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(54) Title: ANTI-4-1BB ANTIBODIES AND METHODS OF MAKING AND USING THEREOF

(57) Abstract:

ANTI-4-1BB ANTIBODIES AND METHODS OF MAKING AND USING THEREOF

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of U.S. Provisional Patent Application No. 62551065, filed August 28, 2017, U.S. Provisional Patent Application No. 62551032 filed August 28, 2017, U.S. Provisional Patent Application No. 62524554 filed June 25, 2017, U.S. Provisional Patent Application No. 62524557 filed June 25, 2017, U.S. Provisional Patent Application No. 62524558 filed June 25, 2017, U.S. Provisional Patent Application No. 62545603 filed August 15, 2017, U.S. Provisional Patent Application No. 62551032 filed August 28, 2017, and U.S. Provisional Patent Application No. 62551035 filed August 28, 2017, the entire disclosures of which are expressly incorporated by reference herein.

TECHNICAL FIELD

The present disclosure generally relates to the technical field of antibodies, and more particularly relates to making and using anti-4-1BB antibodies, and applications of the antibodies in cancer treatment and therapy.

BACKGROUND

Cancer is a major health problem across the world. In the United States alone it is estimated that in 2016 there were 1,685,210 new cases of cancer diagnosed and 595,690 deaths from the disease (http://www.cancer.gov). As such, any pharmaceutical agent that can reduce the severity or mortality rate from cancer is desirable.

In the immune system, resting T-cells can be activated to respond to antigen through a primary signal delivered through the T-cell receptor (TCR) by foreign antigen peptides presented by antigen-presenting cells (APCs). In addition to this primary signal, there are secondary positive and negative co-stimulatory signals that further influence the response of the T-cells. A secondary positive signal is required for full T-cell activation ((Lafferty et al., Ausl. J. Exp. Biol. Med. Sci. 53: 27-42 (1975)). Negative secondary signals can result in T-cell suppression and tolerance.

4-1BB is a co-stimulatory immune checkpoint molecule with the ability to active T cells. 4-1BB, also named as CD137, tumour necrosis factor receptor superfamily member 9 (TNFRSF9), and induced by lymphocyte activation (ILA), is a member of the tumour necrosis factor (TNF) receptor family. It has been reported that Crosslinking of CD137 enhances T cell proliferation, IL-2 secretion, survival and cytolytic activity. Further, it can enhance immune activity to eliminate tumours in mice.

Pfizer's Utomilumab (PF-05082566) targets 4-1BB, when in combination with Merck's Keytruda, stimulates a more intense immune system attack on cancers in a small clinical trial (https://www.reuters.com/article/us-health-cancer-pfizer-immunotherapy-idUSKCN0Y92W2). And seven clinical trials of PF-05082566 are ongoing. (www.clinicaltrials.gov).

SUMMARY

The present disclosure provides, among others, anti-4-1BB monoclonal antibodies, antigen binding portions thereof, therapeutic compositions thereof and/or nucleic acid encoding the same, and their use to upregulate the function of T-cells to enhance cell-mediated immune responses in the treatment of cancer and other T-cell dysfunctional disorders.

In one embodiment, an isolated monoclonal antibody (mAb) or antigen-binding fragment that binds specifically to human or cynomolgus 4-1BB is provided. In one embodiment, the isolated mAb or antigen-binding fragment include an amino acid sequence having a percentage homology with SEQ ID NO:4, SEQ ID NO:8, SEQ ID NO:12, SEQ ID NO:16, SEQ ID NO:20, SEQ ID NO:24, SEQ ID NO:28, SEQ ID NO:32, SEQ ID NO:36, SEQ ID NO:40, SEQ ID NO:44, SEQ ID NO:48, SEQ ID NO:52, SEQ ID NO:56, SEQ ID NO:60, SEQ ID NO:64, SEQ ID NO:68, SEQ ID NO:72, SEQ ID NO:76, SEQ ID NO:80, SEQ ID NO:84, SEQ ID NO:88, SEQ ID NO:88, SEQ ID NO:92, SEQ ID NO:96, SEQ ID NO:100, SEQ ID NO:104, SEQ ID NO:108, SEQ ID NO:112, SEQ ID NO:116, SEQ ID NO:120, SEQ ID NO:124, SEQ ID NO:128, SEQ ID NO:132, SEQ ID NO:136, SEQ ID NO:140, SEQ ID NO:144, SEQ ID NO:148, SEQ ID NO:152, SEQ ID NO:156, SEQ ID NO:160, SEQ ID NO:164, SEQ ID NO:168, SEQ ID NO:172, SEQ ID NO:176, SEQ ID NO:180, SEQ ID NO:184, SEQ ID NO:188, SEQ ID NO:192, SEQ ID NO:196, SEQ ID NO:200, SEQ ID NO:204, SEQ ID NO:208, SEQ ID NO:212, SEQ ID NO:216, SEQ ID NO:220, SEQ ID NO:224, SEQ ID NO:228, SEQ ID NO:232, SEQ ID NO:236, SEQ ID NO:240, SEQ ID NO:244, SEQ ID NO:248, SEQ ID NO:252, SEQ ID NO:256, SEQ ID NO:260, SEQ ID NO:264, SEQ ID NO:268, or SEQ ID NO:272. The percentage homology is not less than 70%, 80%, 90%, 95%, 98%, or 99%.

In one embodiment, the isolated mAb or antigen-binding fragment, has a binding affinity to human or cynomolgus 4-1BB with a Kd not greater than 30nM, 40nM, 50nM, 60nM, 70nM, 80nM, 90nM, or 100nM.

In one embodiment, the isolated mAb or antigen-binding fragment exhibits one or more functional properties such as, without limitation, high affinity binding to human or cynomolgus 4-1BB, inhibiting human or cynomolgus 4-1BB activity, induction of apoptosis, regulation of EGFR signalling pathway, upregulation of EMT genes, enhancing T cell activation, stimulating antibody response, reversing the suppressive function of an immunosuppressive cell, or a combination thereof. In one embodiment, the immunosuppressive cell comprises a regulatory cell. In one embodiment, the isolated mAb or antigen-binding fragment enhances T-cell activation via mechanisms or pathways including T-cell proliferation, IFN-γ and/or IL-2 secretion, or a combination thereof.

In one embodiment, the isolated mAb or antigen-binding fragment comprises a human framework region. In one embodiment, the isolated mAb or antigen-binding fragment is a humanized antibody, a chimeric antibody, or a recombinant antibody.

In one embodiment, the isolated mAb or antigen-binding fragment is an IgG. In one embodiment, the antigen-binding fragment is a Fv, a Fab, a F(ab')2, a scFV or a scFV2 fragment. In one embodiment, the isolated mAb is a bispecific antibody, tri-specific antibody, or multi-specific antibody.

In one embodiment, the isolated mAb or antigen-binding fragment may include an IgG1 heavy chain. In one embodiment, the IgG1 heavy chain comprises an amino acid sequence having a percentage

homology with SEQ ID NO:7, SEQ ID NO:15, SEQ ID NO:23, SEQ ID NO:31, SEQ ID NO:39, SEQ ID NO:47, SEQ ID NO:55, SEQ ID NO:63, SEQ ID NO:71, SEQ ID NO:79, SEQ ID NO:87, SEQ ID NO:95, SEQ ID NO:103, SEQ ID NO:111, SEQ ID NO:119, SEQ ID NO:127, SEQ ID NO:135, SEQ ID NO:143, SEQ ID NO:151, SEQ ID NO:159, SEQ ID NO:167, SEQ ID NO:175, SEQ ID NO:183, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:207, SEQ ID NO:215, SEQ ID NO:223, SEQ ID NO:231, SEQ ID NO:239, SEQ ID NO:247, SEQ ID NO:255, SEQ ID NO:263, or SEQ ID NO:271. The percentage homology is not less than 70%, 80%, 90%, 95%, 98%, or 99%.

In one embodiment, the isolated mAb or antigen-binding fragment may include a kappa light chain. In one embodiment, the kappa light chain comprises an amino acid sequence having a percentage homology with SEQ ID NO:3, SEQ ID NO:11, SEQ ID NO:19, SEQ ID NO:27, SEQ ID NO:35, SEQ ID NO:43, SEQ ID NO:51, SEQ ID NO:59, SEQ ID NO:67, SEQ ID NO:75, SEQ ID NO:83, SEQ ID NO:91, SEQ ID NO:99, SEQ ID NO:107, SEQ ID NO:115, SEQ ID NO:123, SEQ ID NO:131, SEQ ID NO:139, SEQ ID NO:147, SEQ ID NO:155, SEQ ID NO:163, SEQ ID NO:171, SEQ ID NO:179, SEQ ID NO:187, SEQ ID NO:195, SEQ ID NO:203, SEQ ID NO:211, SEQ ID NO:219, SEQ ID NO:1 SEQ ID NO:227, SEQ ID NO:235, SEQ ID NO:243, SEQ ID NO:257, or SEQ ID NO:263. The percentage homology is not less than 70%, 80%, 90%, 95%, 98%, or 99%.

In one embodiment, the isolated mAb or antigen-binding fragment may include a variable light chain. In one embodiment, the variable light chain comprises an amino acid sequence having a percentage homology with SEQ ID NO:4, SEQ ID NO:12, SEQ ID NO:20, SEQ ID NO:28, SEQ ID NO:36, SEQ ID NO:44, SEQ ID NO:52, SEQ ID NO:60, SEQ ID NO: 68, SEQ ID NO:76, SEQ ID NO:84, SEQ ID NO:92, SEQ ID NO:100, SEQ ID NO:108, SEQ ID NO:116, SEQ ID NO:124, SEQ ID NO:132, SEQ ID NO:140, SEQ ID NO:148, SEQ ID NO:156, SEQ ID NO:164, SEQ ID NO:172, SEQ ID NO:180, SEQ ID NO:188, SEQ ID NO:196, SEQ ID NO:204, SEQ ID NO:212, SEQ ID NO:220, SEQ ID NO:228, SEQ ID NO:236, SEQ ID NO:244, SEQ ID NO:252, SEQ ID NO:260, or SEQ ID NO:268. The percentage homology is not less than 70%, 80%, 90%, 95%, 98%, or 99%.

In one embodiment, the isolated mAb or antigen-binding fragment may include a variable heavy chain. In one embodiment, the variable heavy chain comprises an amino acid sequence having a percentage homology with SEQ ID NO:8, SEQ ID NO:16, SEQ ID NO:24, SEQ ID NO:32, SEQ ID NO:40, SEQ ID NO:48, SEQ ID NO:56, SEQ ID NO:64, SEQ ID NO:72, SEQ ID NO:80, SEQ ID NO:88, SEQ ID NO:96, SEQ ID NO:104, SEQ ID NO:112, SEQ ID NO:120, SEQ ID NO:128, SEQ ID NO:136, SEQ ID NO:144, SEQ ID NO:152, SEQ ID NO:160, SEQ ID NO:168, SEQ ID NO:176, SEQ ID NO:184, SEQ ID NO:192, SEQ ID NO:200, SEQ ID NO:208, SEQ ID NO:216, SEQ ID NO:224, SEQ ID NO:232, SEQ ID NO:240, SEQ ID NO:248, SEQ ID NO:256, SEQ ID NO:264, or SEQ ID NO:272. The percentage homology is not less than 70%, 80%, 90%, 95%, 98%, or 99%.

The application further provides isolated nucleic acids encoding at least a portion of the isolated mAb or antigen-binding fragment disclosed herein. In one embodiments, the nucleic acid encodes an IgG1 heavy chain that includes an amino acid sequence having a percentage homology with SEQ ID NO:7, SEQ ID NO:15, SEQ ID NO:23, SEQ ID NO:31, SEQ ID NO:39, SEQ ID NO:47, SEQ ID NO:55, SEQ ID NO:63, SEQ ID NO:71, SEQ ID NO:79, SEQ ID NO:87, SEQ ID NO:95, SEQ ID NO:103, SEQ ID NO:111, SEQ ID NO:119,

SEQ ID NO:127, SEQ ID NO:135, SEQ ID NO:143, SEQ ID NO:151, SEQ ID NO:159, SEQ ID NO:167, SEQ ID NO:175, SEQ ID NO:183, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:207, SEQ ID NO:215, SEQ ID NO:223, SEQ ID NO:231, SEQ ID NO:239, SEQ ID NO:247, SEQ ID NO:255, SEQ ID NO:263, or SEQ ID NO:271. In one embodiment, the nucleic acid encodes a kappa light chain that comprises an amino acid sequence having a percentage homology with SEQ ID NO:3, SEQ ID NO:11, SEQ ID NO:19, SEQ ID NO:27, SEQ ID NO:35, SEQ ID NO:43, SEQ ID NO:51, SEQ ID NO:59, SEQ ID NO:67, SEQ ID NO:75, SEQ ID NO:83, SEQ ID NO:91, SEQ ID NO:99, SEQ ID NO:107, SEQ ID NO:115, SEQ ID NO:123, SEQ ID NO:131, SEQ ID NO:139, SEQ ID NO:147, SEQ ID NO:155, SEQ ID NO:163, SEQ ID NO:171, SEQ ID NO:179, SEQ ID NO:187, SEQ ID NO:195, SEQ ID NO:203, SEQ ID NO:211, SEQ ID NO:219, SEQ ID NO:1 SEQ ID NO:227, SEQ ID NO:235, SEQ ID NO:243, SEQ ID NO:257, or SEQ ID NO:263. In one embodiment, the nucleic acid encodes a variable light chain that comprises an amino acid sequence having a percentage homology with SEQ ID NO:4, SEQ ID NO:12, SEQ ID NO:20, SEQ ID NO:28, SEQ ID NO:36, SEQ ID NO:44, SEQ ID NO:52, SEQ ID NO:60, SEQ ID NO: 68, SEQ ID NO:76, SEQ ID NO:84, SEQ ID NO:92, SEQ ID NO:100, SEQ ID NO:108, SEQ ID NO:116, SEQ ID NO:124, SEQ ID NO:132, SEQ ID NO:140, SEQ ID NO:148, SEQ ID NO:156, SEQ ID NO:164, SEQ ID NO:172, SEQ ID NO:180, SEQ ID NO:188, SEQ ID NO:196, SEQ ID NO:204, SEQ ID NO:212, SEQ ID NO:220, SEQ ID NO:228, SEQ ID NO:236, SEQ ID NO:244, SEQ ID NO:252, SEQ ID NO:260, or SEQ ID NO:268. In one embodiment, the nucleic acid encodes a variable heavy chain that comprises an amino acid sequence having a percentage homology with SEQ ID NO:8, SEQ ID NO:16, SEQ ID NO:24, SEQ ID NO:32, SEQ ID NO:40, SEQ ID NO:48, SEQ ID NO:56, SEQ ID NO:64, SEQ ID NO:72, SEQ ID NO:80, SEQ ID NO:88, SEQ ID NO:96, SEQ ID NO:104, SEQ ID NO:112, SEQ ID NO:120, SEQ ID NO:128, SEQ ID NO:136, SEQ ID NO:144, SEQ ID NO:152, SEQ ID NO:160, SEQ ID NO:168, SEQ ID NO:176, SEQ ID NO:184, SEQ ID NO:192, SEQ ID NO:200, SEQ ID NO:208, SEQ ID NO:216, SEQ ID NO:224, SEQ ID NO:232, SEQ ID NO:240, SEQ ID NO:248, SEQ ID NO:256, SEQ ID NO:264, or SEQ ID NO:272. The percentage homology is not less than 70%, 80%, 90%, 95%, 98%, or 99%.

In one embodiment, an expression vector is provided comprising at least one of the isolated nucleic acids described *infra*. In one embodiment, the expression vector is expressible in a cell.

In one embodiment, a host cell is provided, comprising at least one of the nucleic acids that is described *infra*. In one embodiment, a host cell is provided, comprising the expression vector described *infra*. In one embodiment, the host cell can be a prokaryotic cell or a eukaryotic cell.

