

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, pazopanib, 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 be 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	PD215A1 Light Chain nucleotide
56	PD215A1 Light Chain amino acid
57	PD220F6 x CT4 nucleotide
58	PD220F6 x CT4 amino acid
59	PD220F6 Light 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
 CCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGAT
 GGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCT
 GCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACT
 GGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAG
 AGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTC
 AGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGA
 CCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAG
 AGAGTTGAGCCCAATCTTGTGACAAAACCTCACACATGCCCACCGTGGCCAGCACCTGAAGCCGCGGGGGCACCGTCAGT
 CTTCTCTTCCCCCAAAACCCAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGA
 GCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAGCCGCGGGAG
 GAGCAGTACAACAGCAGTACCGTGTGGTCAGCGTCTCACCCTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAA
 GTGCGCGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCAC
 AGGTGTACACCCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTAT
 CCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTC
 CGACGGCTCCTTCTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCG

TGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGT
 GGTGGATCCGAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAGC
 CTCTGGATTCTCCCTCAGTAGCTATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTACATCGGCTACA
 TTGGTGATACTACTGGCATAGCCTACGCGAGCTGGGCGAATGGCAGATTACCATCTCAAAGACAATACCAAGAACACG
 GTGGATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGCTGGTCTACTTAGACAT
 CTGGGGCCAAGGGACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCG
 GTGGAGGCGGCTCTGCCCTTGTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT
 TGCCAGGCCAGTCAGAACATTTACAGCAATTTAGCCTGGTATCAGCAGAAACCAGGAAAGTTCTTAAGCTCCTGATCTA
 TCAGGCCTCCACTCTGGCATCTGGGGTCCCATCTCGGTTCAAGTGGCAGTGGATATGGGACAGATTTCACTCTCACCATCA
 GCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCAAGGCGGTTATTATAGTGCTGCCCTTAATACTTTTCGGCGGA
 GGGACCAAGGTGGAGATCAAA

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

QVQLVESGGGVVQPGRLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNKKYYADSVKGRFTI
 SRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGT
 AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNT
 KVDKRVEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVY
 TLPSSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQ
 GNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCTASGFSLSYA
MSWVRQAPGKLEYIGYIGDTTGIAYASWANGRFTISKDNTKNTVDLQMNSLRAEDTAVYYCARGWSYLD
IWGQGLTVTVSSGGGGSGGGGSGGGGSGGGGSALVMTQSPSSLSASVGRVTITCQASQNIYSNLAWYQQ
 KPGKVPKLLIYQASTLASGVPSRFSGSGYGTDFTLTISLQPEDVATYYCQGGYYSAALNTFGGGTKVEI
 K

SEQ ID 03: CT4 kappa light chain nt

GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAAGAGCCACCCTCTCCTGCA
 GGGCCAGTCAGAGTGTGGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCT
 CCTCATCTATGGTGCATTCAGCAGGGCCACTGGCATCCCAGACAGGTTCAAGTGGCAGTGGGTCTGGGACA
 GACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTA
 GCTCACCGTGGACGTTTCGGCCAAGGGACCAAGGTGGAAATCAAA
 CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCT
 CTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCT
 CCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGC
 ACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCC
 TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID 04: CT4 kappa light chain aa

EIVLTQSPGTLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGT
 DFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNF
 YPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKADYEEKHKVYACEVTHQGLSSPVTKSF
 NRGEC

SEQ ID 05: CT4 x PL230C6 nt

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAG
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TCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATAT
 ATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTC
 CTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACA
 GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGGCGCCC
 TGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGT
 GACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC
 AAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCCCACCGTGCCCAGCACCTG
 AAGCCGCGGGGGCACCGTCAGTCTTCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGAC
 CCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTG
 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
 TCAGCGTCTCACCCTGCTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGCGGTCTCCAACAA
 AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
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 GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCC
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 ATCTGGGTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGTGGAATCATTACTTATAGTGGTAGTAGAT
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 AATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGATTATATGAGTGGTTCCAC
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 AGGAGACAGAGTCACCATCAAGTGTGAGGCCAGTGGAGACATTTATAGCTTCTTGGCCTGGTATCAGCAG
 AAACCAGGGAAAGCCCCCTAAGCTCCTGATCCATTCTGCATCCTCTCTGGCATCTGGGGTCCCATCAAGGT
 TCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAAC
 TTAATATTGTCAACAGGGTTATGGTAAAAATAATGTTGATAATGCTTTCGGCGGAGGGACCAAGGTGGAG
 ATCAAA

SEQ ID 06: CT4 x PL230C6 aa

QVQLVESGGGVVQPRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYYADSVKGRFTI
 SRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGT
 AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNT
 KVDKRVEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVY
 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ
 GNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQSVEESGGGLVQPGGSLRLSCTASGIDLNTYDM
 IWVRQAPGKGLEWVGIIITYSGSRYIANWAKGRFTISKDNKNTVYLQMNSLRAEDTAVYYCARDYMSGSH
 LWGQGLTVTVSSGGGGSGGGGSQSSAYDMTQSPSSVSASVGDRVTIKCQASEDIYSFLAWYQQ
 KPGKAPKLLIHSASSLASGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQQGYGKNVNDNAFGGGTKVE
 IK

SEQ ID 07: CT4 x PL221G5 null2 Fc nt

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAG
 CCTCTGGATTACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTG

GGTGACATTTATATCATATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTACCATC
TCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATAT
ATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTC
CTCAGCTAGCACCAAGGGGCCCATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCC
TGACCAGCGGCGTGACACACCTTCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGT
GACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC
AAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAACTCACACATGCCCACCGTGCCCAGCACCTG
AAGCCGCGGGGGCACCGTCAGTCTTCTCTTCCCCCAAACCCAAGGACACCTCATGATCTCCCGGAC
CCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
TCAGCGTCTCACCCTGCTGACCAAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGCGGTCTCCAACAA
AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
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ATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCCTCC
CGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
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TGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGAGGTGCAGCTGTTGGAGTCTGGGGGAGG
CTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCTCCTTCAGTAGCGGGTAC
GACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATTGCTGCTGGTAGTG
CTGGTATCACTTACGACGCGAACTGGGCGAAAGGCCGTTTACCATCTCCAGAGACAATTCCAAGAACAC
GCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGATCGGCGTTT
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CTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGACATCCAGATGACCCAGTCTCC
TTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCAGTCAGAGCATTAGTTCC
CACTTAACTGGTATCAGCAGAAACCAGGGAAGCCCCCTAAGCTCCTGATCTATAAGGCATCCACTCTGG
CATCTGGGGTCCCATCAAGGTTTACGCGGCAGTGGATCTGGGACAGAATTTACTCTCACCATCAGCAGCCT
GCAGCCTGATGATTTTGAACCTTATTACTGCCAACAGGGTTATAGTTGGGGTAATGTTGATAATGTTTTTC
GGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 08: CT4 x PL221G5 null Fc aa

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNKKYYADSVKGRFTI
SRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGT
AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNT
KVDKRVEPKSCDKHTHTCPPCPAPEAAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ
GNVFCSSVMHEALHNHYTQKSLSLSPGGGGSGGGGSEVQLLESGLVQPGGSLRLSCAASGFSFSSGY
DMCWVRQAPGKGLEWIACIAAGSAGITYDANWAKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARSAF
SFDYAMDLWGQGLTVTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSTLSASVGRVTITCQASQSISS
HLNWYQQKPGKAPKLLIYKASTLASGVPSRFSSGSGSGTEFTLTISSLQPDFATYYCQQGYSWGNVDNVF
GGGTKVEIK

SEQ ID 09: CT4 x PL231H2 nt

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAG
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 ATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTC
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 GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCC
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 GACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC
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 CATACTACGCGAGCTGGGCGAAAGGCCGATTACCCCTCTCCAAAGACAATACTCGACCACGGTGGATCT
 GCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGATTTTATTAGTGGTTCC
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 AACTTACTATTGTCAACAGGGTTATAGTAAAAGTAATGTGGATAATGCTTTCGGCGGAGGGACCAAGGTG
 GAGATCAAA

SEQ ID 10: CT4 x PL231H2 aa

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKLEWVTFISYDGN NKYYADSVKGRFTI
 SRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGT
 AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNT
 KVDKRVEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVY
 TLPSSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQ
 GNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQVQLVESGGGLVQPGGSLRLSCTTSGIDLSTYD
 MIWVRQAPGKLEWVGIIISYVGNITYYASWAKGRFTLSKDNTSTTVDLQMNSLRAEDTAVYYCARD FISGS
 HLWGQGLTVTVSSGGGGSGGGSGGGSGGGGSAYDMTQSPSSVSASVGDRTVINCQASES ISSFLSWYQ
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 EIK

SEQ ID 11: CT4 x PL004B5 nt

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAG
CCTCTGGATTACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTG
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CTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACA
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GACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC
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AAGCCGCGGGGACCGTCAGTCTTCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGAC
CCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
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AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
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TATACTACGCGAACTGGGCAAAGGCAGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCT
TCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGATATGTGGGTAATAATGAT
GATTATATTAACCTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAG
GTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGACATCCAGATGACCCAGTCTCCTTCCACCCT
GTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCAGTCAGAGTGTTTATAATGGCTACTGG
TTATCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGGTGCATCCACTCTGGCAT
CTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGAATTCCTCTCACCATCAGCAGCCTGCA
GCCTGATGATTTTGCAACTTATTACTGCCTAGGCAGTTATACTAGTAGTACTGAGAACTCTTTCGGCGGA
GGGACCAAGGTGGAGATCAAA

SEQ ID 12: CT4 x PL004B5 aa

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNKYYADSVKGRFTI
SRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGT
AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT
KVDKRVEPKSCDKHTHTCPPCPAPEAAAGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQ
GNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTLSSYW
MSWVRQAPGKGLEWIGVIDTNVYIYYANWAKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCARYVGNND
DYINLWGQGLTVTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQSPSTLSASVGRVITCQSSQSVYNGYW

LSWYQQKPGKAPKLLIYGASTLASGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCLGSYTSSTENSFGG
 GTKVEIK

SEQ ID 13: CT4 x PL004B9 nt

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAG
 CCTCTGGATTACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTG
 GGTGACATTTATATCATATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTACCATC
 TCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATAT
 ATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTC
 CTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACA
 GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGGCGCCC
 TGACCAGCGGCGTGACACCTTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGT
 GACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC
 AAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAACTCACACATGCCACCGTGCCAGCACCTG
 AAGCCGCGGGGGCACCGTCAGTCTTCTCTTCCCCCAAACCCAAGGACACCCCTCATGATCTCCCGGAC
 CCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
 TCAGCGTCTCACCCTGCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAA
 AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCT
 ATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCCTCC
 CGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
 GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCC
 TGTCTCCGGGTGGCGGTGGAGGTCCGGCGGTGGTGGATCAGAGGTGCAGCTGGTGGAGTCTGGGGGAGG
 CTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAGTGTCTGGAATCGACCTCAGTGTCAAT
 ATGGGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAACCATTAATTATGTTGGTAACA
 CATATTACGCGAGCTGGGCGAAAGGCAGATTACCATCTCCAAAACCTCGACCACGGTGGATCTTAAAAT
 CACCAGTCCGACAACCGAGGACACGGCTGTGTATTACTGTGCGAGAGAATCTGGTACTATTTATTACAGT
 TACTTTAACTTGTGGGGCCAAGGGACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTG
 GTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGCATTGCAATTGACCCAGTCTCCATCCTCCCTGTC
 TGCATCTGTAGGAGACAGAGTCACCATCAAGTGCCAGGCCAGTGAAAGCATTAGCAACTACTTATCCTGG
 TATCAGCAGATTCCAGGGAAAGTTCCTAAGCTCCTGATCTATTATGCATCCAATCTGGCATCTGGGGTCC
 CATCTCGGTTCAAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGA
 TGTTGCAACTTATTACTGTCAAAGCTATTATGGTGGTGGTAGTGCCTATACTTTCGGCGGAGGGACCAAG
 GTGGAGATCAAA

SEQ ID 14: CT4 x PL004B9 aa

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKLEWVTFISYDGNNNKYYADSVKGRFTI
SRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLVTVSSASTKGPSVFPLAPSSKSTSGGT
AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNT
KVDKRVEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQ
GNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCTVSGIDLSVIN
MGWVRQAPGKLEWIGTITYVGNTYYASWAKGRFTISKSTTTVDLKITSPPTTEDTAVYYCARESGTIYY

