

BISPECIFIC ANTIBODIES AND METHODS OF MAKING AND USING THEREOF**CROSS REFERENCE TO RELATED APPLICATIONS**

[0001] This application claims the benefit of U.S. Provisional Patent Application No. 62580845 filed on November 2nd, 2017, titled "BISPECIFIC ANTIBODIES AND METHODS OF MAKING AND USING THEREOF", which are expressly incorporated herein by reference in its entirety.

TECHNICAL FIELD

[0002] The present disclosure generally relates to the technical field of biologic therapeutics, and more particularly relates to making and using bispecific antibodies. All references are incorporated herein by its entirety.

BACKGROUND

[0003] Cancer cells develop various strategies to evade immunosurveillance. Absence of specific tumor antigens and loss of expression of major histocompatibility complex (MHC) molecules hinder the recognition of cancer cells by T lymphocytes. Immunosuppressive tumor microenvironment also contributes to the reduced recognition of tumor cells by the immune system. The tumor microenvironment is presented by immunosuppressive cellular populations composed of regulatory T cells, myeloid derived suppressor cells, tumor associated macrophages, suppressive B cells, immunosuppressive cytokines produced by tumor or stroma cells such as TGF-beta or IL-10, and immune checkpoint molecules that regulate T cell function [Marshall HT et al., Front Oncol 2018, 8:315].

[0004] Engaging a patient own immune system has been shown to be effective at controlling tumor growth and specific elimination of tumor cells while leaving normal tissue intact. Immunotherapy has provided an additional angle to treating cancer [Khalil DN et al., Adv Cancer Res 2015, 128:1-68].

[0005] Combining multiple modulators of the immune system is a new rapidly developing area of the immuno-oncology field. New therapeutic agents that can modulate immune response to tumor cells via multiple pathways can be greatly beneficial for cancer patient by increasing the patient response rate and in some cases decreasing toxicity.

[0006] Combination therapy with more than one monoclonal antibody targeting the immune system have been shown to be more efficacious in the treatment of cancer than treatments with single agents [Hellman MD et al., Adv Immunol 2016, 130: 251-77]. In addition to the increased efficacy and response rate, the combination therapy often has greater toxicity than a single agent treatment. Bispecific agents that modulate the immune system can be less toxic to patients and/or more potent, have additional

mechanisms of action than treatments comprised of a combination of monoclonal antibodies with identical specificities.

SUMMARY

[0007] The current disclosure relates to the bispecific antibodies, specifically, the bispecific antibodies that contain an IgG component therefore overcome fast clearance of BiTE molecule, having an advantage over CAR-T cell therapy as an off-the-shelf therapy that does not require *ex vivo* expansion of patients' immune cells. Another advantage of the bispecific antibodies is the enhanced ability to overcome suppressive tumor microenvironment by simultaneous engagement of two checkpoint receptors.

[0008] The bispecific antibodies in the current disclosure can be combined with other agents, for instance T-cell engagers, and further enhance their activity.

[0009] The present disclosure relates to bispecific antibodies that bind to two distinct targets expressed on immune and tumor cells. Both targets may be checkpoint antigens. In one embodiment, both targets may be checkpoint antigens on immune cells. In one embodiment, both targets may be checkpoint antigens on tumor cells. In one embodiment, one target is a checkpoint antigen on immune cells and another target is a checkpoint antigen on tumor cells. In one embodiment, the checkpoint antigen may be selected from PD-1, PD-L1 and CTLA4. In one embodiment, the targets may include any combination of PD-1, PD-L1 and CTLA4.

[0010] The disclosure further provides the composition of the bispecific agents and their therapeutic use for treatment of cancer and autoimmune deficiencies.

[0011] In one embodiment, the application discloses a bispecific antibody comprising IgG heavy chains and light chains, and two scFv components being connected to either C terminal of the heavy chains or N terminal of the light chains, wherein the IgG has the binding specificity to a first antigen, wherein the scFv components have the binding specificity to a second antigen, and wherein the first antigen and the second antigen are different and are independently selected from α -CTLA4, α -PD-1, and α -PD-L1.

[0012] In one embodiment, the bispecific antibody has the two scFv components connected to the C terminal of the heavy chain. In one embodiment, the first antigen comprises α -CTLA4 and the second antigen comprises α -PD-1 or α -PD-L1. In another embodiment, the first antigen comprises α -PD-1 or α -PD-L1 and the second antigen comprises α -CTLA4.

[0013] In one embodiment, the bispecific antibody has the two scFv components connected to the N terminal of the light chain. In one embodiment, the first antigen comprises α -PD-1 or α -PD-L1 and the

second antigen comprises α -CTLA4. In another embodiment, the first antigen comprises α -CTLA4 and the second antigen comprises α -PD-1 or α -PD-L1.

[0014] In one embodiment, the bispecific antibody is an isolated monoclonal antibody.

[0015] In one embodiment, the bispecific antibody comprises an antigenic peptide sequence having a sequence as disclosed herein. In one embodiment, the bispecific antibody may have an antigenic peptide sequence having at least 70%, 80%, 90%, 95%, 98%, or 99% similarity with the disclosed amino acid sequences.

[0016] In one embodiment, the bispecific antibody comprises an antigen-binding fragment having a sequence as disclosed herein. In one embodiment, the bispecific antibody may have an antigen-binding fragment having a sequence with at least 70%, 80%, 90%, 98%, or 99% similarity with the disclosed antibody sequences.

[0017] In one embodiment, the bispecific antibody may have a binding affinity to α -CTLA4, α -PD-1 or α -PD-L1 with a Kd not greater than 70nM, 50nM, 40nM, 30nM, 20nM, 10nM, or 5nM.

[0018] In one embodiment, the bispecific antibody may have a binding affinity to α -CTLA4 and α -PD-1 with a Kd not greater than 70nM, 50nM, 40nM, 30nM, 20nM, 10nM, or 5nM.

[0019] In one embodiment, the bispecific antibody may have a binding affinity to α -CTLA4 and α -PD-L1 with a Kd not greater than 70nM, 50nM, 40nM, 30nM, 20nM, 10nM, or 5nM.

[0020] In one embodiment, the bispecific antibody may have a binding affinity to two of α -CTLA4, α -PD-1, or α -PD-L1 with a Kd not greater than 70nM, 50nM, 40nM, 30nM, 20nM, 10nM, or 5nM.

[0021] In one embodiment, the bispecific antibody may exhibit one or more functional properties selected from high affinity binding to α -CTLA4, α -PD-1, or α -PD-L1, inhibiting binding of PD-L1 to PD-1, enhancing T cell activation, the ability to stimulate antibody responses and/or the ability to reverse the suppressive function of immunosuppressive cells, such as T regulatory cells.

[0022] In one embodiment, enhancing T-cell activation comprises T-cell proliferation, IFN- γ and/or IL-2 secretion, or a combination thereof.

[0023] In one embodiment, the bispecific antibody comprising a human framework region.

[0024] In one embodiment, the bispecific antibody may be a humanized antibody, a chimeric antibody, or a recombinant antibody.

[0025] In one embodiment, the bispecific antibody comprises an IgG1 constant region to extend the circulating half-life of the bispecific molecules. In one embodiment, the IgG1 constant region of the bispecific antibody comprises an amino acid sequence having at least 98% similarity with SEQ ID No.136.

[0026] In one embodiment, the application discloses an isolated bispecific antibody selected from the group consisting of those clones described or having the described characteristics as disclosed herein.

[0027] In one embodiment, the application discloses an IgG1 heavy chains for the bispecific antibody, comprising an amino acid sequence selected from sequences as disclosed herein. In one embodiment, the IgG1 heavy chains may have an amino acid sequence having at least 70%, 80%, 90%, 98%, or 99% similarity with SEQ ID NO. 02, 06, 08, 10, 12, 14, 16, 18, 20, 22, 26, 30, 34, 38, 42, 46, 50, 54, 58, 62, 72, 92, 96, 100, 104, 108, 112, 116, 120, 124, 128, or 132.

[0028] In one embodiment, the application discloses a kappa light chain for the bispecific antibody. In one embodiment, the kappa light chain may have an amino acid sequence having at least 70%, 80%, 90%, 98%, or 99% similarity with SEQ ID NO. 04, 28, 32, 36, 40, 44, 48, 52, 56, 60, and 64.

[0029] In one embodiment, the application discloses a variable light chain for the bispecific antibody, comprising an amino acid sequence as disclosed herein. In one embodiment, the variable light chain may have an amino acid sequence having at least 70%, 80%, 90%, 98%, or 99% similarity with SEQ ID NO. 94, 98, 102, 106, 110, 114, 118, 122, 126, 130, or 134.

[0030] In one embodiment, the application discloses a variable heavy chain for the bispecific antibody, comprising an amino acid sequence as disclosed herein. In one embodiment, the variable heavy chain may have an amino acid sequence having at least 70%, 80%, 90%, 98%, or 99% similarity with SEQ ID NO. 92, 96, 100, 104, 108, 112, 116, 120, 124, 128, or 132.

[0031] In one embodiment, the application discloses an isolated nucleic acid encoding the bispecific antibody, comprising the IgG1 heavy chain disclosed herein, the kappa light chain disclosed herein, the variable light chain disclosed herein, or the variable heavy chain disclosed herein. In one embodiment, the application discloses an isolated nucleic acid encoding the bispecific antibody, comprising the IgG1 heavy chain having an amino acid sequence having at least 70%, 80%, 90%, 98%, or 99% similarity with SEQ ID NO. 02, 06, 08, 10, 12, 14, 16, 18, 20, 22, 26, 30, 34, 38, 42, 46, 50, 54, 58, 62, 72, 92, 96, 100, 104, 108, 112, 116, 120, 124, 128, or 132, the kappa light chain having an amino acid sequence having at least 70%, 80%, 90%, 98%, or 99% similarity with SEQ ID NO. 04, 28, 32, 36, 40, 44, 48, 52, 56, 60, and 64, the variable light chain having an amino acid sequence having at least 70%, 80%, 90%, 98%, or 99% similarity with SEQ ID NO. 94, 98, 102, 106, 110, 114, 118, 122, 126, 130, or 134, or the variable heavy chain having an amino acid sequence having at least 70%, 80%, 90%, 98%, or 99% similarity with SEQ ID NO. 92, 96, 100, 104, 108, 112, 116, 120, 124, 128, or 132.

[0032] In one embodiment, the application discloses an expression vector comprising the isolated nucleic acid disclosed herein. In one embodiment, the expression vector comprises an isolated nucleic

acid having a sequence having at least 70%, 80%, 90%, 98%, or 99% similarity with the nucleic acid sequence disclosed herein.

[0033] In one embodiment, the expression vector is expressible in a cell.

[0034] In one embodiment, the application discloses a host cell comprising the nucleic acid of disclosed herein.

[0035] In one embodiment, the application discloses a host cell comprising the expression vector.

[0036] In some embodiments, the application discloses the host cell, wherein the host cell is a prokaryotic cell or a eukaryotic cell.

[0037] In some embodiments, the application discloses a method of producing an antibody comprising culturing the host cell provided thereof so that the antibody is produced.

[0038] In some embodiments, the application discloses an immunoconjugate comprising the bispecific antibody and a cytotoxic agent. In some embodiments, the cytotoxic agent is a chemotherapeutic agent, a growth inhibitory agent, a toxin, or a radioactive isotope.

[0039] In one embodiment, the application discloses a pharmaceutical composition, comprising the bispecific antibody and a pharmaceutically acceptable carrier. In one embodiment, the application discloses a pharmaceutical composition, comprising the immunoconjugate and a pharmaceutically acceptable carrier. In one embodiment, the pharmaceutical composition further comprises radioisotope, radionuclide, a toxin, a therapeutic agent, a chemotherapeutic agent or a combination thereof.

[0040] In one embodiment, the application discloses a method of treating a subject with a cancer, comprising administering to the subject an effective amount of the bispecific antibody disclosed herein. In one embodiment, the cancer comprises breast cancer, colorectal cancer, pancreatic cancer, head and neck cancer, melanoma, ovarian cancer, prostate cancer, non-small lung cell cancer, small cell lung cancer, glioma, esophageal cancer, nasopharyngeal cancer, kidney cancer, gastric cancer, liver cancer, bladder cancer, cervical cancer, brain cancer, lymphoma, leukaemia, myeloma.

[0041] In one embodiment, the application discloses the method of treating a subject with a cancer, wherein the cancer comprises cells expressing PD-L1.

[0042] In one embodiment, the application discloses the method of treating a subject with a cancer, further comprising co-administering an effective amount of a therapeutic agent. In some embodiments, the therapeutic agent comprises an antibody, a chemotherapy agent, an enzyme, or a combination thereof.

[0043] In some embodiments, the therapeutic agent comprises capecitabine, cisplatin, trastuzumab, fulvestrant, tamoxifen, letrozole, exemestane, anastrozole, aminoglutethimide, testolactone, vorozole, formestane, fadrozole, letrozole, erlotinib, lapatinib, dasatinib, gefitinib, imatinib, pazopininib, lapatinib, sunitinib, nilotinib, sorafenib, nab-palitaxel, a derivative or a combination thereof.

[0044] In one embodiment, the application discloses the method of treating a subject with a cancer, wherein the subject is a human.

[0045] In one embodiment, the application discloses a solution comprising an effective concentration of the bispecific antibody disclosed herein, wherein the solution is blood plasma in a subject.

[0046] Still other embodiments of the present application will become readily apparent to those skilled in the art from the following detailed description, wherein is described embodiments of the application by way of illustrating the best mode contemplated for carrying out the application. As will be realized, the application is capable of other and different embodiments and its several details are capable of modifications in various obvious respects, all without departing from the spirit and the scope of the present application. Accordingly, the drawings and detailed description are to be regarded as illustrative in nature and not as restrictive.

BRIEF DESCRIPTION OF THE DRAWINGS

[0047] The foregoing and other features of this disclosure may become more fully apparent from the following description and appended claims, taken in conjunction with the accompanying drawings. Understanding that these drawings depict only several embodiments arranged in accordance with the disclosure and are, therefore, not to be considered limiting of its scope, the disclosure may be described with additional specificity and detail through use of the accompanying drawings, in which:

[0048] Figure 1 shows a diagram of example bispecific antibodies targeting CTLA4, PD-1 and PD-L1 antigens;

[0049] Figure 2 shows binding of example anti-PD-1 antibodies to PD-1 antigen expressed on the surface of CHO cell line;

[0050] Figure 3 depicts results from a biochemical assay assessing the ability of the representative bispecific antibodies to block the interaction between CTLA4 and CD80;

[0051] Figure 4 shows stimulation of PBMC with super antigen SEB; Figure 4A shows the treatment with PD224D1 x CT4 IgG1 null and PL230C6 x CT4 IgG1 null; Figure 4B shows the treatment with CT4 x PD224D1 IgG1 null, CT4 x PL221G5 IgG1 and CT4 x PL221G5 IgG1 null;

[0052] Figure 5 shows results from a signaling assay for PD-1/PDL-1 pathway;

[0053] Figure 6 shows results from Dendritic Cell Mixed Lymphocytes Reaction study;

- [0054]** Figure 7 shows results from regulatory T cell suppression assay; Figure 7A shows the proliferation of CD8+ T cells; and Figure 7B shows IFN γ production;
- [0055]** Figure 8 shows CD8 T cell degranulation in response to treatment with example bispecific antibodies;
- [0056]** Figure 9 shows results from MiXeno HCC287 mouse tumor model;
- [0057]** Figure 10 shows effect of example bispecific antibodies on proliferation of Flu-specific CD8 T cells;
- [0058]** Figure 11 shows results from PBMC memory response to CEFT peptide pool; and
- [0059]** Figure 12 shows enhancement of Redirected T Cell Cytotoxicity by example bispecific antibodies.

DETAILED DESCRIPTION

[0060] In the following detailed description of embodiments of the application, reference is made to the accompanying drawings in which like references indicates similar elements, and in which is shown by way of illustration, specific embodiments in which the application may be practiced. These embodiments are described in sufficient detail to enable those skilled in the art to practice the application. In other instances, well-known circuits, structures, and techniques have not been shown in detail in order not to obscure the understanding of this description. The following detailed description is, therefore, not to be taken in a limiting sense, and the scope of the application is defined only by the appended claims.

[0061] The disclosure relates to bispecific antibodies that specifically bind to human CTLA4, PD-1 or PD-L1. In some embodiments, the bispecific antibody comprises of a first arm that binds to CTLA4 and a second arm that binds to PD-1 or PD-L1. In some embodiments, the bispecific antibody comprises of a first arm that binds to PD-1 or PD-L1 and a second arm that binds to CTLA4. Examples of domains that comprise the arms include, but are not limited to, Fab and scFv domains. Each arm contains two antigen-binding domains and is connected to another arm via Fc domain. The Fc domain can be of human IgG1, IgG2, IgG3, IgG4 or an engineered isotype.

[0062] The bispecific antibodies of this application (Figure 1) target human CTLA4, human PD-1 and human PD-L1. Each of these targeted bispecific antibodies carry an anti-CTLA4 (SEQ IDs 91, 93) and an anti-human PD-1 (SEQ IDs 95, 97, 131, 133) or PD-L1 binding domains (SEQ IDs 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129). Either one of the binding domains was converted to scFv (VH-VL orientation) for placement at the C-terminus, or scFv (VL-VH orientation) for placement at the N-terminus (Figure 1 A and B respectively).