The application further provides methods for producing the isolated mAb or antigen-binding fragment disclosed herein. In one embodiment, the method uses the host cell described above. In one embodiment, the method includes the steps of providing a host cell that contains an expression vector expressible in the host cell, wherein the expression vector comprises at least one of the nucleic acids that is described *infra*, and culturing the host cells to produce an antibody by the expression of the nucleic acids.

The application further provides an immuno-conjugate that comprises a drug unit or an imaging agent linked to an isolated mAb or antigen-binding fragment with the sequences disclosed herein through a linker. The linker may be cleavable or noncleavable. In one embodiment, the linker is a chemical linker. In one embodiment, the linker comprises a covalent bond such as an ester bond, an ether bond, an amine

bond, an amide bond, a disulphide bond, an imide bond, a sulfone bond, a phosphate bond, a phosphorus ester bond, a peptide bond, a hydrazone bond or a combination thereof. In one embodiment, the linker comprises a hydrophobic poly(ethylene glycol) linker. In one embodiment, the linker comprises a peptide bond.

In one embodiment, the drug unit in the immuno-conjugate comprises a chemotherapeutic agent, a growth inhibitory agent, a cytotoxic agent from class of calicheamicin, an antimitotic agent, a toxin, a radioactive isotope, a therapeutic agent, or a combination thereof. In one embodiment, the therapeutic agent comprises an antibody, an enzyme, or a combination thereof. In one embodiment, the drug unit comprises a calicheamicin, ozogamicin, monomethyl auristatin E, emtansine, a derivative or a combination thereof.

In one embodiment, the drug unit is selected from a cytotoxic agent, an immune regulatory reagent, an imaging agent or a combination thereof. In one embodiment, the cytotoxic agent is selected from a growth inhibitory agent or a chemotherapeutic agent from a class of tubulin binders, DNA intercalators, DNA alkylators, enzyme inhibitors, immune modulators, antimetabolite agents, radioactive isotopes, or a combination thereof. In one embodiment, the cytotoxic agent is selected from a calicheamicin, ozogamicin, monomethyl auristatin E, emtansine, a derivative or a combination thereof. In one embodiment, the immune regulatory reagents activate or suppress immune cells, T cell, NK cell, B cell, macrophage, or dendritic cell.

In one embodiment, the imaging agent may be a radionuclide, a florescent agent, a quantum dots, or a combination thereof.

The application further provides pharmaceutical compositions. In one embodiment, a pharmaceutical composition comprises the isolated mAb or antigen-binding disclosed herein and a pharmaceutically acceptable carrier. In one embodiment, a pharmaceutical composition comprises the immuno-conjugate and pharmaceutically acceptable carrier.

In a further aspect, the application provides methods for treating cancer. In one embodiment, the method comprising administering to the subject an effective amount of the isolated mAb or antigen-binding fragment with the sequences disclosed herein. In one embodiment, the method includes directly injecting into the tumour site an effective amount of the monoclonal antibodies, the antigen-binding fragment thereof, and the immuno-conjugates and disclosed herein.

In some embodiments of the disclosure, the cancer has cells that express 4-1BB. Example cancer can be treated using the disclosed mAbs or their antigen-binding fragments include without limitation breast cancer, colorectal cancer, pancreatic cancer, head and neck cancer, melanoma, ovarian cancer, prostate cancer, non-small lung cell cancer, glioma, esophageal cancer, nasopharyngeal cancer, anal cancer, rectal cancer, gastric cancer, bladder cancer, cervical cancer, or brain cancer.

In one embodiment, the method further includes co-administering an effective amount of a therapeutic agent. In one embodiment, the therapeutic agent can include an antibody, a chemotherapy agent, an enzyme, or a combination thereof. In one embodiment, the therapeutic agent may be capecitabine,

cisplatin, trastuzumab, fulvestrant, tamoxifen, letrozole, exemestane, anastrozole, aminoglutethimide, testolactone, vorozole, formestane, fadrozole, letrozole, erlotinib, lafatinib, dasatinib, gefitinib, imatinib, pazopinib, lapatinib, sunitinib, nilotinib, sorafenib, nab-palitaxel, calicheamicin, antimitotic agent, monomethyl auristatin E, emtansine, ozogamicin, or a derivative or a combination thereof.

The subject receiving the treatment may be a human. In one embodiment, a solution is provided that comprises an effective concentration of the isolated mAb or an antigen-binding disclosed herein, wherein the solution is blood plasma in a subject.

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

BRIEF DESCRIPTION OF THE DRAWINGS

The foregoing and other features of this disclosure will 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 will be described with additional specificity and detail through use of the accompanying drawings, in which:

FIGURE 1 Immunization schedule for rabbit cohorts no.1 and 2 with human 41BB or cynomolgus 41BB transiently transfected HEK293 cells.

FIGURE 2 41BB-specific rabbit IgG antibodies in B cell culture supernatant enhance activation of anti-CD3 activated human T cells and corresponding binding of chimeric rabbit/human IgG 41BB-specific antibodies rescued from the parental B cell culture wells to recombinant human and cynomolgus 41BB protein.

FIGURE 3 Chimeric rabbit/human IgG antibodies specific for 41BB enhance T cell activation, proliferation, and gamma interferon secretion.

FIGURE 4. Octet analysis of dissociation rate for humanized 41BB-specific IgG antibodies.

FIGURE 5. Humanized 41BB-specific IgG antibodies enhance T cell activation, proliferation, and gamma interferon secretion.

FIGURE 6. Serum from rabbits immunized with human or cynomolgus 41BB expressing HEK293's analyzed for 41BB-specific IgG antibody binding to parental CHO or human or cynomolgus 41BB-transfected CHO cells.[

FIGURE 7. Correlation of 41BB-specific IgG antibody in B cell culture supernatant enhancement of Gamma interferon secretion versus proliferation of human T cells.

DETAILED DESCRIPTION

In the following detailed description, reference is made to the accompanying drawings, which form a part hereof. In the drawings, similar symbols typically identify similar components, unless context dictates otherwise. The illustrative embodiments described in the detailed description, drawings, and claims are not meant to be limiting. Other embodiments may be utilized, and other changes may be made, without departing from the spirit or scope of the subject matter presented herein. It will be readily understood that the aspects of the present disclosure, as generally described herein, and illustrated in the Figures, can be arranged, substituted, combined, separated, and designed in a wide variety of different configurations, all of which are explicitly contemplated herein.

The disclosure provides, among others, isolated antibodies, methods of making such antibodies, bispecific or multi-specific molecules, antibody-drug conjugates and/or immuno-conjugates composed from such antibodies or antigen binding fragments and pharmaceutical compositions containing the antibodies, bispecific or multi-specific molecules, antibody-drug conjugates and/or immuno-conjugates.

In one aspect, the disclosure provides isolated monoclonal antibodies that bind to human or cynomolgus 4-1BB. The antibodies may exhibit one or more desirable functional properties, such as high affinity binding to 4-1BB, the ability to enhance T cell activation including proliferation, IFN-γ and/or CD3+ T cell proliferation, IL-2 secretion, survival and cytolytic activity, the ability to stimulate antibody responses and/or the ability to reverse the suppressive function of immunosuppressive cells, such as T regulatory cells. In addition, the antibodies of the disclosure are derived from specific heavy and light chain amino acid sequences and/or structural features such as complementarity determining regions (CDRs) composed of specific amino acid sequences.

The term “antibody” is used in the broadest sense and specifically covers single monoclonal antibodies (including agonist and antagonist antibodies), antibody compositions with polyepitopic specificity, as well as antibody fragments (e.g., Fab, $F(ab')_2$, and Fv), so long as they exhibit the desired biological activity. In some embodiments, the antibody may be monoclonal, polyclonal, chimeric, single chain, bispecific or bi-effective, simianized, human and humanized antibodies as well as active fragments thereof. Examples of active fragments of molecules that bind to known antigens include Fab, $F(ab')_2$, scFv and Fv fragments, including the products of an Fab immunoglobulin expression library and epitope-binding fragments of any of the antibodies and fragments mentioned above. In some embodiments, antibody may include immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, i.e. molecules that contain a binding site that immunospecifically bind an antigen. The immunoglobulin can be of any type (IgG, IgM, IgD, IgE, IgA and IgY) or class (IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2) or subclasses of immunoglobulin molecule. In one embodiment, the antibody may be whole antibodies and any antigen-binding fragment derived from the whole antibodies. A typical antibody refers to heterotetrameric protein comprising typically of two heavy (H) chains and two light (L) chains. Each heavy chain is comprised of a heavy chain variable domain (abbreviated as VH) and a

heavy chain constant domain. Each light chain is comprised of a light chain variable domain (abbreviated as VL) and a light chain constant domain. The VH and VL regions can be further subdivided into domains of hypervariable complementarity determining regions (CDR), and more conserved regions called framework regions (FR). Each variable domain (either VH or VL) is typically composed of three CDRs and four FRs, arranged in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4 from amino-terminus to carboxy-terminus. Within the variable regions of the light and heavy chains there are binding regions that interacts with the antigen.

The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally occurring mutations that may be present in minor amounts. Monoclonal antibodies are highly specific, being directed against a single antigenic site. Furthermore, in contrast to conventional (polyclonal) antibody preparations which typically include different antibodies directed against different determinants (epitopes), each monoclonal antibody is directed against a single determinant on the antigen. In addition to their specificity, the monoclonal antibodies are advantageous in that they are synthesized by the hybridoma culture, uncontaminated by other immunoglobulins. The modifier "monoclonal" indicates the character of the antibody as being obtained from a substantially homogeneous population of antibodies, and is not to be construed as requiring production of the antibody by any particular method. For example, the monoclonal antibodies to be used in accordance with the present disclosure may be made by the hybridoma method first described by Kohler & Milstein, Nature, 256:495 (1975), or may be made by recombinant DNA methods (see, e.g., U.S. Pat. No. 4,816,567).

The monoclonal antibodies may include "chimeric" antibodies (immunoglobulins) in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, so long as they exhibit the desired biological activity (U.S. Pat. No. 4,816,567; and Morrison et al., Proc. Natl. Acad. Sci. USA, 81:6851-6855 [1984]).

Monoclonal antibodies can be produced using various methods including mouse hybridoma or phage display (see Siegel. Transfus. Clin. Biol. 9:15-22 (2002) for a review) or from molecular cloning of antibodies directly from primary B cells (see Tiller. New Biotechnol. 28:453-7 (2011)). In the present disclosure antibodies were created by the immunization of rabbits with cells transiently expressing human or cynomolgus 4-1BB on the cell surface. Rabbits are known to create antibodies of high affinity, diversity and specificity (Weber et al. Exp. Mol. Med. 49:e305). B cells from immunized animals were cultured in vitro and screened for the production of anti-4-1BB antibodies. The antibody variable genes were isolated using recombinant DNA techniques and the resulting antibodies were expressed recombinantly and further screened for desired features such as the ability to enhance human T-cell activation. This general method of antibody discovery is similar to that described in Seeber et al. PLOS One. 9:e86184 (2014).

The term "antigen- or epitope-binding portion or fragment" refers to fragments of an antibody that are capable of binding to an antigen (4-1BB in this case). These fragments may be capable of the antigen-binding function and additional functions of the intact antibody. Examples of binding fragments include, but are not limited to, a single-chain Fv fragment (scFv) consisting of the VL and VH domains of a single arm of an antibody connected in a single polypeptide chain by a synthetic linker or a Fab fragment which is a monovalent fragment consisting of the VL, constant light (CL), VH and constant heavy 1 (CH1) domains. Antibody fragments can be even smaller subfragments and can consist of domains as small as a single CDR domain, in particular the CDR3 regions from either the VL and/or VH domains (for example see Beiboer et al., J. Mol. Biol. 296:833-49 (2000)). Antibody fragments are produced using conventional methods known to those skilled in the art. The antibody fragments are can be screened for utility using the same techniques employed with intact antibodies.

The "antigen-or epitope-binding fragments" can be derived from an antibody of the present disclosure by a number of art-known techniques. For example, purified monoclonal antibodies can be cleaved with an enzyme, such as pepsin, and subjected to HPLC gel filtration. The appropriate fraction containing Fab fragments can then be collected and concentrated by membrane filtration and the like. For further description of general techniques for the isolation of active fragments of antibodies, see for example, Khaw, B. A. et al. J. Nucl. Med. 23:1011-1019 (1982); Rousseaux et al. Methods Enzymology, 121:663-69, Academic Press, 1986.

Papain digestion of antibodies produces two identical antigen binding fragments, called "Fab" fragments, each with a single antigen binding site, and a residual "Fc" fragment, whose name reflects its ability to crystallize readily. Pepsin treatment yields an $F(ab')_2$ fragment that has two antigen combining sites and is still capable of cross-linking antigen.

The Fab fragment may contain the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab' fragments differ from Fab fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. $F(ab')_2$ antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other, chemical couplings of antibody fragments are also known.

"Fv" is the minimum antibody fragment which contains a complete antigen recognition and binding site. This region consists of a dimer of one heavy and one light chain variable domain in tight, non-covalent association. It is in this configuration that the three CDRs of each variable domain interact to define an antigen binding site on the surface of the VH-VL dimer. Collectively, the six CDRs confer antigen binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

The “light chains” of antibodies (immunoglobulins) from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda (λ), based on the amino acid sequences of their constant domains.

Depending on the amino acid sequence of the constant domain of their heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG and IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG-1, IgG-2, IgG-3, and IgG-4; IgA-1 and IgA-2. The heavy chain constant domains that correspond to the different classes of immunoglobulins are called α, delta, epsilon, γ, and μ, respectively. The subunit structures and three-dimensional configurations of different classes of immunoglobulins are well known.

A “humanized antibody” refers to a type of engineered antibody having its CDRs derived from a non-human donor immunoglobulin, the remaining immunoglobulin-derived parts of the molecule being derived from one (or more) human immunoglobulin(s). In addition, framework support residues may be altered to preserve binding affinity. Methods to obtain “humanized antibodies” are well known to those skilled in the art. (see, e.g., Queen et al., Proc. Natl Acad Sci USA, 86:10029-10032 (1989), Hodgson et al., Bio/Technology, 9:421 (1991)).

The terms “polypeptide”, “peptide”, and “protein”, as used herein, are interchangeable and are defined to mean a biomolecule composed of amino acids linked by a peptide bond.

The terms “a”, “an” and “the” as used herein are defined to mean “one or more” and include the plural unless the context is inappropriate.

By “isolated” is meant a biological molecule free from at least some of the components with which it naturally occurs. "Isolated," when used to describe the various polypeptides disclosed herein, means a polypeptide that has been identified and separated and/or recovered from a cell or cell culture from which it was expressed. Ordinarily, an isolated polypeptide will be prepared by at least one purification step. An "isolated antibody," refers to an antibody which is substantially free of other antibodies having different antigenic specificities.

"Recombinant" means the antibodies are generated using recombinant nucleic acid techniques in exogeneous host cells.

The term “antigen” refers to an entity or fragment thereof which can induce an immune response in an organism, particularly an animal, more particularly a mammal including a human. The term includes immunogens and regions thereof responsible for antigenicity or antigenic determinants.

Also as used herein, the term “immunogenic” refers to substances which elicit or enhance the production of antibodies, T-cells or other reactive immune cells directed against an immunogenic agent and contribute to an immune response in humans or animals. An immune response occurs when an individual produces sufficient antibodies, T-cells and other reactive immune cells against administered immunogenic compositions of the present disclosure to moderate or alleviate the disorder to be treated.

"Specific binding" or "specifically binds to" or is "specific for" a particular antigen or an epitope means binding that is measurably different from a non-specific interaction. Specific binding can be measured, for example, by determining binding of a molecule compared to binding of a control molecule, which generally is a molecule of similar structure that does not have binding activity. For example, specific binding can be determined by competition with a control molecule that is similar to the target.