YFNLWGQGLTVTVSSGGGGSGGGSGGGSGGGGSAFELTQSPSSLSASVGDRVTIKCQASESISNYLSW
YQQIPGKVPKLLIYYASNLASGVPSRFSSGSGSGTDFTLTISSLQPEDVATYYCQSYYGGGSAYTFGGGTK
VEIK

SEQ ID 15: CT4 x PD206F12 nt

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAG
CCTCTGGATTACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTG
GGTGACATTTATATCATATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTACCATC
TCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATAT
ATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTC
CTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGGCGCCC
TGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGT
GACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC
AAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCCACCGTGCCACGACCTG
AAGCCGCGGGGGCACCGTCAGTCTTCTCTTCCCCCAAACCCAAGGACACCCCTCATGATCTCCCGGAC
CCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTG
GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
TCAGCGTCTCACCCTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAA
AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCT
ATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCC
CGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCC
TGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGAGGTGCAGCTGGTGGAGTCTGGGGGAGG
CTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTTCGACTTCAGTAGCGGCTAC
TGGATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTTGATCGCATGCATTTATGCTGGTACTA
GTGGTAGTACTTCTACGCGAGCTGGGCGAGAGGCAGATTACCATCTCCGAAACCTCCAAGAACACGGT
GACTCTTCAAATGAACAGCCTGAGAGCCGAGGACTCGGCTGTGTATTACTGTGCGAGAAATCTTTACACT
TACAATAGCTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTG
GTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGACATCCAGATGACCCAGTCTCCTTCCACCCTGTC
TGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCAGTCAGAGTGTTTATGATAACAACCTGGTTA
GCCTGGTATCAGCAGAAACCAGGGAAAGCCCTAAGCTCCTGATCTATACAGTATCCACTCTGGCATCTG
GGTCCCATCAAGGTTTACGCGCAGTGGATCTGGGACAGAATTCATCTCACCATCAGCAGCCTGCAGCC
TGATGATTTTGCAACTTATTACTGCCAAGGCACTTATTATAGTAGTGGTTGGAACCTTTGCTTTCGGCGGA
GGGACCAAGGTGGAGATCAAA

SEQ ID 16: CT4 x PD206F12 aa

QVQLVESGGGVVQPGPSLRRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYYADSVKGRFTI
SRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGT
AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
KVDKRVEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ
GNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCAASGFDSSGY

WICWVRQAPGKGLELIACIYAGTSGSTSYASWARGRFTISETSKNTVTLQMNSLRAEDSAVYYCARNLYT
YNSLWGQGTTLVTVSSGGGSGGGGSGGGGSGGGSDIQMTQSPSTLSASVGDRVITITCQSSQSVYDNNWL
AWYQQKPGKAPKLLIYTVSTLASGVPSRFSGSGSGTEFTLTISLQPDDEFATYYCQGTYYSSGWNFAFGG
 GTKVEIK

SEQ ID 17: CT4 x PD215A1 nt

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAG
 CCTCTGGATTCACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTG
 GGTGACATTTATATCATATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTCACCATC
 TCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATAT
 ATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTC
 CTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACA
 GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCC
 TGACCAGCGGCGTGACACCTTCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGT
 GACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC
 AAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAACTCACACATGCCACCGTGCCAGCACCTG
 AAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCTCATGATCTCCCGGAC
 CCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
 TCAGCGTCCCTCACCGTCTTGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAA
 AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCT
 ATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCCTCC
 CGTGCTGGACTCCGACGGCTCCTTCTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
 GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCC
 TGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCACAGGAGCAGCTGTTGGAGTCTGGGGGAGG
 CTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAGCCTCTGGATTCTCCTTTAGCAGCTACTGG
 ATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGATGCATTACGACTGGTAGTGGTA
 GCACTTACTACGCGAGCTGGGCGAAGCGCCGGTTACCATCTCCAAAGACAATCCAAGAACACGGTGAC
 TCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTACGAGAGCATTTGACTTGTGG
 GGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCG
 GCTCCGGTGGAGGCGGCTCTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGA
 CAGAGTCACCATCACTTGCCAGGCCAGTCAGAGCATTTACAGCTACTTAAACTGGTATCAGCAGAAACCA
 GGGAAAGCCCCTAAGCTCCTGATCTATGGTGCATCCAATCTGGCATCTGGGGTCCCATCAAGGTTTCAGTG
 GCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTTGCAACTTACTA
 CTGTCAAAGCAGTTGGTTGAGTGGTGTCTGTTGGTAATGCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 18: CT4 x PD215A1 aa

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKLEWVTFISYDGNNKYYADSVKGRFTI
 SRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGTTLVTVSSASTKGPSVFPLAPSSKSTSGGT
 AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
 KVDKRVEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVY
 TLPSPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ
 GNVFSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSQEQLLESGGGLVQPGGSLRLSCTASGFSSSYW

MCWVRQAPGKGLEWIGCITTGSGSTYYASWAKRRFTISKDNSKNTVTLQMNSLRAEDTAVYYCTRAFDLW
GQGTLVTVSSGGGSGGGGSGGGGSGGGSDIQMTQSPSSLSASVGDRVITITCQASQSIYSYLNWYQQKP
GKAPKLLIYGASNLASGVPSRFSSGSGSGTDFTLTISSLQPEDFATYYCQSSWLSGAVGNAFGGGTKVEIK

SEQ ID 19: CT4 x PD220F6 nt

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAG
 CCTCTGGATTACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTG
 GGTGACATTTATATCATATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTACCATC
 TCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATAT
 ATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTC
 CTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACA
 GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGGCGCCC
 TGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGT
 GACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC
 AAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCCACCGTGCCACGACCTG
 AAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCAAACCCAAGGACACCCCTCATGATCTCCCGGAC
 CCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTG
 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
 TCAGCGTCTCACCCTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAA
 AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCT
 ATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCC
 CGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
 GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCC
 TGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCACAGGAGCAGGTGAAGGAGACCGGGGGAGG
 CTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCATCAGCAGCTATGGA
 GTGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTGCGATTGATTTTTCCCGGGATTGGTT
 TCAAAGACTACGCGAGCTGGGTGAATGGCCGGTTCACCCTCTCCAGCGACAACGCCCAAGAACTGTGGA
 ACTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGAGATTTGGACTTGTGG
 GGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCG
 GCTCCGGTGGAGGCGGCTCTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGA
 CAGAGTCACCATCACTTGCCAGTCCAGTCCGAGTGTATATAGTAACCTACTTATCCTGGTATCAGCAGAAA
 CCAGGGAAAGTTCTAAGCTCCTGATCTATTATGCATCCACTCTGGCATCTGGGGTCCCATCTCGGTTCA
 GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTA
 TTAAGTGTGCAGGCGGTTATAGTAGTAGTACTCGTGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 20: CT4 x PD220F6 aa

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKLEWVTFISYDGNNKYYADSVKGRFTI
SRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFFDYWGQTLVTVSSASTKGPSVFPLAPSSKSTSGGT
AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNT
KVDKRVEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQ
GNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQEQVKETGGGLVQPGGSLRLSCAASGFTISSYG
VSWVRQAPGKLEWVALIFPGIGFKDYASWVNGRFTLSSDNAQNTVELQMNSLRAEDTAVYYCARDLDLW

GQGTLLVTVSSGGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVITITCQSSPSVYSNYLSWYQQK
 PGKVPKLLIYYASTLASGVPSRFSGSGSGTDFTLTISLQPEDVATYYCAGGYSSSTRAFGGGTKVEIK

SEQ ID 21: CT4 x PD225G11 nt

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAG
 CCTCTGGATTACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTG
 GGTGACATTTATATCATATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTACCATC
 TCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATAT
 ATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTC
 CTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACA
 GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCC
 TGACCAGCGGCGTGCACACCTTCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGT
 GACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC
 AAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAACTCACACATGCCACCGTGCCAGCACCTG
 AAGCCGCGGGGGCACCGTCAGTCTTCTCTTCCCCCAAACCCAAGGACACCCCTCATGATCTCCCGGAC
 CCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
 TCAGCGTCTCACCCTGCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAA
 AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCT
 ATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCCTCC
 CGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
 GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCC
 TGTCTCCGGGTGGCGGTGGAGGTCCGGCGGTGGTGGATCAGAGGTGCAGCTGTTGGAGTCTGGGGGAGG
 CTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTTAGCAGCAGCCAC
 TGGATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATTTATACTGGTAGTA
 TTGATGTCTTTTACTACGCGAGCTGGGCGAAAGGCCGTTTACCATCTCCAGAGACAATTCCAAGAACAC
 GCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGAGCCGCTAAT
 ACTGATACTACCTACTTTAACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGAT
 CTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGCCTATGATATGACCCAGTCTCC
 ATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAGGCCAGTCAGAGCATTAACAAC
 CAACTATCCTGGTATCAGCAGAAACCAGGGAAGTTCCTAAGCTCCTGATCTATGGTGCATCCACTCTGG
 CATCTGGGGTCCCATCTCGGTTTACCAGGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCT
 GCAGCCTGAAGATGTTGCAACTTATTACTGTCATGTTTATTATTGCAGTGGTGGTAGTTGTTTTTGGGCT
 TTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 22: CT4 x PD225G11 aa

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNNKYYADSVKGRFTI
 SRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGTLLVTVSSASTKGPSVFPLAPSSKSTSGGT
 AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNT
 KVDKRVEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVY
 TLPSSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQ
 GNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSEVQLLESGLLVQPGGSLRLSCAASGFTFSSSH
WICWVRQAPGKGLEWIACIYTGSIDVFYASWAKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARAA

TDDTTYFNLWGQGLVTVSSGGGSGGGGSGGGGSGGGGSAYDMTQSPSSLSASVGDRVTINCQASQSINN
QLSWYQQKPGKVPKLLIYGASTLASGVPSRFTGSGSGTDFTLTISSLQPEDVATYYCHVHYCSGGSCFWA
FGGGTKVEIK

SEQ ID 23: G4S x 4 nt

GGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCT

SEQ ID 24: G4S x 4 aa

GGGSGGGGSGGGGSGGGGS

SEQ ID 25: PL230C6 x CT4 nt

CAGTCGGTGGAGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACCGCCT
CTGGAATCGACCTTAATACCTACGACATGATCTGGGTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGT
TGGAATCATTACTTATAGTGGTAGTAGATACTACGCGAACTGGGCGAAAGGCCGATTACCATCTCCAAA
GACAATACCAAGAACACGGTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACT
GTGCGAGAGATTATATGAGTGGTTCCTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGCTAG
CACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTG
GGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCCTGACCAGCG
GCGTGACACCTTCCCGGTGTCTTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC
CTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGAC
AAGAGAGTTGAGCCCAAATCTTGTGACAAACTCACACATGCCACCGTGCCAGCACCTGAAGCCGCGG
GGGCACCGTCAGTCTTCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGT
CACATGCGTGGTGGTGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTG
GAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCC
TCACCGTCTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCC
AGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCC
CCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCG
ACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTGGA
CTCCGACGGCTCCTTCTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC
TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGG
GTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGTCCA
GCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATACTATGCACTGG
GTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACAATAAATACT
ACGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATCCAAGAACACGCTGTATCTGCAAAT
GAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGTGGCTGGGGCCCTTTGAC
TACTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGTTTACGGCGGAGGTGGAAGTGGTG
GTGGCGGCTCTGGAGGCGGCGGATCTGAAATTGTGTGACGAGTCTCCAGGCACCCTGTCTTTGTCTCC
AGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTGGCAGCAGCTACTTAGCCTGGTACCAG
CAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATTACAGCAGGGCCACTGGCATCCCAGACA
GGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGC
AGTGTATTACTGTCAGCAGTATGGTAGCTCACCGTGGACGTTTCGGCCAAGGGACCAAGGTGGAAATCAAA