[0063] In some embodiments, scFv molecules described herein contain a 20-amino acid flexible gly-gly-gly-gly-ser (G4S) X4 linker that operably links the VH and VL, regardless of the V-region orientation (LH or HL). The remaining positions in the bispecific antibody may consist of a human IgG1 Fc or IgG1 null Fc heavy chain, VH-CH1-Hinge-CH2-CH3, and its corresponding kappa light chain, VL-CL. scFv domains were genetically linked through a 10-amino acid (G4S) x 2 linker to either N-terminal or C-terminal of IgG1 heavy chain, resulting in a contiguous ~ 100 kDa heavy chain monomer peptide. When co-transfected with the appropriate light chain, the final symmetric bispecific molecule may be purified through the human IgG1 Fc (Protein A) and assayed to assess functional activity.

[0064] Heavy and light chain gene “cassettes” were previously constructed such that V-regions could be cloned using either restriction enzyme sites (Figure 1A example: HindIII/NotI for the heavy chain and HindIII/BsiWI for the light chain). In one embodiment, “restriction-free cloning” NEBuilder (NEB, Ipswich, MA) was used.

[0065] Bispecific antibodies are produced through a process that involves design of the intact molecule, synthesis and cloning of the nucleotide sequences for each domain, expression in mammalian cells and purification of the final product. Nucleotide sequences were assembled using the Geneious 10.2.3 software package (Biomatters, Auckland, NZ) and broken up into their component domains for gene synthesis (Genewiz, South Plainsfield, NJ). In one example (Figure 1A), the heavy chain of CT4 x PD224D1 IgG1 null bispecific antibody (SEQ ID 2) consists of the anti-CTLA4 VH domain fused to the human IgG1 null Fc domain (hinge, CH1, and CH2), followed by a 10-amino acid (G4S) x 2 linker fused to the anti-PD-1 scFv domain (clone PD224D1). Using NEBuilder web-based tools, 5' and 3' nucleotides were appended to each of the domains so that each domain overlaps its flanking domains by 20-30 nucleotides, which direct site-specific recombination, thus genetically fusing each domain in a single gene assembly step.

[0066] The light chain of CT4 x PD224D1 IgG1 null consists of the anti-CTLA4 VL domain fused to the human C kappa domain. A synthesized gene fragment was digested with the restriction enzymes HindIII and BsiWI and was then ligated in-frame with the human C kappa domain. For both constructs, a small aliquot was transformed into *E.coli* DH10b (Invitrogen, Carlsbad, CA) and plated on TB + carbenicillin 100ug/ml plates (Teknova, Hollister, CA) and incubated at 37C overnight. Resultant colonies were selected and 2ml overnight cultures inoculated in TB + carbenicillin. DNA was prepared (Thermo-Fisher, Carlsbad, CA) from overnight cultures and subsequently sequenced (Genewiz, South Plainsfield, NJ) using sequencing primers (Sigma, St. Louis, MO) flanking each domain. All DNA sequences were assembled and analysed in Geneious.

EXAMPLES

[0067] Example 1: Binding of anti-PD-L1 antibodies to PD-L1 antigen

[0068] Binding affinities and kinetics of anti-PD-L1 antibodies to PD-L1 recombinant protein were assessed via Surface Plasmon Resonance on ForteBio Octet RED96 instrument. The antigen was immobilized on the sensor chip surface and the tested antibodies were flown over the immobilized antigens. All molecules showed strong binding to the antigen as shown in **Table 1** for examples.

[0069] Table 1. Binding of Anti-PD-L1 Antibodies to PD-L1 Antigen

	mAb			scFv-Fc			Fc-scFv		
Sample ID	KD (M)	kon(1/Ms)	kdis(1/s)	KD (M)	kon(1/Ms)	kdis(1/s)	KD (M)	kon(1/Ms)	kdis(1/s)
PL004B9	1.37E-09	5.08E+05	6.95E-04	1.42E-09	3.87E+05	5.50E-04	1.54E-09	3.07E+05	4.71E-04
PL221G5	4.83E-10	5.72E+05	2.76E-04	5.97E-10	5.08E+05	3.03E-04	4.12E-10	4.14E+05	1.71E-04
PL230C6	7.69E-10	6.09E+05	4.68E-04	9.17E-10	5.03E+05	4.61E-04	8.68E-10	4.18E+05	3.62E-04
PL231H2	7.81E-10	5.01E+05	3.91E-04	9.99E-10	4.20E+05	4.19E-04	4.62E-10	8.40E+05	3.89E-04

[0070] Example 2: Binding of anti-PD-1 antibodies to PD-1 antigen

Binding of the bispecific antibodies and their components to PD-1 antigen expressed on the surface of CHO cell line was assessed using FACS method. The bispecific antibodies were incubated with CHO cell line expressing PD-1 antigen and then detected with secondary anti-human antibodies directly conjugated to Alexa Fluor 647 fluorochrome. Cellular binding of the test antibodies was analyzed on a flow cytometer BD LSRFortessa. All tested antibodies bound to the antigen with a KD in a single digit nanomolar range (Figure 2).

[0071] Example 3: Blockade of interaction between CTLA4 and CD80

[0072] Ability of the bispecific antibodies to block the interaction between CTLA4 and its ligand CD80 was tested in a biochemical interaction assay (Cisbio). Briefly, a bispecific antibody was incubated with CTLA4 and CD80 proteins. Detection antibodies recognizing CTLA4 and CD80 proteins and labeled with HTRF donor/acceptor fluorescent pair then were added to the mixture. The interaction between CTLA4 and CD80 was assessed via FRET efficiency. All bispecific antibodies tested were able to block the interaction between CTLA4 and CD80 (Figure 3).

[0073] Example 4: Stimulation of PBMC with superantigen SEB

[0074] Ability of the bispecific antibodies to enhance cytokine release from human Peripheral Blood Mononuclear Cells (PBMC) after stimulation with superantigen SEB was assessed. All bispecific

molecules were able to significantly enhance the production of IL-2 by PBMC upon stimulation with SEB, as shown in Figure 4A and Figure 4B.

[0075] Example 5: PD-1/PD-L1 pathway signaling

[0076] The bispecific antibodies were tested for their ability to block PD-1/PD-L1 pathway. Briefly, the test molecules were incubated with Jurkat reporter cell line expressing PD-1 receptor and luciferase NFAT reporter and CHO-PD-L1 cell line (Promega). The ability of the test antibodies to block the signaling through the PD-1/PD-L1 pathway was assessed via an increase in NFAT signaling. The NFAT signaling in turn was monitored via activity of luciferase reporter gene. The assay was read on a plate reader (Clariostar, BMG). All tested bispecific antibodies and monoclonal antibody controls were able to block PD-1/PD-L1 signaling (Figure 5).

[0077] Example 6: Dendritic cell Mixed Leukocyte Reaction

[0078] The bispecific antibodies were tested for their ability to enhance Dendritic cell Mixed Leukocyte Reaction (MLR). The test molecules were incubated for 6 days with dendritic cells from one donor and T cells isolated from another donor. Dendritic cells were differentiated *in vitro* from monocytes in the presence of GM-CSF and IL-4. Monocytes and T cell populations were isolated from PBMC with StemCell isolation kits. The ability of the test molecules to enhance MLR was assessed via secreted IFN γ . All tested bispecific antibodies were able to augment production of IFN γ as shown on Figure 6.

[0079] Example 7: Suppression of CD8 T cells by regulatory T cells

[0080] The bispecific antibodies were tested for their ability to block suppressive effect of regulatory T cells on effector CD8 T cell proliferation and cytokine production. CD8 T cells were isolated with StemCell isolation kit and labeled with CellTrace dye (ThermoFisher). Dendritic cells were prepared as described earlier in the MLR study. Regulatory T cells were isolated from PBMC with StemCell isolation kit and expanded *in vitro*. The bispecific antibody was incubated with effector CD8 T cells, dendritic cells and regulatory T cells for 4 days. The ability of the bispecific antibody to rescue effector CD8 T cell function in the presence of regulatory T cells was assessed via proliferation of effector CD8 T cells (Figure 7A) and secreted IFN γ (Figure 7 B).

[0081] Example 8: CD8 T cell degranulation

[0082] Ability of bispecific molecules to have an effect on cytotoxic CD8 T cells was assessed in this study. Briefly, CD8 T cells were purified with StemCell isolation kit and stimulated with CEFT peptide pool (JPT Peptide Technologies) in the presence of the bispecific test molecules. The media was supplemented with IL-7 and IL-21. On day 11 CD8 T cells were re-stimulated with the peptides in the presence of Brefeldin and Monensin and anti-CD107a antibody directly labeled with a fluorochrome. 24

hours later CD8 T cells were stained with anti-IFN γ antibodies directly conjugated to a fluorochrome and assessed on a flow cytometer BD LSRFortessa. As shown on Figure 8, all tested bispecific antibodies were able to increase the number of cytotoxic IFN γ positive T cells.

[0083] Example 9: MiXeno mouse tumor model

[0084] Humanized mouse model was used to assess the ability of bispecific antibodies of this class to inhibit tumor growth *in vivo*. Briefly, NOG mice were reconstituted with human PBMC (5×10^6 cells per mouse). On day 3 the animals were subcutaneously inoculated with a human lung cancer cell line HCC827 (0.5×10^6 cells/animal) and started on a biweekly treatment with a bispecific antibody and control antibodies. Tumor volumes were measured every 2-3 days. Animal weight was monitored. The tested bispecific antibody was able to inhibit tumor growth better than the control antibodies (Figure 9).

[0085] Example 10: Proliferation of Flu-specific T cells

[0086] Ability of the bispecific antibodies to augment proliferation of antigen specific CD8 T cells was assessed in this study. CD8 T cells were purified from PBMC with StemCell isolation kit, pulsed with influenza specific peptides (JPT Peptide Technologies) and incubated in the presence of the bispecific antibodies for 14 days. The media was supplemented with IL-7 and IL-21. On day 15 the cells were stained with a peptide specific MHC dextramers (Immudex) and assessed on a flow cytometer BD LSRFortessa. All tested bispecific antibodies were able to increase the number of antigen specific CD8 T cells (Figure 10).

[0087] Example 11: PBMC memory response to CEFT peptide pool

[0088] Ability of the bispecific antibodies to augment T cell memory response was assessed. Briefly, PBMC were incubated for 4-5 days in the presence of peptides specific for CMV, EBV, Influenza and Tetanus (JPT Peptide Technologies). The amount of secreted IFN γ was quantified. The bispecific CT4 x PD224D1, shown on Figure 11, was able to enhance production of IFN γ several fold over the control treatment.

[0089] Example 12: Enhancement of Redirected T cell Cytotoxicity

[0090] The bispecific antibodies were tested for their ability to enhance Redirected T cell Cytotoxicity (RTCC) against a tumor cell line target. The tumor cell line was stably expressing nucleus-localized Red Fluorescent Protein (RFP) delivered via lentiviral transduction (Sartorius). The tumor cells were co-cultured with PBMC and a T cell engager molecule specific for the given tumor cell line. The bispecific antibodies were added to the co-cultures. Lysis of tumor cells was assessed by counting RFP labeled tumor cell nuclei. Images were acquired on live cell imager IncuCyte (Sartorius). Activity of the antibodies were assessed after 96 hours of incubation. Four PBMC donors were tested in this study. All

bispecific antibodies tested were able to enhance RTCC activity in at least one PBMC donor tested (Figure 12).

[0091] While the present disclosure has been described with reference to particular embodiments or examples, it may be understood that the embodiments are illustrative and that the disclosure scope is not so limited. Alternative embodiments of the present disclosure may become apparent to those having ordinary skill in the art to which the present disclosure pertains. Such alternate embodiments are considered to be encompassed within the scope of the present disclosure. Accordingly, the scope of the present disclosure is defined by the appended claims and is supported by the foregoing description. All references cited or referred to in this disclosure are hereby incorporated by reference in their entireties.

SEQUENCE LISTING

SEQ ID	Description
1	CT4 x PD224D1 nucleotide
2	CT4 x PD224D1 amino acid
3	CT4 Light Chain nucleotide
4	CT4 Light Chain amino acid
5	CT4 x PL230C6 nucleotide
6	CT4 x PL230C6 amino acid
7	CT4 x PL221G5 nucleotide
8	CT4 x PL221G5 amino acid
9	CT4 x PL231H2 nucleotide
10	CT4 x PL231H2 amino acid
11	CT4 x PL004B5 nucleotide
12	CT4 x PL004B5 amino acid
13	CT4 x PL004B9 nucleotide
14	CT4 x PL004B9 amino acid
15	CT4 x PD206F12 nucleotide
16	CT4 x PD206F12 amino acid
17	CT4 x PD215A1 nucleotide
18	CT4 x PD215A1 amino acid
19	CT4 x PD220F6 nucleotide
20	CT4 x PD220F6 amino acid
21	CT4 x PD225G11 nucleotide
22	CT4 x PD225G11 amino acid
23	Gly 4 Ser x 4 nucleotide

24	Gly 4 Ser x 4 amino acid
25	PL230C6 x CT4 nucleotide
26	PL230C6 x CT4 amino acid
27	PL230C6 Light Chain nucleotide
28	PL230C6 Light Chain amino acid
29	PD224D1 x CT4 nucleotide
30	PD224D1 x CT4 amino acid
31	PD224D1 Light Chain nucleotide
32	PD224D1 Light Chain amino acid
33	PL221G5 x CT4
34	PL221G5 x CT4
35	PL221G5 Light Chain
36	PL221G5 Light Chain
37	PL231H2 x CT4 nucleotide
38	PL231H2 x CT4 amino acid
39	PL231H2 Light Chain nucleotide
40	PL231H2 Light Chain amino acid
41	PL004B5 x CT4 nucleotide
42	PL004B5 x CT4 amino acid
43	PL004B5 Light Chain nucleotide
44	PL004B5 Light Chain amino acid
45	PL004B9 x CT4 nucleotide
46	PL004B9 x CT4 amino acid
47	PL004B9 Light Chain nucleotide
48	PL004B9 Light Chain amino acid

49	PD206F12 x CT4 nucleotide
50	PD206F12 x CT4 amino acid
51	PD206F12 Light Chain nucleotide
52	PD206F12 Light Chain amino acid
53	PD215A1 x CT4 nucleotide
54	PD215A1 x CT4 amino acid
55	PD215A1Light Chain nucleotide
56	PD215A1 Light Chain amino acid
57	PD220F6 x CT4 nucleotide
58	PD220F6 x CT4 amino acid
59	PD220F6Light Chain nucleotide
60	PD220F6 Light Chain amino acid
61	PD225G11 x CT4 nucleotide
62	PD225G11 x CT4 amino acid
63	PD225G11 Light Chain nucleotide
64	PD225G11 Light Chain amino acid
65	CT4 signal peptide nucleotide
66	CT4 signal peptide amino acid
67	Heavy Chain signal peptide nucleotide
68	Heavy Chain signal peptide amino acid
69	Light Chain signal peptide nucleotide
70	Light Chain signal peptide amino acid
71	CT4 scFv nucleotide
72	CT4 scFv amino acid
73	PD224D1 scFv nucleotide

74	PD224D1 scFv amino acid
75	PD206F12 scFv nucleotide
76	PD206F12 scFv amino acid
77	PD215A1 scFv nucleotide
78	PD215A1 scFv amino acid
79	PD225G11 scFv nucleotide
80	PD225G11 scFv amino acid
81	PL230C6 scFv nucleotide
82	PL230C6 scFv amino acid
83	PL231H2 scFv nucleotide
84	PL231H2 scFv amino acid
85	PL221G5 scFv nucleotide
86	PL221G5 scFv amino acid
87	PL004B5 scFv nucleotide
88	PL004B5 scFv amino acid
89	PL004B9 scFv nucleotide
90	PL004B9 scFv amino acid
91	CT4 VH nucleotide
92	CT4 VH amino acid
93	CT4 VL nucleotide
94	CT4 VL amino acid
95	PD224D1 VH nucleotide
96	PD224D1 VH amino acid
97	PD224D1 VL nucleotide
98	PD224D1 VL amino acid

99	PD206F12 VH nucleotide
100	PD206F12 VH amino acid
101	PD206F12 VL nucleotide
102	PD206F12 VL amino acid
103	PD215A1 VH nucleotide
104	PD215A1 VH amino acid
105	PD215A1 VL nucleotide
106	PD215A1 VL amino acid
107	PD225G11 VH nucleotide
108	PD225G11 VH amino acid
109	PD225G11 VL nucleotide
110	PD225G11 VL amino acid
111	PL230C6 VH nucleotide
112	PL230C6 VH amino acid
113	PL230C6 VL nucleotide
114	PL230C6 VL amino acid
115	PL231H2 VH nucleotide
116	PL231H2 VH amino acid
117	PL231H2 VL nucleotide
118	PL231H2 VL amino acid
119	PL221G5 VH nucleotide
120	PL221G5 VH amino acid
121	PL221G5 VL nucleotide
122	PL221G5 VL amino acid
123	PL004B5 VH nucleotide