Specific binding for a particular antigen or an epitope can be exhibited, for example, by an antibody having a KD for an antigen or epitope of at least about 10^{-4} M, at least about 10^{-5} M, at least about 10^{-6} M, at least about 10^{-7} M, at least about 10^{-8} M, at least about 10^{-9} M, alternatively at least about 10^{-10} M, at least about 10^{-11} M, at least about 10^{-12} M, or greater, where KD refers to a dissociation rate of a particular antibody-antigen interaction. Typically, an antibody that specifically binds an antigen will have a KD that is 20-, 50-, 100-, 500-, 1000-, 5,000-, 10,000- or more times greater for a control molecule relative to the antigen or epitope.

Also, specific binding for a particular antigen or an epitope can be exhibited, for example, by an antibody having a KA or Ka for an antigen or epitope of at least 20-, 50-, 100-, 500-, 1000-, 5,000-, 10,000- or more times greater for the epitope relative to a control, where KA or Ka refers to an association rate of a particular antibody-antigen interaction.

“Homology” between two sequences is determined by sequence identity. If two sequences which are to be compared with each other differ in length, sequence identity preferably relates to the percentage of the nucleotide residues of the shorter sequence which are identical with the nucleotide residues of the longer sequence. Sequence identity can be determined conventionally with the use of computer programs. The deviations appearing in the comparison between a given sequence and the above-described sequences of the disclosure may be caused for instance by addition, deletion, substitution, insertion or recombination.

In another aspect, the application provides pharmaceutical composition including the mAbs and their antigen-binding fragments disclosed herein. In one embodiment, the pharmaceutical composition includes the mAbs or their antigen-binding fragments and a pharmaceutically acceptable carrier. In one embodiment, the pharmaceutical composition includes the immuno-conjugate and a pharmaceutically acceptable carrier. Formulation of the pharmaceutical composition according to the disclosure can be accomplished according to standard methodology know to those of ordinary skill in the art.

The antibodies or immuno-conjugates according to the disclosure can be prepared in a physiologically acceptable formulation and may comprise a pharmaceutically acceptable carrier, diluent and/or excipient using known techniques. For example, the antibody according to the disclosure may include any functionally equivalent antibody or functional parts thereof, in particular, the monoclonal antibody including any functionally equivalent antibody or functional parts thereof is combined with a pharmaceutically acceptable carrier, diluent and/or excipient to form a therapeutic composition. Suitable pharmaceutical carriers, diluents and/or excipients are well known in the art and include, for example, phosphate buffered saline solutions, water, emulsions such as oil/water emulsions.

"Pharmaceutically acceptable" refers to those compounds, materials, compositions, and dosage forms which are, within the scope of sound medical judgment, suitable for use contact with the tissues of human beings or animals without excessive toxicity, irritation, or other problem or complication, commensurate with a reasonable benefit/risk ratio.

In one embodiment, the pharmaceutical composition may comprise proteinaceous carriers such as, for example, serum albumin or immunoglobulin, particularly of human origin. Further biologically active agents may be present in the pharmaceutical composition of the disclosure dependent on the intended use. Proteinaceous pharmaceutically active matter may be present in amounts between 1 ng and 10 mg per dose. Generally, the regime of administration should be in the range of between 0.1 μg and 10 mg of the antibody according to the disclosure, particularly in a range 1.0 μg to 1.0 mg, and more particularly in a range of between 1.0 μg and 100 μg, with all individual numbers falling within these ranges also being part of the disclosure. If the administration occurs through continuous infusion a more proper dosage may be in the range of between 0.01 μg and 10 mg units per kilogram of body weight per hour with all individual numbers falling within these ranges also being part of the disclosure.

In a further aspect, the disclosure provide method for treating cancer using anti-4-1BB antibodies or other molecules containing the antigen-binding portion of an anti-4-1BB antibody. In one embodiment, the method is used to inhibit growth of tumour cells. In one embodiment, the method is used to stimulate a protective autoimmune response, to modify an immune response or to stimulate antigen-specific immune responses.

In one embodiment, the method for treating cancer includes administering to a subject in need of such treatment an effective amount of the mAbs, their antigen-binding fragments as disclosed herein. In one embodiment, the composition may be administered in combination with other compositions comprising a biologically active substance or compound. In one embodiment, the biologically active substance may include capecitabine, cisplatin, trastuzumab, fulvestrant, tamoxifen, letrozole, exemestane, anastrozole, aminoglutethimide, testolactone, vorozole, formestane, fadrozole, letrozole, erlotinib, lafatinib, dasatinib, gefitinib, imatinib, pazopinib, lapatinib, sunitinib, nilotinib, sorafenib, nab-palitaxel, a derivative or a combination thereof.

The compositions of the present disclosure may be administered to a subject in the form of a solid, liquid or aerosol at a suitable, pharmaceutically effective dose. Examples of solid compositions include pills, creams, and implantable dosage units. Pills may be administered orally. Therapeutic creams may be administered topically. Implantable dosage units may be administered locally, for example, at a tumour site, or may be implanted for systematic release of the therapeutic composition, for example, subcutaneously. Examples of liquid compositions include formulations adapted for injection intramuscularly, subcutaneously, intravenously, intra-arterially, and formulations for topical and intraocular administration. Examples of aerosol formulations include inhaler formulations for administration to the lungs.

The compositions may be administered by standard routes of administration. For example, the composition may be administered by topical, oral, rectal, nasal, interdermal, intraperitoneal, or

parenteral (for example, intravenous, subcutaneous, or intramuscular) routes. In one embodiment, administration may be parenterally, e.g. intravenously. Preparations for parenteral administration include sterile aqueous or non-aqueous solutions, suspensions and emulsions. Non-aqueous solvents include without being limited to it, propylene glycol, polyethylene glycol, vegetable oil such as olive oil, and injectable organic esters such as ethyl oleate. Aqueous solvents may be chosen from the group consisting of water, alcohol/aqueous solutions, emulsions or suspensions including saline and buffered media. Parenteral vehicles include sodium chloride solution, Ringer's dextrose, dextrose and sodium chloride, lactated Ringer's, or fixed oils. Intravenous vehicles include fluid and nutrient replenishers, electrolyte replenishers (such as those based on Ringer's dextrose) and others. Preservatives may also be present such as, for example, antimicrobials, anti-oxidants, chelating agents, inert gases, etc.

In one embodiment, the composition may be incorporated into sustained release matrices such as biodegradable polymers, the polymers being implanted in the vicinity of where delivery is desired, for example, at the site of a tumour. The method includes administration of a single dose, administration of repeated doses at predetermined time intervals, and sustained administration for a predetermined period of time.

It is known to those of ordinary skill in the art that the dosage of the composition will depend on various factors such as, for example, the condition of being treated, the particular composition used, and other clinical factors such as weight, size, sex and general health condition of the patient, body surface area, the particular compound or composition to be administered, other drugs being administered concurrently, and the route of administration.

In one embodiment, the term “therapeutically effective amount” refers to the amount of antibody which, when administered to a human or animal, elicits a response which is sufficient to result in a therapeutic effect in said human or animal. The effective amount is readily determined by one of ordinary skill in the art following routine procedures.

Varieties of cancer may be treated using the mAbs, their antigen-binding fragments, and compositions disclosed herein. Example cancer including without limitation breast cancer, colorectal cancer, pancreatic cancer, head and neck cancer, melanoma, ovarian cancer, prostate cancer, non-small lung cell cancer, glioma, esophageal cancer, nasopharyngeal cancer, anal cancer, rectal cancer, gastric cancer, bladder cancer, cervical cancer, or brain cancer. In one embodiment, the cancer may express 4-1BB genes. Inhibition of 4-1BB activity with anti-4-1BB monoclonal antibodies or antigen-binding fragment provides therapeutic effect. In one embodiment, administering a therapeutically effective amount of composition comprising anti-4-1BB monoclonal antibodies or antigen-binding fragment may cure, prevent, ameliorate, and delay the development or metastasis of cancers, through the effect of the drug unit.

The present disclosure may be understood more readily by reference to the following detailed description of specific embodiments included herein. Although the present disclosure has been described with reference to specific details of certain embodiments thereof, it is not intended that such details should be regarded as limitations upon the scope of the disclosure.

EXAMPLES

Example 1: Generation of Anti-4-1BB Antibodies

Monoclonal antibodies against human or cynomolgus 4-1BB were developed by immunizing New Zealand white rabbits. As shown in FIGURE 1, animals were immunized with recombinant human embryonic kidney 293 (HEK) cells transiently transfected with human or cynomolgus 4-1BB mixed 1:1 v/v with Titermax Gold (Cohort 1) or Complete or incomplete Freund's adjuvant (Cohort 2) alternating with Alhydrogel 2% (Alum) plus CpG 2007 and were performed by subcutaneous injection. Blood samples were drawn at different timepoints during the immunization schedule as shown in FIGURE 1. Serum which was drawn from all 4 animals on day 62 was analyzed for human or cynomolgus 4-1BB-specific IgG by FACS analysis as shown in FIGURE 6. All 4 animals developed human or cynomolgus-specific IgG after immunization.

Antigen-specific B cells were labeled with biotinylated human and cynomolgus 4-1BB recombinant protein followed by streptavidin-alexafluor647 and then sorted into multiple 96 well tissue culture plates at 1 antigen-specific IgG+ B cell per well and cultured for 9 days to allow their differentiation into plasma cells and for secretion of antibodies. The supernatants from these B cell culture (BCC) plates were screened by ELISA and functional assay for the presence of 4-1BB-specific antibodies in the assays as listed below:

Binding to recombinant human and cynomolgus 4-1BB - IgG ELISA

Enhancement of CD3-induced T cell activation of purified human CD3+ T cells – detection of gamma interferon secretion by ELISA and quantitation of CD3+ T cell proliferation by alamar blue cell viability assay

A total of 693 wells from the BCC plates had human and cynomolgus 4-1BB-specific IgG. The 4-1BB-specific antibody from these 693 BCC wells were then analyzed for agonist activity to enhance anti-CD3-induced activation of CD3+ human T cells. A fixed concentration of a control anti-human CD3-specific antibody was combined with a fixed concentration of 4-1BB-specific antibody from the BCC supernatants and then captured on and ELISA plate that was previously coated with a goat anti-rabbit IgG Fc polyclonal antibody. Purified human CD3+ T cells were added at 100,000 per each assay well and the plate was incubated for 5 days. On day 5 of the assay the contents of each assay well were collected and analyzed for the amount of gamma interferon secreted into the culture supernatant and for the number of CD3+ T cells in each assay well which is shown in FIGURE 7. From these data the best 92 BCC wells were advanced to molecular rescue of the rabbit antibody heavy and light chain variable regions by RT-PCR.

On day 9 of B cell culture the supernatants were separated from the B cells and stored in a separate plate for later analysis. RNAlater tissue storage reagent was added to each well in the B cell culture plate to preserve the RNA in the B cells for RT-PCR amplification of antibody variable regions. The set of 92 BCC wells were advanced to molecular "rescue" of the antibody variable regions. The light and heavy chain variable sequences were amplified by multiplex RT-PCR using degenerate primers designed to

anneal to leader sequences and the constant regions of rabbit IgG and rabbit kappa sequences. Secondary PCR was performed separately for the light and heavy chains using nested primers containing restriction sites. Amplicons from the variable heavy chain PCR were cloned into an expression vector containing human IgG1. Light chain amplicons were cloned into an expression vector containing human IgK. Resulting clones were sequenced and analyzed.

The heavy and light chain expression plasmids generated from each well were transiently co-transfected to produce rabbit/human chimeric antibodies. Recombinant antibody supernatants were confirmed to contain antibodies specific for human and cynomolgus 4-1BB using bio-layer interferometry analysis on a ForteBio Octet Red 96 instrument. Anti-human Fc biosensors (Pall ForteBio) were used to capture antibodies in the supernatants. Association to human or cynomolgus 4-1BB was observed by real-time interferometry by placing the biosensors in wells containing recombinant human or cynomolgus 4-1BB extracellular domain protein. Dissociation was measured after transfer of the biosensors into wells containing 10X kinetics buffer (Pall ForteBio). The software provided by the manufacturer was used to analyze the interferometry data. A summary of the primary BCC screening data and the corresponding screening data for 34 recombinant chimeric rabbit/human IgG antibodies is shown in FIGURE 2. From the original 92 BCC wells 34 chimeric antibodies were rescued and were shown to bind human and cynomolgus recombinant 4-1BB protein (FIGURE 2)

The panel of 34 chimeric rabbit/human IgG antibodies specific for human and cynomolgus 4-1BB were then assayed for agonist activity which enhanced the anti-CD3-induced activation of human CD3+ T cells. As shown in FIGURE 3, EC_{50} for secretion of gamma interferon were calculated for each chimeric antibody as well as the fold-over-background of the enhancement of proliferation of human CD3+ T cells. Proliferation of human CD3+ T cells with anti-CD3 antibody alone, without additional 4-1BB antibody, is set to the background value of 1.0 and then the fold-over-background is calculated at different concentrations of the chimeric 4-1BB antibodies are tested. From these data 18 chimeric 4-1BB-specific antibodies were advanced to humanization.

From the panel of 34 chimeric rabbit/human IgG antibodies specific for human and cynomolgus 4-1BB that were advanced to humanization 18 were successfully humanized as shown in FIGURE 4 where binding to human and recombinant 4-1BB by octet assay was performed. These 18 humanized antibodies specific for human or cynomolgus 4-1BB were then assayed for agonist activity which enhanced the anti-CD3-induced activation of human CD3+ T cells. As shown in FIGURE 5, EC_{50} for secretion of gamma interferon were calculated for each humanized antibody as well as the fold-over-background of the enhancement of proliferation of human CD3+ T cells. Proliferation of human CD3+ T cells with anti-CD3 antibody alone, without additional 4-1BB antibody, is set to the background value of 1.0 and then the fold-over-background is calculated at different concentrations of the humanized 4-1BB antibodies are tested. From these data 17 of the 18 humanized 4-1BB-specific antibodies showed enhancement of anti-CD3-induced activation of human CD3+ T cells.

While the disclosure has been particularly shown and described as referenced to the embodiments thereof, those skilled in the art will understand that the foregoing and other changes in form and detail

may be made therein without departing from the spirit and scope. All references cited or referred to in this disclosure are hereby incorporated by reference in their entireties.