SEQ ID 26: PL230C6 x CT4 aa

QSVEESGGGLVQPGGSLRLSCTASGIDLNTYDMIWVRQAPGKGLEWVGIIITYSGSRYANWAKGRFTISK
 DNTKNTVYLQMNLSRAEDTAVYYCARDYMSGSHLWGQGT LVT VSSASTKGPSVFPLAPSSKSTSGGTAAL
 GCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVD
 KRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGV
 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTL P
 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV
 FSCSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSQVQLVESGGGVVQPGRSRLRLSCAASGFTFSSYTMHW
 VRQAPGKGLEWVTFISYDGN NKYYADSVKGRFTISRDN SKNTLYLQMNLSRAEDTAIYYCARTGWLGPFD
 YWGQGT LVT VSSGGGGSGGGGSGGGGSGGGGSEIVLTQSPGTL SLSLSPGERATLSCRASQSVGSSYLAWYQ
 QKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK

SEQ ID 27: PL230C6 kappa light chain nt

GCCTATGATATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCAAGTGTC
 AGGCCAGTGAGGACATTTATAGCTTCTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT
 GATCCATTCTGCATCCTCTCTGGCATCTGGGGTCCCATCAAGGTT CAGCGGCAGTGGATCTGGGACAGAT
 TTTACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGGTTATGGTA
 AAAATAATGTTGATAATGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA
 CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCT
 CTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCT
 CCAATCGGGTA ACTCCCAGGAGAGTGT CACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGC
 ACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCC
 TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID 28: PL230C6 kappa light chain aa

AYDMTQSPSSVSASVGDRTIKCQASEDIYSFLAWYQQKPGKAPKLLIHSASSLASGVPSRFSGSGSGTD
 FTLTISSLQPEDFATYYCQQGYGKNVDNAFGGGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVCLLN
 NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTK
 SFNRGEC

SEQ ID 29: PD224D1 x CT4 nt

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAG
 CCTCTGGATTCTCCCTCAGTAGCTATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTA
 CATCGGCTACATTGGTGATACTACTGGCATAGCCTACGCGAGCTGGGCGAATGGCAGATTACCATCTCC
 AAAGACAATACCAAGAACACGGTGGATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATT
 ACTGTGCGAGAGGCTGGTCTTACTTAGACATCTGGGGCCAAGGGACCCTGGTCACCGTCTCGAGCGCTAG
 CACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTG
 GGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAAGTCAAGCGCCCTGACCAGCG
 GCGTGACACACTTCCCCGGCTGTCCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC
 CTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGAC
 AAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCCACCGTGCCAGCACCTGAAGCCGCGG
 GGGACCGTCACTCTTCTCTTCCCCCAAAACCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGT
 CACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTG
 GAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCC
 TCACCGTCTGACACAGGACTGGCTGAATGGCAAGGAGTACAAGTGC GCGGTCTCCAACAAAGCCCTCCC

AGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCC
 CCATCCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCG
 ACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGA
 CTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC
 TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGG
 GTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCCAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGTCCA
 GCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATACTATGCACTGG
 GTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACAATAAATACT
 ACGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAAT
 GAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGAC
 TACTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCGGGCG
 GTGGCGGCTCCGGTGGAGGCGGTTCTGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCC
 AGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTGGCAGCAGCTACTTAGCCTGGTACCAG
 CAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATTACAGCAGGGCCACTGGCATCCCAGACA
 GGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGC
 AGTGTATTACTGTCAGCAGTATGGTAGCTCACCGTGGACGTTTCGGCCAAGGGACCAAGGTGGAAATCAAA

SEQ ID 30: PD224D1 x CT4 aa

EVQLVESGGGLVQPGGSLRLSCTASGFSLSYAMSWVRQAPGKLEYIGYIGDITGIIAYASWANGRFTIS
 KDNTKNTVDLQMNSLRAEDTAVYYCARGWSYLDIWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAAL
 GCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVD
 KRVEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGV
 EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLTP
 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV
 FSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHW
 VRQAPGKGLEWVTFISYDGNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCARTGWLGPFD
 YWGQGLTVTVSSGGGGSGGGSGGGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVGSSYLAWYQ
 QKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEIK

SEQ ID 31: PD224 light chain nt

GCCCTTGTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCC
 AGGCCAGTCAGAACATTTACAGCAATTTAGCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCT
 GATCTATCAGGCCTCCACTCTGGCATCTGGGGTCCCATCTCGGTTTCAGTGGCAGTGGATATGGGACAGAT
 TTCCTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCAAGGCGGTTATTATA
 GTGCTGCCCTTAATACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA
 CGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCT
 CTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCT
 CCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGC
 ACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCC
 TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID 32: PD224 light chain aa

ALVMTQSPSSLSASVGRVITTCQASQNIYSNLAWYQQKPGKVPKLLIYQASTLASGVPSRFSGSGYGTD
 FTLTISSLQPEDVATYYCQGGYYSAAALNTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNN

FYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKS
FNRGEC

SEQ ID 33: PL221G5 x CT4 null Fc nt

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAG
CCTCTGGATTCTCCTTCAGTAGCGGGTACGACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGA
GTGGATCGCATGCATTGCTGCTGGTAGTGCTGGTATCACTTACGACGCGAACTGGGCGAAAGGCCGGTTC
ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGG
CCGTATATTACTGTGCGAGATCGGCGTTTTTCGTTGACTACGCCATGGACCTCTGGGGCCAGGGAACCCCT
GGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACC
TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGA
ACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCT
CAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAG
CCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCCAATCTTGTGACAAAACCTCACACATGCCACCGT
GCCCAGCACCTGAAGCCGCGGGGGGCACCGTCAGTCTTCTCTTCCCCCCTTCCCAAGGACACCCCTCAT
GATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC
AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCA
CGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGC
GGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAA
CCACAGGTGTACACCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGACCTGCCTGG
TCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAATACTACAA
GACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGC
AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGA
AGAGCCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCCAGGTGCAATTGGTGGA
GTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTC
AGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCAT
ATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTACCACATCTCCAGAGACAATTCCAA
GAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACC
GGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGAT
CTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGTCTGAAATTGTGTTGACGCAGTCTCC
AGGCACCCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTGGCAGC
AGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATTACAGCA
GGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAG
ACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCACCGTGGACGTTCGGCCAA
GGGACCAAGGTGGAAATCAAA

SEQ ID 34: PL221G5 x CT4 null Fc aa

EVQLLESGLVQPGGSLRLSCAASGFSFSSGYDMCWVRQAPGKGLEWIAACIAAGSAGITYDANWAKGRF
TISRDN SKNTLYLQMN SLRAEDTAVYYCARSAFSFDYAMD LWGQGLVTVSSASTKGPSVFPLAPSSKST
SGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
PSNTKVDKRVEPKSCDKHTCTPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF
NWWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPRE
PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS
RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQVQLVESGGGVVQPGRSLRLSCAASGFTF

SSYTMHWVRQAPGKGLEWVTFISYDGNKNKYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCART
GWLGPFDYWGQGLTVTVSSGGGSGGGGSGGGGSGGGSEIVLTQSPGTLSPGERATLSCRASQSVGS
SYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWF
FGQ
GTKVEIK

SEQ ID 35: PL221G5 Light Chain nt

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCC
AGGCCAGTCAGAGCATTAGTTCCCACTTAAACTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT
GATCTATAAGGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTCAGCGGCAGTGGATCTGGGACAGAA
TTTACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAACAGGGTTATAGTT
GGGGTAATGTTGATAATGTTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATC
TGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGTGCCTGCTGAAT
AACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGG
AGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGC
AGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAG
AGCTTCAACAGGGGAGAGTGT

SEQ ID 36: PL221G5 Light Chain aa

DIQMTQSPSTLSASVGDRVTITCQASQSISSHLNWYQQKPGKAPKLLIYKASTLASGVPSRFSGSGSGTE
FTLTISSLPDDFATYYCQQGYSWGNVDNVFGGGKVEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLN
NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTK
SFNRGEC

SEQ ID 37: PL231H2 x CT4 null Fc nt

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGGGCTCCCTGAGACTCTCCTGTACAA
CTTCTGGAATCGACCTTAGTACCTACGACATGATCTGGGTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTG
GGTGGGAATCATTAGTTATGTTGGTAACACATACTACGCGAGCTGGGCGAAAGGCCGATTACCCCTCTCC
AAAGACAATACCTCGACCACGGTGGATCTGCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATT
ACTGTGCGAGAGATTTTATTAGTGGTTCCCACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGC
TAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCC
CTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAACCTCAGGCGCCCTGACCA
GCGGCGTGCACACCTTCCCGGCTGTCTTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGT
GCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG
GACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAAGCCG
CGGGGGCACCGTCAGTCTTCTCTTCCCCCAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGA
GGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
GTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCG
TCCTCACCGTCTTGACACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCT
CCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG
CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA
GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGCT
GGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAC
GTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTC
CGGGTGGCGGTGGAGGGTCCGCGGTGGTGGATCCCAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGT

CCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATACTATGCAC
 TGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACAATAAAT
 ACTACGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCA
 AATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTT
 GACTACTGGGGCCAGGGAACCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCG
 GCGGTGGCGGCTCCGGTGGAGGCGGTTCTGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTC
 TCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTGGCAGCAGCTACTTAGCCTGGTAC
 CAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATTACAGCAGGGCCACTGGCATCCCAG
 ACAGGTTCACTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTT
 TGCAGTGTATTACTGTCAGCAGTATGGTAGCTCACCGTGGACGTTTCGGCCAAGGGACCAAGGTGGAAATC
 AAA

SEQ ID 38: PL231H2 x CT4 null Fc aa

QVQLVESGGGLVQPGGSLRLSCTTSGIDLSTYDMIWVRQAPGKGLEWVGIIISYVGNTYYASWAKGRFTLS
 KDNTSTTVDLQMNSLRAEDTAVYYCARDFISGSHLWGQTLVTVSSASTKGPSVFPLAPSSKSTSGGTAA
 LGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKV
 DKRVEPKSCDKHTHTCPPCPAPEAAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG
 VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTL
 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGN
 VFSCSVMEALHNHYTQKSLSLSPGGGGSGGGGSQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMH
 WVRQAPGKGLEWVTFISYDGNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPF
DYWGQTLVTVSSGGGGSGGGSGGGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVGSSYLAWY
 QQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKVEI
 K

SEQ ID 39: PL231H2 Light Chain nt

GCCTATGATATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGTC
 AGGCCAGTGAGAGCATTAGTAGCTTCTTATCCTGGTATCAGCAGAAACCAGGGAAAGCCCTAAGCTCCT
 GATCTTTTCTGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTACGCGGCAGTGGATCTGGGACAGAT
 TTAATCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGGTTATAGTA
 AAAGTAATGTGGATAATGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATC
 TGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAAT
 AACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGG
 AGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGC
 AGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAG
 AGCTTCAACAGGGGAGAGTGT

SEQ ID 40: PL231H2 Light Chain aa

AYDMTQSPSSVSASVGDRTVINCQASESISSEFLSWYQQKPGKAPKLLIFASATLASGVPSRFSGSGSGTD
 FTLTIISSLPEDFATYYCQQGYSKSNVDNAFGGGTKVEIKRTVAAPSVFIFFPSDEQLKSGTASVCLLN
 NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTK
 SFNRGEC

SEQ ID 41: PL004B5 x CT4 nt

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAG
 CCTCTGGATTCTCCCTCAGTAGCTACTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTG
 GATCGGAGTCATTGATACTAATGTTTATATATACTACGCGAACTGGGCAAAAGGCAGATTCACCATCTCC
 AGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATT
 ACTGTGCGAGATATGTGGTAATAATGATGATTATATTAACCTTGTGGGGCCAGGGAACCCCTGGTCACCGT
 CTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGC
 ACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACCTCAGGCG
 CCCTGACCAGCGGCGTGACACCTTCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGT
 GGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAAC
 ACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCCACCGTGCCAGCAC
 CTGAAGCCGCGGGGGCACCGTCAGTCTTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCG
 GACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
 GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTG
 TGGTCAGCGTCTCACCCTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAA
 CAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTG
 TACACCCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCT
 TCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAAACAACCTACAAGACCACGCC
 TCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCCTGGACAAGAGCAGGTGGCAG
 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCT
 CCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCCAGGTGCAATTGGTGGAGTCTGGGGG
 AGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTAT
 ACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAA
 ACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAAGAACACGCT
 GTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTG
 GGGCCCTTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAG
 GTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGTTCTGAAATTGTGTTGACGCAGTCTCCAGGCACCCCT
 GTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTGGCAGCAGCTACTTA
 GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATTACAGCAGGGCCACTG
 GCATCCCAGACAGGTTCACTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCC
 TGAAGATTTTGAGTGTATTACTGTCAGCAGTATGGTAGCTCACCGTGGACGTTCCGCCAAGGGACCAAG
 GTGGAAATCAAA

