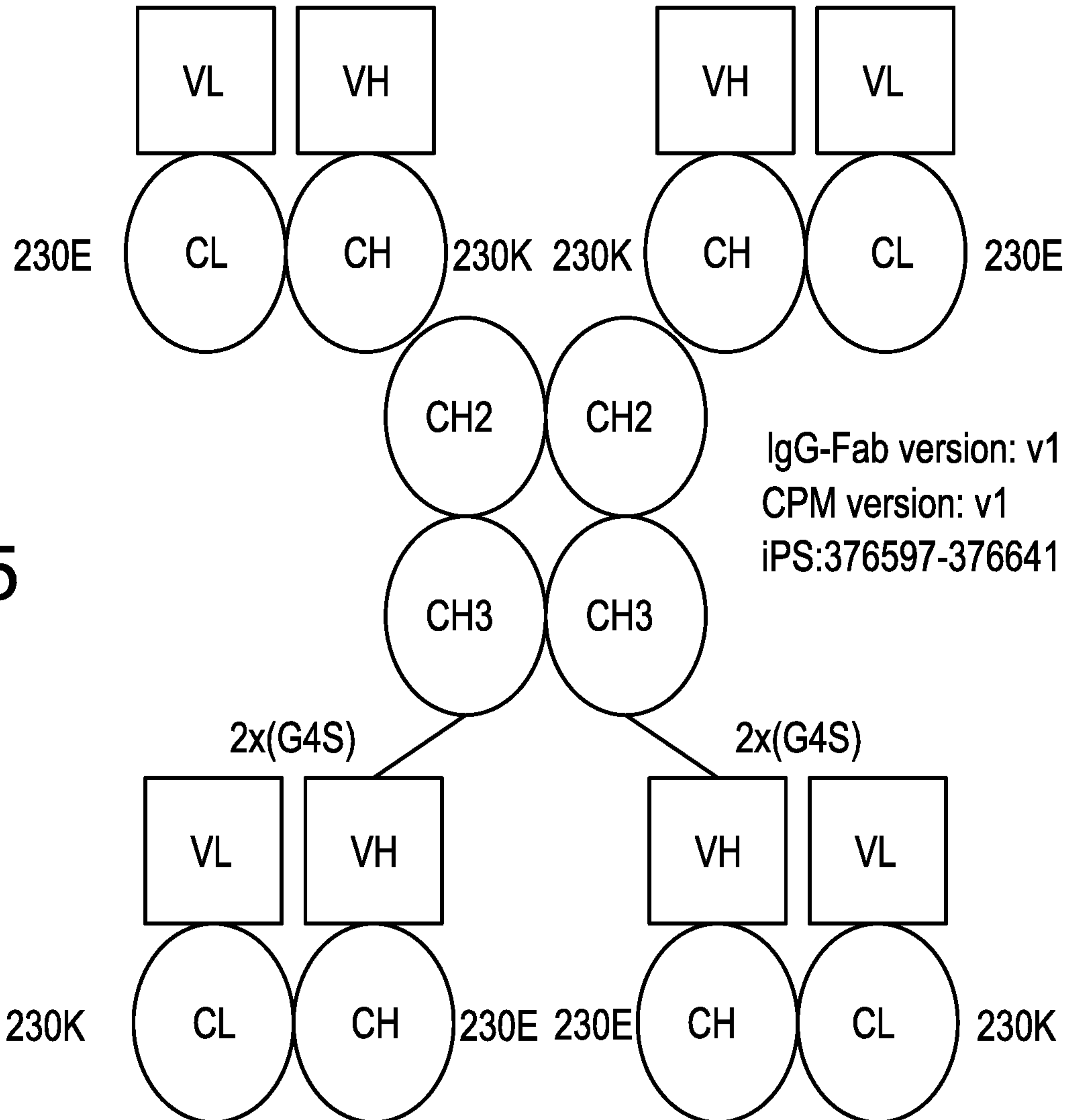
IPS:376601
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IPS:376651
IPS:376659
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IPS:376709
IPS:376721
IPS:376729
IPS:376739
IPS:376750
IPS:376760
IPS:376770
IPS:376779
IPS:376789
IPS:376797
IPS:376806
IPS:376817
IPS:376826
IPS:376834
IPS:376842
IPS:376850
IPS:376858
IPS:376867
IPS:376879
IPS:376889
IPS:376902
IPS:376913
IPS:376925
IPS:376937
IPS:376949
IPS:376962
IPS:376972
IPS:376983
IPS:376995
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IPS:377015
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IPS:377036
IPS:377045
IPS:377056
IPS:377064
IPS:377073
IPS:377082
IPS:377092
IPS:377102
IPS:377112
IPS:377121
IPS:377133
IPS:377142
IPS:377152
IPS:377162
IPS:377172
IPS:377182
IPS:377193
IPS:377208
IPS:377217
IPS:377229
IPS:377241
IPS:377252
IPS:377261
IPS:377272
IPS:377281
IPS:377290

IPS

FIG. 23
IgG-Fab TNF α Potency: CPMs
TNF α



IgG-Fab CPMv1



IgG-Fab version: v1 (no swap)
CPM version: v1
iPS:376597-376641

FIG. 5