124	PL004B5 VH amino acid
125	PL004B5 VL nucleotide
126	PL004B5 VL amino acid
127	PL004B9 VH nucleotide
128	PL004B9 VH amino acid
129	PL004B9 VL nucleotide
130	PL004B9 VL amino acid
131	PD220F6 VH nucleotide
132	PD220F6 VH amino acid
133	PD220F6 VL nucleotide
134	PD220F6 VL amino acid
135	Human IgG1 Constant Domain nucleotide
136	Human IgG1 Constant Domain amino acid
137	Human IgG1 Constant Domain null nucleotide
138	Human IgG1 Constant Domain null amino acid
139	PD220F6 scFv nucleotide
140	PD220F6 scFv amino acid

SEQ ID 01: CT4 x PD224D1 nucleotide sequence (nt)

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCA
 CTTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGAT
 GGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATCCAAGAACACGCTGTATCT
 GCAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACT
 GGGGCCAGGGAACCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAG
 AGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTC
 AGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGA
 CCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAG
 AGAGTTGAGCCCAATCTTGTGACAAAACCTCACACATGCCACCGTGCCGAGCACCTGAAGCCGCGGGGGCACCGTCAGT
 CTTCCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGA
 GCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAG
 GAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCACCCTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAA
 GTGCGCGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCAC
 AGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCAAGAACCAGGTGAGCTGACCTGCCTGGTCAAAGGCTTCTAT
 CCCAGCGACATCGCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCCTCCCGTGTCTGGACTC
 CGACGGCTCCTTCTTCTATAGCAAGCTCACCCTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG

TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGT
 GGTGGATCCGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAGC
 CTCTGGATTCTCCCTCAGTAGCTATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTACATCGGCTACA
 TTGGTGATACTACTGGCATAGCCTACGCCAGCTGGGCGAATGGCAGATTCACCATCTCCAAAGACAATACCAAGAACAG
 GTGGATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGCTGGTCTCTACTTAGACAT
 CTGGGGCCAAGGGACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTCCGGCGGTGGCGGCTCCG
 GTGGAGGCGGCTCTGCCCTTGTGATGACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGAGACAGAGTACCATCACT
 TGCCAGGCCAGTCAGAACATTTACAGCAATTTAGCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTA
 TCAGGCCTCCACTCTGGCATCTGGGTCCCATCTCGGTTCACTGGCAGTGGATATGGGACAGATTTCACTCTCACCATCA
 GCAGCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCAAGGCGGTTATTATAGTGCTGCCCTTAATACTTTTCGGCGGA
 GGGACCAAGGTGGAGATCAAA

SEQ ID 02: CT4 x PD224D1 amino acid sequence (aa)

QVQLVESGGGVVQPGSRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNKYYADSVKGRFTI
 SRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGT
 AALGLCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
 KVDKRVEPKSCDKHTCTPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDNLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVY
 TLPSPRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ
 GNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCTASGFSLSYA
MSWVRQAPGKLEYIGYIGDTTGIAYASWANGRFTISKDNTKNTVDLQMNSLRAEDTAVYYCARGWSYLD
IWGQGLTVTVSSGGGGSGGGGSGGGGSALVMTQSPSSLSASVGRVTITCQASQNIYSNLAWYQQ
 KPGKVPKLLIYQASTLASGVPSRFSGSGYGTDFTLTISLQPEDVATYYCQGGYYSAALNTFGGGTKVEI
 K

SEQ ID 03: CT4 kappa light chain nt

GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCA
 GGGCCAGTCAGAGTGTGGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCT
 CCTCATCTATGGTGCATTACAGCAGGGCCACTGGCATCCCAGACAGGTTCACTGGCAGTGGGTCTGGGACA
 GACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTGACAGTATGGTA
 GCTCACCGTGGACGTTCCGCCAAGGGACCAAGGTGGAAATCAAA
 CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCT
 CTGTTGTGTGCCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCCT
 CCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGC
 ACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCC
 TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID 04: CT4 kappa light chain aa

EIVLTQSPGTLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGT
 DFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNF
 YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSF
 NRGEC

SEQ ID 05: CT4 x PL230C6 nt

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAG
 CCTCTGGATTACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTG
 GGTGACATTTATATCATATGATGGAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTACCATC

TCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATAT
ATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTC
CTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCC
TGACCAGCGGCGTGCACACCTTCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGT
GACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC
AAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCCACCGTGCCAGCACCTG
AAGCCGCGGGGGCACCGTCAGTCTTCTCTTCCCCCAAACCCAAGGACACCCCTCATGATCTCCCGGAC
CCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
TCAGCGTCTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGC GCGGTCTCCAACAA
AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
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GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCC
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GGTCCAGCCTGGGGGGTCCCTGAGACTCTCTGTACCGCTCTGGAATCGACCTAATACCTACGACATG
ATCTGGGTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGTGGAATCATTACTTATAGTGGTAGTAGAT
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AATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGATTATATGAGTGGTTCCAC
TTGTGGGGCCAGGGAACCCTGGTCACCGTCTCTTCCGGTGGAGGCGGTTGAGGCGGAGGTGGAAGTGGTG
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AGGAGACAGAGTCACCATCAAGTGTGAGGCCAGTGAGGACATTTATAGCTTCTTGGCCTGGTATCAGCAG
AAACCAGGGAAAGCCCCCTAAGCTCCTGATCCATTCTGCATCCTCTCTGGCATCTGGGGTCCCATCAAGGT
TCAGCGGCAGTGGATCTGGGACAGATTTACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAAC
TTACTATTGTCAACAGGGTTATGGTAAAAATAATGTTGATAATGCTTTTCGGCGGAGGGACCAAGGTGGAG
ATCAAA

SEQ ID 06: CT4 x PL230C6 aa

QVQLVESGGGVVQPGRLRLSCAASGFTFSSYTMHWVRQAPGKLEWVTFISYDGNKKYYADSVKGRFTI
SRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLVTVSSASTKGPSVFPLAPSSKSTSGGT
AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
KVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ
GNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQSVESGGGLVQPGGSLRLSCTASGIDLNTYDM
IWVRQAPGKLEWVGIIITYSGSRYANWAKGRFTISKDNTKNTVYLQMNSLRAEDTAVYYCARDYMSGSH
LWGQGLVTVSSGGGGSGGGSGGGSGGGGSAYDMTQSPSSVSASVGDRTIKCQASEDIYSFLAWYQQ
KPGKAPKLLIHSASSLASGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQGYGKNNVDNAFGGGTKVE
IK

SEQ ID 07: CT4 x PL221G5 null2 Fc nt

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAG
CCTCTGGATTACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTG

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TCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATAT
ATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTC
CTCAGCTAGCACCAAGGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCC
TGACCAGCGGCGTGCACACCTTCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGT
GACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC
AAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCCACCGTGCCAGCACCTG
AAGCCGCGGGGGCACCGTCAGTCTTCTCTTCCCCCAAACCAAGGACACCCCTCATGATCTCCCGGAC
CCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
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AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
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ATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAGAACAACCTACAAGACCACGCCTCC
CGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
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GACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATTGCTGCTGGTAGTG
CTGGTATCACTTACGACGCGAACTGGGCGAAAGGCCGTTTACCATCTCCAGAGACAATTCCAAGAACAC
GCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGATCGGCGTTT
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CTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGACATCCAGATGACCCAGTCTCC
TTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCAGTCAGAGCATTAGTTCC
CACTTAAACTGGTATCAGCAGAAACCAGGGAAAGCCCTAAGCTCCTGATCTATAAGGCATCCACTCTGG
CATCTGGGGTCCCATCAAGGTTTACGCGGCAGTGGATCTGGGACAGAATTTACTCTCACCATCAGCAGCCT
GCAGCCTGATGATTTTGAACCTTATTACTGCCAACAGGGTTATAGTTGGGGTAATGTTGATAATGTTTTT
GGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 08: CT4 x PL221G5 null Fc aa

QVQLVESGGGVVQPGKSLRLSCAASGFTFSSYTMHWVRQAPGKLEWVTFISYDGNKYYADSVKGRFTI
SRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWQGTLLTVSSASTKGPSVFPLAPSSKSTSGGT
AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNT
KVDKRVPEPKSCKDTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQ
GNVFSCSVMHEALHNHYTQKSLSLSPGSGGGSGGGGSEVQLLESGLLVQPGGSLRLSCAASGFSFSSGY
DMCWVRQAPGKLEWVIAAAGSAGITYDANWAKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARSAF
SFDYAMD~~LD~~WGQGTLLTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSTLSASVGRVTITCQASQSISS
HLN~~WY~~QKPGKAPKLLIYKASTLASGVPSRFSGSGSGTEFTLTISSLQPD~~F~~ATYYCQQGYSWGNDNVF
GGGKVEIK

SEQ ID 09: CT4 x PL231H2 nt

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAG
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 ATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTC
 CTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACA
 GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAAGTCAAGGCGCCC
 TGACCAGCGGCGTGCACACCTTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGT
 GACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC
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 CCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
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 TGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCACAGGTGCAGCTGGTGGAGTCTGGGGGAGG
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 CATACTACGCGAGCTGGGCGAAAGGCCGATTCACCCCTCTCCAAAGACAATACTCGACCACGGTGGATCT
 GCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGATTTTATTAGTGGTTCC
 CACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCG
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 TGTAGGAGACAGAGTCACCATCAATTGTCAGGCCAGTGAGAGCATTAGTAGCTTCTTATCCTGGTATCAG
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 GGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGC
 AACTTACTATTGTCAACAGGGTTATAGTAAAAGTAATGTGGATAATGCTTTCGGCGGAGGGACCAAGGTG
 GAGATCAA

SEQ ID 10: CT4 x PL231H2 aa

QVQLVESGGGVVQPRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNKYYADSVKGRFTI
 SRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLVTVSSASTKGPSVFPLAPSSKSTSGGT
 AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT
 KVDKRVEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVY
 TLPSSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQ
 GNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSQVQLVESGGGLVQPGGSLRLSCTTSGIDLSTYD
MIWVRQAPGKGLEWVGIIISYVGNTYYASWAKGRFTLSKDNTSTTVDLQMNSLRAEDTAVYYCARDFISGS
HLWGQGLVTVSSGGGGSGGGSGGGSGGGGSAYDMTQSPSSVSASVGRVNTINCQASESISFSLSWYQ
QKPGKAPKLLIFSASTLASGVPSRFSSGSGSGTDFTLTISSLPEDFATYYCQQGYSKSNVDNAFGGGTKV
 EIK

SEQ ID 11: CT4 x PL004B5 nt

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAG
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TCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATAT
ATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTC
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GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCC
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TATACTACGCGAACTGGGCAAAAGGCAGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCT
TCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGATATGTGGGTAATAATGAT
GATTATATTAACCTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAG
GTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGACATCCAGATGACCCAGTCTCCTTCCACCCT
GTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCAGTCAGAGTGTTTATAATGGCTACTGG
TTATCCTGGTATCAGCAGAAACCAGGGAAGCCCCCTAAGCTCCTGATCTATGGTGCATCCACTCTGGCAT
CTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGAATTCACCTCTACCATCAGCAGCCTGCA
GCCTGATGATTTTGCAACTTATTACTGCCTAGGCAGTTATACTAGTAGTACTGAGAACTCTTTCGGCGGA
GGGACCAAGGTGGAGATCAAA

SEQ ID 12: CT4 x PL004B5 aa

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGN NKYYADSVKGRFTI
SRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGT
AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
KVDKRVEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQ
GNVFSCSVMHEALHNHYTQKSLSLSPGGGGGGGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLSYW
MSWVRQAPGKLEWIGVIDTNVYIYYANWAKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARYVGNND
DYINLWGQGLTVTVSSGGGGSGGGSGGGSGGGSGGGSDIQMTQSPSTLSASVGDRVTITCQSSQSVYNGYW

LSWYQQKPGKAPKLLIYGASTLASGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCLGSYTSSTENSFGG
 GTKVEIK

SEQ ID 13: CT4 x PL004B9 nt

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAG
 CCTCTGGATTACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTG
 GGTGACATTTATATCATATGATGGAACAATAAAATACTACGCAGACTCCGTGAAGGGCCGATTACCATC
 TCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATAT
 ATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTC
 CTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACA
 GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCC
 TGACCAGCGGCGTGCACACCTTCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGT
 GACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC
 AAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCCACCGTGCCACGACCTG
 AAGCCGCGGGGGCACCGTCAGTCTTCTCTTCCCCCAAAAACCAAGGACACCCCTCATGATCTCCCGGAC
 CCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
 TCAGCGTCTCTACCGTCTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAA
 AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCT
 ATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCC
 CGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
 GGGAAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCC
 TGTCTCCGGGTGGCGGTGGAGGTCCGGCGGTGGTGGATCAGAGGTGCAGCTGGTGGAGTCTGGGGGAGG
 CTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAGTGTCTGGAATCGACCTCAGTGTCAAT
 ATGGGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAACCATTACTTATGTTGGTAACA
 CATATTACGCGAGCTGGGCGAAAGGCAGATTACCATCTCCAAAACCTCGACCACGGTGGATCTTAAAT
 CACCAGTCCGACAACCGAGGACACGGCTGTGTATTACTGTGCGAGAGAATCTGGTACTATTTATTACAGT
 TACTTTAACTTGTGGGGCCAAGGGACCCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTG
 GTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGCATTGGAATTGACCCAGTCTCCATCCTCCCTGTC
 TGCATCTGTAGGAGACAGAGTCACCATCAAGTGCCAGGCCAGTGAAAGCATTAGCAACTACTTATCCTGG
 TATCAGCAGATTCCAGGGAAAGTTCCTAAGCTCCTGATCTATTATGCATCCAATCTGGCATCTGGGGTCC
 CATCTCGGTTTCAAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGA
 TGTGCAACTTATTACTGTCAAAGCTATTATGGTGGTGGTAGTGCCTATACTTTCGGCGGAGGGACCAAG
 GTGGAGATCAAA

SEQ ID 14: CT4 x PL004B9 aa

QVQLVESGGGVVQPRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYYADSVKGRFTI
 SRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLVTVSSASTKGPSVFPLAPSSKSTSGGT
 AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
 KVDKRVEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVY
 TLPSPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ
 GNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCTVSGIDLSVIN
 MGWVRQAPGKGLEWIGTITYVGNTYYASWAKGRFTISKSTSTVDLKITSPTTEDTAVYYCARESGTIYYS

YFNLWGQGLVTVSSGGGSGGGGSGGGGSGGGGSAFELTQSPSSLSASVGDVRTIKQASESISNYLSW
YQQIPGKVPKLLIYYASNLASGVPSRFSGSGSGTDFTLTISSLPEDVATYYCQSYYGGSAYTFGGGTK
VEIK

SEQ ID 15: CT4 x PD206F12 nt

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAG
CCTCTGGATTACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTG
GGTGACATTTATATCATATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTACCATC
TCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATAT
ATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCTGGTCACCGTCTC
CTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCC
TGACCAGCGGCGTGCACACCTTCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGT
GACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC
AAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCCACCGTGCCCAGCACCTG
AAGCCGCGGGGGCACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGAC
CCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
TCAGCGTCTCACCCTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAA
AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCT
ATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCC
CGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCC
TGTCTCCGGGTGGCGGTGGAGGTCCGGCGGTGGTGGATCAGAGGTGCAGCTGGTGGAGTCTGGGGGAGG
CTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTGCACTTCAGTAGCGGCTAC
TGGATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTTGATCGCATGCATTTATGCTGGTACTA
GTGGTAGTACTTCTACGCGAGCTGGGCGAGAGGCAGATTACCCTCTCCGAAACCTCCAAGAACACGGT
GACTCTTCAAATGAACAGCCTGAGAGCCGAGGACTCGGCTGTGTATTACTGTGCGAGAAATCTTTACACT
TACAATAGCTTGTGGGGCCAGGGAACCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTG
GTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGACATCCAGATGACCCAGTCTCCTTCCACCCTGTC
TGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCAGTCAGAGTGTTTATGATAACAACCTGGTTA
GCCTGGTATCAGCAGAAACCAGGGAAGCCCCTAAGCTCCTGATCTATACAGTATCCACTCTGGCATCTG
GGTCCCATCAAGGTTGAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAGCC
TGATGATTTTGCAACTTATTACTGCCAAGGCACTTATTATAGTAGTGGTTGGAACCTTGCTTTCGGCGGA
GGGACCAAGGTGGAGATCAAA

SEQ ID 16: CT4 x PD206F12 aa

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYYADSVKGRFTI
SRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLVTVSSASTKGPSVFPLAPSSKSTSGGT
AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
KVDKRVEPKSCDKHTCTPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQ
GNVFSCSVMEALHNHYTQKSLSLSPGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFDSSGY

WICWVRQAPGKGLELIACIYAGTSGSTSYASWARGRFTISETSKNTVTLMNSLRAEDSAVYYCARNLYT
YNSLWGQGLVTVSSGGGSGGGSGGGSGGGSDIQMTQSPSTLSASVGDRVTITCQSSQSVYDNNWL
AWYQQKPGKAPKLLIYTVSTLASGVPSRFSGSGSGTEFTLTISLQPDDFATYYCQGTYYSSGWNFAFGG
GTKVEIK