SEQ ID 42: PL004B5 x CT4 aa

EVQLVESGGGLVQPGGSLRLSCAASGFSLSYWMSWVRQAPGKGLEWIGVIDTNVYIYYANWAKGRFTIS
 RDNSKNTLYLQMNSLRAEDTAVYYCARYVGNNDYINLWGQGLVTVSSASTKGPSVFPLAPSSKSTSGG
 TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSN
 TKVDKRVPEKSCDKHTCPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQV
 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQ
 QGNVVFSCVMHEALHNHYTQKSLSLSPGGGGSGGGGSQVQLVESGGGVVQPGRSRLSCAASGFTFSSY
 TMHWVRQAPGKGLEWVTFISYDGNNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAIYYCARTGWL
 GPFIDYWGQGLVTVSSGGGGSGGGSGGGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVGSSYL
 AWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWFVFGQGTK
 VEIK

SEQ ID 43: PL004B5 Light Chain nt

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCC
AGTCCAGTCAGAGTGTTTATAATGGCTACTGGTTATCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAA
GCTCCTGATCTATGGTGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGG
ACAGAATTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCTAGGCAGTT
ATACTAGTAGTACTGAGAACTCTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACC
ATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTG
AATAACTTCTATCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCC
AGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAA
AGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACA
AAGAGCTTCAACAGGGGAGAGTGT

SEQ ID 44: PL004B5 Light Chain aa

DIQMTQSPSTLSASVGDRTITCQSSQSVYNGYWLSWYQQKPGKAPKLLIYGASTLASGVPSRFSGSGSG
TEFTLTISLQPDDEFATYYCLGSYTSSTENSFGGGTKVEIKRTVAAPSVFI FPPSDEQLKSGTASVCLL
NNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVT
KSFNRGEC

SEQ ID 45: PL004B9 x CT4 nt

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAG
TGTCTGGAATCGACCTCAGTGTCAATATGGGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTG
GATCGGAACCATTACTTATGTTGGTAACACATATTACGCGAGCTGGGCGAAAGGCAGATTACCATCTCC
AAAACCTCGACCACGGTGGATCTTAAAATCACCAGTCCGACAACCGAGGACACGGCTGTGTATTACTGTG
CGAGAGAATCTGGTACTATTTATTACAGTTACTTTAACTTGTGGGGCCAAGGGACCCTGGTCACCGTCTC
GAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGGAAGTCAAGCGCCC
TGACCAGCGGCGTGCACACCTTCCCGGTGTCTTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGT
GACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC
AAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAACTCACACATGCCCCACCGTGCCAGCACCTG
AAGCCGCGGGGGCACCGTCAGTCTTCTCTTCCCCCAAAACCCAAGGACACCCCTCATGATCTCCCGGAC
CCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
TCAGCGTCTCACCCTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGCGTCTCCAACAA
AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCT
ATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACTACAAGACCACGCCTCC
CGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCC
TGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCCAGGTGCAATTGGTGGAGTCTGGGGGAGG
CGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATACT
ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACA
ATAAATACTACGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTA
TCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTGGGG
CCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTG

GTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGTTCTGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTC
 TTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTGGCAGCAGCTACTTAGCC
 TGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATTACAGCAGGGCCACTGGCA
 TCCCAGACAGGTTTCACTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGA
 AGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCACCGTGGACGTTTCGGCCAAGGGACCAAGGTG
 GAAATCAAA

SEQ ID 46: PL004B9 x CT4 aa

EVQLVESGGGLVQPGGSLRLSCTVSGIDLSVINMGWVRQAPGKGLEWIGTITYVGNTYYASWAKGRFTIS
 KTSTTVDLKITSPTTEDTAVYYCARESGTIYYSYFNLWGQGLVTVSSASTKGPSVFPLAPSSKSTSGGT
 AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
 KVDKRVEPKSCDKHTHTCPPCPAPEAAAGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYV
 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVY
 TLPSSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ
 GNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQVQLVESGGGVVQPGPSLRSLSCAASGFTFSSYT
 MHWVRQAPGKGLEWVTFISYDGNKYYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAIYYCARTGWLG
 PFDYWGQGLVTVSSGGGGSGGGSGGGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVGSSYLA
 WYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKV
 EIK

SEQ ID 47: PL004B9 Light Chain nt

GCATTGGAATTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAAGTGCC
 AGGCCAGTGAAAGCATTAGCAACTACTTATCCTGGTATCAGCAGATTCCAGGGAAAGTTCCTAAGCTCCT
 GATCTATTATGCATCCAATCTGGCATCTGGGGTCCCATCTCGGTTCACTGGCAGTGGATCTGGGACAGAT
 TTTACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCAAAGCTATTATGGTG
 GTGGTAGTGCCTATACTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGT
 CTTTCATCTTCCC GCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAAC
 TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGA
 GTGTACACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGA
 CTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGC
 TTCAACAGGGGAGAGTGT

SEQ ID 48: PL004B9 Light Chain aa

AFELTQSPSSLSASVGDRVTIKQASESISNYLSWYQQIPGKVPKLLIYYASNLASGVPSRFSGSGSGTD
 FTLTISLQPEDVATYYCQSYYGGSAYTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNN
 FYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKS
 FNRGEC

SEQ ID 49: PD206F12 x CT4 nt

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAG
 CCTCTGGATTCGACTTCAGTAGCGGCTACTGGATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGA
 GTTGATCGCATGCATTTATGCTGGTACTAGTGGTAGTACTTCTACGCGAGCTGGGCGAGAGGCAGATTC
 ACCATCTCCGAAACCTCCAAGAACACGGTGACTCTTCAAATGAACAGCCTGAGAGCCGAGGACTCGGCTG

TGTATTACTGTGCGAGAAATCTTTACACTTACAATAGCTTGTGGGGCCAGGGAACCCTGGTCACCGTCTC
GAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCC
TGACCAGCGGCGTGACACCTTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGT
GACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC
AAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTG
AAGCCGCGGGGGCACCGTCAGTCTTCCCTCTTCCCCCAAACCCAAGGACACCCCTCATGATCTCCCGGAC
CCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
TCAGCGTCTCTACCGTCTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAA
AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCT
ATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCC
CGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG
GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCC
TGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCAGGTGCAATTGGTGGAGTCTGGGGGAGG
CGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATACT
ATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACA
ATAAATACTACGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTA
TCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGTGGCTGGGG
CCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTG
GTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGTTCTGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTC
TTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTGGCAGCAGCTACTTAGCC
TGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATTACAGCAGGGCCACTGGCA
TCCCAGACAGGTTTCAAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGA
AGATTTTGCAGTGTATTACTGTGAGCAGTATGGTAGCTCACCGTGGACGTTTCGGCCAAGGGACCAAGGTG
GAAATCAAA

SEQ ID 50: PD206F12 x CT4 aa

EVQLVESGGGLVQPGLSLRLSCAASGFDSSGYWICWVRQAPGKGLLELIACIYAGTSGSTSYASWARGRF
TISETSKNTVTLQMNSLRAEDSAVYYCARNLYTNSLWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGT
AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
KVDKRVEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ
GNVFSCSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYT
MHWVRQAPGKGLEWVTFISYDGNKYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAIYYCARTGWLG
PFDYWGQGLTVTVSSGGGGSGGGSGGGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVGSSYLA
WYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPWTFGQGTKV
EIK

SEQ ID 51: PD206F12 Light Chain nt

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCC
AGTCCAGTCAGAGTGTTTATGATAACAACCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAA

GCTCCTGATCTATACAGTATCCACTCTGGCATCTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGG
ACAGAATTCACCTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAAGGCACTT
ATTATAGTAGTGGTTGGAACCTTTGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGC
ACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTG
CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAACT
CCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAG
CAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTC
ACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID 52: PD206F12 Light Chain aa

DIQMTQSPSTLSASVGRVITTCQSSQSVYDNNWLAWYQQKPGKAPKLLIYTVSTLASGVPSRFSGSGSG
TEFTLTISLQPDDEFATYYCQGTYYSSGWNFAFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCL
LNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSSLTLSKADYEKHKVYACEVTHQGLSSPV
TKSFNRGEC

SEQ ID 53: PD215A1 x CT4 nt

CAGGAGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAG
CCTCTGGATTCTCCTTTAGCAGCTACTGGATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTG
GATCGGATGCATTACGACTGGTAGTGGTAGCACTTACTACGCGAGCTGGGCGAAGCGCCGGTTCACCATC
TCCAAAGACAATTCCAAGAACACGGTGACTCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTAT
ATTACTGTACGAGAGCATTTGACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCAA
GGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGC
CTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAAGTCAAGGCGCCCTGACCAGCGGCGTGC
ACACCTTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG
CAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGA
GTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAAGCCGCGGGGGCAC
CGTCAGTCTTCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACATG
CGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTG
CATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCG
TCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCCAGCCCC
CATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC
CGGGATGAGCTGACCAAGAACCAGGTACGCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCG
CCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAACTACAAGACCACGCCTCCCGTGCTGGACTCCGA
CGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA
TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTGGCG
GTGGAGGGTCCGGCGGTGGTGGATCCCAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGG
GAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATACTATGCACTGGGTCCGC
CAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACAATAAATACTACGCAG
ACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAG
CCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGG
GGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCG
GCTCCGGTGGAGGCGGTCTGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGA
AAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTGGCAGCAGCTACTTAGCCTGGTACCAGCAGAAA
CCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATTACAGCAGGGCCACTGGCATCCCAGACAGGTTCA

GTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTA
TTACTGTCAGCAGTATGGTAGCTCACCGTGGACGTTCGGCCAAGGGACCAAGGTGGAATCAAA

SEQ ID 54: PD215A1 x CT4 aa

QEQLLES~~GGGLVQPGGSLRLSCTASGFSF~~SSYWMCWVRQAPGKGLEWIGCITTGSGSTYYASWAKRRFTI
SKDNSKNTVTLQMNSLRAEDTAVYYCTRA~~FDL~~WGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC
LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKR
VEPKSCDKHTCTPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV
HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
CSVMHEALHNHYTQKSLSLSPGGGGGSGGGGSQVQLVESGGGVVQPGRSLRLSCAASGFTF~~SSY~~TMHWVR
QAPGKGLEWVTFISYDGNKYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYW
GQGLTVTVSSGGGGSGGGSGGGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVGSSYLAWYQQK
PGQAPRLLIYGA~~FSRAT~~GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQ~~QY~~GSSPWF~~FGQGT~~KVEIK

SEQ ID 55: PD215A1 Light Chain nt

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCC
AGGCCAGTCAGAGCATTTACAGCTACTTAACTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT
GATCTATGGTGCATCCAATCTGGCATCTGGGGTCCCATCAAGGTTCAAGTGGCAGTGGATCTGGGACAGAT
TTCATCTCACCATCAGCAGTCTGCAACCTGAAGATTTTGCAACTTACTACTGTCAAAGCAGTTGGTTGA
GTGGTGCTGTTGGTAATGCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATC
TGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGTGCCTGCTGAAT
AACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGG
AGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGC
AGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAG
AGCTTCAACAGGGGAGAGTGT

SEQ IF 56: PD215A1 Light Chain aa

DIQMTQSPSSLSASVGDRVTITCQASQSIYSYLNWYQQKPGKAPKLLIYGASNLASGVPSRFSGSGSGTD
FTLTIS~~SLQPEDFATYYCQSSWLSGAVGNA~~FGGGTKVEIKRTVAAPSVFI~~FPPSDEQLKSGTASV~~VCLLN
NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTK
SFNRGEC

SEQ ID 57: PD220F6 x CT4 nt

CAGGAGCAGGTGAAGGAGACCGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGAGACTCTCCTGTGCAG
CCTCTGGATTACCATCAGCAGCTATGGAGTGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGCTGGAGTG
GGTCGCATTGATTTTTCCCGGGATTGGTTTCAAAGACTACGCGAGCTGGGTGAATGGCCGGTTCACCTC
TCCAGCGACAACGCCCAGAACACTGTGGAACCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTAT
ATTACTGTGCGAGAGATTTGGACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCAA
GGGCCCATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGC
CTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGC
ACACCTTCCCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAG
CAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGA

GTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAAGCCGCGGGGGCAC
 CGTCAGTCTTCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACATG
 CGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTG
 CATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACC
 TCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGC GCGGTCTCCAACAAAGCCCTCCCAGCCCC
 CATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC
 CGGGATGAGCTGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCG
 CCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGTGGACTCCGA
 CGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCA
 TGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTGGCG
 GTGGAGGGTCCGGCGGTGGTGGATCCCAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGG
 GAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTCAGTAGCTATACTATGCACTGGGTCCGC
 CAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGATGGAAACAATAAATACTACGCAG
 ACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAATGAACAG
 CCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGGTGGCTGGGGCCCTTTGACTACTGG
 GGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCG
 GCTCCGGTGGAGGCGGTCTGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGA
 AAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTGGCAGCAGCTACTTAGCCTGGTACCAGCAGAAA
 CCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATTACAGCAGGGCCACTGGCATCCCAGACAGGTTCA
 GTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTA
 TTA CTGTCAGCAGTATGGTAGCTCACCGTGGACGTTCCGCCAAGGGACCAAGGTGGAAATCAAA

SEQ ID 58: PD220F6 x CT4 aa

QEQVKETGGGLVQPGSLRLSCAASGFTISSYGVSWVRQAPGKGLEWVALIFPGIGFKDYASWVNGRFTL
 SSDNAQNTVELQMNSLRAEDTAVYYCARDLDLWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC
 LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVKDR
 VEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV
 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS
 CSVMHEALHNHYTQKSLSLSPGGGGSGGGGSQVQLVESGGGVVQPGRLRLSCAASGFTFSSYTMHWVR
 QAPGKGLEWVTFISYDGNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYW
 GQGLTVTVSSGGGGSGGGSGGGSGGGGSEIVLTQSPGTLSPGERATLSCRASQSVGSSYLAWYQQK
 PGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGS SPWTFGQGTKVEIK

SEQ ID 59: PD220F6 Light Chain nt

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCC
 AGTCCAGTCCGAGTGTTTATAGTAACTACTTATCCTGGTATCAGCAGAAACCAGGGAAAGTTCCCTAAGCT
 CCTGATCTATTATGCATCCACTCTGGCATCTGGGGTCCCATCTCGGTTCA GTGGCAGTGGATCTGGGACA
 GATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTGCAGGCGGTTATA
 GTAGTAGTACTCGTGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGT
 CTT CATCTTCCC GCCATCTGATGAGCAGTTGAAATCTGGA ACTGCCTCTGTTGTGTGCCTGCTGAATAAC
 TTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGA
 GTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGA

CTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGC
TTCAACAGGGGAGAGTGT

SEQ ID 60: PD220F6 Light Chain aa

DIQMTQSPSSLSASVGDRTITCQSSPSVYSNYLSWYQQKPGKVPKLLIYYASTLASGVPSRFSGSGSGT
DFTLTISSLPEDVATYYCAGGYSSSTRAFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNN
FYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKS
FNRGEC

SEQ ID 61: PD225G11 x CT4 nt

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAG
CCTCTGGATTACCTTTAGCAGCAGCCACTGGATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGA
GTGGATCGCATGCATTTATACTGGTAGTATTGATGTCTTTTACTACGCGAGCTGGGCGAAAGGCCGGTTC
ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGG
CCGTATATTACTGTGCGAGAGCCGCTAATACTGATACTACCTACTTTAACTTGTGGGGCCAGGGAACCCCT
GGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACC
TCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGA
ACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCT
CAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAG
CCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCCAATCTTGTGACAAAACCTCACACATGCCACCGT
GCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCTCTTCCCCCAAACCCAAGGACACCCTCAT
GATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC
AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCA
CGTACCGTGTGGTCAGCGTCTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGC
GGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAA
CCACAGGTGTACACCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGACCTGCCTGG
TCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACCTACAA
GACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGC
AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGA
AGAGCCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCCAGGTGCAATTGGTGGGA
GTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCTTC
AGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCAT
ATGATGGAAACAATAAAATACTACGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAA
GAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACC
GGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCCCTGGTCACCGTCTCGAGCGGTGGAGGCGGAT
CTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGTTCTGAAATTGTGTTGACGCAGTCTCC
AGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTGGCAGC
AGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATTCAGCA
GGGCCACTGGCATCCCAGACAGGTTCACTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAG
ACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCACCGTGGACGTTCCGGCCAA
GGGACCAAGGTGGAAATCAAA

SEQ ID 62: PD225G11 x CT4 aa

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSSHWICWVRQAPGKGLEWIACIYTGSIDVFYYASWAKGRF
 TISRDN SKNTLYLQMN SLRAEDTAVYYCARAANTDTTYFNLWGQGT LVT VSSASTKGPSVFPLAPSSKST
 SGGTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
 PSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF
 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQPRE
 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGSGGGSGGGGSQVQLVESGGGVVQPGRSLRLSCAASGFTF
SSYTMHWVRQAPGKGLEWVTFISYDGNNKYIADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAIYYCART
GWLGPFFDYWGQGT LVT VSSGGGSGGGGSGGGGSGGGGSEIVLTQSPGTL SLSLSPGERATLSCRASQSVGS
SYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQYGS SPWTFGQ
 GTKVEIK

SEQ ID 63: PD225G11 Light Chain nt

GCCTATGATATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCC
 AGGCCAGTCAGAGCATTAACAACCAACTATCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCT
 GATCTATGGTGCATCCACTCTGGCATCTGGGGTCCCATCTCGGTTACCGGCAGTGGATCTGGGACAGAT
 TTCCTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCATGTTTATTATTGCA
 GTGGTGGTAGTTGTTTTTGGGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACC
 ATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTG
 AATAACTTCTATCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCC
 AGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAA
 AGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACA
 AAGAGCTTCAACAGGGGAGAGTGT

SEQ ID 64: PD225G11 Light Chain aa

AYDMTQSPSSLSASVGDRVTINQASQSINNQLSWYQQKPGKVPKLLIYGASTLASGVPSRFTGSGSGTD
 FTLTISSLQPEDVATYYCHVHYCSGGSCFWAFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL
 NNFYFPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVT
 KSFNRGEC

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

ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCTGTCC

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

MKHLWFFLLLVAAAPRWVLS

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

ATGGCTGTCTTGGGGCTGCTCTTCTGCCTGGTGACATTCCCAAGCTGTGTCCTATCC

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

MAVLGLLFLCLVTFPSCVLS

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

ATGAGGGCCCCTGCTCAGTTTCTTGGCTTCTTGTCTTTCTGGATTCCAGCCTCCAGAAGT

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

MRAPAQFLGFLFWIPASRS

SEQ ID 71: CT4 scFv nt

CAGGTGCAATTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAG
 CCTCTGGATTACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTG
 GGTGACATTTATATCATATGATGGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTACCATC
 TCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATAT
 ATTACTGTGCGAGGACCGGCTGGCTGGGGCCCTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTC
 GAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGTCTGAAATT
 GTGTTGACGCAGTCTCCAGGCACCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCA
 GTCAGAGTGTTGGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCAT
 CTATGGTGCATTACAGCAGGGCCACTGGCATCCCAGACAGGTTCACTGGCAGTGGGTCTGGGACAGACTTC
 ACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATGGTAGCTCAC
 CGTGGACGTTCCGCCAAGGGACCAAGGTGGAAATCAAA

SEQ ID 72: CT4 scFv aa

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKGLEWVTFISYDGNKKYYADSVKGRFTI
 SRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLVTVSSGGGSGGGGSGGGGSGGGGSEI
 VLTQSPGTLSLSPGERATLSCRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGTDF
 TLTISRLEPEDFAVYYCQQYGSSPWF^{FGQGTKVEIK}

SEQ ID73: PD224D1 scFv nt

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAGC
 CTCTGGATTCTCCCTCAGTAGCTATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTACATCGGCTACA
 TTGGTGATACTACTGGCATAGCCTACGCGAGCTGGGCGAATGGCAGATTACCATCTCCAAAGACAATACCAAGAACACG
 GTGGATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGCTGGTCCCTACTTAGACAT
 CTGGGGCCAAGGGACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCG
 GTGGAGGCGGCTCTGCCCTTGTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACT
 TGCCAGGCCAGTCAGAACATTTACAGCAATTTAGCCTGGTATCAGCAGAAACCAGGGAAGTTCCCTAAGCTCCTGATCTA
 TCAGGCCTCCACTCTGGCATCTGGGGTCCCATCTCGGTTCACTGGCAGTGGATATGGGACAGATTTCACTCTCACCATCA
 GCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCAAGGCGGTATTATAGTGCTGCCCTTAATACTTTTCGGCGGA
 GGGACCAAGGTGGAGATCAAA

SEQ ID 74: PD224D1 scFv aa

EVQLVESGGGLVQPGGSLRLSCTASGFSLSYAMSWVRQAPGKLEYIGYIGD^{TTGIAYASWANG}RFTISKDNTKNTVDLQMN
 S LRAEDTAVYYCARGWSYLDI^{WGQGLVTVSSGGGSGGGGSGGGGSGGGG}SALVMTQSPSSLSASVGRVITITCQASQNIYSN
 LAWYQQKPGKVPKLLIYQASTLASGVPSRFSGSGYGTDFTLTISLQPEDVATYYCQGGYYSALNTF^{GGG}GTKVEIK

SEQ ID 75: PD206F12 scFv nt

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAG
 CCTCTGGATTCTGACTTCAGTAGCGGCTACTGGATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGA
 GTTGATCGCATGCATTTATGCTGGTACTAGTGGTAGTACTTCTACGCGAGCTGGGCGAGAGGCAGATTC
 ACCATCTCCGAAACCTCCAAGAACACGGTGA^{CTCTTCAAATGAACAGCCTGAGAGCCGAGGACTCGGCTG}
 TGTATTACTGTGCGAGAAATCTTTACACTTACAATAGCTTGTGGGGCCAGGGAACCCTGGTCACCGTCTC

GAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGACATC
 CAGATGACCCAGTCTCCTTCCACCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCA
 GTCAGAGTGTTTATGATAACAACTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCCTAAGCTCCT
 GATCTATACAGTATCCACTCTGGCATCTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGAA
 TTCCTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAAGGCAGTATTATATA
 GTAGTGGTTGGAACCTTGGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 76: PD206F12 scFv aa

EVQLVESGGGLVQPGGSLRLSCAASGFDSSGYWICWVRQAPGKGLELIACIYAGTSGSTSYASWARGRF
 TISETSKNTVTLQMNSLRAEDSAVYYCARNLYTNSLWGQGLVTVSSGGGSGGGGSGGGGSGGGGSDI
 QMTQSPSTLSASVGDRVTITCQSSQSVYDNNWLAWYQQKPGKAPKLLIYTVSTLASGVPSRFSGSGSGTE
 FTLTISSLQPEDFATYYCQGTYYSSGWNFAFGGGTKVEIK

SEQ ID 77: PD215A1 scFv nt

CAGGAGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAG
 CCTCTGGATTCTCCTTTAGCAGCTACTGGATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTG
 GATCGGATGCATTACGACTGGTAGTGGTAGCACTTACTACGCGAGCTGGGCGAAGCGCCGGTTCACCATC
 TCCAAAGACAATTCCAAGAACACGGTGACTCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTAT
 ATTACTGTACGAGAGCATTTGACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGG
 ATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGACATCCAGATGACCCAGTCT
 CCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCAGTCAGAGCATTTACA
 GCTACTTAACTGGTATCAGCAGAAACCAGGGAAGCCCCCTAAGCTCCTGATCTATGGTGCATCCAATCT
 GGCATCTGGGGTCCCATCAAGGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGT
 CTGCAACCTGAAGATTTTGCACTTACTACTGTCAAAGCAGTTGGTTGAGTGGTGTCTGTTGGTAATGCTT
 TCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 78: PD215A1 scFv aa

QEQLLESGGGLVQPGGSLRLSCTASGFSFSSYWMCWVRQAPGKGLEWIGCITTGSGSTIYYASWAKRRFTI
 SKDNSKNTVTLQMNSLRAEDTAVYYCTRAFDLWGQGLVTVSSGGGSGGGGSGGGGSGGGGSDIQMTQS
 PSSLSASVGDRVTITCQASQSIYSYLNWYQQKPGKAPKLLIYGASNLASGVPSRFSGSGSGTDFTLTISS
 LQPEDFATYYCQSSWLSGAVGNFAFGGGTKVEIK