SEQUENCE LISTING

SEQ ID NO:1

411H11 CHIMERIC LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GATGTTGTGATGACCCAGACTCCAGCCTCCGTGTCTGAACCTGTGAGAGCCACAGTCACCATCAAGTGCCAGGCCA
GTCAGAGCATTGGTGCTGATTTAGCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTACAGGG
CATCCACTCTGGCCTCTGGGGTCCCATCGCGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAG
CGACCTGGAGTGTGCCGATGCTGCCACTTACTACTGTCAATGTATTTATTATGGTACTGATGATGTCATATACCATA
CTTTCGGCGGAGGGACCGAGGTGGTGTTCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGA
TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAG
TGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCAC
CTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCAC
CCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:2

411H11 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GATGTTGTGATGACCCAGACTCCAGCCTCCGTGTCTGAACCTGTGAGAGCCACAGTCACCATCAAGTGCCAGGCCA
GTCAGAGCATTGGTGCTGATTTAGCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTACAGGG
CATCCACTCTGGCCTCTGGGGTCCCATCGCGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAG
CGACCTGGAGTGTGCCGATGCTGCCACTTACTACTGTCAATGTATTTATTATGGTACTGATGATGTCATATACCATA
CTTTCGGCGGAGGGACCGAGGTGGTGTTCAAA

SEQ ID NO:3

411H11 CHIMERIC LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

DVVMTQTPASVSEPVRATVTIKCQASQSIGADLAWYQQKPGQPPKLLIYRASTLASGVPSRFSGSGSGTEFTLTISDLEC
ADAATYYCQCIYYGTDDVIYHTFGGGTEVVFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:4

411H11 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

DVVMTQTPASVSEPVRATVTIKCQASQSIGADLAWYQQKPGQPPKLLIYRASTLASGVPSRFSGSGSGTEFTLTISDLEC
ADAATYYCQCIYYGTDDVIYHTFGGGTEVVFK

SEQ ID NO:5

411H11 CHIMERIC HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

CAGTCGGTGGAGGAGTCCGGGGGTCGCCTGGTCACGCCTGGGACACCCCTAACACTCACCTGCACAGTATCTGGA
TTCACCATCAGTAGCCACCACATGATCTGGGTCCGCCAGGCTCCAGGAGAGGGGCTGCAATACATCGGATTCATTA
ATGATGGTGACTATACATACTACACGAACTGGGCAAAAGGCCGATTCACCATCTCCAGAACCTCGACTACGGTGG
ACCTGAAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCTGTGCCAGAGGGGTTGATGGTACTAGTT
ATCCTGGCTTGTGGGGCCCAGGCACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCT
GGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACC
GGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGG
ACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCG
TGCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCT
CCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
TCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCC
TCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCC
CATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCG
CCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGC
TCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGA
TGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:6

411H11 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

CAGTCGGTGGAGGAGTCCGGGGGTCGCCTGGTCACGCCTGGGACACCCCTAACACTCACCTGCACAGTATCTGGA
TTCACCATCAGTAGCCACCACATGATCTGGGTCCGCCAGGCTCCAGGAGAGGGGCTGCAATACATCGGATTCATTA
ATGATGGTGACTATACATACTACACGAACTGGGCAAAAGGCCGATTCACCATCTCCAGAACCTCGACTACGGTGG
ACCTGAAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCTGTGCCAGAGGGGTTGATGGTACTAGTT
ATCCTGGCTTGTGGGGCCCAGGCACCCTGGTCACCGTCTCGAGC

SEQ ID NO:7

411H11 CHIMERIC HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

QSVEESGGRLVTPGTPLTLTCTVSGFTISSHHMIWVRQAPGEGLQYIGFINDGDYTYYTNWAKGRFTISRTSTTVDLKM
TSLTAADTATYFCARGVDGTSYPGLWGPGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS
GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSV
FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
YKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL
DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:8

411H11 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

QSVEESGGRLVTPGTPLTLTCTVSGFTISSHHMIWVRQAPGEGLQYIGFINDGDYTYYTNWAKGRFTISRTSTTVDLKM
TSLTAADTATYFCARGVDGTSYPGLWGPGTLVTVSS

SEQ ID NO:9

413F3 CHIMERIC LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GACGTCGTGATGACCCAGACTCCAGCCTCCGTGGAGGCAGCTGTGGGAGGCACAGTCACCATCAAGTGCCAGGC
CAGTCAGAGCATTTACAGCAATTTAGCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAACTCCTAATCTATTCT
ACATCCACTCTGGCATCTGGGGTCCCATCGCGGTTCAGCGGCAGTGGATCCGGGACAGAGTTCACTCTCACCATCA
GCGACCTGGAGTGTGCCGATGCTGCCACTTACTACTGTCAAAACTATTATGGTAGTAGTACTGATAGTTATGGGAA
TCCTTTCGGCGGAGGCACCGAGGTGGTGTTCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCT
GATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTAC
AGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGC
ACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTC
ACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:10

413F3 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GACGTCGTGATGACCCAGACTCCAGCCTCCGTGGAGGCAGCTGTGGGAGGCACAGTCACCATCAAGTGCCAGGC
CAGTCAGAGCATTTACAGCAATTTAGCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAACTCCTAATCTATTCT
ACATCCACTCTGGCATCTGGGGTCCCATCGCGGTTCAGCGGCAGTGGATCCGGGACAGAGTTCACTCTCACCATCA
GCGACCTGGAGTGTGCCGATGCTGCCACTTACTACTGTCAAAACTATTATGGTAGTAGTACTGATAGTTATGGGAA
TCCTTTCGGCGGAGGCACCGAGGTGGTGTTCAAA

SEQ ID NO:11

413F3 CHIMERIC LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

DVVMTQTPASVEAAVGGTVTIKCQASQSIYSNLAWYQQKPGQPPKLLIYSTSTLASGVPSRFSGSGSGTEFTLTISDLEC
ADAATYYCQNYYGSSTDSYGNPFGGGTEVVFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:12

413F3 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

DVVMTQTPASVEAAVGGTVTIKCQASQSIYSNLAWYQQKPGQPPKLLIYSTSTLASGVPSRFSGSGSGTEFTLTISDLEC
ADAATYYCQNYYGSSTDSYGNPFGGGTEVVFK

SEQ ID NO:13

413F3 CHIMERIC HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

CAGTCGCTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGAGGGATCCCTGACACTCACCTGCACAGGCTCTGG
AATCGACTTCAGTAGCAACTACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCAT
TTATGGTGATAGTAGTGATAATAGTTACTCCGCGAGCTGGGCGAAAGGGCGATTCACCATCTCCAAAACCTCGTCG
ACCACGGTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCTGTGCGAGATCTGGTTATA
GCTATTTAGGCTACTTTAACTTGTGGGGCCCAGGGACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATC
GGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
CTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTA
CAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCT
GCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACA
CATGCCCACCGTGCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC
CCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTT
CAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG
TACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCC
AACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA
GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGAC
TCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCAT
GCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:14

413F3 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

CAGTCGCTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGAGGGATCCCTGACACTCACCTGCACAGGCTCTGG
AATCGACTTCAGTAGCAACTACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCAT
TTATGGTGATAGTAGTGATAATAGTTACTCCGCGAGCTGGGCGAAAGGGCGATTCACCATCTCCAAAACCTCGTCG
ACCACGGTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCTGTGCGAGATCTGGTTATA
GCTATTTAGGCTACTTTAACTTGTGGGGCCCAGGGACCCTGGTCACCGTCTCGAGC

SEQ ID NO:15

413F3 CHIMERIC HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

QSLEESGGDLVKPEGSLTLTCTGSGIDFSSNYMCWVRQAPGKGLEWIACIYGDSSDNSYSASWAKGRFTISKTSSTTVTL
QMTSLTAADTATYFCARSGYSYLGYFNLWGPGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAG
APSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL

NGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:16

413F3 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

QSLEESGGDLVKPEGSLTLTCTGSGIDFSSNYMCWVRQAPGKGLEWIACIYGDSSDNSYSASWAKGRFTISKTSSTTVTL
QMTSLTAADTATYFCARSGYSYLGYFNLWGPGTLVTVSS

SEQ ID NO:17

416F8 CHIMERIC LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GCGCAAGTGCTGACCCAGACTGCATCGTCCGTGTCTGCACCTGTGGGCGGCACAGTCACCATCAGTTGCCAGTCCA
GTCAGACTGTTTATAATAACAACTTGTTATCCTGGTATCAGCAGAAACCAGGGCAGCGTCCCAAGCTCCTGATCTA
TTATGCATCCACTCTGGCATTTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGAGTTCACTCTCACC
ATCAGCGACCTGGAGTGTGACGATGCTGCCACTTACTTCTGTCAAGGCGGTTATAGTGGTTGGATTTATGTTTTCG
GCGGAGGCACCGAGGTGGAGGTCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGC
AGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAA
GGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACA
GCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATC
AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:18

416F8 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GCGCAAGTGCTGACCCAGACTGCATCGTCCGTGTCTGCACCTGTGGGCGGCACAGTCACCATCAGTTGCCAGTCCA
GTCAGACTGTTTATAATAACAACTTGTTATCCTGGTATCAGCAGAAACCAGGGCAGCGTCCCAAGCTCCTGATCTA
TTATGCATCCACTCTGGCATTTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGAGTTCACTCTCACC
ATCAGCGACCTGGAGTGTGACGATGCTGCCACTTACTTCTGTCAAGGCGGTTATAGTGGTTGGATTTATGTTTTCG
GCGGAGGCACCGAGGTGGAGGTCAAA

SEQ ID NO:19

416F8 CHIMERIC LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

AQVLTQTASSVSAPVGGTVTISCQSSQTVYNNNLLSWYQQKPGQRPKLLIYYASTLAFGVPSRFKGSGSGTEFTLTISDLE
CDDAATYFCQGGYSGWIYVFGGGTEVEVKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS
GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:20

416F8 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

AQVLTQTASSVSAPVGGTVTISCQSSQTVYNNNLLSWYQQKPGQRPKLLIYYASTLAFGVPSRFKGSGSGTEFTLTISDLE CDDAATYFCQGGYSGWIYVFGGGTEVEVK

SEQ ID NO:21

416F8 CHIMERIC HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

CAGTCGCTGGAGGAGTCCGGGGGTCGCCTGGTCACGCCTGGGACACCCCTGACACTCACCTGCACAGCCTCTGGA
TTCTCCCTCAGTAACTACTACATGAACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAATACATCGGAATCATTA
GTAGTAGTGGTAGCGCATACTACGCGAGCTGGGCTAAAGGCCGATTCACCATCTCCAGAACCTCGACCACGGTGG
ACCTGAGAATCACCAGTCCGACAACCGAGGACACGGCCACCTATTTCTGTGCCAGAGGGGACTACGGCATGGACC
TCTGGGGCCAAGGGACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTC
CTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGT
GTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCC
CTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCC
AGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA
CCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCC
CTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
GTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCT
CACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCCAGCCCC
CATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGA
TGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTG
GGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCT
CTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGC
TCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:22

416F8 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

CAGTCGCTGGAGGAGTCCGGGGGTCGCCTGGTCACGCCTGGGACACCCCTGACACTCACCTGCACAGCCTCTGGA
TTCTCCCTCAGTAACTACTACATGAACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAATACATCGGAATCATTA
GTAGTAGTGGTAGCGCATACTACGCGAGCTGGGCTAAAGGCCGATTCACCATCTCCAGAACCTCGACCACGGTGG
ACCTGAGAATCACCAGTCCGACAACCGAGGACACGGCCACCTATTTCTGTGCCAGAGGGGACTACGGCATGGACC
TCTGGGGCCAAGGGACCCTGGTCACCGTCTCGAGC

SEQ ID NO:23

416F8 CHIMERIC HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

QSLEESGGRLVTPGTPLTLTCTASGFSLSNYYMNWVRQAPGKGLEYIGIISSSGSAYYASWAKGRFTISRTSTTVDLRITSP
TTEDTATYFCARGDYGMDLWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPK
PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAV
SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS
FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:24

416F8 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

QSLEESGGRLVTPGTPLTLTCTASGFSLSNYYMNWVRQAPGKGLEYIGIISSSGSAYYASWAKGRFTISRTSTTVDLRITSP
TTEDTATYFCARGDYGMDLWGQGTLVTVSS

SEQ ID NO:25

416G1 CHIMERIC LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GACGTCGTGATGACCCAGACTCCAGCCTCCGTGTCTGAACCTGTGGGAGGCGCAGTCACCATCAAGTGCCAGGCC
AGTCAGAGCATTGGTAGTGATTTAGCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTACAGG
GCATCCACTCTGGCATCTGGGGTCTCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCA
GCGACCTGGAGTGTGCCGATGCTGCCACTTACTACTGTCAATGTATTTATTATGGTAGTGATGATGTCATATACCAT
ACTTTCGGCGGAGGGACCGAGGTGGTGGTCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTG
ATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA
GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCA
CCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA
CCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:26

416G1 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GACGTCGTGATGACCCAGACTCCAGCCTCCGTGTCTGAACCTGTGGGAGGCGCAGTCACCATCAAGTGCCAGGCC
AGTCAGAGCATTGGTAGTGATTTAGCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTACAGG
GCATCCACTCTGGCATCTGGGGTCTCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCA
GCGACCTGGAGTGTGCCGATGCTGCCACTTACTACTGTCAATGTATTTATTATGGTAGTGATGATGTCATATACCAT
ACTTTCGGCGGAGGGACCGAGGTGGTGGTCAAA

SEQ ID NO:27

416G1 CHIMERIC LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

DVVMTQTPASVSEPVGGAVTIKCQASQSIGSDLAWYQQKPGQPPKLLIYRASTLASGVSSRFKGSGSGTEFTLTISDLEC
ADAATYYCQCIYYGSDDVIYHTFGGGTEVVVKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:28

416G1 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

DVVMTQTPASVSEPVGGAVTIKCQASQSIGSDLAWYQQKPGQPPKLLIYRASTLASGVSSRFKGSGSGTEFTLTISDLEC
ADAATYYCQCIYYGSDDVIYHTFGGGTEVVVK

SEQ ID NO:29

416G1 CHIMERIC HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

CAGTCGGTGGAGGAGTCCGGGGGTCGCCTGGTCACGCCTGGGACACCCCTGACACTCACCTGCACAGTCTCTGGA
TTCACTATCAATAGCTACCACATGATCTGGGTCCGCCAGGCTCCAGGGGAGGGGCTGGAATACATCGGATTCATTA
ATGATGGTGGTTTCACATACTACGCGAGCTGGGCAAAAGGCCGATTTATCATCTCCAGAACCTCGACCACGGTGG
ATCTGAAAATGACCAGTCTGACAGTCGCGGACACGGCCACCTATTTCTGTGCCAGAGGGGTTGATGGTACTAGTT
ATCCTGACTTATGGGGCCCGGGCACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCT
GGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACC
GGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGG
ACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT
CACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCG
TGCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCT
CCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
TCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCC
TCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCC
CATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCG
CCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGC
TCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGA
TGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:30

416G1 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

CAGTCGGTGGAGGAGTCCGGGGGTCGCCTGGTCACGCCTGGGACACCCCTGACACTCACCTGCACAGTCTCTGGA
TTCACTATCAATAGCTACCACATGATCTGGGTCCGCCAGGCTCCAGGGGAGGGGCTGGAATACATCGGATTCATTA
ATGATGGTGGTTTCACATACTACGCGAGCTGGGCAAAAGGCCGATTTATCATCTCCAGAACCTCGACCACGGTGG
ATCTGAAAATGACCAGTCTGACAGTCGCGGACACGGCCACCTATTTCTGTGCCAGAGGGGTTGATGGTACTAGTT
ATCCTGACTTATGGGGCCCGGGCACCCTGGTCACCGTCTCGAGC

SEQ ID NO:31

416G1 CHIMERIC HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

QSVEESGGRLVTPGTPLTLTCTVSGFTINSYHMIWVRQAPGEGLEYIGFINDGGFTYYASWAKGRFIISRTSTTVDLKMTS
LTVADTATYFCARGVDGTSYPDLWGPGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA
LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLF
PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK
CAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:32

416G1 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

QSVEESGGRLVTPGTPLTLTCTVSGFTINSYHMIWVRQAPGEGLEYIGFINDGGFTYYASWAKGRFIISRTSTTVDLKMTS
LTVADTATYFCARGVDGTSYPDLWGPGTLVTVSS

SEQ ID NO:33

418E10 CHIMERIC LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GCCCTGGTGATGACCCAGACTCCATCCCCTGTGTCTGCGGCTGTGGGAGGCACAGTCACCATCAACTGCCAGGCC
AGTCAGAGCATTGGTAGTAACTTGAACTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATTTATTATG
TATCCACTCTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGAGTACACTCTCACCATCAG
CGGCGTGCAGTGTGACGATGCTGCCACTTACTACTGCCTAGGTGTTTGGAATTATTGGGGTGATGACGGTACTGCT
TTCGGCGGAGGCACCGAGGTGGAGGTCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATG
AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTG
GAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCT
ACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCC
ATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:34

418E10 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GCCCTGGTGATGACCCAGACTCCATCCCCTGTGTCTGCGGCTGTGGGAGGCACAGTCACCATCAACTGCCAGGCC
AGTCAGAGCATTGGTAGTAACTTGAACTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATTTATTATG
TATCCACTCTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGAGTACACTCTCACCATCAG
CGGCGTGCAGTGTGACGATGCTGCCACTTACTACTGCCTAGGTGTTTGGAATTATTGGGGTGATGACGGTACTGCT
TTCGGCGGAGGCACCGAGGTGGAGGTCAAA