SEQ ID 17: CT4 x PD215A1 nt

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAG
CCTCTGGATTACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTG
GGTGACATTTATATCATATGATGGAACAATAAACTACGCAGACTCCGTGAAGGGCCGATTACCATC
TCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATAT
ATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTC
CTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCC
TGACCAGCGGCGTGCACACCTTCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGT
GACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC
AAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCCACCGTGCCCAGCACCTG
AAGCCGCGGGGGCACCGTCAGTCTTCTCTTCCCCCAAAACCCAAGGACACCCCTCATGATCTCCCGGAC
CCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
TCAGCGTCTCACCCTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGC GCGGTCTCCAACAA
AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCT
ATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCC
CGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCC
TGTCTCCGGGTGGCGGTGGAGGTCGCGCGGTGGTGGATCACAGGAGCAGCTGTTGGAGTCTGGGGGAGG
CTTGGTACAGCCTGGGGGTCCCTGAGACTCTCCTGTACAGCCTCTGGATTCTCCTTTAGCAGCTACTGG
ATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGATGCATTACGACTGGTAGTGGTA
GCACTTACTACGCGAGCTGGGCGAAGCGCCGTTTACCATCTCCAAAGACAATTCCAAGAACACGGTGAC
TCTGCAAATGAACAGCCTGAGAGCCGAGGACACGCCGTATATTACTGTACGAGAGCATTTGACTTGTGG
GGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCGGGCGGTGGCG
GCTCCGGTGGAGGCGGCTCTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGA
CAGAGTCACCATCACTTGCCAGGCCAGTCAGAGCATTTACAGCTACTTAACTGGTATCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCTATGGTGCATCCAATCTGGCATCTGGGTCCCATCAAGGTTTCAGTG
GCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTTGCACTTACTA
CTGTCAAAGCAGTTGGTTGAGTGGTGTCTGTTGGTAATGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 18: CT4 x PD215A1 aa

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGN NKYYADSVKGRFTI
SRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLVTVSSASTKGPSVFPLAPSSKSTSGGT
AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
KVDKRVEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQ
GNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQEQLLESGGGLVQPGGSLRLSCTASGFSFSSYW

MCWVRQAPGKGLEWIGCITTGSGSTYYASWAKRRFTISKDNSKNTVTLQMNSLRAEDTAVYYCTRAFDLW
GQGTLLVTVSSGGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCQASQSIYSYLNWYQQKP
GKAPKLLIYGASNLASGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQSSWLSGAVGNAFGGGTKVEIK

SEQ ID 19: CT4 x PD220F6 nt

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAG
CCTCTGGATTACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTG
GGTGACATTTATATCATATGATGGAAACAATAAACTACGCAGACTCCGTGAAGGGCCGATTACCATC
TCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATAT
ATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTC
CTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCC
TGACCAGCGGCGTGCACACCTTCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGT
GACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC
AAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCCACCGTGCCCAGCACCTG
AAGCCGCGGGGGCACCGTCAGTCTTCTCTTCCCCCAAAAACCAAGGACACCTCATGATCTCCCGGAC
CCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
TCAGCGTCTCACCCTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGCGGTCTCCAACAA
AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCT
ATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCC
CGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCC
TGTCTCCGGGTGGCGGTGGAGGTCGCGCGGTGGTGGATCACAGGAGCAGGTGAAGGAGACCGGGGGAGG
CTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCATCAGCAGCTATGGA
GTGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTGCGATTGATTTTTCCCGGGATTGGTT
TCAAAGACTACGCGAGCTGGGTGAATGGCCGTTTACCCTCTCCAGCGACAACGCCCAGAACACTGTGGA
ACTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGAGATTTGGACTTGTGG
GGCCAGGGAACCTTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCG
GCTCCGGTGGAGGCGGCTCTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGA
CAGAGTCACCATCACTTGCCAGTCCAGTCCGAGTGTTTATAGTAACTACTTATCCTGGTATCAGCAGAAA
CCAGGGAAAGTTCCCTAAGCTCCTGATCTATTATGCATCCACTCTGGCATCTGGGGTCCCATCTCGGTTCA
GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTA
TACTGTGCAGGCGGTTATAGTAGTAGTACTCGTGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 20: CT4 x PD220F6 aa

QVQLVESGGGVVQPRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNKYYADSVKGRFTI
SRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLLVTVSSASTKGPSVFPLAPSSKSTSGGT
AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
KVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQ
GNVFCSSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSQEQVKETGGGLVQPGGSLRLSCAASGFTISSYG
VSWVRQAPGKGLEWVALIFPGIGFKDYASWVNGRFTLSSDNAQNTVELQMNSLRAEDTAVYYCARDLDELW

GQGT^{LV}TVSSGGGGSGGGSGGGSGGGSDIQMTQSPSSLSASVGDRVTITCQSSPSVYSNYLSWYQQK
PGKVPKLLIYYASTLASGVPSRFSGSGSGTDFTLTISSLPEDVATYYCAGGYSSSTRAFGGGTKVEIK

SEQ ID 21: CT4 x PD225G11 nt

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAG
CCTCTGGATTACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTG
GGTGACATTTATATCATATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTACCATC
TCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATAT
ATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTC
CTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCC
TGACCAGCGGCGTGCACACCTTCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGT
GACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC
AAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCCACCGTGCCCAGCACCTG
AAGCCGCGGGGGCACCGTCAGTCTTCTCTTCCCCCAAAAACCAAGGACACCTCATGATCTCCCGGAC
CCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
TCAGCGTCTCTACCGTCTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAA
AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCT
ATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCC
CGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCC
TGTCTCCGGGTGGCGGTGGAGGTCCGGCGGTGGTGGATCAGAGGTGCAGCTGTTGGAGTCTGGGGGAGG
CTTGGTACAGCCTGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTTAGCAGCAGCCAC
TGGATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATTTATACTGGTAGTA
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GCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGAGCCGCTAAT
ACTGATACTACCTACTTTAACTTGTGGGGCCAGGGAACCTGGTCACCGTCTCGAGCGGTGGAGGCGGAT
CTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGCCTATGATATGACCCAGTCTCC
ATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAGGCCAGTCAGAGCATTAAACAAC
CAACTATCCTGGTATCAGCAGAAACCAGGGAAGTTCTAAGCTCCTGATCTATGGTGCATCCACTCTGG
CATCTGGGGTCCCATCTCGGTTACCCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCT
GCAGCCTGAAGATGTTGCAACTTATTACTGTCTATGTTTATTTGCAGTGGTGGTAGTTGTTTTTGGGCT
TTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 22: CT4 x PD225G11 aa

QVQLVESGGGVVQPRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGN^{NY}YADSVKGRFTI
SRD^{NS}SKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGT^{LV}TVSSASTKGPSVFPLAPSSKSTSGGT
AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN^{HK}PSNT
KVDKRV^{EP}KSCDKHTCTPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQ
GNVFC^{SV}MHEALHNHYTQKSLSLSPGGGGSGGGGSEVQLLES^{GG}GLVQPGGSLRLSCAASGFTFSSSH
WICWVRQAPGKLEWIA^{CI}YTGSDIVFY^{AS}WAKGRFTISR^{DN}SKNTLYLQMNSLRAEDTAVYYCARA^{AN}

TDTTYFNLWGQGLVTVSSGGGSGGGGSGGGGSGGGGSAYDMTQSPSSLSASVGDRVTINCQASQSINN
QLSWYQQKPGKVPKLLIYGASTLASGVPSRFTGSGSGTDFTLTISLQPEDVATYYCHVHYCSGGSCFWA
FGGGTKVEIK

SEQ ID 23: G4S x 4 nt

GGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCT

SEQ ID 24: G4S x 4 aa

GGGGSGGGGSGGGGSGGGGS

SEQ ID 25: PL230C6 x CT4 nt

CAGTCGGTGGAGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACCGCCT
CTGGAATCGACCTTAATACCTACGACATGATCTGGGTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGT
TGGAATCATTACTTATAGTGGTAGTAGATACTACGCCAACTGGGCGAAAGGCCGATTACCATCTCCAAA
GACAATACCAAGAACACGGTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACT
GTGCGAGAGATTATATGAGTGGTTCCCACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGCTAG
CACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTG
GGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCCTGACCAGCG
GCGTGCACACCTTCCCGGTGTCTTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC
CTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGAC
AAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAAGCCGCGG
GGGCACCGTCAGTCTTCTTCTTCCCCCAAACCCAAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGT
CACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTG
GAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAAGCTCC
TCACCGTCTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCC
AGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCGAGCCCCGAGAACCACAGGTGTACACCCTGCCC
CCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCG
ACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA
CTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGACAAAGAGCAGGTGGCAGCAGGGGAACGTC
TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGG
GTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGTCCA
GCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATACTATGCACTGG
GTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACAATAAATACT
ACGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAAT
GAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGAC
TACTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGTTTCAGGCGGAGGTGGAAGTGGTG
GTGGCGGCTCTGGAGGCGGCGGATCTGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCC
AGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTGGCAGCAGCTACTTAGCCTGGTACCAG
CAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATTTCAGCAGGGCCACTGGCATCCCAGACA
GGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGC
AGTGTATTACTGTACAGCAGTATGGTAGCTCACCGTGGACGTTTCGGCCAAGGGACCAAGGTGGAAATCAAA

SEQ ID 26: PL230C6 x CT4 aa

QSVESGGGLVQPGGSLRLSCTASGIDLNTYDMIWVRQAPGKGLEWVGIIITYSGSRYANWAKGRFTISK
 DNTKNTVYLQMNLSRAEDTAVYYCARDYMSGSHLWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAAL
 GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVD
 KRVEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGV
 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLTP
 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV
 FSCSVMHEALHNHYTQKSLSLSPGSGGGGSGGGGSQVQLVESGGSVQVQGRSLRLSCAASGFTFSSYTMHW
 VRQAPGKGLEWVTFISYDGNNKYADSVKGRFTISRDN SKNTLYLQMNLSRAEDTAIYYCARTGWLGPFD
 YWGQGLTVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVGSSYLAWYQ
 QKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKEIK

SEQ ID 27: PL230C6 kappa light chain nt

GCCTATGATATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCAAGTGTC
 AGGCCAGTGAGGACATTTATAGCTTCTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT
 GATCCATTCTGCATCCTCTCTGGCATCTGGGGTCCCATCAAGGTTACAGCGGCAGTGATCTGGGACAGAT
 TTCCTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGGTTATGGTA
 AAAATAATGTTGATAATGCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA
 CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCT
 CTGTTGTGTGCCTGCTGAATAACTTCTATCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCT
 CCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGC
 ACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCC
 TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID 28: PL230C6 kappa light chain aa

AYDMTQSPSSVSASVGDRTIKCQASEDIYSFLAWYQQKPGKAPKLLIHSASSLASGVPSRFSGSGSGTD
 FTLTIISSLPEDFATYYCQQYGKNNVDNAFGGGTKVEIKRTVAAPSVEIFPPSDEQLKSGTASVVCLLN
 NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTK
 SFNRGEC

SEQ ID 29: PD224D1 x CT4 nt

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAG
 CCTCTGGATTCTCCCTCAGTAGCTATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTA
 CATCGGCTACATTGGTGATACTACTGGCATAGCCTACGCGAGCTGGGCGAATGGCAGATTACCATCTCC
 AAAGACAATAACCAAGAACACGGTGGATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATT
 ACTGTGCGAGAGGCTGGTCTTACTTAGACATCTGGGGCCAAGGGACCCTGGTCAACGCTCTCGAGCGCTAG
 CACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTG
 GGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAAGTCAAGGCGCCCTGACCAGCG
 GCGTGACACCTTCCCGGCTGTCTTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC
 CTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGAC
 AAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCCACCGTGCCAGCACCTGAAGCCGCGG
 GGGCACCGTCAGTCTTCTTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGT
 CACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTG
 GAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAAGCTCC
 TCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCC

AGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCC
 CCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCG
 ACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAATAACAAGACCACGCCTCCCGTGCTGGA
 CTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC
 TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGG
 GTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCCAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGTCCA
 GCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATACTATGCACCTGG
 GTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACAATAAATACT
 ACGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAAT
 GAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGAC
 TACTGGGGCCAGGGAACCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCGGGCG
 GTGGCGGCTCCGGTGGAGGCGGTCTGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCC
 AGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTGGCAGCAGCTACTTAGCCTGGTACCAG
 CAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATTGAGCAGGGCCACTGGCATCCCAGACA
 GGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGC
 AGTGTATTACTGTGTCAGCAGTATGGTAGCTCACCGTGGACGTTTCGGCCAAGGGACCAAGGTGGAATCAAA

SEQ ID 30: PD224D1 x CT4 aa

EVQLVESGGGLVQPGGSLRLSCTASGFSLSYAMSWVRQAPGKLEYIGYIGDITGIIAYASWANGRFTIS
 KDNTKNTVDLQMNLSRAEDTAVYYCARGWSYLDIWGQGLVTVSSASTKGPSVFPLAPSSKSTSGGTAAL
 GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVD
 KRVEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLT
 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV
 FSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQVQLVESGGGVVQPRSLRLSCAASGFTFSSYTMHW
 VRQAPGKLEWVTFISYDGNKKYYADSVKGRFTISRDN SKNTLYLQMNLSRAEDTAIYYCARTGWLGPFD
 YWGQGLVTVSSGGGSGGGSGGGSGGGSEIVLTQSPGTLSPGERATLSCRASQSVGSSYLAWYQ
 QKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGGSSPWTFGQGTKVEIK

SEQ ID 31: PD224 light chain nt

GCCCTTGTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCC
 AGGCCAGTCAGAACATTTACAGCAATTTAGCCTGGTATCAGCAGAAACCAGGGAAAGTTCTTAAGCTCCT
 GATCTATCAGGCCTCCACTCTGGCATCTGGGGTCCCATCTCGGTTTCAGTGGCAGTGGATATGGGACAGAT
 TTCCTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCAAGGCGGTTATTATA
 GTGCTGCCCTTAATACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA
 CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCT
 CTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCCT
 CCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGC
 ACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCC
 TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID 32: PD224 light chain aa

ALVMTQSPSSLSASVGDRVTITCQASQNIYSNLAWYQQKPGKVPKLLIYQASTLASGVPSRFSGSGYGTD
 FTLTISLQPEDVATYYCQGGYYSAALNTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNN

FYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKS
FNRGEC

SEQ ID 33: PL221G5 x CT4 null Fc nt

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAG
CCTCTGGATTCTCCTTCAGTAGCGGGTACGACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGA
GTGGATCGCATGCATTGCTGCTGGTAGTGCTGGTATCACTTACGACGCGAACTGGGCGAAAGGCCGGTTC
ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGG
CCGTATATTACTGTGCGAGATCGGCGTTTTTCGTTGACTACGCCATGGACCTCTGGGGCCAGGGAACCCCT
GGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACC
TCTGGGGGCACAGCGGCCCTGGGCTGCCGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGA
ACTCAGGCGCCCTGACCAGCGCGTGCACACCTTCCCGGTGTCTACAGTCCTCAGGACTCTACTCCCT
CAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTGGGGACCCAGACCTACATCTGCAACGTGAATCACAAG
CCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCCACCGT
GCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCAAAAACCAAGGACACCCCTCAT
GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC
AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCA
CGTACCGTGTGGTCAGCGTCCTCACCCTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGC GC
GGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAA
CCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGACCTGCCTGG
TCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAA
GACCACGCCTCCCGTGTCTGGACTCCGACGGCTCCTTCTCCTCTATAGCAAGCTCACCGTGGACAAGAGC
AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGA
AGAGCCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCCAGGTGCAATTGGTGGGA
GTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTC
AGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCAT
ATGATGGAAACAATAATACTACGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAA
GAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACC
GGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCTGGTCACCGTCTCGAGCGGTGGAGGCGGAT
CTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGTCTGAAATTGTGTTGACGCAGTCTCC
AGGCACCCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTGGCAGC
AGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATCTATGGTGCATTACAGCA
GGGCCACTGGCATCCAGACAGGTTCAAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAG
ACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTGAGCAGTATGGTAGCTCACCGTGGACGTTTCGCCAA
GGGACCAAGGTGGAAATCAAA

SEQ ID 34: PL221G5 x CT4 null Fc aa

EVQLLESGLVQPGGSLRLSCAASGFSFSSGYDMCWVRQAPGKGLEWIAACIAAGSAGITYDANWAKGRF
TISRDNKNTLYLQMNSLRAEDTAVYYCARSAFSDYAMD~~LD~~WGQGLVTVSSASTKGPSVFPLAPSSKST
SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHK
PSNTKVDKRVEPKSCDKHTCTPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT~~LV~~LHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS
RWQQGNVFCSCVMHEALHNHYTQKSLSLSPGGGGGSGGGGQQVQLVESGGGVVQPGRSRLRLSCAASGFTF

SSYTMHWVRQAPGKGLEWVTFISYDGNKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAIYYCART
GWLGPFDYWGQGLVTVSSGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVGS
SYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSDFTLTISRLEPEDFAVYYCQQYGSSPWFQ
GTKVEIK