SEQ ID 79: PD225G11 scFv nt

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAG
 CCTCTGGATTACCTTTAGCAGCAGCCACTGGATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGA
 GTGGATCGCATGCATTTATACTGGTAGTATTGATGTCTTTTACTACGCGAGCTGGGCGAAAGCCGGTTC
 ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGG
 CCGTATATTACTGTGCGAGAGCCGCTAATACTGATACTACCTACTTTAACTTGTGGGGCCAGGGAACCCT
 GGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGC
 GGCTCTGCCTATGATATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCA
 ATTGCCAGGCCAGTCAGAGCATTAACAACCAACTATCCTGGTATCAGCAGAAACCAGGGAAGTTCTCTAA
 GCTCCTGATCTATGGTGCATCCACTCTGGCATCTGGGGTCCCATCTCGGTTACCGGCAGTGGATCTGGG

ACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCATGTTTCATT
ATTGCAGTGGTGGTAGTTGTTTTTGGGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 80: PD225G11 scFv aa

EVQLLES^{GGGLVQPGGSLRLSCAASGFTFSS}SSHWICWVRQAPGKGLEWIACIYTGSI^{DVFYYASWAKGRF}
TISRDN^{SKNTLYLQMN}SLRAEDTAVYYCARAANTDTTYFNLWGQGLVTVSSGGGSGGGGSGGGGSGGG
GSAYDMTQSPSSLSASV^{GDRVTINCQASQSINNQLSWYQQKPGKVPKLLIY}GASTLASGVPSRFTGSGSG
TDFTLTIS^{SLQPEDVATYYCHVHYCSGGSCFWAF}GGGTKEIK

SEQ ID 81: PL230C6 scFv nt

CAGTCGGTGGAGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACCGCCT
CTGGAATCGACCTTAATACCTACGACATGATCTGGGTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGT
TGGAATCATTACTTATAGTGGTAGTAGATACTACGCGAACTGGGCGAAAGGCCGATTACCATCTCCAAA
GACAATACCAAGAACACGGTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACT
GTGCGAGAGATTATATGAGTGGTTCCTCACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCTTCCGGTGG
AGGCGGTTCAGGCGGAGGTGGAAGTGGTGGTGGCGGCTCTGGAGGCGGCGGATCTGCCTATGATATGACC
CAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCAAGTGTGAGGCCAGTGAGGACA
TTTATAGCTTCTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCCATTCTGCATC
CTCTCTGGCATCTGGGGTCCCATCAAGGTTGAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATC
AGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGGTTATGGTAAAAATAATGTTGATA
ATGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 82: PL230C6 scFv aa

QSVEESGGGLVQPGGSLRLSCTASGIDLNTYDMIWVRQAPGKGLEWVGIITYSGSRYYANWAKGRFTISK
DNTKNTVYLQMN^{SLRAEDTAVYYCARDYMSGSHLWGQGLVTVSSGGGSGGGGSGGGGSGGGGSAYDMT}
QSPSSVSASV^{GDRVTIKCQASEDIYSFLAWYQQKPGKAPKLLIHSASSLASGVPSRFS}SGSGSGTDFTLT
ISLQPEDFATYYCQQGYGKNNVDNAFGGGTKEIK

SEQ ID 83: PL231H2 scFv nt

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAA
CTTCTGGAATCGACCTTAGTACCTACGACATGATCTGGGTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTG
GGTGGGAATCATTAGTTATGTTGGTAACATACTACGCGAGCTGGGCGAAAGGCCGATTACCCCTCTCC
AAAGACAATACCTCGACCACGGTGGATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATT
ACTGTGCGAGAGATTTTATTAGTGGTTCCTCACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGG
TGGAGGCGGATCTGGCGGAGGTGGTTCGGCGGCTGGCGGCTCCGGTGGAGGCGGTTCTGCCTATGATATG
ACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGTGAGGCCAGTGAGA
GCATTAGTAGCTTCTTATCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTTTTCTGC
ATCCACTCTGGCATCTGGGGTCCCATCAAGGTTGAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACC
ATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGGTTATAGTAAAAGTAATGTGG
ATAATGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 84: PL231H2 scFv aa

QVQLVESGGGLVQPGGSLRLSCTTSGIDLSTYDMIWVRQAPGKGLEWVGIIISYVGNTYYASWAKGRFTLS
KDNTSTTVDLQMN^{SLRAEDTAVYYCARDFISGSHLWGQGLVTVSSGGGSGGGGSGGGGSGGGGSAYDM}

TQSPSSVSASVGDRVITINCQASESIS~~SSFLSWYQQKPGKAPKLLIF~~SASTLASGVPSRFSSGSGSGTDFTLT
 ISSLQPEDFATYYCQQGYSKSNVDNAFGGGTKVEIK

SEQ ID 85: PL221G5 scFv nt

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAG
 CCTCTGGATTCTCCTTCAGTAGCGGGTACGACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGA
 GTGGATCGCATGCATTGCTGCTGGTAGTGCTGGTATCACTTACGACGCGAACTGGGCGAAAGGCCGGTTC
 ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGG
 CCGTATATTACTGTGCGAGATCGGCGTTTTTCGTTGACTACGCCATGGACCTCTGGGGCCAGGGAACCCT
 GGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGC
 GGCTCTGACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCA
 CTTGCCAGGCCAGTCAGAGCATTAGTTCCCACTTAACTGGTATCAGCAGAAACCAGGGAAAGCCCCTAA
 GCTCCTGATCTATAAGGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTGAGCGGCAGTGGATCTGGG
 ACAGAATTTACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAACAGGGTT
 ATAGTTGGGGTAATGTTGATAATGTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 86: PL221G5 scFv aa

EVQLLES~~GGGLVQPGGSLRLSCAASGFSFSSGYDMCWVRQAPGKGLEW~~IACIAAGSAGITYDANWAKGRF
 TISRDN~~SKNTLYLQMNSLRAEDTAVYYCARSAF~~SFDYAMDLWGQGLTVTVSSGGGGSGGGGSGGGGSGGG
 GSDIQMTQSPSTLSASVGDRVITITCQASQSI~~SSHLN~~WYQQKPGKAPKLLIYKASTLASGVPSRFS~~SGSG~~
 TEFTLTISSLQPD~~DFATYYCQQGY~~SWGNVDNVFGGGTKVEIK

SEQ ID 87: PL004B5 scFv nt

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAG
 CCTCTGGATTCTCCCTCAGTAGCTACTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTG
 GATCGGAGTCATTGATACTAATGTTTATATATACTACGCGAACTGGGCAAAAGGCAGATTACCATCTCC
 AGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATT
 ACTGTGCGAGATATGTGGGTAATAATGATGATTATATTAAGTGTGGGGCCAGGGAACCCTGGTCACCGT
 CTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGAC
 ATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGT
 CCAGTCAGAGTGTTTATAATGGCTACTGGTTATCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCT
 CCTGATCTATGGTGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTGAGCGGCAGTGGATCTGGGACA
 GAATTCACCTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCTAGGCAGTTATA
 CTAGTAGTACTGAGAACTCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 88: PL004B5 scFv aa

EVQLVESGGGLVQPGGSLRLSCAASGFS~~SLSSY~~WMSWVRQAPGKLEWIGVIDTNVYIYANWAKGRFTIS
 RDNSKNTLYLQMNSLRAEDTAVYYCARYVGNNDYINLWGQGLTVTVSSGGGGSGGGGSGGGGSGGGGSD
 IQMTQSPSTLSASVGDRVITITCQSSQSVYNGY~~WLSWYQQKPGKAPKLLIY~~GASTLASGVPSRFSSGSGSGT
 EFTLTISSLQPD~~DFATYYCLGSYTS~~TENSFGGGTVEIK

SEQ ID 89: PL004B9 scFv nt

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAG
 TGTCTGGAATCGACCTCAGTGTCAATATGGGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTG

GATCGGAACCATTACTTATGTTGGTAACACATATTACGCGAGCTGGGCGAAAGGCAGATTACCATCTCC
AAAACCTCGACCACGGTGGATCTTAAAATCACCAGTCCGACAACCGAGGACACGGCTGTGTATTACTGTG
CGAGAGAATCTGGTACTATTTATTACAGTTACTTTAACTTGTGGGGCCAAGGGACCCTGGTCACCGTCTC
GAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGCATTC
GAATTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAAGTGCCAGGCCA
GTGAAAGCATTAGCAACTACTTATCCTGGTATCAGCAGATTCCAGGGAAAGTTCCTAAGCTCCTGATCTA
TTATGCATCCAATCTGGCATCTGGGGTCCCATCTCGGTTCACTGGCAGTGGATCTGGGACAGATTTCACT
CTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCACTTATTACTGTCAAAGCTATTATGGTGGTGGTA
GTGCCTATACTTTCCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 90: PL004B9 scFv aa

EVQLVESGGGLVQP^{GGSLRLS}CTVSGIDLSVINMGWVRQAPGKGLEWIGTITYVGNTYYASWAKGRFTIS
KTSTTVDLKITSPTTEDTAVYYCARESGTIYYSYFNLWGQGLVTVSSGGGGSGGGSGGGGSAF
ELTQSPSSLSASVGRVTIKCQASESISNYLSWYQQIPGKVPKLLIYYASNLASGVPSRFSGSGSGTDFT
LTISSLQPEDVATYYCQSYYGGSAYTFGGGTKEIK

SEQ ID 91: CT4 VH nt

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCA
CCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGACATTTATATCATATGAT
GGAAACAATAAATACTACGCAGACTCCGTGAAGGGCCGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCT
GCAAATGAACAGCCTGAGAGCTGAGGACACGGCTATATATTACTGTGCGAGGACCGCTGGCTGGGGCCCTTTGACTACT
GGGGCCAGGGAACCTGGTCACCGTCTCCTCA

SEQ ID 92: CT4 VH aa

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYTMHWVRQAPGKLEWVTFISYDGNMKYYADSVKGRFTI
SRDNSKNTLYLQMNSLRAEDTAIYYCARTGWLGPFDYWGQGLVTVSS

SEQ ID 93: CT4 VL nt

GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCA
GGGCCAGTCAGAGTGTGGCAGCAGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCT
CCTCATCTATGGTGCATTACAGCAGGGCCACTGGCATCCCAGACAGGTTCACTGGCAGTGGGTCTGGGACA
GACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCTCAGCAGTATGGTA
GCTCACCGTGGACGTTCCGCCAAGGGACCAAGGTGGAAATCAAA

SEQ ID 94: CT4 VL aa

EIVLTQSPGTL^{SLSPGERATLS}CRASQSVGSSYLAWYQQKPGQAPRLLIYGAFSRATGIPDRFSGSGSGT
DFTLTISRLEPEDFAVYYCQYIGSSPWF^{FGQ}GTKVEIK

SEQ ID 95: PD224D1 VH nt

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAG
CCTCTGGATTCTCCCTCAGTAGCTATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGCTGGAGTA
CATCGGCTACATTGGTGATACTACTGGCATAGCCTACGCGAGCTGGGCGAATGGCAGATTACCATCTCC
AAAGACAATAACCAAGAACACGGTGGATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATT
ACTGTGCGAGAGGCTGGTCCTACTTAGACATCTGGGGCCAAGGGACCCTGGTCACCGTCTCGAGC

SEQ ID 96: PD224D1 VH aa

EVQLVESGGGLVQPGGSLRLSCTASGFSLSSYAMSWVRQAPGKLEYIGYIGDTTGIAYASWANGRFTIS
 KDNTKNTVDL
 QMNSLRAEDTAVYYCARGWSYLDIWGQGLTVTVSS

SEQ ID 97: PD224D1 VL nt

GCCCTTGTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCC
 AGGCCAGTCAGAACATTTACAGCAATTTAGCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCT
 GATCTATCAGGCCTCCACTCTGGCATCTGGGGTCCCATCTCGGTTCAAGTGGCAGTGGATATGGGACAGAT
 TTCCTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCAAGGCGGTTATTATA
 GTGCTGCCCTTAATACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 98: PD224D1 VL aa