SEQ ID NO:35

418E10 CHIMERIC LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

ALVMTQTPSPVSAAVGGTVTINCQASQSIGSNLNWYQQKPGQPPKLLIYYVSTLASGVPSRFKGSGSGTEYTLTISGVQ
CDDAATYYCLGVWNYWGDDGTAFGGGTEVEVKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVD
NALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:36

418E10 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

ALVMTQTPSPVSAAVGGTVTINCQASQSIGSNLNWYQQKPGQPPKLLIYYVSTLASGVPSRFKGSGSGTEYTLTISGVQ
CDDAATYYCLGVWNYWGDDGTAFGGGTEVEVK

SEQ ID NO:37

418E10 CHIMERIC HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

CAGTCGCTGGAGGAGTCCGGGGGTCGCCTGGTCACGCCTGGGACACCCCTGACACTCACCTGCACAGCCTCTGAT
TTCTCCCTCAGTACCTATTATATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAAGTATT
TATGATAGTGGTGCCGCATACTACGCGACCTGGGCGAAGGGCCGATTCACCATCTCCAGAACGTCGACCACGGTG
GATCTGAGAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCTGTGCCAGAGATCCTATTAATAATGCCA
TCTGGGGCCAAGGGACCCTCGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTC
CTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGT
GTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCC
CTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCC
AGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA
CCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCC
CTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
GTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCT
CACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCCAGCCCC
CATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGA
TGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTG
GGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCT
CTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGC
TCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:38

418E10 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

CAGTCGCTGGAGGAGTCCGGGGGTCGCCTGGTCACGCCTGGGACACCCCTGACACTCACCTGCACAGCCTCTGAT
TTCTCCCTCAGTACCTATTATATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAAGTATT
TATGATAGTGGTGCCGCATACTACGCGACCTGGGCGAAGGGCCGATTCACCATCTCCAGAACGTCGACCACGGTG
GATCTGAGAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCTGTGCCAGAGATCCTATTAATAATGCCA
TCTGGGGCCAAGGGACCCTCGTCACCGTCTCGAGC

SEQ ID NO:39

418E10 CHIMERIC HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

QSLEESGGRLVTPGTPLTLTCTASDFSLSTYYMSWVRQAPGKGLEWIGSIYDSGAAYYATWAKGRFTISRTSTTVDLRM
TSLTAADTATYFCARDPINNAIWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT
SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCA
VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:40

418E10 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

QSLEESGGRLVTPGTPLTLTCTASDFSLSTYYMSWVRQAPGKGLEWIGSIYDSGAAYYATWAKGRFTISRTSTTVDLRM
TSLTAADTATYFCARDPINNAIWGQGTLVTVSS

SEQ ID NO:41

418E4 CHIMERIC LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GCCCTGGTGATGACCCAGACTCCATCCCCTGTGTCTGCGGCTGTGGGAGGCACAGTCACCATCAACTGCCAGGCC
AGTCAGAGTATTGCTACTAACTTGAACTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTATTATA
CATCCAGTCTGGCATCTGGGGTCCCATCGCGGTTCAGCGGCAGTGGATCTGGCACAGAGTTCACTCTCACCATCAG
CGGTGTGCAGTGTGACGATGCTGCCACTTACTACTGCCTAGGTGTTTGGAATTATTGGGGTGATGATGGTACTGCT
TTCGGCGGAGGGACCGAGGTGGAGTTCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATG
AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTG
GAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCT
ACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCC
ATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:42

418E4 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GCCCTGGTGATGACCCAGACTCCATCCCCTGTGTCTGCGGCTGTGGGAGGCACAGTCACCATCAACTGCCAGGCC
AGTCAGAGTATTGCTACTAACTTGAACTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTATTATA

CATCCAGTCTGGCATCTGGGGTCCCATCGCGGTTCAGCGGCAGTGGATCTGGCACAGAGTTCACTCTCACCATCAG
CGGTGTGCAGTGTGACGATGCTGCCACTTACTACTGCCTAGGTGTTTGGAATTATTGGGGTGATGATGGTACTGCT
TTCGGCGGAGGGACCGAGGTGGAGTTCAAA

SEQ ID NO:43

418E4 CHIMERIC LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

ALVMTQTPSPVSAAVGGTVTINCQASQSIATNLNWYQQKPGQPPKLLIYYTSSLASGVPSRFSGSGSGTEFTLTISGVQC
DDAATYYCLGVWNYWGDDGTAFGGGTEVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:44

418E4 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

ALVMTQTPSPVSAAVGGTVTINCQASQSIATNLNWYQQKPGQPPKLLIYYTSSLASGVPSRFSGSGSGTEFTLTISGVQC
DDAATYYCLGVWNYWGDDGTAFGGGTEVEFK

SEQ ID NO:45

418E4 CHIMERIC HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

CAGTCGCTGGAGGAGTCCGGGGGTCGCCTGGTCACGCCTGGGACACCCCTGACACTCACCTGCACAGCCTCTGAA
TTCTCCCTCAGTAGCTACTACATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAATGGATCGGAAGTATT
TATGCTAGTGGTAGCGCATACTACGCGAGTTGGGCGAAGGGCCGATTCACCATCTCCAGAACGTCGACCACGGTG
GATCTGAAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCTGTGTCAGAGATCCTATTAACAATGACA
TCTGGGGCCCAGGCACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTC
CTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGT
GTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCC
CTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCC
AGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA
CCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCC
CTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
GTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCT
CACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCCAGCCCC
CATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGA
TGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTG
GGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCT
CTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGC
TCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:46

418E4 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

CAGTCGCTGGAGGAGTCCGGGGGTCGCCTGGTCACGCCTGGGACACCCCTGACACTCACCTGCACAGCCTCTGAA
TTCTCCCTCAGTAGCTACTACATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAATGGATCGGAAGTATT
TATGCTAGTGGTAGCGCATACTACGCGAGTTGGGCGAAGGGCCGATTCACCATCTCCAGAACGTCGACCACGGTG
GATCTGAAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCTGTGTCAGAGATCCTATTAACAATGACA
TCTGGGGCCCAGGCACCCTGGTCACCGTCTCGAGC

SEQ ID NO:47

418E4 CHIMERIC HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

QSLEESGGRLVTPGTPLTLTCTASEFSLSSYYMSWVRQAPGKGLEWIGSIYASGSAYYASWAKGRFTISRTSTTVDLKMT
SLTAADTATYFCVRDPINNDIWGPGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPPK
PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAV
SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS
FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:48

418E4 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

QSLEESGGRLVTPGTPLTLTCTASEFSLSSYYMSWVRQAPGKGLEWIGSIYASGSAYYASWAKGRFTISRTSTTVDLKMT
SLTAADTATYFCVRDPINNDIWGPGTLVTVSS

SEQ ID NO:49

418H5 CHIMERIC LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GCCCAAGTGCTGACCCAGACTCCAGCCTCCGTGTCTGCAACTGTGGGAAGCACAGTCACCATCAGTTGCCAGTCCA
GTCCGAGTGTTTATAAGAACAACCAATTAGCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAACTCCTGATCTA
TCTGGCATCTACTCTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGAGTTCACTCTCACC
ATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTACTGTGCAGGCGGTTATAGTAGTAGTAGTGATACTGCTT
TCGGCGGAGGGACCGAGGTGGAGGTCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATG
AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTG
GAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCT
ACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCC
ATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:50

418H5 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GCCCAAGTGCTGACCCAGACTCCAGCCTCCGTGTCTGCAACTGTGGGAAGCACAGTCACCATCAGTTGCCAGTCCA
GTCCGAGTGTTTATAAGAACAACCAATTAGCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAACTCCTGATCTA
TCTGGCATCTACTCTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGAGTTCACTCTCACC
ATCAGCGACCTGGAGTGTGCCGATGCTGCCACTTACTACTGTGCAGGCGGTTATAGTAGTAGTAGTGATACTGCTT
TCGGCGGAGGGACCGAGGTGGAGGTCAAA

SEQ ID NO:51

418H5 CHIMERIC LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

AQVLTQTPASVSATVGSTVTISCQSSPSVYKNNQLAWYQQKPGQPPKLLIYLASTLASGVPSRFKGSGSGTEFTLTISDLE
CADAATYYCAGGYSSSSDTAFGGGTEVEVKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS
GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:52

418H5 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

AQVLTQTPASVSATVGSTVTISCQSSPSVYKNNQLAWYQQKPGQPPKLLIYLASTLASGVPSRFKGSGSGTEFTLTISDLE
CADAATYYCAGGYSSSSDTAFGGGTEVEVK

SEQ ID NO:53

418H5 CHIMERIC HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

CAGTCGCTGGAGGAGTCCGGGGGTCGCCTGGTCACGCCTGGGACACCCCTGACACTCACCTGCACAGTCTCTGGA
ATCGACCTCAGTGCCTACCACATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAATACATCGGAATGATT
GGTAGTAGTGGTACCATACACTACGCGAACTGGGCGAAAGGCCGATTCACCATCTCCAAAACCTCGACCACGGTG
GATCTGAAAATCACCAGTCCGACAACCGAGGACACGGCCACCTATTTCTGTGCCAGGGACAGTTATAATAGTGATT
ATGCCTTTAACTTATGGGGCCCAGGGACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCC
CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGA
ACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC
AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTG
AATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCA
CCGTGCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA
TCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGT
ACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGT
GGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGC
CCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCC

CCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATC
GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGG
CTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTG
ATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:54

418H5 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

CAGTCGCTGGAGGAGTCCGGGGGTCGCCTGGTCACGCCTGGGACACCCCTGACACTCACCTGCACAGTCTCTGGA
ATCGACCTCAGTGCCTACCACATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAATACATCGGAATGATT
GGTAGTAGTGGTACCATACACTACGCGAACTGGGCGAAAGGCCGATTCACCATCTCCAAAACCTCGACCACGGTG
GATCTGAAAATCACCAGTCCGACAACCGAGGACACGGCCACCTATTTCTGTGCCAGGGACAGTTATAATAGTGATT
ATGCCTTTAACTTATGGGGCCCAGGGACCCTGGTCACCGTCTCGAGC

SEQ ID NO:55

418H5 CHIMERIC HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

QSLEESGGRLVTPGTPLTLTCTVSGIDLSAYHMSWVRQAPGKGLEYIGMIGSSGTIHYANWAKGRFTISKTSTTVDLKITS
PTTEDTATYFCARDSYNSDYAFNLWGPGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG
ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFL
FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:56

418H5 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

QSLEESGGRLVTPGTPLTLTCTVSGIDLSAYHMSWVRQAPGKGLEYIGMIGSSGTIHYANWAKGRFTISKTSTTVDLKITS
PTTEDTATYFCARDSYNSDYAFNLWGPGTLVTVSS

SEQ ID NO:57

419D9 CHIMERIC LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GCTCAAGTGCTGACCCAGACTGCATCGCCCGTGTCTGCCGCTGTGGGAGGCACAGTCACCATCAACTGCCAGTCCA
GTCAGAGTGTTTATAGTAACTGGTTATCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCGCCTGATCTATTC
TGCATCCACTCTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACACAGTTCACTCTCACCATC
AGCGACCTGGAGTGTGACGATGCTGCCACTTACTACTGTGCAGGCGGTTATAATACTGTTACTGATACTTTTGCTTT
CGGCAGAGGCACCGAGGTGGAGGTCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGA
GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGG
AAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTA

CAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCA
TCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:58

419D9 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GCTCAAGTGCTGACCCAGACTGCATCGCCCGTGTCTGCCGCTGTGGGAGGCACAGTCACCATCAACTGCCAGTCCA
GTCAGAGTGTTTATAGTAACTGGTTATCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCGCCTGATCTATTC
TGCATCCACTCTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACACAGTTCACTCTCACCATC
AGCGACCTGGAGTGTGACGATGCTGCCACTTACTACTGTGCAGGCGGTTATAATACTGTTACTGATACTTTTGCTTT
CGGCAGAGGCACCGAGGTGGAGGTCAAA

SEQ ID NO:59

419D9 CHIMERIC LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

AQVLTQTASPVSAAVGGTVTINCQSSQSVYSNWLSWYQQKPGQPPKRLIYSASTLASGVPSRFKGSGSGTQFTLTISDL
ECDDAATYYCAGGYNTVTDTFAFGRGTEVEVKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:60

419D9 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

AQVLTQTASPVSAAVGGTVTINCQSSQSVYSNWLSWYQQKPGQPPKRLIYSASTLASGVPSRFKGSGSGTQFTLTISDL
ECDDAATYYCAGGYNTVTDTFAFGRGTEVEVK

SEQ ID NO:61

419D9 CHIMERIC HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACTCACCTGCACAGCCTCTGGA
TTCTCCTTCAGTAGCAGGCACTACATGTGTTGGGTCCGCCAGGCTCCAGGGGAGGGGCTGGAGTGGATCGCATGC
ATTTATACTGGTAGTAGTGGTACTCCTCACTACGCGAGCTGGGCGAAAGGCCGATTCACCATCTCCCAAACCTCGT
CGACCACGGTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCTGTTCGAGCGAAGGTA
ACCTGTGGGGCCCAGGCACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACC
CTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGAC
GGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTAC
TCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGC
CCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAG
CACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGAC
CCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACG
GCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTC

CTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCCAGCC
CCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGG
GATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAG
TGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTC
CTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG
GCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:62

419D9 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACTCACCTGCACAGCCTCTGGA
TTCTCCTTCAGTAGCAGGCACTACATGTGTTGGGTCCGCCAGGCTCCAGGGGAGGGGCTGGAGTGGATCGCATGC
ATTTATACTGGTAGTAGTGGTACTCCTCACTACGCGAGCTGGGCGAAAGGCCGATTCACCATCTCCCAAACCTCGT
CGACCACGGTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCTGTTCGAGCGAAGGTA
ACCTGTGGGGCCCAGGCACCCTGGTCACCGTCTCGAGC

SEQ ID NO:63

419D9 CHIMERIC HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

QSLEESGGDLVKPGASLTLTCTASGFSFSSRHYMCWVRQAPGEGLEWIACIYTGSSGTPHYASWAKGRFTISQTSSTTV
TLQMTSLTAADTATYFCSSEGNLWGPGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA
LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLF
PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK
CAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:64

419D9 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

QSLEESGGDLVKPGASLTLTCTASGFSFSSRHYMCWVRQAPGEGLEWIACIYTGSSGTPHYASWAKGRFTISQTSSTTV
TLQMTSLTAADTATYFCSSEGNLWGPGTLVTVSS

SEQ ID NO:65

420H5 CHIMERIC LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GCCCTTGTGATGACCCAGACTCCAGCCTCCGTGTCTGCAGCTGTGGGAGGCACAGTCACCATCAATTGCCAGGCCA
GTGAGGACATTGATACCTATTTAGCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTTTTATGC
ATCCGATCTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGC
GGTGTGCAGTGTGACGATGCTGCCACTTACTACTGTCAAGGCGGTTACTATACTAGTAGTGCTGATACGAGGGGT
GCTTTCGGCGGAGGCACCGAGGTGGTGGTCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTG

ATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA
GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCA
CCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA
CCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:66

420H5 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GCCCTTGTGATGACCCAGACTCCAGCCTCCGTGTCTGCAGCTGTGGGAGGCACAGTCACCATCAATTGCCAGGCCA
GTGAGGACATTGATACCTATTTAGCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTTTTATGC
ATCCGATCTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGC
GGTGTGCAGTGTGACGATGCTGCCACTTACTACTGTCAAGGCGGTTACTATACTAGTAGTGCTGATACGAGGGGT
GCTTTCGGCGGAGGCACCGAGGTGGTGGTCAAA