SEQ ID 35: PL221G5 Light Chain nt

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCC
AGGCCAGTCAGAGCATTAGTTCCCACTTAACTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT
GATCTATAAGGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTACAGCGGCAGTGATCTGGGACAGAA
TTTACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAACAGGGTTATAGTT
GGGGTAATGTTGATAATGTTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATC
TGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGTGCCTGCTGAAT
AACTTCTATCCAGAGAGGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACCTCCAGG
AGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGC
AGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAG
AGCTTCAACAGGGGAGAGTGT

SEQ ID 36: PL221G5 Light Chain aa

DIQMTQSPSTLSASVGDRVTITCQASQSISSHLNHWYQQKPGKAPKLLIYKASTLASGVPSRFSGSGSGTE
FTLTISSLPDDFATYYCQQGYSWGNDNVFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN
NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTK
SFNRGEC

SEQ ID 37: PL231H2 x CT4 null Fc nt

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGGGCTCCCTGAGACTCTCCTGTACAA
CTTCTGGAATCGACCTTAGTACCTACGACATGATCTGGGTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTG
GGTGGGAATCATTAGTTATGTTGGTAACACATACTACGCGAGCTGGGCGAAAGGCCGATTACCCCTCTCC
AAAGACAATACCTCGACCACGGTGGATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATT
ACTGTGCGAGAGATTTTATTAGTGGTTCCCACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGC
TAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCC
CTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCCTGACCA
GCGGCGTGCACACCTTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGT
GCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG
GACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAAGCCG
CGGGGGCACCGTCAGTCTTCTCTTCCCCCAAACCCAAGGACACCCCTCATGATCTCCCGGACCCCTGA
GGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
GTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCG
TCCTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCT
CCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACACAGGTGTACACCCTG
CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCTATCCCA
GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACTACAAGACCACGCCTCCCGTGTCT
GGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAC
GTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAACCTACACGCAGAAGAGCCTCTCCCTGTCTC
CGGGTGGCGGTGGAGGTCGCGCGGTGGTGGATCCAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGT

CCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATACTATGCAC
 TGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACAATAAAT
 ACTACGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCA
 AATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTT
 GACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCG
 GCGGTGGCGGCTCCGGTGGAGGCGGTTCTGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTC
 TCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTGGCAGCAGCTACTTAGCCTGGTAC
 CAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATCTATGGTGCATTCAGCAGGGCCACTGGCATCCCAG
 ACAGGTTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTT
 TGCAGTGTATTACTGTGACAGTATGGTAGCTCACCGTGGACGTTCCGCCAAGGGACCAAGGTGGAAATC
 AAA

SEQ ID 38: PL231H2 x CT4 null Fc aa

QVQLVESGGGLVQPGGSLRLSCTTSGIDLSYDMIWVRQAPGKGLEWVGIIISYVGNITYYASWAKGRFTLS
 KDNTSTTVDLQMNSLRAEDTAVYYCARDFISGSHLWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAA
 LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTPVSSSLGTQTYICNVNHKPSNTKV
 DKRVEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDG
 VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTL
 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGN
 VFSCSVMHEALHNHYTQKSLSLSPGGGGGGGGGGSGVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMH
 WVRQAPGKGLEWVTFISYDGNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCARTGWLGP
F
DIWGQGLTVTVSSGGGGGGGGGGSGGGGGGGGGSEIVLTQSPGTL
SLSPGERATL
SCRASQSVGSSYLAWY
 QQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGS
SPWTFGQGT
 K

SEQ ID 39: PL231H2 Light Chain nt

GCCTATGATATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGTC
 AGGCCAGTGAGAGCATTAGTAGCTTCTTATCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT
 GATCTTTTCTGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTTCAGCGGCAGTGATCTGGGACAGAT
 TTA CTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGGTTATAGTA
 AAAGTAATGTGGATAATGCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATC
 TGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAAT
 AACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGG
 AGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGC
 AGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAG
 AGCTTCAACAGGGGAGAGTGT

SEQ ID 40: PL231H2 Light Chain aa

AYDMTQSPSSVSASVGDRTVINCQASESISFSLSWYQQKPGKAPKLLIFSASTLASGVPSR
FSGSGSGTD
 FTLTISSLQPEDFATYYCQQGYSKSNVDNAFGGGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVCLLN
 NFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTK
 SFNRGEC

SEQ ID 41: PL004B5 x CT4 nt

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAG
 CCTCTGGATTCTCCCTCAGTAGCTACTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTG
 GATCGGAGTCATTGATACTAATGTTTATATATACTACGCGAACTGGGCAAAAGGCAGATTACCATCTCC
 AGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATT
 ACTGTGCGAGATATGTGGTAATAATGATGATTATTAACCTTGTGGGGCCAGGGAACCTGGTCACCGT
 CTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGC
 ACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCG
 CCCTGACCAGCGGCTGCACACCTTCCCGGCTGTCTTACAGTCTCAGGACTCTACTCCCTCAGCAGCGT
 GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAAC
 ACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCAC
 CTGAAGCCGCGGGGGCACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCG
 GACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTAC
 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG
 TGGTCAGCGTCCTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGC GCGGTCTCCAA
 CAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTG
 TACACCTGCCCCCATCCCGGGATGAGCTGACCAAGAACAGGTGAGCCTGACCTGCCTGGTCAAAGGCT
 TCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCC
 TCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCT
 CCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCAGGTGCAATTGGTGGAGTCTGGGGG
 AGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTAT
 ACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAA
 ACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAAGAACACGCT
 GTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGTGGCTG
 GGGCCCTTTGACTACTGGGGCCAGGGAACCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAG
 GTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGTTCTGAAATTGTGTTGACGCAGTCTCCAGGCACCT
 GTCTTTGTCTCCAGGGGAAGAGCCACCTCTCCTGCAGGGCCAGTCAGAGTGTTGGCAGCAGCTACTTA
 GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATTGAGCAGGGCCACTG
 GCATCCCAGACAGGTTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCC
 TGAAGATTTTGCAGTGATTACTGTGTCAGCAGTATGGTAGCTCACCGTGGACGTTCCGGCAAGGGACCAAG
 GTGGAAATCAAA

SEQ ID 42: PL004B5 x CT4 aa

EVQLVESGGGLVQPGGSLRLSCAASGFSLSYWMSWVRQAPGKLEWIGVIDTNVYIYYANWAKGRFTIS
 RDNSKNTLYLQMNSLRAEDTAVYYCARYVGNDDYINLWGQGLVTVVSSASTKGPSVFPLAPSSKSTSGG
 TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSN
 TKVDKRVPEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWY
 VDGEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQV
 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
 QGNVFSCSVMEALHNHYTQKSLSLSPGGGGSGGGGSQVQLVESGGGVVQPGRSLRLSCAASGFTFSSY
TMHWVRQAPGKLEWVTFISYDGNNKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAIYYCARTGWL
GFPDYWGQGLVTVVSSGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVGSSYL
AWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTK
 VEIK

SEQ ID 43: PL004B5 Light Chain nt

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCC
AGTCCAGTCAGAGTGTATAATGGCTACTGGTTATCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAA
GCTCCTGATCTATGGTGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTTACGCGGCAGTGGATCTGGG
ACAGAATTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCTAGGCAGTT
ATACTAGTAGTACTGAGAACTCTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACC
ATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTG
AATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAACTCCC
AGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAA
AGCAGACTACGAGAAACACAAAGTCTACGCCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACA
AAGAGCTTCAACAGGGGAGAGTGT

SEQ ID 44: PL004B5 Light Chain aa

DIQMTQSPSTLSASVGDRTITCQSSQSVYNGYWLSWYQQKPKAPKLLIYGASTLASGVPSRFSGSGSG
TEFTLTITSSLPDDFATYYCLGSYTSSTENSFGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL
NNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVT
KSFNRGEC

SEQ ID 45: PL004B9 x CT4 nt

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAG
TGTCTGGAATCGACCTCAGTGTCAATATGGGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTG
GATCGGAACCATTAATTATGTTGGTAACACATATTACGCGAGCTGGGCGAAAGGCAGATTACCATCTCC
AAAACCTCGACACGGTGGATCTTAAAATCACCAGTCCGACAACCGAGGACACGGCTGTGTATTACTGTG
CGAGAGAATCTGGTACTATTTATTACAGTTACTTTAACTTGTGGGGCCAAGGGACCCTGGTCACCGTCTC
GAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAAGTCAAGCGCCC
TGACCAGCGGCTGCACACCTTCCCGGCTGTCTTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGT
GACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCAGCAACACC
AAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCCACCGTGCCAGCACCTG
AAGCCGCGGGGGCACCGTCACTCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGAC
CCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTG
GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
TCAGCGTCTCACCCTGCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAA
AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCT
ATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACTACAAGACCACGCCTCC
CGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCC
TGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCAGGTGCAATTGGTGGAGTCTGGGGGAGG
CGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATACT
ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACA
ATAAATACTACGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTA
TCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTGGGG
CCCTTTGACTACTGGGGCCAGGGAACCCCTGGTCAACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTG

GTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGTTCTGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTC
 TTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTGGCAGCAGCTACTTAGCC
 TGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATTACAGCAGGGCCACTGGCA
 TCCCAGACAGGTTTCACTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGA
 AGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCACCGTGGACGTTTCGGCCAAGGGACCAAGGTG
 GAAATCAAA

SEQ ID 46: PL004B9 x CT4 aa

EVQLVESGGGLVQPGGSLRLSCTVSGIDLSVINMGWRQAPGKGLEWIGTITYVGNITYYASWAKGRFTIS
 KTSTTVDLKITSPTTEDTAVYYCARESGTIYYSYFNLWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGT
 AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNT
 KVDKRVEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVY
 TLPSSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ
 GNVFSCSVMHREALHNHYTQKSLSLSPGGGGSGGGGSQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYT
 MHWVRQAPGKGLEWVTFISYDGNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCARTGWLG
 PFDYWGQGLTVTVSSGGGGSGGGSGGGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVGSSYLA
 WYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKV
 EIK

SEQ ID 47: PL004B9 Light Chain nt

GCATTGCAATTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAAGTGCC
 AGGCCAGTGAAAGCATTAGCAACTACTTATCCTGGTATCAGCAGATTCCAGGGAAAGTTCCTAAGCTCCT
 GATCTATTATGCATCCAATCTGGCATCTGGGGTCCCATCTCGGTTCACTGGCAGTGGATCTGGGACAGAT
 TTCCTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCAAAGCTATTATGGTG
 GTGGTAGTGCTATACTTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGT
 CTTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAAC
 TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGA
 GTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGA
 CTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCCTCACAAAGAGC
 TTCAACAGGGGAGAGTGT

SEQ ID 48: PL004B9 Light Chain aa

AFELTQSPSSLSASVGDRVTIKCQASESISNYLSWYQQIPGKVPKLLIYYASNLASGVPSRFSGSGSGTD
 FTLTISSLQPEDVATYYCQSYYGGSAYTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNN
 FYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSSLTLSKADYEKHKVYACEVTHQGLSSPVTKS
 FNRGEC

SEQ ID 49: PD206F12 x CT4 nt

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAG
 CCTCTGGATTGACTTCAGTAGCGGCTACTGGATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGA
 GTTGATCGCATGCATTTATGCTGGTACTAGTGGTAGTACTTCCTACGCGAGCTGGGCGAGAGGCAGATTC
 ACCATCTCCGAAACCTCCAAGAACACGGTGACTCTTCAAATGAACAGCCTGAGAGCCGAGGACTCGGCTG

TGTATTACTGTGCGAGAAATCTTTACACTTACAATAGCTTGTGGGGCCAGGGAACCCTGGTCACCGTCTC
 GAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACA
 GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCC
 TGACCAGCGGCGTGCACACCTTCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGT
 GACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC
 AAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTG
 AAGCCGCGGGGGCACCGTCAGTCTTCTCTTCCCCCAAACCCAAAGGACACCCCTCATGATCTCCCGGAC
 CCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
 TCAGCGTCTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGC GCGGTCTCCAACAA
 AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
 ACCCTGCCCCCATCCCGGATGAGCTGACCAAGAACCAGGTGACCGTGACCTGCCTGGTCAAAGGCTTCT
 ATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCC
 CGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
 GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCC
 TGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCCAGGTGCAATTGGTGGAGTCTGGGGGAGG
 CGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGACGCTCTGGATTACCTTCAGTAGCTATACT
 ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGTGGAGTGGGTGACATTTATATCATATGATGGAAACA
 ATAAATACTACGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTA
 TCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTGGGG
 CCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTG
 GTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGTCTGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTC
 TTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTGGCAGCAGCTACTTAGCC
 TGGTACCAGCAGAAACCTGGCCAGGCTCCAGGCTCCTCATCTATGGTGCATTACAGCAGGGCCACTGGCA
 TCCAGACAGGTTAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGA
 AGATTTTGCAGTGTATTACTGTGACAGTATGGTAGCTCACCGTGGACGTTCCGGCCAAGGGACCAAGGTG
 GAAATCAAA

SEQ ID 50: PD206F12 x CT4 aa

EVQLVESGGGLVQPGGSLRLSCAASGFDSSGYWICWVRQAPGKGLELIACIYAGTSGSTSYASWARGRF
 TISETSKNTVTLQMNSLRAEDSAVYYCARNLYTNSLWGQGLVTVSSASTKGPSVFPLAPSSKSTSGGT
 AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT
 KVDKRVEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVY
 TLPSSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ
 GNVFSCSVSMHEALHNHYTQKSLSLSPGGGGGSGGGGSQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYT
MHWVRQAPGKGLEWVTFISYDGNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCARTGWLG
PFDYWGQGLVTVSSGGGGSGGGSGGGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVGSSYLA
WYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKV
 EIK

SEQ ID 51: PD206F12 Light Chain nt

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCC
 AGTCCAGTCAGAGTGTATTATGATAACAACCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCCTAA

GCTCCTGATCTATACAGTATCCACTCTGGCATCTGGGGTCCCATCAAGGTTTACGCGGCAGTGGATCTGGG
ACAGAATTCCTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAAGGCACTT
ATTATAGTAGTGGTTGGAACCTTGTCTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGC
ACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGTGCCTG
CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAACCT
CCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAG
CAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTC
ACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID 52: PD206F12 Light Chain aa

DIQMTQSPSTLSASVGRVITTCQSSQSVYDNNWLAWYQQKPKAPKLLIYTVSTLASGVPSRFSGSGSG
TEFTLTISLQPDFFATYYCQGTYYSSGWNFAFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC
LNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPV
TKSFNRGEC

SEQ ID 53: PD215A1 x CT4 nt

CAGGAGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAG
CCTCTGGATTCTCCTTTAGCAGCTACTGGATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTG
GATCGGATGCATTACGACTGGTAGTGGTAGCACTTACTACGCGAGCTGGGCGAAGCGCCGGTTCACCATC
TCCAAAGACAATTCCAAGAACACGGTGACTCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTAT
ATTACTGTACGAGAGCATTTGACTTGTGGGGCCAGGGAACCTTGGTCACCGTCTCGAGCGCTAGCACCAA
GGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGC
CTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGC
ACACCTTCCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG
CAGCTTGGGACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGA
GTTGAGCCCCAAATCTTGTGACAAAACCTACACATGCCACCGTGCCAGCACCTGAAGCCGCGGGGGCAC
CGTCAGTCTTCTCTTCCCCC AAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCACATG
CGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGAGGTG
CATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCACC
TCTGACACAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCCAGCCCC
CATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCATCC
CGGGATGAGCTGACCAAGAACCAGGTACGCTGACCTGCTGGTCAAAGGCTTCTATCCCAGCGACATCG
CCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGA
CGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA
TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTGGCG
GTGGAGGGTCCGGCGGTGGTGGATCCCAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGG
GAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATACTATGCACTGGGTCCGC
CAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACAATAAATACTACGCAG
ACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAG
CCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGCTGGCTGGGGCCCTTTGACTACTGG
GGCCAGGGAACCTTGGTACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCGGCGGTGGCG
GCTCCGGTGGAGGCGGTTCTGAAATTGTGTTGACGCAGTCTCCAGGCACCCCTGTCTTTGTCTCCAGGGGA
AAGAGCCACCCCTCTCCTGCAGGGCCAGTCAGAGTGTGGCAGCAGCTACTTAGCCTGGTACCAGCAGAAA
CCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATTACAGCAGGGCCACTGGCATCCAGACAGGTTCA

GTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTA
TTACTGTCAGCAGTATGGTAGCTCACCGTGGACGTTTCGCCAAGGGACCAAGGTGGAAATCAAA

SEQ ID 54: PD215A1 x CT4 aa

QEQLLESGGGLVQPGGSLRLSCTASGFSFSSYWMCWVRQAPGKGLEWIGCITTGSGSTYYASWAKRRFTI
SKDNSKNTVTTLQMNSLRAEDTAVYYCTRAFDLWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC
LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKR
VEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTKAKGQPREPQVYTLPPS
RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
CSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQVQLVESGGGVVQPRSLRLSCAASGFTFSSYTMHWVR
QAPGKGLEWVTFISYDGNNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYW
GQGLTVTVSSGGGGSGGGSGGGSGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQK
PGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGGSPWTFGQGTKVEIK

SEQ ID 55: PD215A1 Light Chain nt

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCC
AGGCCAGTCAGAGCATTTACAGCTACTTAACTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT
GATCTATGGTGCATCCAATCTGGCATCTGGGGTCCCATCAAGGTTCAAGTGGCAGTGGATCTGGGACAGAT
TTCATCTCACCATCAGCAGTCTGCAACCTGAAGATTTGCAACTTACTACTGTCAAAGCAGTTGGTTGA
GTGGTGTCTGTTGGTAATGCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATC
TGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAAT
AACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGG
AGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGC
AGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAG
AGCTTCAACAGGGGAGAGTGT

SEQ IF 56: PD215A1 Light Chain aa

DIQMTQSPSSLSASVGDRTITCQASQSIYSYLNWYQQKPGKAPKLLIYGASNLASGVPSRFRSGSGSGTD
FTLTISSLQPEDFATYYCQSSWLSGAVGNAFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLN
NFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTK
SFNRGEC

SEQ ID 57: PD220F6 x CT4 nt

CAGGAGCAGGTGAAGGAGACCGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAG
CCTCTGGATTACCATCAGCAGCTATGGAGTGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTG
GGTCGCATTGATTTTTCCCGGATTGGTTTCAAAGACTACGCGAGCTGGGTGAATGGCCGGTTACCCCTC
TCCAGCGACAACGCCCAGAACACTGTGGAAGTCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTAT
ATTACTGTGCGAGAGATTTGGACTTGTGGGGCCAGGGAACCTTGGTCACCGTCTCGAGCGCTAGCACCAA
GGGCCCATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGC
CTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAAGTCAAGCGCCCTGACCAGCGGCGTGC
ACACCTTCCCGGCTGTCTTACAGTCTCAGGACTTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCAG
CAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGA

GTTGAGCCCAAATCTTGTGACAAACTCACACATGCCACCGTGCCAGCACCTGAAGCCGCGGGGGCAC
CGTCAGTCTTCCTCTTCCCCCAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATG
CGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGAGGTG
CATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCCAGCTCCTACCG
TCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGCGGTCTCCAACAAAGCCCTCCAGCCCC
CATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCATCC
CGGGATGAGCTGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCG
CCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGTGGACTCCGA
CGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA
TGCTCCGTGATGCATGAGGCTCTGCACAACACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTGGCG
GTGGAGGGTCCGGCGGTGGTGGATCCCAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGG
GAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATACTATGCACTGGGTCCGC
CAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACAATAAATACTACGCAG
ACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAG
CCTGAGAGCTGAGGACACGGCTATATATTACTGTGCAGGACCGGCTGGCTGGGGCCCTTTGACTACTGG
GGCCAGGGAACCCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCGGGCGGTGGCG
GCTCCGGTGGAGGCGGTTCTGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGA
AAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTGGCAGCAGCTACTTAGCCTGGTACCAGCAGAAA
CCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATTACAGAGGGCCACTGGCATCCCAGACAGGTTCA
GTGGCAGTGGGTCTGGGACAGACTTCACTCTACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTA
TTACTGTCAGCAGTATGGTAGCTCACCGTGGACGTTCCGCCAAGGGACCAAGGTGGAAATCAAA

SEQ ID 58: PD220F6 x CT4 aa

QEQQKETGGGLVQPGGSLRLSCAASGFTISSYGVSWVRQAPGKGLEWVALIFPGIGFKDYASWVNGRFTL
SSDNAQNTVELQMNSLRAEDTAVYYCARDLDLWGQGLTIVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC
LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHKPSNTKVKDR
VEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGFSFLYSKLTVDKSRWQQGNVFS
CSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQVQLVESGGGVVQPRSLRLSCAASGFTFSSYTMHWVR
QAPGKGLEWVTFISYDGNKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYW
GQGLTIVTVSSGGGGSGGGSGGGSGGGSEIVLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQK
PGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK

SEQ ID 59: PD220F6 Light Chain nt

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCC
AGTCCAGTCCGAGTGTATATAGTAACACTTATCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCT
CCTGATCTATTATGCATCCACTCTGGCATCTGGGGTCCCATCTCGGTTCAGTGGCAGTGGATCTGGGACA
GATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTGCAGGCGGTTATA
GTAGTAGTACTCGTGCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGT
CTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAATGCCTCTGTTGTGTGCCTGCTGAATAAC
TTCTATCCCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGA
GTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGA

CTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCCTCACAAAGAGC
TTCAACAGGGGAGAGTGT

SEQ ID 60: PD220F6 Light Chain aa

DIQMTQSPSSLSASVGDRVTITCQSSPSVYSNYLSWYQQKPKVKPLLIYYASTLASGVPSRFSGSGSGT
DFTLTISLQPEDVATYYCAGGYSSSTRAFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNN
FYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKS
FNRGEC

SEQ ID 61: PD225G11 x CT4 nt

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAG
CCTCTGGATTACCTTTAGCAGCAGCCACTGGATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGA
GTGGATCGCATGCATTTATACTGGTAGTATTGATGTCTTTACTACGCGAGCTGGGCGAAAGGCCGTTTC
ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGG
CCGTATATTACTGTGCGAGAGCCGCTAATACTGATACTACCTACTTTAACTTGTGGGGCCAGGGAACCCCT
GGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCC
TCTGGGGGACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGA
ACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCT
CAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAG
CCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTGTGACAAAACCTCACACATGCCACCGT
GCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCAAACCCAAGGACACCCTCAT
GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC
AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCA
CGTACCGTGTGGTCAGCGTCTCACCCTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGC
GGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAA
CCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGACCTGCCTGG
TCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAA
GACCACGCCTCCCGTGTCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGC
AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGA
AGAGCCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCCAGGTGCAATTGGTGG
GTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTC
AGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCAT
ATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAA
GAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACC
GGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCGAGCGGTGGAGGCGGAT
CTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGTCTGAAATTGTGTTGACGCAGTCTCC
AGGCACCCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCCTCTCCTGCAGGGCCAGTCAGAGTGTGGCAGC
AGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATTACAGCA
GGGCCACTGGCATCCAGACAGGTTCAAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAG
ACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTGAGCAGTATGGTAGCTCACCGTGGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAA

SEQ ID 62: PD225G11 x CT4 aa

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSSHWICWVRQAPGKGLEWIACTITGSDIVFYIASWAKGRF
TISRDN SKNTLYLQMN SLRAEDTAVYYCARAANTDTTYFNLWGQGLVTVSSASTKGPSVFPLAPSSKST
SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHK
PSNTKVDKRVEPKSCDKHTCTPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF
NWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKS
RWQQGNVFCSSVMHEALHNHYTQKSLSLSPGGGGSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVGS
SSYTMHWVRQAPGKGLEWVTFISYDGN NKYYADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAIYYCART
GWLGPFDYWGQGLVTVSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVGS
SYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWF
FGQ
GTKVEIK

SEQ ID 63: PD225G11 Light Chain nt

GCCTATGATATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCC
AGGCCAGTCAGAGCATTAAACAACCAACTATCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCT
GATCTATGGTGCATCCACTCTGGCATCTGGGGTCCCATCTCGGTTACACGGCAGTGATCTGGGACAGAT
TTCATCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCATGTTCAATTATTGCA
GTGGTGGTAGTTGTTTTTGGGCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACC
ATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTG
AATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCC
AGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAA
AGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACA
AAGAGCTTCAACAGGGGAGAGTGT

SEQ ID 64: PD225G11 Light Chain aa

AYDMTQSPSSLSASVGDRVTINCQASQSINNQLSWYQQKPGKVPKLLIYGASTLASGVPSRFTGSGSGTD
FTLTISSLPEDVATYYCHVHYCSGGSCFWAFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL
NNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVT
KSFNRGEC

SEQ ID 65: CT4 heavy chain signal peptide nucleotide sequence nt

ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGTCCCAGATGGGTCTGTCC

SEQ ID 66: CT4 heavy chain signal peptide nucleotide sequence aa

MKHLWFFLLLVAAAPRWVLS

SEQ ID 67: PL230/PD224 Heavy chain signal peptide nt

ATGGCTGTCTTGGGGCTGCTCTTCTGCCTGGTGACATTCCAAGCTGTGTCTATCC

SEQ ID 68: PL230/PD224 Heavy chain signal peptide aa

MAVLGLLFCLVTFPSCVLS

SEQ ID 69: PL230/PD224 Light chain signal peptide nt

ATGAGGGCCCTGCTCAGTTTCTTGGCTTCTTGCTTTTCTGGATTCCAGCCTCCAGAAGT

SEQ ID 70: PL230/PD224 Light chain signal peptide aa

MRAPAQFLGFLLFWIPASRS

SEQ ID 71: CT4 scFv nt

CAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAG
CCTCTGGATTACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTG
GGTGACATTTATATCATATGATGGAAACAATAAACTACGCAGACTCCGTGAAGGGCCGATTACCATC
TCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATAT
ATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTC
GAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCGGCGGTGGCGGCTCCGGTGGAGGCGGTTCTGAAATT
GTGTTGACGCAGTCTCCAGGCACCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCA
GTCAGAGTGTGGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCAT
CTATGGTGCATTACAGCAGGGCCACTGGCATCCCAGACAGGTTCACTGGCAGTGGGTCTGGGACAGACTTC
ACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTGACAGTATGGTAGCTCAC
CGTGGACGTTTCGGCCAAGGGACCAAGGTGGAAATCAA

SEQ ID 72: CT4 scFv aa

QVQLVESGGGVVQPGRSRLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNKYYADSVKGRFTI
SRDNSKNTLYLQMNLSRAEDTAIYYCARTGWLGPFDYWGQGLVTVSSGGGSGGGGSGGGGSGGGGSEI
VLTQSPGTLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDF
TLTISRLEPEDFAVYYCQYGSPPWTFGQGTKVEIK

SEQ ID 73: PD224D1 scFv nt

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGTCCCTGAGACTCTCCTGTACAGC
CTCTGGATTCTCCCTCAGTAGCTATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTACATCGGCTACA
TTGGTGATACTACTGGCATAGCCTACGCGAGCTGGGCGAATGGCAGATTACCATCTCCAAAGACAATACCAAGAACACG
GTGGATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGCTGGTCTACTTAGACAT
CTGGGGCCAAGGGACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCGGCGCGGTGGCGGCTCCG
GTGGAGGCGGCTCTGCCCTGTGATGACCCAGTCTCCATCCTCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT
TGCCAGGCCAGTCAGAACATTTACAGCAATTTAGCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTA
TCAGGCCTCCACTCTGGCATCTGGGTCCCATCTCGGTTCACTGGCAGTGGATATGGGACAGATTTCACTCTCACCATCA
GCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCAAGGCGGTTATTATAGTGCTGCCCTTAATACTTTTCGGCGGA
GGGACCAAGGTGGAGATCAA

SEQ ID 74: PD224D1 scFv aa

EVQLVESGGGLVQPGGSLRLSCTASGFSLSSYAMSWVRQAPGKLEYIGYIGDTTGIAYASWANGRFTISKDNTKNTVDLQMN
LRAEDTAVYYCARGWSYLDIWQGLVTVSSGGGSGGGGSGGGGSGGGGSSALVMTQSPSSLSASVGDRTITCQASQNIYSN
LAWYQQKPGKVPKLLIYQASTLASGVPSRFSGSGYGTDFTLTISLQPEDVATYYCQGGYSAALNTFGGGTKVEIK

SEQ ID 75: PD206F12 scFv nt

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGTCCCTGAGACTCTCCTGTGCAG
CCTCTGGATTGCACTTCAGTAGCGGCTACTGGATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGA
GTTGATCGCATGCATTTATGCTGGTACTAGTGGTAGTACTTCCTACGCGAGCTGGGCGAGAGGCAGATT
ACCATCTCCGAAACCTCCAAGAACACGGTGACTCTTCAAATGAACAGCCTGAGAGCCGAGGACTCGGCTG
TGTATTACTGTGCGAGAAATCTTTACACTTACAATAGCTTGTGGGGCCAGGGAACCCTGGTCACCGTCTC

GAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGACATC
 CAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCA
 GTCAGAGTGTATGATAACAACCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCCTAAGCTCCT
 GATCTATACAGTATCCACTCTGGCATCTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGAA
 TTCCTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAAGGCACTTATTATA
 GTAGTGGTTGGAACCTTTGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 76: PD206F12 scFv aa

EVQLVESGGGLVQPGGSLRLSCAASGFDSSGYWICWVRQAPGKGLELIACIYAGTSGSTSYASWARGRF
 TISETSKNTVTLMNSLRAEDSAVYYCARNLYTNSLWGQGLVTVSSGGGSGGGGSGGGGSGGGGSDI
 QMTQSPSTLSASVGDRTITCQSSQSVYDNNWLAWYQQKPKAPKLLIYTVSTLASGVPSRFSGSGSGTE
 FTLTISLQPDDEFATYYCQGTYYSSGWNFAFGGGTKVEIK

SEQ ID 77: PD215A1 scFv nt

CAGGAGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAG
 CCTCTGGATTCTCCTTTAGCAGCTACTGGATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTG
 GATCGGATGCATTACGACTGGTAGTGGTAGCACTTACTACGCGAGCTGGGCGAAGCGCCGGTTCACCATC
 TCCAAAGACAATTCCAAGAACACGGTGACTCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTAT
 ATTACTGTACGAGAGCATTTGACTTGTGGGGCCAGGGAACCTGGTCACCGTCTCGAGCGGTGGAGGCGG
 ATCTGGCGGAGGTGGTTCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGACATCCAGATGACCCAGTCT
 CCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCAGTCAGAGCATTTACA
 GCTACTTAAACTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGGTGCATCCAATCT
 GGCATCTGGGGTCCCATCAAGGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGT
 CTGCAACCTGAAGATTTTGCAACTTACTACTGTCAAAGCAGTTGGTTGAGTGGTGTGTTGGTAATGCTT
 TCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 78: PD215A1 scFv aa

QEQLLESGGGLVQPGGSLRLSCTASGFSFSSYWMCWVRQAPGKGLEWIGCITTGSGSTYYASWAKRRFTI
 SKDNSKNTVTLMNSLRAEDTAVYYCTRAFDLWGQGLVTVSSGGGSGGGGSGGGGSGGGGSDIQMTQS
 PSSLSASVGDRTITCQASQSIYSYLNWYQQKPKAPKLLIYGASNLASGVPSRFSGSGSGTDFTLTIS
 LQPEDFATYYCQSSWLSGAVGNAFGGGTKVEIK

SEQ ID 79: PD225G11 scFv nt

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAG
 CCTCTGGATTACCTTTAGCAGCAGCCACTGGATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGA
 GTGGATCGCATGCATTTATACTGGTAGTATTGATGTCTTTTACTACGCGAGCTGGGCGAAAGGCCGGTTC
 ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGG
 CCGTATATTACTGTGCGAGAGCCGCTAATACTGATACTACCTACTTTAACTTGTGGGGCCAGGGAACCT
 GGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCGGCGGTGGCGGCTCCGGTGGAGGC
 GGCTCTGCCTATGATATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCA
 ATTGCCAGGCCAGTCAGAGCATTAACAACCACTATCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAA
 GCTCCTGATCTATGGTGCATCCACTCTGGCATCTGGGGTCCCATCTCGGTTACCGGCAGTGGATCTGGG

ACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCATGTTTCATT
ATTGCAGTGGTGGTAGTTGTTTTTGGGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 80: PD225G11 scFv aa

EVQLLES^{GGGLVQPGGSLRLSCAASGFTFSSSHWICWVRQAPGKGLEW}IACIYTGSIDVFYYASWAKGRF
TISRDN^{SKNTLYLQMNSLRAEDTAVYYCARAANTDTTYFNLWGQ}GLVTVSSGGGSGGGGSGGGGSGGGG
GSAYDMTQSPSSLSASV^{GDRTINCQASQSINNQLSWYQQKPGKVPKLLIYGASTLASGVPSRFTGSGSG}
TDFTLTIS^{SLQPEDVATYYCHVHYCSGGSCFWAFGGGT}KVEIK

SEQ ID 81: PL230C6 scFv nt

CAGTCGGTGGAGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACCGCCT
CTGGAATCGACCTTAATACCTACGACATGATCTGGGTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGT
TGGAATCATTACTTATAGTGGTAGTAGATACTACGCGAACTGGGCGAAAGGCCGATTACCATCTCCAAA
GACAATACCAAGAACACGGTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACT
GTGCGAGAGATTATATGAGTGGTTCCTTGTGGGGCCAGGGAACCTGGTCACCGTCTCTTCCGGTGG
AGGCGGTTTCAGGCGGAGGTGGAAGTGGTGGTGGCGGCTCTGGAGGCGGCGGATCTGCCTATGATATGACC
CAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCAAGTGTGAGGCCAGTGAGGACA
TTTATAGCTTCTTGGCCTGGTATCAGCAGAAACCAGGGAAGCCCCCTAAGCTCCTGATCCATTCTGCATC
CTCTCTGGCATCTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATC
AGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGGTTATGGTAAAAATAATGTTGATA
ATGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 82: PL230C6 scFv aa