ALVMTQSPSSLSASVGDRVITITCQASQNIYSNLAWYQQKPGKVPKLLIYQASTLASGVPSRFSGSGYGT
 DFTLTISLQ
 EDVATYYCQGGYSAALNTFGGGTKVEIK

SEQ ID 99: PD206F12 VH nt

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAG
 CCTCTGGATTCTGACTTCAGTAGCGGCTACTGGATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGA
 GTTGATCGCATGCATTTATGCTGGTACTAGTGGTAGTACTTCCTACGCGAGCTGGGCGAGAGGCAGATTC
 ACCATCTCCGAAACCTCCAAGAACACGGTGACTCTTCAAATGAACAGCCTGAGAGCCGAGGACTCGGCTG
 TGTATTACTGTGCGAGAAATCTTTACTTACAATAGCTTGTGGGGCCAGGGAACCCTGGTCACCGTCTC
 GAGC

SEQ ID 100: PD206F12 VH aa

EVQLVESGGGLVQPGGSLRLSCAASGFDSSGYWICWVRQAPGKLELIACIYAGTSGSTSYASWARGRF
 TISETSKNTVTLQMNSLRAEDSAVYYCARNLYTNSLWGQGLTVTVSS

SEQ ID 101: PD206F12 VL nt

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCC
 AGTCCAGTCAGAGTGTTTATGATAACAACCTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAA
 GCTCCTGATCTATACAGTATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAAGCGGCAGTGGATCTGGG
 ACAGAATTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAAGGCACTT
 ATTATAGTAGTGGTTGGAACCTTGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 102: PD206F12 VL aa

DIQMTQSPSTLSASVGDRVITITCQSSQSVYDNNWLAWYQQKPGKAPKLLIYTVSTLASGVPSRFSGSGSG
 TEFTLTISLQPDDEFATYYCQGTYYSSGWNFAFGGGTKVEIK

SEQ ID 103: PD215A1 VH nt

CAGGAGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAG
 CCTCTGGATTCTCCTTTAGCAGCTACTGGATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTG
 GATCGGATGCATTACGACTGGTAGTGGTAGCACTTACTACGCGAGCTGGGCGAAGCGCCGGTTCACCATC
 TCCAAAGACAATTCCAAGAACACGGTGACTCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTAT
 ATTACTGTACGAGAGCATTTGACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

SEQ ID 104: PD215A1 VH aa

QEQLLES^{GGGLVQPGGSLRLSCTASGFSF}SSYWMCWVRQAPGKGLEWIGCITTGSGSTYYASWAKRRFTI
SKDNSKNTVTLQMNSLRAEDTAVYYCTRAFDLWGQGLTVTVSS

SEQ ID 105: PD215A1 VL nt

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCC
AGGCCAGTCAGAGCATTTACAGCTACTTAACTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT
GATCTATGGTGCATCCAATCTGGCATCTGGGGTCCCATCAAGGTCAGTGGCAGTGGATCTGGGACAGAT
TTCATCTCACCATCAGCAGTCTGCAACCTGAAGATTTTGCAACTTACTACTGTCAAAGCAGTTGGTTGA
GTGGTGTCTGTTGGTAATGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 106: PD215A1 VL aa

DIQMTQSPSSLSASVGDRVTITCQASQSIYSYLNWYQQKPGKAPKLLIYGASNLASGVPSRFSGSGSGTD
FTLTISSLQPEDFATYYCQSSWL^{SGAVGNA}FGGGTKVEIK

SEQ ID 107: PD225G11 VH nt

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGAGACTCTCCTGTGCAG
CCTCTGGATTACCTTTAGCAGCAGCCACTGGATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGA
GTGGATCGCATGCATTTATACTGGTAGTATTGATGTCTTTTACTACGCGAGCTGGGCGAAAGCCGGTTC
ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGG
CCGTATATTACTGTGCGAGAGCCGCTAATACTGATACTACCTACTTTAACTTGTGGGGCCAGGGAACCCT
GGTCACCGTCTCGAGC

SEQ ID 108: PD225G11 VH aa

EVQLLES^{GGGLVQPGGSLRLSCAASGFTFSSSHWICWVRQAPGKGLEW}IACIYTGSIDVFYYASWAKGRF
TISRDNKNTLYLQMNSLRAEDTAVYYCARAANTDTTYFNLWGQGLTVTVSS

SEQ ID 109: PD225G11 VL nt

GCCTATGATATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCC
AGGCCAGTCAGAGCATTAACAACCAACTATCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCT
GATCTATGGTGCATCCACTCTGGCATCTGGGGTCCCATCTCGGTTACCGGCAGTGGATCTGGGACAGAT
TTCATCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTATGTTTATTATTGCA
GTGGTGGTAGTTGTTTTTGGGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 110: PD225G11 VL aa

AYDMTQSPSSLSASVGDRVTINCQASQSINNQLSWYQQKPGKVPKLLIYGASTLASGVPSRFTGSGSGTD
FTLTISSLQPEDVATYYCHVHYCSGGSCFWAFGGGTKVEIK

SEQ ID 111: PL230C6 VH nt

CAGTCGGTGGAGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGTCCCTGAGACTCTCCTGTACCGCCT
CTGGAATCGACCTTAATACCTACGACATGATCTGGGTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTGGGT
TGGAATCATTACTTATAGTGGTAGTAGATACTACGCGAACTGGGCGAAAGGCCGATTCACCATCTCCAAA
GACAATACCAAGAACACGGTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACT
GTGCGAGAGATTATATGAGTGGTTCCTCACTTGTGGGGCCAGGGAACCCTGGTCAACCGTCTCTTCC

SEQ ID 112: PL230C6 VH aa

QSVEESGGGLVQPGGSLRLSCTASGIDLNTYDMIWVRQAPGKGLEWVGIIITYSGSRYIANWAKGRFTISK
DNTKNTVYLQMNSLRAEDTAVYYCARDYMSGSHLWGQGLTVTVSS

SEQ ID 113: PL230C6 VL nt

GCCTATGATATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCAAGTGTC
 AGGCCAGTGAGGACATTTATAGCTTCTTGGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT
 GATCCATTCTGCATCCTCTCTGGCATCTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGAT
 TTCCTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGGTTATGGTA
 AAAATAATGTTGATAATGCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 114: PL230C6 VL aa

AYDMTQSPSSVSASVGDRVTIKCQASEDIYSFLAWYQQKPGKAPKLLIHSASSLASGVPSRFSGSGSGTD
 FTLTISSLQP
 EDFATYYCQQGYGKNNVDNAFGGGTKVEIK

SEQ ID 115: PL231H2 VH nt

CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGGGCTCCCTGAGACTCTCCTGTACAA
 CTTCTGGAATCGACCTTAGTACCTACGACATGATCTGGGTCCGCCAGGCTCCAGGCAAGGGGCTAGAGTG
 GGTGGGAATCATTAGTTATGTTGGTAACACATACTACGCGAGCTGGGCGAAAGGCCGATTACCCCTCTCC
 AAAGACAATACCTCGACCACGGTGGATCTGCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATT
 ACTGTGCGAGAGATTTTATTAGTGGTTCCCACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

SEQ ID 116: PL231H2 VH aa

QVQLVESGGGLVQPGGSLRLSCTTSGIDLSTYDMIWVRQAPGKGLEWVGIIISYVGNTYYASWAKGRFTLS
 KDNTSTTVDLQMNSLRAEDTAVYYCARDFISGSHLWGQGLVTVSS

SEA ID 117: PL231H2 VL nt

GCCTATGATATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGTC
 AGGCCAGTGAGAGCATTAGTAGCTTCTTATCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT
 GATCTTTTCTGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGAT
 TTCCTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGGTTATAGTA
 AAAGTAATGTGGATAATGCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 118: PL231H2 VL aa

AYDMTQSPSSVSASVGDRVTINCQASESISSELSWYQQKPGKAPKLLIFSASTLASGVPSRFSGSGSGTD
 FTLTISSLQPEDFATYYCQQGYSKSNVDNAFGGGTKVEIK

SEQ ID 119: PL221G5 VH nt

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGCTCCCTGAGACTCTCCTGTGCAG
 CCTCTGGATTCTCCTTCAGTAGCGGGTACGACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGA
 GTGGATCGCATGCATTGCTGCTGGTAGTGCTGGTATCACTTACGACGCGAACTGGGCGAAAGGCCGGTTC
 ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGG
 CCGTATATTACTGTGCGAGATCGGCGTTTTTCGTTGACTACGCCATGGACCTCTGGGGCCAGGGAACCCT
 GGTACACCGTCTCGAGC

SEA ID 120: PL221G5 VH aa

EVQLLES^{GGGLVQPGGSLRLSCAASGFSFSSGYDMCWVRQAPGKGLEW}IACIAAGSAGITYDANWAKGRF
TISRDN^{SKNTLYLQMNSLRAEDTAVYYCARSAF}SFDYAMDLWGQGLVTVSS

SEQ ID 121: PL221G5 VL nt

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCC
AGGCCAGTCAGAGCATTAGTTCCCACTTAACTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCT
GATCTATAAGGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGAA
TTTACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAACAGGGTTATAGTT
GGGGTAATGTTGATAATGTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEA ID 122: PL221G5 VL aa

DIQMTQSPSTLSASVGDRVTITCQASQSISSHLNWYQQKPGKAPKLLIYKASTLASGVPSRFSGSGSGTE
FTLTISSLQPD^{DFATYYCQ}QGYSWGNDNVFGGGTKVEIK

SEA ID 123: PL004B5 VH nt

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAG
CCTCTGGATTCTCCCTCAGTAGCTACTGGATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTG
GATCGGAGTCATTGATACTAATGTTTATATATACTACGCGAACTGGGCAAAAGGCAGATTACCATCTCC
AGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATT
ACTGTGCGAGATATGTGGGTAATAATGATGATTATATTA^{ACTTGTGGGGCCAGGGAAC}CCTGGTCACCGT
CTCGAGC

SEQ ID 124: PL004B5 VH aa

EVQLVESGGGLVQPGGSLRLSCAASGFSLSYWMSWVRQAPGKGLEWIGVIDTNVYIYYANWAKGRFTIS
RDNSKNTLYLQMNSLRAEDTAVYYCARYVGNND^{DYINLW}QGLTVTVSS

SEQ ID 125: PL004B5 VL nt

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCC
AGTCCAGTCAGAGTGTTTATAATGGCTACTGGTTATCCTGGTATCAGCAGAAACCAGGGAAAGCCCCCTAA
GCTCCTGATCTATGGTGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTTCAGCGGCAGTGGATCTGGG
ACAGAATTC^{ACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCTAGGCAGTT}
ATACTAGTAGTACTGAGA^{ACTCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAA}

SEQ ID 126: PL004B5 VL aa

DIQMTQSPSTLSASVGDRVTITCQSSQSVYNGYWLSWYQQKPGKAPKLLIYGASTLASGVPSRFSGSGSG
TEFTLTISSLQPD^{DFATYYCLGSYTSSTENS}FGGGTKEIK

SEA ID 127: PL004B9 VH nt

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAG
TGTCTGGAATCGACCTCAGTGTCAATATGGGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTG
GATCGGAACCATTA^{CTTATGTTGGTAACACATATTACGCGAGCTGGGCGAAAGGCAGATTACCATCTCC}
AAAACCTCGACCACGGTGGATCTTAA^{AATCACCAGTCCGACAACCGAGGACACGGCTGTGTATTACTGTG}
CGAGAGAATCTGGTACTATTTATTACAGT^{TACTTTAACTTGTGGGGCCAAGGGACCCTGGTCACCGTCTC}
GAGC

SEQ ID 128: PL004B9 VH aa

EVQLVESGGGLVQPGGSLRLSCTVSGIDLSVINMGWVRQAPGKGLEWIGTITYVGNTYYASWAKGRFTIS
 KTSTTVDLKITSPTTEDTAVYYCARESGTIIYYSYFNLWGQGTLLTVSS

SEQ ID 129: PL004B9 VL nt

GCATTTCGAATTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAAGTGCC
 AGGCCAGTGAAAGCATTAGCAACTACTTATCCTGGTATCAGCAGATTCCAGGGAAAGTTCCTAAGCTCCT
 GATCTATTATGCATCCAATCTGGCATCTGGGGTCCCATCTCGGTTCAAGTGGCAGTGGATCTGGGACAGAT
 TTCCTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCAAAGCTATTATGGTG
 GTGGTAGTGCCTATACTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 130: PL004B9 VL aa