SEQ ID NO:67

420H5 CHIMERIC LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

ALVMTQTPASVSAAVGGTVTINCQASEDIDTYLAWYQQKPGQPPKLLIFYASDLASGVPSRFKGSGSGTEFTLTISGVQC
DDAATYYCQGGYYTSSADTRGAFGGGTEVVVKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA
LQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:68

420H5 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

ALVMTQTPASVSAAVGGTVTINCQASEDIDTYLAWYQQKPGQPPKLLIFYASDLASGVPSRFKGSGSGTEFTLTISGVQC
DDAATYYCQGGYYTSSADTRGAFGGGTEVVVK

SEQ ID NO:69

420H5 CHIMERIC HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACTCACCTGCACAGCCTCTGGA
TTCTCCTTCAGTAGCAACTACTGGATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGC
ATTTATGTTGGTAGTAGTGGTGACACTTACTACGCGAGCTGGGCGAAAGGCCGATTCACCATCTCCAAAACCTCGT
CGACCACGGTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCTGTGCGAGAGATAGTA
GTAGTTATTATATGTTTAACTTGTGGGGCCAGGGGACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATC
GGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
CTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTA
CAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCT
GCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACA
CATGCCCACCGTGCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC

CCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTT
CAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG
TACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCC
AACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA
GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGAC
TCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCAT
GCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:70

420H5 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACTCACCTGCACAGCCTCTGGA
TTCTCCTTCAGTAGCAACTACTGGATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGC
ATTTATGTTGGTAGTAGTGGTGACACTTACTACGCGAGCTGGGCGAAAGGCCGATTCACCATCTCCAAAACCTCGT
CGACCACGGTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCTGTGCGAGAGATAGTA
GTAGTTATTATATGTTTAACTTGTGGGGCCAGGGGACCCTGGTCACCGTCTCGAGC

SEQ ID NO:71

420H5 CHIMERIC HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

QSLEESGGDLVKPGASLTLTCTASGFSFSSNYWICWVRQAPGKGLEWIACIYVGSSGDTYYASWAKGRFTISKTSSTTVT
LQMTSLTAADTATYFCARDSSSYYMFNLWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAG
APSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL
NGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:72

420H5 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

QSLEESGGDLVKPGASLTLTCTASGFSFSSNYWICWVRQAPGKGLEWIACIYVGSSGDTYYASWAKGRFTISKTSSTTVT
LQMTSLTAADTATYFCARDSSSYYMFNLWGQGTLVTVSS

SEQ ID NO:73

420H6 CHIMERIC LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GCTCAAGTGCTGACCCAGACTGCATCGCCCGTGTCTGCCGCTGTGGGAGGCACAGTCACCATCAACTGCCAGGCC
AGTCAGAGTGTTTATAGTAACTGGTTATCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCGCCTGATCTATT
CTGCATCCACTCTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACACAGTTCACTCTCACCAT

TAGCGACCTGGAGTGTGACGATGCTGCCACTTACTACTGTGCAGGCGGTTACAATACTGTTATTGATACTTTTGCTT
TCGGCGGAGGCACCGAGGTGGAGTTCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGA
GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGG
AAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTA
CAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCA
TCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:74

420H6 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GCTCAAGTGCTGACCCAGACTGCATCGCCCGTGTCTGCCGCTGTGGGAGGCACAGTCACCATCAACTGCCAGGCC
AGTCAGAGTGTTTATAGTAACTGGTTATCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCGCCTGATCTATT
CTGCATCCACTCTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACACAGTTCACTCTCACCAT
TAGCGACCTGGAGTGTGACGATGCTGCCACTTACTACTGTGCAGGCGGTTACAATACTGTTATTGATACTTTTGCTT
TCGGCGGAGGCACCGAGGTGGAGTTCAAA

SEQ ID NO:75

420H6 CHIMERIC LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

AQVLTQTASPVSAAVGGTVTINCQASQSVYSNWLSWYQQKPGQPPKRLIYSASTLASGVPSRFKGSGSGTQFTLTISDL
ECDDAATYYCAGGYNTVIDTFAFGGGTEVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:76

420H6 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

AQVLTQTASPVSAAVGGTVTINCQASQSVYSNWLSWYQQKPGQPPKRLIYSASTLASGVPSRFKGSGSGTQFTLTISDL
ECDDAATYYCAGGYNTVIDTFAFGGGTEVEFK

SEQ ID NO:77

420H6 CHIMERIC HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

CAGCAGCAGCTGGAGGAGTCCGGGGGAGGCCTGGTCAAGCCTGGAGGAACCCTGACACTCACCTGCAAAGCCTC
TGGAATTGACTTCAGTAGTAGTTACTACATGTGCTGGGTCCGCCAGGCTCCAGGGGAGGGGCTGGAGTGGATCGC
ATGCATTTATACTGGTGGTAGTGGTACTCCTCACTACGCGAGCTGGGCGAAAGGCCGATTCACCATCTCCCAAACC
TCGTCGACCACGGTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCTGTGCGAGAGAA
GGTAGCCTGTGGGGCCAGGGCACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTG
GCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG
GTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGA
CTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATC

ACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGT
GCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTC
CCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGT
GGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTC
AGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTC
CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA
TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTC
CTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATG
CATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:78

420H6 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

CAGCAGCAGCTGGAGGAGTCCGGGGGAGGCCTGGTCAAGCCTGGAGGAACCCTGACACTCACCTGCAAAGCCTC
TGGAATTGACTTCAGTAGTAGTTACTACATGTGCTGGGTCCGCCAGGCTCCAGGGGAGGGGCTGGAGTGGATCGC
ATGCATTTATACTGGTGGTAGTGGTACTCCTCACTACGCGAGCTGGGCGAAAGGCCGATTCACCATCTCCCAAACC
TCGTCGACCACGGTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCTGTGCGAGAGAA
GGTAGCCTGTGGGGCCAGGGCACCCTGGTCACCGTCTCGAGC

SEQ ID NO:79

420H6 CHIMERIC HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

QQQLEESGGGLVKPGGTLTLTCKASGIDFSSSYYMCWVRQAPGEGLEWIACIYTGGSGTPHYASWAKGRFTISQTSSTT
VTLQMTSLTAADTATYFCAREGSLWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG
ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFL
FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:80

420H6 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

QQQLEESGGGLVKPGGTLTLTCKASGIDFSSSYYMCWVRQAPGEGLEWIACIYTGGSGTPHYASWAKGRFTISQTSSTT
VTLQMTSLTAADTATYFCAREGSLWGQGTLVTVSS

SEQ ID NO:81

459F1 CHIMERIC LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GCTCAAGTGCTGACCCAGACTGCATCGCCCGTGTCTGCCGCTGTGGGAGGCACAGTCACCATCAACTGCCAGTCCA
GTCAGAGTGTTTATAGTAACTGGTTCTCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTATTCT
GCATCCACTCTGGCATCTGGGGTCCCCTCGCGGTTTAAAGGCAGTGGATCTGGGACACAGTTCACTCTCACCATCA
GCGACCTGGAGTGTGACGATGCTGCCACTTACTACTGTGCAGGCGGTTACAATACTGTAACTGATACTTTTGCTTTC
GGCGGAGGCACCGAGGTGGAGTTCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAG
CAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGA
AGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTAC
AGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCAT
CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:82

459F1 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GCTCAAGTGCTGACCCAGACTGCATCGCCCGTGTCTGCCGCTGTGGGAGGCACAGTCACCATCAACTGCCAGTCCA
GTCAGAGTGTTTATAGTAACTGGTTCTCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTATTCT
GCATCCACTCTGGCATCTGGGGTCCCCTCGCGGTTTAAAGGCAGTGGATCTGGGACACAGTTCACTCTCACCATCA
GCGACCTGGAGTGTGACGATGCTGCCACTTACTACTGTGCAGGCGGTTACAATACTGTAACTGATACTTTTGCTTTC
GGCGGAGGCACCGAGGTGGAGTTCAAA

SEQ ID NO:83

459F1 CHIMERIC LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

AQVLTQTASPVSAAVGGTVTINCQSSQSVYSNWFSWYQQKPGQPPKLLIYSASTLASGVPSRFKGSGSGTQFTLTISDLE
CDDAATYYCAGGYNTVTDTFAFGGGTEVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:84

459F1 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

AQVLTQTASPVSAAVGGTVTINCQSSQSVYSNWFSWYQQKPGQPPKLLIYSASTLASGVPSRFKGSGSGTQFTLTISDLE
CDDAATYYCAGGYNTVTDTFAFGGGTEVEFK

SEQ ID NO:85

459F1 CHIMERIC HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACTCACCTGCACAGCCTCTGG
AATCGACTTCAGTAGGAGATACTACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCAT
GCATGTATACTGGTAGCCGCGATACTCCTCACTACGCGAGCTGGGCGAAAGGCCGGTTCACCATCTCCCAAACCTC
GTCGACCACGGTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCTGTGCGAGAGAAGG
TAACCTGTGGGGCCCGGGGACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGC

ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGT
GACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACT
CTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCAC
AAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGC
CCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC
GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCA
GCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCC
CAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCAT
CCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCG
TGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
TTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGC
ATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:86

459F1 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

GAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACTCACCTGCACAGCCTCTGG
AATCGACTTCAGTAGGAGATACTACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCAT
GCATGTATACTGGTAGCCGCGATACTCCTCACTACGCGAGCTGGGCGAAAGGCCGGTTCACCATCTCCCAAACCTC
GTCGACCACGGTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCTGTGCGAGAGAAGG
TAACCTGTGGGGCCCGGGGACCCTGGTCACCGTCTCGAGC

SEQ ID NO:87

459F1 CHIMERIC HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

ESLEESGGDLVKPGASLTLTCTASGIDFSRRYYMCWVRQAPGKGLEWIACMYTGSRDTPHYASWAKGRFTISQTSSTTV
TLQMTSLTAADTATYFCAREGNLWGPGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA
LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLF
PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK
CAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:88

459F1 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

ESLEESGGDLVKPGASLTLTCTASGIDFSRRYYMCWVRQAPGKGLEWIACMYTGSRDTPHYASWAKGRFTISQTSSTTV
TLQMTSLTAADTATYFCAREGNLWGPGTLVTVSS

SEQ ID NO:89

460C3 CHIMERIC LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GCCCAAGTGCTGACCCAGACTCCATCGTCCGTGTCTGCAGCTGTGGGAGGCACAGTCAGCATCAGTTGCCAGTCC
AGTCAGAGTGTTTATAGTAACTGGTTCTCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTATT
CTGCATCCACTCTGGCATCTGGGGTCCCCTCGCGGTTTAAAGGCAGTGGATCTGGGACACAGTTCACTCTCACCAT
CAGCGACCTGGAGTGTGACGATGCTGCCACTTACTACTGTGCAGGCGGTTACAATACTGTTATTGATACTTTTGCTT
TCGGCGGAGGCACCGAGGTGGAGTTCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGA
GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGG
AAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTA
CAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCA
TCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:90

460C3 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GCCCAAGTGCTGACCCAGACTCCATCGTCCGTGTCTGCAGCTGTGGGAGGCACAGTCAGCATCAGTTGCCAGTCC
AGTCAGAGTGTTTATAGTAACTGGTTCTCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTATT
CTGCATCCACTCTGGCATCTGGGGTCCCCTCGCGGTTTAAAGGCAGTGGATCTGGGACACAGTTCACTCTCACCAT
CAGCGACCTGGAGTGTGACGATGCTGCCACTTACTACTGTGCAGGCGGTTACAATACTGTTATTGATACTTTTGCTT
TCGGCGGAGGCACCGAGGTGGAGTTCAAA

SEQ ID NO:91

460C3 CHIMERIC LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

AQVLTQTPSSVSAAVGGTVSISCQSSQSVYSNWFSWYQQKPGQPPKLLIYSASTLASGVPSRFKGSGSGTQFTLTISDLE
CDDAATYYCAGGYNTVIDTFAFGGGTEVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ
SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:92

460C3 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

AQVLTQTPSSVSAAVGGTVSISCQSSQSVYSNWFSWYQQKPGQPPKLLIYSASTLASGVPSRFKGSGSGTQFTLTISDLE
CDDAATYYCAGGYNTVIDTFAFGGGTEVEFK

SEQ ID NO:93

460C3 CHIMERIC HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACTCACCTGCACAGCCTCTGGA
ATCGACTTCAGTAGGAGATACTACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATG
CATATATACTGGTAGCCGCGATACTCCTCACTACGCGAGCTGGGCGAAAGGCCGATTCACCATCTCCCAAACCTCG

TCGACCACGGTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCTGTGCGAGAGAAGGT
AGCCTGTGGGGCCAGGGCACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCA
CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTG
ACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCT
ACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAA
GCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCC
AGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGG
ACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGA
CGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC
GTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCCA
GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCC
CGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG
GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTT
CTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCA
TGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:94

460C3 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

CAGTCGTTGGAGGAGTCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACTCACCTGCACAGCCTCTGGA
ATCGACTTCAGTAGGAGATACTACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATG
CATATATACTGGTAGCCGCGATACTCCTCACTACGCGAGCTGGGCGAAAGGCCGATTCACCATCTCCCAAACCTCG
TCGACCACGGTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCTGTGCGAGAGAAGGT
AGCCTGTGGGGCCAGGGCACCCTGGTCACCGTCTCGAGC

SEQ ID NO:95

460C3 CHIMERIC HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

QSLEESGGDLVKPGASLTLTCTASGIDFSRRYYMCWVRQAPGKGLEWIACIYTGSRDTPHYASWAKGRFTISQTSSTTV
TLQMTSLTAADTATYFCAREGSLWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA
LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLF
PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK
CAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:96

460C3 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

QSLEESGGDLVKPGASLTLTCTASGIDFSRRYYMCWVRQAPGKGLEWIACIYTGSRDTPHYASWAKGRFTISQTSSTTV
TLQMTSLTAADTATYFCAREGSLWGQGTLVTVSS

SEQ ID NO:97

464D11 CHIMERIC LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GCGCAAGTGCTGACCCAGACTCCATCGCCTGTGTCTGCAGCTGTGGGAGGCACAGTCACCATCAATTGCCAGTCCA
GTCAGAGTGTTTATAGTAACAGCTTCTTATCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCGCCTGATCTA
TTCTGCATCCGATCTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACACAGTTCACTCTCACC
ATCAGCGACCTGGAGTGTGACGATGCTGCCACTTACTACTGTGCAGGCGTTTATAGTGATAATACTTATGTTTTCG
GCGGAGGCACCGAGGTGGAGTTCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGC
AGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAA
GGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACA
GCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATC
AGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:98

464D11 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GCGCAAGTGCTGACCCAGACTCCATCGCCTGTGTCTGCAGCTGTGGGAGGCACAGTCACCATCAATTGCCAGTCCA
GTCAGAGTGTTTATAGTAACAGCTTCTTATCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCGCCTGATCTA
TTCTGCATCCGATCTGGCATCTGGGGTCCCATCGCGGTTCAAAGGCAGTGGATCTGGGACACAGTTCACTCTCACC
ATCAGCGACCTGGAGTGTGACGATGCTGCCACTTACTACTGTGCAGGCGTTTATAGTGATAATACTTATGTTTTCG
GCGGAGGCACCGAGGTGGAGTTCAAA

SEQ ID NO:99

464D11 CHIMERIC LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

AQVLTQTPSPVSAAVGGTVTINCQSSQSVYSNSFLSWYQQKPGQPPKRLIYSASDLASGVPSRFKGSGSGTQFTLTISDL
ECDDAATYYCAGVYSDNTYVFGGGTEVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ
SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:100

464D11 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

AQVLTQTPSPVSAAVGGTVTINCQSSQSVYSNSFLSWYQQKPGQPPKRLIYSASDLASGVPSRFKGSGSGTQFTLTISDL
ECDDAATYYCAGVYSDNTYVFGGGTEVEFK

SEQ ID NO:101

464D11 CHIMERIC HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

CAGTCGGTGGAGGAGTCCGGCGGTCGCCTGGTAAAGCCTGACGAATCCCTGACACTCACCTGCACAGCCTCTGGA
TTCTCCCTCAGTCACTACTGGATGACTTGGGTCCGACAGGCTCCAGGGAAGGGACTGGAATACATCGGATTCATTA