QSVEESGGGLVQPGGSLRLSCTASGID^{LN}TYDMIWVRQAPGKGLEWVGIITYSGSRYANWAKGRFTISK
DNTKNTVYLQMNSLRAEDTAVYYCARDYMSG^{SHLWGQ}GLVTVSSGGGSGGGGSGGGGSGGGGSAYDMT
QSPSSVSASVGDRTIKCQASEDIYSFLAWYQQKPGKAPKLLIHSASSLASGVPSRFSGSGSGTDFTLTI
SSLQPEDFATYYCQQGYGKNNVDNAFGGGTKVEIK

SEQ ID 83: PL231H2 scFv nt

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGGGCTCCCTGAGACTCTCCTGTACAA
CTTCTGGAATCGACCTTAGTACCTACGACATGATCTGGGTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTG
GGTGGGAATCATTAGTTATGTTGGTAACACATACTACGCGAGCTGGGCGAAAGGCCGATTACCCCTCTCC
AAAGACAATACCTCGACCACGGTGGATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATT
ACTGTGCGAGAGATTTTATTAGTGGTTCCTTGTGGGGCCAGGGAACCTGGTCACCGTCTCGAGCGG
TGGAGGCGGATCTGGCGGAGGTGGTTCGGCGGTGGCGGCTCCGGTGGAGGCGGTTCTGCCTATGATATG
ACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGTGAGGCCAGTGAGA
GCATTAGTAGCTTCTTATCCTGGTATCAGCAGAAACCAGGGAAGCCCCCTAAGCTCCTGATCTTTTCTGC
ATCCACTCTGGCATCTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACC
ATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGGTTATAGTAAAAGTAATGTGG
ATAATGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 84: PL231H2 scFv aa

QVQLVESGGGLVQPGGSLRLSCTTS^{GID}LNSTYDMIWVRQAPGKGLEWVGIIISYVGN^{TY}YASWAKGRFTLS
KDNTSTTV^{DLQMNSLRAEDTAVYYCARD}FISGSHLWGQGLVTVSSGGGSGGGGSGGGGSGGGGSAYDM

TQSPSSVSASVGDRVTINCQASESIS~~SS~~FLSWYQQKPGKAPKLLIF~~S~~SASTLASGVPSRFSGSGSGTDFTLT
ISSLQPEDFATYYC~~QQGY~~SKSNVDNAFGGGTKVEIK

SEQ ID 85: PL221G5 scFv nt

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAG
CCTCTGGATTCTCCTTCAGTAGCGGGTACGACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGA
GTGGATCGCATGCATTGCTGCTGGTAGTGTGCTGGTATCACTTACGACGCGAACTGGGCGAAAGGCCGGTTC
ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGG
CCGTATATTACTGTGCGAGATCGGCGTTTTCTGTTGCGACTACGCCATGGACCTCTGGGGCCAGGGAACCCCT
GGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGC
GGCTCTGACATCCAGATGACCCAGTCTCCTTCCACCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCA
CTTGCCAGGCCAGTCAGAGCATTAGTTCCCACTTAACTGGTATCAGCAGAAACCAGGGAAAGCCCCCTAA
GCTCCTGATCTATAAGGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTTACGCGGCAGTGGATCTGGG
ACAGAATTTACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAACAGGGTT
ATAGTTGGGGTAATGTTGATAATGTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 86: PL221G5 scFv aa

EVQLLES~~GGGLVQPGG~~SLRLSCAASGFSFSSGYDMCWVRQAPGKGLEWIA~~CIA~~AGSAGITYDANWAKGRF
TISRDN~~SKNTLYLQMN~~SLRAEDTAVYYCARSAF~~SFDY~~AMD~~LWGQ~~TLVTVSSGGGSGGGGSGGGGSGGG
GSDIQMTQSPSTLSASVGDRVTITCQASQ~~SISS~~HLN~~WYQQKPGKAPKLLIY~~KASTLASGVPSRFSGSGSG
TEFTLT~~ISSLQPD~~DFATYYC~~QQGY~~SWGNVDN~~V~~FGGGTKVEIK

SEQ ID 87: PL004B5 scFv nt

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAG
CCTCTGGATTCTCCCTCAGTAGCTACTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTG
GATCGGAGTCATTGATACTAATGTTTATATATACTACGCGAACTGGGCAAAAGGCAGATTACCATCTCC
AGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATT
ACTGTGCGAGATATGTGGGTAATAATGATGATTATATTA~~ACTTGTGGGGCCAGGGAACCC~~TGGTCACCGT
CTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGAC
ATCCAGATGACCCAGTCTCCTTCCACCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGT
CCAGTCAGAGTGTTTATAATGGCTACTGGTTATCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCT
CCTGATCTATGGTGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTTACGCGGCAGTGGATCTGGGACA
GAATTC~~ACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCTAGGCAGTTATA~~
CTAGTAGTACTGAGAACTCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 88: PL004B5 scFv aa

EVQLVES~~GGGLVQPGG~~SLRLSCAASGFS~~LS~~SYWMSWVRQAPGKLEWIG~~VID~~TNVYIYYANWAKGRFTIS
RDNSKNTLYLQMN~~SLRAEDTAVYYCARYVGN~~NDYINLWGQTLVTVSSGGGSGGGGSGGGGSGGGGSD
IQMTQSPSTLSASVGDRVTITCQSSQSVYNGY~~WLSWYQQKPGKAPKLLIY~~GASTLASGVPSRFSGSGSGT
EFTLT~~ISSLQPD~~DFATYYC~~LG~~SYTSSTENSFGGGTKVEIK

SEQ ID 89: PL004B9 scFv nt

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAG
TGTCTGGAATCGACCTCAGTGTCAATATGGGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTG

GATCGGAACCATTACTTATGTTGGTAACACATATTACGCGAGCTGGGCGAAAGGCAGATTACCATCTCC
 AAAACCTCGACCACGGTGGATCTTAAAATCACCAGTCCGACAACCGAGGACACGGCTGTGTATTACTGTG
 CGAGAGAATCTGGTACTATTTATTACAGTTACTTTAACTTGTGGGGCCAAGGGACCCTGGTCACCGTCTC
 GAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGCATTC
 GAATTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAAGTGCCAGGCCA
 GTGAAAGCATTAGCAACTACTTATCCTGGTATCAGCAGATTCCAGGGAAAGTTCCTAAGCTCCTGATCTA
 TTATGCATCCAATCTGGCATCTGGGGTCCCATCTCGGTTCACTGGCAGTGGATCTGGGACAGATTTCACT
 CTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCAAAGCTATTATGGTGGTGGTA
 GTGCCTATACTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 90: PL004B9 scFv aa

EVQLVESGGGLVQPGGSLRLSCTVSGIDLSVINMGWRQAPGKGLEWIGTITYVGNITYYASWAKGRFTIS
 KTSTTVDLKITSPTTEDTAVYYCARESGTIYYSYFNLWGQGLVTVSSGGGGSGGGSGGGSGGGSAF
 ELTQSPSSLSASVGDRTIKCQASESISNYLSWYQQIPGKVPKLLIYYASNLASGVPSRFSGSGSGTDF
 LTISSLQPEDVATYYCQSYYGGSAYTFGGGTKVEIK

SEQ ID 91: CT4 VH nt

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCA
 CCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGAT
 GGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATCCAAGAACACGCTGTATCT
 GCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACT
 GGGGCCAGGGAACCTGGTCACCGTCTCCTCA

SEQ ID 92: CT4 VH aa

QVQLVESGGGVVQPGSRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNKKYYADSVKGRFTI
 SRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLVTVSS

SEQ ID 93: CT4 VL nt

GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCA
 GGGCCAGTCAGAGTGTGGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCT
 CCTCATCTATGGTGCATTACAGCAGGGCCACTGGCATCCCAGACAGGTTCACTGGCAGTGGGTCTGGGACA
 GACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTGAGCAGTATGGTA
 GCTCACCGTGGACGTTTCGGCCAAGGGACCAAGGTGGAAATCAAA

SEQ ID 94: CT4 VL aa

EIVLTQSPGTLISLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGT
 DFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK

SEQ ID 95: PD224D1 VH nt

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGTCCCTGAGACTCTCCTGTACAG
 CCTCTGGATTCTCCCTCAGTAGCTATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTA
 CATCGGCTACATTGGTGATACTACTGGCATAGCCTACGCGAGCTGGGCGAATGGCAGATTACCATCTCC
 AAAGACAATAACCAAGAACACGGTGGATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATT
 ACTGTGCGAGAGGCTGGTCCTACTTAGACATCTGGGGCCAAGGGACCCTGGTCACCGTCTCGAGC

SEQ ID 96: PD224D1 VH aa

EVQLVESGGGLVQPGGSLRLSCTASGFSLSSYAMSWVRQAPGKLEYIGYIGDTTGIAYASWANGRFTIS
KDNTKNTVDL
QMNSLRAEDTAVYYCARGWSYLDIWGQGTTLTVSS

SEQ ID 97: PD224D1 VL nt

GCCCTTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCC
AGGCCAGTCAGAACATTTACAGCAATTTAGCCTGGTATCAGCAGAAACCAGGGAAAGTTCTTAAGCTCCT
GATCTATCAGGCCTCCACTCTGGCATCTGGGGTCCCATCTCGGTTCACTGGCAGTGGATATGGGACAGAT
TTCCTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCAAGGCGGTTATTATA
GTGCTGCCCTTAATACTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 98: PD224D1 VL aa

ALVMTQSPSSLSASVGDRTITCQASQNIYSNLAWYQQKPGKVPKLLIYQASTLASGVPSRFSGSGYGTD
FTLTISSLQP
EDVATYYCQGGYYSAALNTFGGGTKVEIK

SEQ ID 99: PD206F12 VH nt

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAG
CCTCTGGATTTCGACTTCAGTAGCGGCTACTGGATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGA
GTTGATCGCATGCATTTATGCTGGTACTAGTGGTAGTACTTCCTACGCGAGCTGGGCGAGAGGCAGATTC
ACCATCTCCGAAACCTCCAAGAACACGGTGACTCTTCAAATGAACAGCCTGAGAGCCGAGGACTCGGCTG
TGTATTACTGTGCGAGAAATCTTTACACTTACAATAGCTTGTGGGGCCAGGGAACCCTGGTCACCGTCTC
GAGC

SEQ ID 100: PD206F12 VH aa

EVQLVESGGGLVQPGGSLRLSCAASGFDFSSGYWICWVRQAPGKLELIACIYAGTSGSTSYASWARGRF
TISETSKNTVTLMNSLRAEDSAVYYCARNLYTYNSLWGQGTTLTVSS

SEQ ID 101: PD206F12 VL nt

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCC
AGTCCAGTCAGAGTGTATGATAACAACCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAA
GCTCCTGATCTATACAGTATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAAGCGCAGTGGATCTGGG
ACAGAATTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAAGGCACTT
ATTATAGTAGTGGTTGGAACCTTGCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 102: PD206F12 VL aa

DIQMTQSPSTLSASVGDRTITCQSSQSVYDNNWLAWYQQKPGKAPKLLIYTVSTLASGVPSRFSGSGSG
TEFTLTISSLQPDDEFATYYCQGTYYSSGWNFAFGGGTKVEIK

SEQ ID 103: PD215A1 VH nt

CAGGAGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAG
CCTCTGGATTCTCCTTTAGCAGCTACTGGATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTG
GATCGGATGCATTACGACTGGTAGTGGTAGCACTTACTACGCGAGCTGGGCGAAGCGCCGGTTCAACATC
TCCAAAGACAATTCCAAGAACACGGTGACTCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTAT
ATTACTGTACGAGAGCATTTGACTTGTGGGGCCAGGGAACCCTGGTCAACCGTCTCGAGC

SEQ ID 104: PD215A1 VH aa

QEQLLESGGGLVQPGGSLRLSCTASGFSFSSYWMCWVRQAPGKGLEWIGCITTGSGSTYYASWAKRRFTI
SKDNSKNTVTLLQMNSLRAEDTAVYYCTRAFDLWGQGLVTVSS

SEQ ID 105: PD215A1 VL nt

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCC
AGGCCAGTCAGAGCATTTACAGCTACTTAACTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT
GATCTATGGTGCATCCAATCTGGCATCTGGGGTCCCATCAAGGTTTCAGTGGCAGTGGATCTGGGACAGAT
TTCACCTCTCACCATCAGCAGTCTGCAACCTGAAGATTTTGCAACTTACTACTGTCAAAGCAGTTGGTTGA
GTGGTGCTGTTGGTAATGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 106: PD215A1 VL aa

DIQMTQSPSSLSASVGDRTITCQASQSIYSYLNWYQQKPGKAPKLLIYGASNLASGVPSRFSGSGSGTD
FTLTISLQPEDFATYYCQSSWLSGAVGNAFGGGTKVEIK

SEQ ID 107: PD225G11 VH nt

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAG
CCTCTGGATTACCTTTTAGCAGCAGCCACTGGATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGA
GTGGATCGCATGCATTTATACTGGTAGTATTGATGTCTTTACTACGCGAGCTGGGCGAAAGGCCGGTTC
ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGG
CCGTATATTACTGTGCGAGAGCCGCTAATACTGATACTACCTACTTTAACTTGTGGGGCCAGGGAACCCCT
GGTCACCGTCTCGAGC

SEQ ID 108: PD225G11 VH aa

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSSHWICWVRQAPGKGLEWIIACIYTGSIDVFYYASWAKGRF
TISRDNKNTLYLLQMNSLRAEDTAVYYCARAANTDTTYFNLWGQGLVTVSS

SEQ ID 109: PD225G11 VL nt

GCCTATGATATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCC
AGGCCAGTCAGAGCATTAACAACCAACTATCCTGGTATCAGCAGAAACCAGGGAAAGTTTCTAAGCTCCT
GATCTATGGTGCATCCACTCTGGCATCTGGGGTCCCATCTCGGTTACCCGGCAGTGGATCTGGGACAGAT
TTCACCTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCTGTTTATTATTGCA
GTGGTGGTAGTTGTTTTTGGGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 110: PD225G11 VL aa

AYDMTQSPSSLSASVGDRTINCQASQSINNQLSWYQQKPGKVPKLLIYGASTLASGVPSRFTGSGSGTD
FTLTISLQPEDVATYYCHVHYCSGGSCFWAFGGGTKVEIK

SEQ ID 111: PL230C6 VH nt

CAGTCGGTGGAGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACCGCCT
CTGGAATCGACCTTAATACCTACGACATGATCTGGTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGT
TGGAATCATTACTTATAGTGGTAGTAGATACTACGCGAACTGGGCGAAAGGCCGATTACCATCTCCAAA
GACAATAACCAAGAACACGGTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACT
GTGCGAGAGATTATATGAGTGGTTCCCACTTGTGGGGCCAGGGAACCCCTGGTCACCGTCTCTTCC

SEQ ID 112: PL230C6 VH aa

QSVEESGGGLVQPGGSLRLSCTASGIDLNTYDMIWVRQAPGKGLEWVGIIITYSGSRYYANWAKGRFTISK
DNTKNTVYLLQMNSLRAEDTAVYYCARDYMSGSHLWGQGLVTVSS

SEQ ID 113: PL230C6 VL nt

GCCTATGATATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCAAGTGTC
AGGCCAGTGAGGACATTTATAGCTTCTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT
GATCCATTCTGCATCCTCTCTGGCATCTGGGGTCCCATCAAGGTTTCAGCGGCAGTGATCTGGGACAGAT
TTCATCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGGTTATGGTA
AAAATAATGTTGATAATGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 114: PL230C6 VL aa

AYDMTQSPSSVSASVGDRVTIKCQASEDIYSFLAWYQQKPGKAPKLLIHSASSLASGVPSRFSGSGSGTD
FTLTISSLQP
EDFATYYCQQGYGKNNVDNAFGGGTKVEIK

SEQ ID 115: PL231H2 VH nt

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGGGCTCCCTGAGACTCTCCTGTACAA
CTTCTGGAATCGACCTTAGTACCTACGACATGATCTGGGTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTG
GGTGGGAATCATTAGTTATGTTGGTAACACATACTACGCGAGCTGGGCGAAAGGCCGATTACCCCTCTCC
AAAGACAATACCTCGACCACGGTGGATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATT
ACTGTGCGAGAGATTTTATTAGTGGTTCCTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

SEQ ID 116: PL231H2 VH aa

QVQLVESGGGLVQPGGSLRLSCTTSGIDLSTYDMIWVRQAPGKGLEWVGIIISYVGNITYYASWAKGRFTLS
KDNTSTTVDLQMNSLRAEDTAVYYCARDFISGSHLWGQTLTVSS

SEA ID 117: PL231H2 VL nt

GCCTATGATATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGTC
AGGCCAGTGAGAGCATTAGTAGCTTCTTATCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT
GATCTTTTCTGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTTCAGCGGCAGTGATCTGGGACAGAT
TTCATCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGGTTATAGTA
AAAGTAATGTGGATAATGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 118: PL231H2 VL aa