AFELTQSPSSLSASVGDRVTIKCQASESISNYLSWYQQIPGKVPKLLIYYASNLASGVPSRFSGSGSGTD
 FTLTISSLQPEDVATYYCQSYYGGSAYTFGGGTKEIK

SEQ ID 131: PD220F6 VH nt

CAGGAGCAGGTGAAGGAGACCGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAG
 CCTCTGGATTCCACCATCAGCAGCTATGGAGTGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTG
 GGTCGCATTGATTTTTCCCGGGATTGGTTTCAAAGACTACGCGAGCTGGGTGAATGGCCGGTTCACCCCTC
 TCCAGCGACAACGCCCAGAACACTGTGGAAGTCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTAT
 ATTACTGTGCGAGAGATTTGGACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

SEQ ID 132: PD220F6 VH aa

QEQQKETGGGLVQPGGSLRLSCAASGFTISSYGVSWVRQAPGKGLEWVALIFPGIGFKDYASWVNGRFTL
 SSDNAQNTVELQMNSLRAEDTAVYYCARDLLDLWGQGTLLTVSS

SEQ ID 133: PD220F6 VL nt

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCC
 AGTCCAGTCCGAGTGTTTATAGTAAGTACTTATCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCT
 CCTGATCTATTATGCATCCACTCTGGCATCTGGGGTCCCATCTCGGTTCAAGTGGCAGTGGATCTGGGACA
 GATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTGCAGGCGGTTATA
 GTAGTAGTACTCGTGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 134: PD220F6 VL aa

DIQMTQSPSSLSASVGDRVTITCQSSPSVSYNYLSWYQQKPGKVPKLLIYYASTLASGVPSRFSGSGSGT
 DFTLTISSLQPEDVATYYCAGGYSSSTRAFGGGTKEIK

SEQ ID 135: human IgG1 constant region nt

GCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG
 CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAAGTCAAGGCGCCCTGAC
 CAGCGGCGTGACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACC
 GTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGG
 TGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCCACCGTGCCAGCACCTGAACT
 CCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCT
 GAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACG
 GCGTGAGGTTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAG
 CGTCCCTACCGTCTGACACAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCC
 CTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACACAGGTGTACACCC

TGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC
CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTG
CTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGA
ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTC
TCCGGGT

SEQ ID 136: human IgG1 constant region aa

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT
VPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRT
EPTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA
LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
LDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG

SEQ ID 137: human IgG1 effector null nt

GCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGG
CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACCTAGGCGCCCTGAC
CAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACC
GTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGG
TGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCCAACCGTGGCCAGCACCTGAAGC
CGCGGGGGCACCGTCAGTCTTCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCT
GAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTCAACTGGTACGTGGACG
GCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAG
CGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCC
CTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCC
TGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC
CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTG
CTGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGA
ACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTC
TCCGGGT

SEQ ID 138: human IgG1 effector null aa

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT
VPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRT
EPTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKA
LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
LDSDGSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPG

SEQ ID 139: PD220F6 scFv nt

CAGGAGCAGGTGAAGGAGACCGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAG
CCTCTGGATTCAACATCAGCAGCTATGGAGTGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTG
GGTCGCATTGATTTTTCCCGGATTGGTTTTCAAAGACTACGCGAGCTGGGTGAATGGCCGGTTCACCTC
TCCAGCGACAACGCCCAGAACACTGTGGAACCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTAT
ATTACTGTGCGAGAGATTTGGACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGG
ATCTGGCGGAGGTGGTTCCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGACATCCAGATGACCCAGTCT
CCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCAGTCCGAGTGTTTATA

GTAAC TACTTATCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTATTATGCATCCAC
TCTGGCATCTGGGGTCCCATCTCGGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGC
AGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTGCAGGCGGTTATAGTAGTAGTACTCGTGCTTTTCG
GCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID 140: PD220F6 scFv aa

QEQVKETGGGLVQPGGSLRLSCAASGFTISSYGVSWVRQAPGKGLEWVALIFPGIGFKDYASWVNGRFTL
SSDNAQNTVELQMNSLRAEDTAVYYCARDLDLWGQGLTVTVSSGGGGSGGGGSGGGGSGGGGSDIQMTQS
PSSLASVGDRTITCQSSPSVYSNYLSWYQQKPGKVPKLLIYYASTLASGVPSRFSGSGSGTDFTLTIS
SLQPEDVATYYCAGGYSSSTRAFGGGTKVEIK

SEQ ID 141: CT4 VH CDR1 aa

SSYTMH

SEQ ID 142: CT4 VH CDR2 aa

FISYDGNNKYYADSVKG

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
QQGYSWGNDNV

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
QASESISSFLS

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
TITYVGNTYYASWAKG

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
QGTYYS SGWNFA

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
SSYGV

SEQ ID 196: PD220F6 VH CDR2 aa
LIFPGIGFKDYASWNG

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	CDR 3		
CT4	CTLA4	SSYTMH Seq ID 141	FISYDGNKKYADSVKG Seq ID 142	TGWLGPFDY Seq ID 143	RASQSVGSSVLA Seq ID 144	GAFSRAT Seq ID 145	QQYGSSPWT Seq ID 146		
PL230C6	PD-L1	NTYDMI Seq ID 147	IITYSGSRYVANWAKG Seq ID 148	DYMSGHL Seq ID 149	QASEDIYSFLA Seq ID 150	SASSLAS Seq ID 151	QQGYGKNNVDNA Seq ID 152		
PD224D1	PD-1	SSYAMS Seq ID 153	YIGDTTGIAYASWANG Seq ID 154	GWSYLDI Seq ID 155	QASQNIYSNLA Seq ID 156	QASTLAS Seq ID 157	QGGYSAALNT Seq ID 158		
PL221G5	PD-L1	SGYDMC Seq ID 159	CIAAGSAGITYDANWAKG Seq ID 160	SAFSFDYAMD Seq ID 161	QASQSISSHLN Seq ID 162	KASTLAS Seq ID 163	QQGYSWGNNVDNV Seq ID 164		
PL231H2	PD-L1	STYDMI Seq ID 165	IISYVGNTYYASWAKG Seq ID 166	DFISGSHL Seq ID 167	QASESISSFLS Seq ID 168	SASTLAS Seq ID 169	QQGYSKSNVDNA Seq ID 170		
PL004B5	PD-L1	SSYWMS Seq ID 171	VIDTNVVIYANWAKG Seq ID 172	YVGNDDYINL Seq ID 173	QSSQSVYNGWLS Seq ID 174	GASTLAS Seq ID 175	LGSYTSSTENS Seq ID 176		
PL004B9	PD-L1	SVINMG Seq ID 177	TITYVGNNTYYASWAKG Seq ID 178	ESGTIYYSYFNL Seq ID 179	QASESISNYLS Seq ID 180	YASNLAS Seq ID 181	QSYYGGSAYT Seq ID 182		
PD206F12	PD-1	SGYWIC Seq ID 183	CIYAGTSGTSYASWARG Seq ID 184	NLYTYNSL Seq ID 185	QSSQSVYDNNWLA Seq ID 186	TVSTLAS Seq ID 187	QGTYYSSGWNFA Seq ID 188		
PD215A1	PD-1	SSYWMC Seq ID 189	CITTGSGTYYASWAKR Seq ID 190	AFDL Seq ID 191	QASQSIYSYLN Seq ID 192	GASNLAS Seq ID 193	QSSWLSGAVGNA Seq ID 194		
PD220F6	PD-1	SSYGVS Seq ID 195	LIFPGIGFKDYASWVNG Seq ID 196	DLDL Seq ID 197	QSSPSVYSNYLS Seq ID 198	YASTLAS Seq ID 199	AGGYSSSTRA Seq ID 200		
PD225G11	PD-1	SSHWIC Seq ID 201	CIYTGSDVFFYASWAKG Seq ID 202	AANTDTTYFNL Seq ID 203	QASQSINNQLS Seq ID 204	GASTLAS Seq ID 205	HVHYCSGGSCFWA Seq ID 206		

CLAIMS

What is claimed is:

1. A bispecific antibody, comprising IgG domains having 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 domains have a first binding specificity to α -CTLA4, wherein the scFv components have a second binding specificity to α -PD-1 or α -PD-L1, and wherein the bispecific antibody comprises:
 - i. the 3 complementarity determining regions (CDRs) of SEQ ID No. 94, the 3 CDRs of SEQ ID No. 92, the 3 CDRs of SEQ ID No. 96 and the 3 CDRs of SEQ ID No. 98; or
 - ii. the 3 complementarity determining regions (CDRs) of SEQ ID No. 94, the 3 CDRs of SEQ ID No. 92, the 3 CDRs of SEQ ID No. 120 and the 3 CDRs of SEQ ID No. 122.
2. The bispecific antibody of claim 1, wherein:
 - i. the scFv components comprise an amino acid sequence having at least 98% sequence identity to SEQ ID No. 96 and 98, and the IgG domains comprise an amino acid sequence having at least 98% identity to SEQ ID No. 92 and 94; or
 - ii. the scFv components comprise an amino acid sequence having at least 98% sequence identity to SEQ ID No. 120 and 122, and the IgG variable domains comprise an amino acid sequence having at least 98% identity to SEQ ID No. 92 and 94.
3. The bispecific antibody of claim 1, comprising:
 - i. an amino acid sequence having at least 98% sequence identity to SEQ ID No. 2 and an amino acid sequence having at least 98% sequence identity to SEQ ID No. 4; or
 - ii. an amino acid sequence having at least 98% sequence identity to SEQ ID No. 8 and an amino acid sequence having at least 98% sequence identity to SEQ ID No. 4.
4. The bispecific antibody of any one of claims 1 to 3, wherein the two scFv components are connected to the C terminal of the heavy chain.
5. The bispecific antibody of any one of claims 1 to 3, wherein the two scFv components are connected to the N terminal of the light chain.
6. The bispecific antibody of any one of claims 1 to 5, wherein the bispecific antibody is an isolated monoclonal antibody.

7. The bispecific antibody of any one of claims 1 to 6, wherein neither the first nor the second binding specificity has a K_d greater than 70nM.
8. The bispecific antibody of any one of claims 1 to 7, comprising a human framework region.
9. The bispecific antibody of any one of claims 1 to 8, wherein the antibody is a humanized antibody, a chimeric antibody, or a recombinant antibody.
10. The bispecific antibody of any one of claims 1 to 9, wherein the IgG domain comprises an IgG1 constant region, wherein the IgG1 constant region comprises an amino acid sequence having at least 98% similarity with SEQ ID No. 136.
11. An isolated nucleic acid encoding the bispecific antibody of any one of claims 1 to 10.
12. An expression vector comprising the isolated nucleic acid of claim 11.
13. The expression vector of claim 12, wherein the vector is expressible in a cell.
14. A host cell comprising the nucleic acid of claim 11.
15. A host cell comprising the expression vector of claim 12.
16. The host cell of claim 14 or 15, wherein the host cell is a prokaryotic cell or a eukaryotic cell.
17. A method of producing a bispecific antibody, comprising culturing the host cell of any one of claims 14 to 16 so that the bispecific antibody is produced.
18. An immunoconjugate comprising the bispecific antibody of any one of claims 1 to 10 and a cytotoxic agent.
19. The immunoconjugate of claim 18, wherein the cytotoxic agent comprises a chemotherapeutic agent, a growth inhibitory agent, a toxin, or a radioactive isotope.
20. A pharmaceutical composition, comprising the bispecific antibody of any one of claims 1 to 10 and a pharmaceutically acceptable carrier.
21. The pharmaceutical composition of claim 20, further comprising radioisotope, radionuclide, a toxin, a therapeutic agent, a chemotherapeutic agent or a combination thereof.
22. A pharmaceutical composition, comprising the immunoconjugate of claim 18 or 19 and a pharmaceutically acceptable carrier.

23. Use of the bispecific antibody of any one of claims 1 to 10 in the manufacture of a medicament for the treatment of a subject with a cancer that is responsive to regulation of CTLA4 and PD-1 or PD-L1 checkpoint antigens.
24. The use of claim 23, wherein the cancer comprises cells expressing PD-L1.
25. The use of claim 23, wherein 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, or myeloma.
26. The use of claim 23, wherein the subject is a human.