ATGTTGGTGGTGACACATCTTACGCGAGCTGGTCGAAAGGCCGATTCACCATCTCCAAGGCCTCGACCACGGTGG
ATCTGAAGATCAGTAGTCTGACAACCGAGGACACGGCCACCTATTTCTGTGGCAGAGGTGGTCTGACTTTTGGTTG
GGACTTGTGGGGCCCAGGGACCCTCGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGC
ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGT
GACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACT
CTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCAC
AAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGC
CCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCC
GGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG
GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCA
GCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCC
CAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCAT
CCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCG
TGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCC
TTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGC
ATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:102

464D11 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

CAGTCGGTGGAGGAGTCCGGCGGTCGCCTGGTAAAGCCTGACGAATCCCTGACACTCACCTGCACAGCCTCTGGA
TTCTCCCTCAGTCACTACTGGATGACTTGGGTCCGACAGGCTCCAGGGAAGGGACTGGAATACATCGGATTCATTA
ATGTTGGTGGTGACACATCTTACGCGAGCTGGTCGAAAGGCCGATTCACCATCTCCAAGGCCTCGACCACGGTGG
ATCTGAAGATCAGTAGTCTGACAACCGAGGACACGGCCACCTATTTCTGTGGCAGAGGTGGTCTGACTTTTGGTTG
GGACTTGTGGGGCCCAGGGACCCTCGTCACCGTCTCGAGC

SEQ ID NO:103

464D11 CHIMERIC HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

QSVEESGGRLVKPDESLTLTCTASGFSLSHYWMTWVRQAPGKGLEYIGFINVGGDTSYASWSKGRFTISKASTTVDLKIS
SLTTEDTATYFCGRGGLTFGWDLWGPGTLVTVSSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG
ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFL
FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
KCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:104

464D11 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

QSVEESGGRLVKPDESLTLTCTASGFSLSHYWMTWVRQAPGKGLEYIGFINVGGDTSYASWSKGRFTISKASTTVDLKIS
SLTTEDTATYFCGRGGLTFGWDLWGPGTLVTVSS

SEQ ID NO:105

466F6 CHIMERIC LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GATGTTGTGATGACCCAGACTCCAGCCTCCGTGTCTGAACCTGTGGGAGGCACAGTCACCATCAAGTGCCAGGCC
AGTCAGAACATTAGGACTTACTTATCCTGGTATCAGCAGAAACCAGGGCAGCGTCCCAAGCTCCTGATCTATGCTG
CAGCCAATCTGGCATCTGGGGTCCCATCGCGGTTCAGTGGCAGTAGATCTGGGACAGAGTTCACTCTCACCATCAG
CGACCTGGAGTGTGCCGATGCTGCCACTTACTATTGTCAGTGTACCTATCTTGGTACTGATTATGTTGGCGGTGCTT
TCGGCGGAGGCACCGAGGTGGAGTTCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGA
GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGG
AAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTA
CAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCA
TCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:106

466F6 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GATGTTGTGATGACCCAGACTCCAGCCTCCGTGTCTGAACCTGTGGGAGGCACAGTCACCATCAAGTGCCAGGCC
AGTCAGAACATTAGGACTTACTTATCCTGGTATCAGCAGAAACCAGGGCAGCGTCCCAAGCTCCTGATCTATGCTG
CAGCCAATCTGGCATCTGGGGTCCCATCGCGGTTCAGTGGCAGTAGATCTGGGACAGAGTTCACTCTCACCATCAG
CGACCTGGAGTGTGCCGATGCTGCCACTTACTATTGTCAGTGTACCTATCTTGGTACTGATTATGTTGGCGGTGCTT
TCGGCGGAGGCACCGAGGTGGAGTTCAAA

SEQ ID NO:107

466F6 CHIMERIC LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

DVVMTQTPASVSEPVGGTVTIKCQASQNIRTYLSWYQQKPGQRPKLLIYAAANLASGVPSRFSGSRSGTEFTLTISDLEC
ADAATYYCQCTYLGTDYVGGAFGGGTEVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:108

466F6 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

DVVMTQTPASVSEPVGGTVTIKCQASQNIRTYLSWYQQKPGQRPKLLIYAAANLASGVPSRFSGSRSGTEFTLTISDLEC
ADAATYYCQCTYLGTDYVGGAFGGGTEVEFK

SEQ ID NO:109

466F6 CHIMERIC HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

CGGTCGCTGGAGGAGTCCGGGGGTCGCCTGGTCACGCCTGGGACACCCCTGACACTCACCTGCACAGCCTCTGGA
TTCACCATCAGTAGCTACCACATGCAGTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAATACATCGGAACCATT
AGTAGTGGTGGTAATGTATACTACGCGAGCTGGGCGAGAGGCCGATTCACCATCTCCAGACCCTCGTCGACCACG
GTGGATCTGAAGATGACCAGTCTGACAACCGAGGACACGGCCACCTATTTCTGTGCCAGAGACTCTGGTTATAGT
GATCCTATGTGGGGCCCGGGCACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTG
GCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG
GTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGA
CTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATC
ACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGT
GCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTC
CCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGT
GGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTC
AGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTC
CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA
TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTC
CTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATG
CATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:110

466F6 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

CGGTCGCTGGAGGAGTCCGGGGGTCGCCTGGTCACGCCTGGGACACCCCTGACACTCACCTGCACAGCCTCTGGA
TTCACCATCAGTAGCTACCACATGCAGTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAATACATCGGAACCATT
AGTAGTGGTGGTAATGTATACTACGCGAGCTGGGCGAGAGGCCGATTCACCATCTCCAGACCCTCGTCGACCACG
GTGGATCTGAAGATGACCAGTCTGACAACCGAGGACACGGCCACCTATTTCTGTGCCAGAGACTCTGGTTATAGT
GATCCTATGTGGGGCCCGGGCACCCTGGTCACCGTCTCGAGC

SEQ ID NO:111

466F6 CHIMERIC HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

RSLEESGGRLVTPGTPLTLTCTASGFTISSYHMQWVRQAPGKGLEYIGTISSGGNVYYASWARGRFTISRPSSTTVDLKM
TSLTTEDTATYFCARDSGYSDPMWGPGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA
LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLF
PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK
CAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:112

466F6 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

RSLEESGGRLVTPGTPLTLTCTASGFTISSYHMQWVRQAPGKGLEYIGTISSGGNVYYASWARGRFTISRPSSTTVDLKM
TSLTTEDTATYFCARDSGYSDPMWGPGTLVTVSS

SEQ ID NO:113

470B6 CHIMERIC LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GCAGCCGTGCTGACCCAGACACCATCGCCCGTGTCTGCAGCTGTGGGAGGCACAGTCACCATCAGTTGCCAGTCC
AGTCAGAGTGTTTATAGTAACAACCAATTATCCTGGTTTCAGCAGAAATCAGGGCAGCCTCCCAAGCTCCTGATCT
ATGATGCATCCAATCTGGCATCTGGGGTCCCATCACGGTTCAGCGGCAGTGGATCTGGGACACAGTTCACTCTCAC
CATCAGCAGCGTGCAGTGTGACGATGCTGCCACTTACCACTGTCTAGGCGGTAGTGATGATGATGGTGATATTGCT
TTCGGCGGAGGCACCGAGGTGGTGTTCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATG
AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTG
GAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCT
ACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCC
ATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:114

470B6 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GCAGCCGTGCTGACCCAGACACCATCGCCCGTGTCTGCAGCTGTGGGAGGCACAGTCACCATCAGTTGCCAGTCC
AGTCAGAGTGTTTATAGTAACAACCAATTATCCTGGTTTCAGCAGAAATCAGGGCAGCCTCCCAAGCTCCTGATCT
ATGATGCATCCAATCTGGCATCTGGGGTCCCATCACGGTTCAGCGGCAGTGGATCTGGGACACAGTTCACTCTCAC
CATCAGCAGCGTGCAGTGTGACGATGCTGCCACTTACCACTGTCTAGGCGGTAGTGATGATGATGGTGATATTGCT
TTCGGCGGAGGCACCGAGGTGGTGTTCAAA

SEQ ID NO:115

470B6 CHIMERIC LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

AAVLTQTPSPVSAAVGGTVTISCQSSQSVYSNNQLSWFQQKSGQPPKLLIYDASNLASGVPSRFSGSGSGTQFTLTISSV
QCDDAATYHCLGGSDDDGDIAFGGGTEVVFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:116

470B6 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

AAVLTQTPSPVSAAVGGTVTISCQSSQSVYSNNQLSWFQQKSGQPPKLLIYDASNLASGVPSRFSGSGSGTQFTLTISSV
QCDDAATYHCLGGSDDDGDIAFGGGTEVVFK

SEQ ID NO:117

470B6 CHIMERIC HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

CAGTCACTGGAGGAGTCCGGGGGTCGCCTGGTCACGCCTGGGACACCCCTGACACTCACCTGCACAGCCTCTGGA
TTCTCCCTCAGTAGCTACTACATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGACTGGAATGGATCGGAAGTATT
TATGGTAGTGGTGCCGCATACTACGCGAGCTGGGCGAAAGGCCGATTCACCATCTCCAGAACGTCGACCACGGTG
GATCTGAAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCTGTGCCAGAGATCCTATTAACAATGCCA
TGTGGGGCCCAGGCACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTC
CTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGT
GTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCC
CTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCC
AGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCA
CCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCC
CTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGC
GTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCT
CACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTCCCAGCCCC
CATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGA
TGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTG
GGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCT
CTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGC
TCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:118

470B6 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

CAGTCACTGGAGGAGTCCGGGGGTCGCCTGGTCACGCCTGGGACACCCCTGACACTCACCTGCACAGCCTCTGGA
TTCTCCCTCAGTAGCTACTACATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGACTGGAATGGATCGGAAGTATT
TATGGTAGTGGTGCCGCATACTACGCGAGCTGGGCGAAAGGCCGATTCACCATCTCCAGAACGTCGACCACGGTG
GATCTGAAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCTGTGCCAGAGATCCTATTAACAATGCCA
TGTGGGGCCCAGGCACCCTGGTCACCGTCTCGAGC

SEQ ID NO:119

470B6 CHIMERIC HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

QSLEESGGRLVTPGTPLTLTCTASGFSLSSYYMSWVRQAPGKGLEWIGSIYGSGAAYYASWAKGRFTISRTSTTVDLKMT
SLTAADTATYFCARDPINNAMWGPGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT
SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLFPP
KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCA
VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:120

470B6 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

QSLEESGGRLVTPGTPLTLTCTASGFSLSSYYMSWVRQAPGKGLEWIGSIYGSGAAYYASWAKGRFTISRTSTTVDLKMT
SLTAADTATYFCARDPINNAMWGPGTLVTVSS

SEQ ID NO:121

470C6 CHIMERIC LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GCCCTTGTGATGACCCAGACTCCAGCCTCCGTGTCTGCAGCTGTGGGAGGCACAGTCACCATCAATTGCCAGGCCA
GTGAGGACATTGATAACTATTTAGCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTTTTATGC
ATCCGATCTGGCATCTGGGGTCCCATCGCGGTTCTCAGGCAGTGGATCTGGGACACAGTTCACTCTCACCATCAGC
GGTGTGCAGTGTGACGATGCTGCCACTTACTACTGTCAAGGCGGTTACTATACTAGTAGTACTGATACGAGGGGT
GCTTTCGGCGGAGGCACCGAGGTGGTGGTCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTG
ATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACA
GTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCA
CCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCA
CCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:122

470C6 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GCCCTTGTGATGACCCAGACTCCAGCCTCCGTGTCTGCAGCTGTGGGAGGCACAGTCACCATCAATTGCCAGGCCA
GTGAGGACATTGATAACTATTTAGCCTGGTATCAGCAGAAACCAGGGCAGCCTCCCAAGCTCCTGATCTTTTATGC
ATCCGATCTGGCATCTGGGGTCCCATCGCGGTTCTCAGGCAGTGGATCTGGGACACAGTTCACTCTCACCATCAGC
GGTGTGCAGTGTGACGATGCTGCCACTTACTACTGTCAAGGCGGTTACTATACTAGTAGTACTGATACGAGGGGT
GCTTTCGGCGGAGGCACCGAGGTGGTGGTCAAA

SEQ ID NO:123

470C6 CHIMERIC LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

ALVMTQTPASVSAAVGGTVTINCQASEDIDNYLAWYQQKPGQPPKLLIFYASDLASGVPSRFSGSGSGTQFTLTISGVQ
CDDAATYYCQGGYYTSSTDTRGAFGGGTEVVVKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:124

470C6 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

ALVMTQTPASVSAAVGGTVTINCQASEDIDNYLAWYQQKPGQPPKLLIFYASDLASGVPSRFSGSGSGTQFTLTISGVQ
CDDAATYYCQGGYYTSSTDTRGAFGGGTEVVVK

SEQ ID NO:125

470C6 CHIMERIC HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

CAGTCATTGGAGGAGGCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACTCACCTGCACAGCCTCTGGC
TTCTCCTTCACTAGCAGCTACTACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGC
ATTTATACTGGTAGTAGTGGTAGCACTTACTACGCGAACTGGGCGAAAGGCCGATTCACCATCTCCAAAACCTCGT
CGACCACGGTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCTGTGCGAGAGATAGTA
GTAGTTATTATATGTTTAACTTGTGGGGCCAGGGCACCCTCGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATC
GGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTA
CTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTA
CAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCT
GCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACA
CATGCCCACCGTGCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACAC
CCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTT
CAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG
TACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCC
AACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTAC
ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA
GCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGAC
TCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCAT
GCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:126

470C6 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

CAGTCATTGGAGGAGGCCGGGGGAGACCTGGTCAAGCCTGGGGCATCCCTGACACTCACCTGCACAGCCTCTGGC
TTCTCCTTCACTAGCAGCTACTACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGC
ATTTATACTGGTAGTAGTGGTAGCACTTACTACGCGAACTGGGCGAAAGGCCGATTCACCATCTCCAAAACCTCGT
CGACCACGGTGACTCTGCAAATGACCAGTCTGACAGCCGCGGACACGGCCACCTATTTCTGTGCGAGAGATAGTA
GTAGTTATTATATGTTTAACTTGTGGGGCCAGGGCACCCTCGTCACCGTCTCGAGC

SEQ ID NO:127

470C6 CHIMERIC HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

QSLEEAGGDLVKPGASLTLTCTASGFSFTSSYYMCWVRQAPGKGLEWIACIYTGSSGSTYYANWAKGRFTISKTSSTTVT
LQMTSLTAADTATYFCARDSSSYYMFNLWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAG
APSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL

NGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:128

470C6 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

QSLEEAGGDLVKPGASLTLTCTASGFSFTSSYYMCWVRQAPGKGLEWIACIYTGSSGSTYYANWAKGRFTISKTSSTTVT
LQMTSLTAADTATYFCARDSSSYYMFNLWGQGTLVTVSS

SEQ ID NO:129

472E4 CHIMERIC LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GCAGCCGTGCTGACCCAGACTCCATCTTCCACGTCTGCAGCTGTGGGAGGCACAGTCACCATCAGTTGCCAGTCCA
GTCAGAGTGTTTATAATAACAATGCTTTAGCCTGGTATCAGAAAAAACCAGGACAGCCTCCCAAGCTCCTGATCTA
TTTGGCTTCCACTCTGGCATCTGGGGTCCCATCGCGGTTCAGCGGCAGTGGATCTGGGACACAGTTCACTCTCACC
ATCAGCGACCTGGAGTGTGACGATGCTGCCACTTATTATTGTCTAGGTGTTTATAATGATGATGTTGATAATGGTTT
CGGCGGAGGCACCGAGGTGGTGTTCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAG
CAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGA
AGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTAC
AGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCAT
CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:130