AYDMTQSPSSVSASVGDRVTINCQASESISSFLSWYQQKPGKAPKLLIFSASTLASGVPSRFSGSGSGTD
FTLTISSLQPEDFATYYCQQGYSKSNVDNAFGGGTKVEIK

SEQ ID 119: PL221G5 VH nt

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAG
CCTCTGGATTCTCCTTCAGTAGCGGGTACGACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGA
GTGGATCGCATGCATTGCTGCTGGTAGTGCTGGTATCACTTACGACGCGAACTGGGCGAAAGGCCGGTTC
ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGG
CCGTATATTACTGTGCGAGATCGGCGTTTTCTGTTGACTACGCCATGGACCTCTGGGGCCAGGGAACCCCT
GGTCACCGTCTCGAGC

SEA ID 120: PL221G5 VH aa

EVQLLES^{GGGLVQPGGSLRLSCAASGFSFSS}SGYDMCWVRQAPGKGLEWIACIAAGSAGITYDANWAKGRF
TISRDNKNTLYLQMNSLRAEDTAVYYCARSSAFSFDYAMDLWGQGLVTVSS

SEQ ID 121: PL221G5 VL nt

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCC
AGGCCAGTCAGAGCATTAGTTCCCACTTAACTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT
GATCTATAAGGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGAA
TTTACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAACAGGGTTATAGTT
GGGTAATGTTGATAATGTTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEA ID 122: PL221G5 VL aa

DIQMTQSPSTLSASVGDRVTITCQASQSISSHLN^{WYQQKPGKAPKLLIY}KASTLASGVPSRFSGSGSGTE
FTLTISLQPD^{DFATYYCQQY}SWGNVDNVFGGGTKVEIK

SEA ID 123: PL004B5 VH nt

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAG
CCTCTGGATTCTCCCTCAGTAGCTACTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTG
GATCGGAGTCATTGATACTAATGTTTATATATACTACGCGAACTGGGCAAAAGGCAGATTCACCATCTCC
AGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATT
ACTGTGCGAGATATGTGGGTAATAATGATGATTATTAACCTGTGGGGCCAGGGAACCCTGGTCACCGT
CTCGAGC

SEQ ID 124: PL004B5 VH aa

EVQLVESGGGLVQPGGSLRLSCAASGFSLS^{SYWMSWVRQAPGKGLEW}I^{GVIDTNVYIYYANWAKGRF}TIS
RDNSKNTLYLQMNSLRAEDTAVYYCARY^{VGNNDY}INLWGQGLVTVSS

SEQ ID 125: PL004B5 VL nt

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCC
AGTCCAGTCAGAGTGTTTATAATGGCTACTGGTTATCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAA
GCTCCTGATCTATGGTGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGG
ACAGAATTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCTAGGCAGTT
ATACTAGTAGTACTGAGAACTCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 126: PL004B5 VL aa

DIQMTQSPSTLSASVGDRVTITCQSSQSVYNGY^{WLSWYQQKPGKAPKLLIY}GASTLASGVPSRFSGSGS
TEFTLTISLQPD^{DFATYYCLGSYTSSTENS}FGGGTKVEIK

SEA ID 127: PL004B9 VH nt

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAG
TGTCTGGAATCGACCTCAGTGTCATCAATATGGGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTG
GATCGGAACCATTA^{CTTATGTTGGTAACACATATTACGCGAGCTGGGCGAAAGGCAGATT}CACCATCTCC
AAAACCTCGACCACGGTGGATCTTAAATCACCAGTCCGACAACCGAGGACACGGCTGTGTATTACTGTG
CGAGAGAATCTGGTACTATTTATTACAGTTACTTTAACTTGTGGGGCCAAGGGACCCTGGTCACCGTCTC
GAGC

SEQ ID 128: PL004B9 VH aa

EVQLVESGGGLVQPGGSLRLSCTVSGIDLSVINMGWVRQAPGKGLEWIGTITYVGN¹TYIASWAKGRFTIS
 KTSTTVDLKITSPTTEDTAVYYCARESGTIYYSYFNLWGQGLTVTVSS

SEQ ID 129: PL004B9 VL nt

GCATTTCGAATTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAAGTGCC
 AGGCCAGTGAAAGCATTAGCAACTACTTATCCTGGTATCAGCAGATTCCAGGGAAAGTTCCTAAGCTCCT
 GATCTATTATGCATCCAATCTGGCATCTGGGGTCCCATCTCGGTTTCAGTGGCAGTGGATCTGGGACAGAT
 TTCCTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCAAAGCTATTATGGTG
 GTGGTAGTGCCTATACTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 130: PL004B9 VL aa

AFELTQSPSSLSASVGDRTIKCQASESISNYLSWYQQIPGKVPKLLIYYASNLASGVPSRFSGSGSGTD
 FTLT¹ISSLQPEDVATYYCQSY²YGGGSAYTFGGGTKEIK

SEQ ID 131: PD220F6 VH nt

CAGGAGCAGGTGAAGGAGACCGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAG
 CCTCTGGATTACCATCAGCAGCTATGGAGTGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTG
 GGTCGCATTGATTTTTCCCGGATTTGGTTTCAAAGACTACGCGAGCTGGGTGAATGGCCGGTTCACCCCT
 TCCAGCGACAACGCCGAGAACACTGTGGAAC¹TGAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTAT
 ATTACTGTGCGAGAGATTTGGACTTGTGGGGCCAGGGAACCTGGTCAACCGTCTCGAGC

SEQ ID 132: PD220F6 VH aa

QEQQKETGGGLVQPGGSLRLSCAASGFTISSYGVSWVRQAPGKGLEWVALIFPGIGFKDYASWVNGRFTL
 SSDNAQNTVELQMNSLRAEDTAVYYCARDL¹DLWGQGLTVTVSS

SEQ ID 133: PD220F6 VL nt

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCC
 AGTCCAGTCCGAGTGTTTATAGTAACTACTTATCCTGGTATCAGCAGAAACCAGGGAAGTTCCTAAGCT
 CCTGATCTATTATGCATCCACTCTGGCATCTGGGGTCCCATCTCGGTTTCAGTGGCAGTGGATCTGGGACA
 GATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTGCAGGCGGTTATA
 GTAGTAGTACTCGTGCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 134: PD220F6 VL aa

DIQMTQSPSSLSASVGDRTITCQSSPSVYSNYLSWYQQKPGKVPKLLIYYASTLASGVPSRFSGSGSGT
 DFTLT¹ISSLQPEDVATYYCAGGYSSSTRAFGGGTKEIK

SEQ ID 135: human IgG1 constant region nt

GCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG
 CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAAC¹TACAGCGCCCTGAC
 CAGCGGCGTGACACCTTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACC
 GTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCAGCAACACCAAGG
 TGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAAC²TACACATGCCCACCGTGCCAGCACCTGAACT
 CCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCAAGGACACCCTCATGATCTCCCGGACCCCT
 GAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACG
 GCGTGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAG
 CGTCTCACCCTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCC
 CTCCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACC

TGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC
CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTG
CTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGA
ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTC
TCCGGGT

SEQ ID 136: human IgG1 constant region aa

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT
VPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE
VTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA
LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
LDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG

SEQ ID 137: human IgG1 effector null nt

GCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG
CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCCTGAC
CAGCGCGTGCACACCTTCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACC
GTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGG
TGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCCACCGTGCCCAGCACCTGAAGC
CGCGGGGGCACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCT
GAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACG
GCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAG
CGTCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCC
CTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCC
TGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC
CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTG
CTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGA
ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTC
TCCGGGT

SEQ ID 138: human IgG1 effector null aa

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT
VPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPE
VTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKA
LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
LDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG

SEQ ID 139: PD220F6 scFv nt

CAGGAGCAGGTGAAGGAGACCGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAG
CCTCTGGATTACCATCAGCAGCTATGGAGTGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTG
GGTCGCATTGATTTTTCCCGGATTGGTTTCAAAGACTACGCGAGCTGGGTGAATGGCCGGTTACCCCTC
TCCAGCGACAACGCCCAGAACACTGTGGAAGTCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTAT
ATTACTGTGCGAGAGATTTGGACTTGTGGGGCCAGGGAACCTGGTCACCGTCTCGAGCGGTGGAGCGG
ATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGTGGAGGCGGCTCTGACATCCAGATGACCCAGTCT
CCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCAGTCCGAGTGTTTATA

GTAAC TACTTATCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTATTATGCATCCAC
TCTGGCATCTGGGGTCCCATCTCGGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGC
AGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTGCAGGCGGTTATAGTAGTAGTACTCGTGCTTTCG
GCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 140: PD220F6 scFv aa

QE QVKETGGGLVQPGGSLRLSCAASGFTISSYGVSWVRQAPGKGLEWVALIFPGIGFKDYASWVNGRFTL
SSDNAQNTVELQMNSLRAEDTAVYYCARDLDLWGQGLTVTVSSGGGGSGGGSGGGSGGGSDIQMTQS
PSSLSASVGDRTITCQSSPSVYSNYLSWYQQKPGKVPKLLIYYASTLASGVPSRFSGSGSGTDFTLTIS
SLQPEDVATYYCAGGYSSSTRAFGGGTKVEIK

SEQ ID 141: CT4 VH CDR1 aa

SSYTMH

SEQ ID 142: CT4 VH CDR2 aa

FISYDGNKYYADSVKG

SEQ ID 143: CT4 VH CDR3 aa

TGWLGPFDY

SEQ ID 144: CT4 VL CDR1 aa

RASQSVGSSYLA

SEQ ID 145: CT4 VL CDR2 aa

GAFSRAT

SEQ ID 146: CT4 VL CDR3 aa

QQYGSSPWT

SEQ ID 147: PL230C6 VH CDR1 aa

NTYDMI

SEQ ID 148: PL230C6VH CDR2 aa

IITYSGSRYANWAKG

SEQ ID 149: PL230C6VH CDR3 aa

DYMSGSHL

SEQ ID 150: PL230C6VL CDR1 aa

QASEDIYSFLA

SEQ ID 151: PL230C6VL CDR2 aa

SASSLAS

SEQ ID 152: PL230C6VL CDR3 aa

QQGYGKNNVDNA

SEQ ID 153: PD224D1 VH CDR1 aa

NTYDMI

SEQ ID 154: PD224D1 CDR2 aa
IITYSGSRYANWAKG

SEQ ID 155: PD224D1 CDR3 aa
DYMSGSHL

SEQ ID 156: PD224D1 CDR1 aa
QASEDIYSFLA

SEQ ID 157: PD224D1 CDR2 aa
SASSLAS

SEQ ID 158: PD224D1 CDR3 aa
QQGYGKNNVDNA

SEQ ID 159: PL221G5 VH CDR1 aa
SGYDMC

SEQ ID 160: PL221G5 CDR2 aa
CIAAGSAGITYDANWAKG

SEQ ID 161: PL221G5 CDR3 aa
SAFSFDYAMD

SEQ ID 162: PL221G5 CDR1 aa
QASQSISSHLN

SEQ ID 163: PL221G5 CDR2 aa
KASTLAS

SEQ ID 164: PL221G5 CDR3 aa
QQGYSWGNVDNV

SEQ ID 165: PL231H2 VH CDR1 aa
STYDMI

SEQ ID 166: PL231H2 VH CDR2 aa
IISYVGNTYYASWAKG

SEQ ID 167: PL231H2 VH CDR3 aa
DFISGSHL

SEQ ID 168: PL231H2 VL CDR1 aa
QASESISFSL

SEQ ID 169: PL231H2 VL CDR2 aa
SASTLAS

SEQ ID 170: PL231H2 VL CDR3 aa

QQGYSKSNVDNA

SEQ ID 171: PL004B5 VH CDR1 aa
SSYWMS

SEQ ID 172: PL004B5 VH CDR2 aa
VIDTNVYIYYANWAKG

SEQ ID 173: PL004B5 VH CDR3 aa
YVGNNDDYINL

SEQ ID 174: PL004B5 VL CDR1 aa
QSSQSVYNGWLS

SEQ ID 175: PL004B5 VL CDR2 aa
GASTLAS

SEQ ID 176: PL004B5 VL CDR3 aa
LGSYTSSTENS

SEQ ID 177: PL004B9 VH CDR1 aa
SVINMG

SEQ ID 178: PL004B9 VH CDR2 aa
TITYVGNITYYASWAKG

SEQ ID 179: PL004B9 VH CDR3 aa
ESGTIYYSYFNL

SEQ ID 180: PL004B9 VL CDR1 aa
QASESISNYLS

SEQ ID 181: PL004B9 VL CDR2 aa
YASNLAS

SEQ ID 182: PL004B9 VL CDR3 aa
QSYYGGSAYT

SEQ ID 183: PD206F12 VH CDR1 aa
SGYWIC

SEQ ID 184: PD206F12 VH CDR2 aa
CIYAGTSGSTSYASWARG

SEQ ID 185: PD206F12 VH CDR3 aa
NLYTYNSL

SEQ ID 186: PD206F12 VL CDR1 aa
QSSQSVYDNNWLA

SEQ ID 187: PD206F12 VL CDR2 aa

TVSTLAS

SEQ ID 188: PD206F12 VL CDR3 aa
QGTYYSSGWNFA

SEQ ID 189: PD215A1 VH CDR1 aa
SSYWMC

SEQ ID 190: PD215A1 VH CDR2 aa
CITTGSGSTYYASWAKR

SEQ ID 191: PD215A1 VH CDR3 aa
AFDL

SEQ ID 192: PD215A1 VL CDR1 aa
QASQSIYSYLN

SEQ ID 193: PD215A1 VL CDR2 aa
GASNLAS

SEQ ID 194: PD215A1 VL CDR3 aa
QSSWLSGAVGNA

SEQ ID 195: PD220F6 VH CDR1 aa
SSYGVs

SEQ ID 196: PD220F6 VH CDR2 aa
LIFPGIGFKDYASWVNG

SEQ ID 197: PD220F6 VH CDR3 aa
DLDL

SEQ ID 198: PD220F6 VL CDR1 aa
QSSPSVYSNYLS

SEQ ID 199: PD220F6 VL CDR2 aa
YASTLAS

SEQ ID 200: PD220F6 VL CDR3 aa
AGGYSSSTRA

SEQ ID 201: PD225G11 VH CDR1 aa
SSHWIC

SEQ ID 202: PD225G11 VH CDR2 aa
CIYTGSIDVFYYASWAKG

SEQ ID 203: PD225G11 VH CDR3 aa
AANTDTTYFNL

SEQ ID 204: PD225G11 VL CDR1 aa
QASQSINNQLS

SEQ ID 205: PD225G11 VL CDR2 aa
GASTLAS

SEQ ID 206: PD225G11 VL CDR3 aa
HVHYCSGGSCFWA

CDR Sequences for anti-CTLA4, anti-PD-1 and anti-PD-L1						
mAb	Target	VH			VL	
		CDR 1	CDR 2	CDR 3	CDR 1	CDR 2
CT4	CTLA4	SSYTMH Seq ID 141	FISYDGNKKYADSVKG Seq ID 142	TGWLGPFDY Seq ID 143	RASQSVGSSVLA Seq ID 144	GAFSRAT Seq ID 145
		NTYDMI Seq ID 147	IITYSGSRYANWAKG Seq ID 148	DYMSGSHL Seq ID 149	QASEDIYSFLA Seq ID 150	SASSLAS Seq ID 151
PL230C6	PD-L1	SSYAMS Seq ID 153	YIGDTTGIAYASWANG Seq ID 154	GWSYLDI Seq ID 155	QASQNIYSNLA Seq ID 156	QASTLAS Seq ID 157
PD224D1	PD-1	SGYDMC Seq ID 159	CIAAGSAGITYDANWAKG Seq ID 160	SAFSFDYAMD Seq ID 161	QASQSISSHLN Seq ID 162	KASTLAS Seq ID 163
PL221G5	PD-L1	STYDMI Seq ID 165	IISYVGNTYYASWAKG Seq ID 166	DFISGSHL Seq ID 167	QASESISSFLS Seq ID 168	SASTLAS Seq ID 169
PL231H2	PD-L1	SSYWMS Seq ID 171	VIDTNVYIYANWAKG Seq ID 172	YVGNNDDYINL Seq ID 173	QSSQSVYNGWLS Seq ID 174	GASTLAS Seq ID 175
PL004B5	PD-L1	SVINMG Seq ID 177	TTITYVGNTYYASWAKG Seq ID 178	ESGTIYYSYFNL Seq ID 179	QASESISNYLS Seq ID 180	YASNLAS Seq ID 181
PL004B9	PD-L1	SGYWIC Seq ID 183	CIYAGTSGSTSYASWARG Seq ID 184	NLYTYNSL Seq ID 185	QSSQSVYDNNWLA Seq ID 186	TVSTLAS Seq ID 187
PD206F12	PD-1	SSYWMC Seq ID 189	CITTGSGSTYYASWAKR Seq ID 190	AFDL Seq ID 191	QASQSIYSYLN Seq ID 192	GASNLAS Seq ID 193
PD215A1	PD-1	SSYGVS Seq ID 195	LIFPGIGFKDYASWVNG Seq ID 196	DLDL Seq ID 197	QSSPSVYSNYLS Seq ID 198	YASTLAS Seq ID 199
PD220F6	PD-1	SSHVIC Seq ID 201	CIYTGSIDVFYYASWAKG Seq ID 202	AANTDTTYFNL Seq ID 203	QASQSINNQLS Seq ID 204	GASTLAS Seq ID 205
PD225G11	PD-1					HVHYCSGGSCFWA Seq ID 206