472E4 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GCAGCCGTGCTGACCCAGACTCCATCTTCCACGTCTGCAGCTGTGGGAGGCACAGTCACCATCAGTTGCCAGTCCA
GTCAGAGTGTTTATAATAACAATGCTTTAGCCTGGTATCAGAAAAAACCAGGACAGCCTCCCAAGCTCCTGATCTA
TTTGGCTTCCACTCTGGCATCTGGGGTCCCATCGCGGTTCAGCGGCAGTGGATCTGGGACACAGTTCACTCTCACC
ATCAGCGACCTGGAGTGTGACGATGCTGCCACTTATTATTGTCTAGGTGTTTATAATGATGATGTTGATAATGGTTT
CGGCGGAGGCACCGAGGTGGTGTTCAAA

SEQ ID NO:131

472E4 CHIMERIC LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

AAVLTQTPSSTSAAVGGTVTISCQSSQSVYNNNALAWYQKKPGQPPKLLIYLASTLASGVPSRFSGSGSGTQFTLTISDLE
CDDAATYYCLGVYNDDVDNGFGGGTEVVFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:132

472E4 CHIMERIC LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

AAVLTQTPSSTSAAVGGTVTISCQSSQSVYNNNALAWYQKKPGQPPKLLIYLASTLASGVPSRFSGSGSGTQFTLTISDLE
CDDAATYYCLGVYNDDVDNGFGGGTEVVFK

SEQ ID NO:133

472E4 CHIMERIC HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

CAGTCGCTGGAGGAGTCCGGGGGTCGCCTGGTCACGCCTGGAGGATCCCTGACACTCACCTGCACCGTCTCTGGA
TTCTCCCTCAATAACAATGCAATAAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAATGGGTTGCAATCATA
CAAAATACTGGTACCACAGACTACGCGAGGTGGGCGAAAGGCCGATTCACCATCTCCAAAACCTCGACCACGGTG
GATTTGAAAATCAACAGTCCGACAACCGAGGACACGGCCACCTATTTCTGTGGCAGAGGGTATGGTTTTGAGTCG
GAGCTTGTCATCTGGGGCCCGGGCACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCC
TGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAAC
CGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAG
GACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAA
TCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACC
GTGCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC
TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
TCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCC
TCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCC
CATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCG
CCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGC
TCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGA
TGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:134

472E4 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

CAGTCGCTGGAGGAGTCCGGGGGTCGCCTGGTCACGCCTGGAGGATCCCTGACACTCACCTGCACCGTCTCTGGA
TTCTCCCTCAATAACAATGCAATAAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAATGGGTTGCAATCATA
CAAAATACTGGTACCACAGACTACGCGAGGTGGGCGAAAGGCCGATTCACCATCTCCAAAACCTCGACCACGGTG
GATTTGAAAATCAACAGTCCGACAACCGAGGACACGGCCACCTATTTCTGTGGCAGAGGGTATGGTTTTGAGTCG
GAGCTTGTCATCTGGGGCCCGGGCACCCTGGTCACCGTCTCGAGC

SEQ ID NO:135

472E4 CHIMERIC HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

QSLEESGGRLVTPGGSLTLTCTVSGFSLNNNAISWVRQAPGKGLEWVAIIQNTGTTDYARWAKGRFTISKTSTTVDLKIN
SPTTEDTATYFCGRGYGFESELVIWGPGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGA
LTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSVFLF
PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK
CAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:136

472E4 CHIMERIC HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

QSLEESGGRLVTPGGSLTLTCTVSGFSLNNNAISWVRQAPGKGLEWVAIIQNTGTTDYARWAKGRFTISKTSTTVDLKIN
SPTTEDTATYFCGRGYGFESELVIWGPGTLVTVSS

SEQ ID NO:137

411H11 HUMANIZED LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GACGTTGTGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACCTGTCAGGCCA
GTCAGAGCATTGGTGCTGATTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATAGGG
CATCCACTCTGGCCTCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAG
CAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAAGCTATTTATTATGGTACTGATGATGTCATATACCATA
CTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGA
TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAG
TGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCAC
CTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCAC
CCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:138

411H11 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GACGTTGTGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACCTGTCAGGCCA
GTCAGAGCATTGGTGCTGATTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATAGGG
CATCCACTCTGGCCTCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAG
CAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAAGCTATTTATTATGGTACTGATGATGTCATATACCATA
CTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID NO:139

411H11 HUMANIZED LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

DVVMTQSPSSVSASVGDRVTITCQASQSIGADLAWYQQKPGKAPKLLIYRASTLASGVPSRFSGSGSGTDFTLTISSLQP
EDFATYYCQAIYYGTDDVIYHTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ
SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:140

411H11 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

DVVMTQSPSSVSASVGDRVTITCQASQSIGADLAWYQQKPGKAPKLLIYRASTLASGVPSRFSGSGSGTDFTLTISSLQP
EDFATYYCQAIYYGTDDVIYHTFGGGTKVEIK

SEQ ID NO:141

411H11 HUMANIZED HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTC
TGGATTCACCATCAGTAGCCACCACATGATCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGCAATACATCGGATT
CATTAATGATGGTGACTATACATACTACACGAACTCCGCAAAAGGCAGATTCACCATCTCCAGAGACAATTCCAAG
AACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGGGTTGAT
GGTACTAGTTATCCTGGCTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCG
GTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACT
TCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTAC
AGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG
CAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACAC
ATGCCCACCGTGCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACC
CTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC
AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGT
ACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCA
ACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACA
CCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAG
CGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACT
CCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCAT
GCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:142

411H11 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTC
TGGATTCACCATCAGTAGCCACCACATGATCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGCAATACATCGGATT
CATTAATGATGGTGACTATACATACTACACGAACTCCGCAAAAGGCAGATTCACCATCTCCAGAGACAATTCCAAG
AACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGGGTTGAT
GGTACTAGTTATCCTGGCTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

SEQ ID NO:143

411H11 HUMANIZED HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

EVQLVESGGGLVQPGGSLRLSCAASGFTISSHHMIWVRQAPGKGLQYIGFINDGDYTYYTNSAKGRFTISRDNSKNTLYL
QMNSLRAEDTAVYYCARGVDGTSYPGLWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAG
APSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL
NGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:144

411H11 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

EVQLVESGGGLVQPGGSLRLSCAASGFTISSHHMIWVRQAPGKGLQYIGFINDGDYTYYTNSAKGRFTISRDNSKNTLYL
QMNSLRAEDTAVYYCARGVDGTSYPGLWGQGTLVTVSS

SEQ ID NO:145

413F3 HUMANIZED LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCA
GTCAGAGCATTTACAGCAATTTAGCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTATTCTAC
ATCCACTCTGGCATCTGGGGTCCCATCTCGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGC
AGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCAAAACTATTATGGTAGTAGTACTGATAGTTATGGGAATC
CTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGA
TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAG
TGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCAC
CTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCAC
CCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:146

413F3 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCA
GTCAGAGCATTTACAGCAATTTAGCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTATTCTAC
ATCCACTCTGGCATCTGGGGTCCCATCTCGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGC
AGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCAAAACTATTATGGTAGTAGTACTGATAGTTATGGGAATC
CTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID NO:147

413F3 HUMANIZED LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

DIQMTQSPSSLSASVGDRVTITCQASQSIYSNLAWYQQKPGKVPKLLIYSTSTLASGVPSRFSGSGSGTDFTLTISSLQPED
VATYYCQNYYGSSTDSYGNPFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS
GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:148

413F3 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

DIQMTQSPSSLSASVGDRVTITCQASQSIYSNLAWYQQKPGKVPKLLIYSTSTLASGVPSRFSGSGSGTDFTLTISSLQPED
VATYYCQNYYGSSTDSYGNPFGGGTKVEIK

SEQ ID NO:149

413F3 HUMANIZED HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTC
TGGAATCGACTTCAGTAGCAACTACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCAT
GCATTTATGGTGATAGTAGTGATAATAGTTACTCCGCGAGCTCCGCTAAAGGCAGATTCACCATCTCCAGAGACAA
TTCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGATCT
GGTTATAGCTATTTAGGCTACTTTAACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGG
GCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAA
GGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGC
TGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACC
TACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAA
ACTCACACATGCCCACCGTGCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCA
AGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGG
TCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAAC
AGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCG
GTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAG
GTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCT
ATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTG
CTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC
TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:150

413F3 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTC
TGGAATCGACTTCAGTAGCAACTACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCAT
GCATTTATGGTGATAGTAGTGATAATAGTTACTCCGCGAGCTCCGCTAAAGGCAGATTCACCATCTCCAGAGACAA
TTCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGATCT
GGTTATAGCTATTTAGGCTACTTTAACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

SEQ ID NO:151

413F3 HUMANIZED HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

EVQLVESGGGLVQPGGSLRLSCAASGIDFSSNYMCWVRQAPGKGLEWIACIYGDSSDNSYSASSAKGRFTISRDNSKNT
LYLQMNSLRAEDTAVYYCARSGYSYLGYFNLWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAA
GAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW
LNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:152

413F3 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

EVQLVESGGGLVQPGGSLRLSCAASGIDFSSNYMCWVRQAPGKGLEWIACIYGDSSDNSYSASSAKGRFTISRDNSKNT
LYLQMNSLRAEDTAVYYCARSGYSYLGYFNLWGQGTLVTVSS

SEQ ID NO:153

416F8 HUMANIZED LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCA
GTCAGACTGTTTATAATAACAACTTGTTATCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTAT
TATGCATCCACTCTGGCATTTGGGGTCCCATCTCGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCAT
CAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCAAGGCGGTTATAGTGGTTGGATTTATGTTTTCGGC
GGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAG
TTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGG
TGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGC
CTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAG
GGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:154

416F8 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCA
GTCAGACTGTTTATAATAACAACTTGTTATCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTAT

TATGCATCCACTCTGGCATTTGGGGTCCCATCTCGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCAT
CAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCAAGGCGGTTATAGTGGTTGGATTTATGTTTTCGGC
GGAGGGACCAAGGTGGAGATCAAA

SEQ ID NO:155

416F8 HUMANIZED LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

DIQMTQSPSSLSASVGDRVTITCQSSQTVYNNNLLSWYQQKPGKVPKLLIYYASTLAFGVPSRFSGSGSGTDFTLTISSLQ
PEDVATYYCQGGYSGWIYVFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS
GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:156

416F8 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

DIQMTQSPSSLSASVGDRVTITCQSSQTVYNNNLLSWYQQKPGKVPKLLIYYASTLAFGVPSRFSGSGSGTDFTLTISSLQ
PEDVATYYCQGGYSGWIYVFGGGTKVEIK

SEQ ID NO:157

416F8 HUMANIZED HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

CAGTCGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGA
TTCTCCCTCAGTAACTACTACATGAACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTACATCGGAATCATT
AGTAGTAGTGGTAGCGCATACTACGCGAGCTCCGCTAAAGGCAGATTCACCATCTCCAGAGACAATTCCAAGAAC
ACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGGGACTACGGC
ATGGACCTCTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTG
GCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG
GTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGA
CTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATC
ACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGT
GCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTC
CCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGT
GGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTC
AGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCCTC
CCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCA
TCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCC
GTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTC
CTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATG
CATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:158

416F8 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

CAGTCGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGA
TTCTCCCTCAGTAACTACTACATGAACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTACATCGGAATCATT
AGTAGTAGTGGTAGCGCATACTACGCGAGCTCCGCTAAAGGCAGATTCACCATCTCCAGAGACAATTCCAAGAAC
ACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGGGACTACGGC
ATGGACCTCTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

SEQ ID NO:159

416F8 HUMANIZED HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

QSLVESGGGLVQPGGSLRLSCAASGFSLSNYYMNWVRQAPGKGLEYIGIISSSGSAYYASSAKGRFTISRDNSKNTLYLQ
MNSLRAEDTAVYYCARGDYGMDLWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS
GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSV
FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
YKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL
DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:160

416F8 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

QSLVESGGGLVQPGGSLRLSCAASGFSLSNYYMNWVRQAPGKGLEYIGIISSSGSAYYASSAKGRFTISRDNSKNTLYLQ
MNSLRAEDTAVYYCARGDYGMDLWGQGTLVTVSS

SEQ ID NO:161

416G1 HUMANIZED LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GACGTTGTGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACCTGTCAGGCCA
GTCAGAGCATTGGTAGTGATTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATAGGG
CATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAG
CAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAATCCATTTATTATGGTAGTGATGATGTCATATACCATA
CTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGA
TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAG
TGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCAC
CTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCAC
CCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:162

416G1 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GACGTTGTGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACCTGTCAGGCCA
GTCAGAGCATTGGTAGTGATTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATAGGG
CATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAG
CAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAATCCATTTATTATGGTAGTGATGATGTCATATACCATA
CTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID NO:163

416G1 HUMANIZED LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

DVVMTQSPSSVSASVGDRVTITCQASQSIGSDLAWYQQKPGKAPKLLIYRASTLASGVPSRFSGSGSGTDFTLTISSLQPE
DFATYYCQSIYYGSDDVIYHTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS
GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:164

416G1 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

DVVMTQSPSSVSASVGDRVTITCQASQSIGSDLAWYQQKPGKAPKLLIYRASTLASGVPSRFSGSGSGTDFTLTISSLQPE
DFATYYCQSIYYGSDDVIYHTFGGGTKVEIK

SEQ ID NO:165

416G1 HUMANIZED HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTC
TGGATTCACTATCAATAGCTACCACATGATCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTACATCGGATT
CATTAATGATGGTGGTTTCACATACTACGCGAGCTCCGCTAAAGGCAGATTCACCATCTCCAGAGACAATTCCAAG
AACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGGGTTGAT
GGTACTAGTTATCCTGACTTATGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCG
GTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACT
TCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTAC
AGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG
CAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACAC
ATGCCCACCGTGCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACC
CTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC
AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGT
ACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCA
ACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACA

CCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAG
CGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACT
CCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCAT
GCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:166

416G1 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTC
TGGATTCACTATCAATAGCTACCACATGATCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTACATCGGATT
CATTAATGATGGTGGTTTCACATACTACGCGAGCTCCGCTAAAGGCAGATTCACCATCTCCAGAGACAATTCCAAG
AACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGGGTTGAT
GGTACTAGTTATCCTGACTTATGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

SEQ ID NO:167

416G1 HUMANIZED HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

EVQLVESGGGLVQPGGSLRLSCAASGFTINSYHMIWVRQAPGKGLEYIGFINDGGFTYYASSAKGRFTISRDNSKNTLYL
QMNSLRAEDTAVYYCARGVDGTSYPDLWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAG
APSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL
NGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:168

416G1 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

EVQLVESGGGLVQPGGSLRLSCAASGFTINSYHMIWVRQAPGKGLEYIGFINDGGFTYYASSAKGRFTISRDNSKNTLYL
QMNSLRAEDTAVYYCARGVDGTSYPDLWGQGTLVTVSS

SEQ ID NO:169

418E10 HUMANIZED LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCA
GTCAGAGCATTGGTAGTAACTTGAACTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATTATGT
ATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGC
AGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCTAGGTGTTTGGAATTATTGGGGTGATGACGGTACTGCTTT
CGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGA
GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGG
AAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTA

CAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCA
TCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:170

418E10 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCA
GTCAGAGCATTGGTAGTAACTTGAACTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATTATGT
ATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGC
AGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCTAGGTGTTTGGAATTATTGGGGTGATGACGGTACTGCTTT
CGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID NO:171

418E10 HUMANIZED LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

DIQMTQSPSTLSASVGDRVTITCQASQSIGSNLNWYQQKPGKAPKLLIYYVSTLASGVPSRFSGSGSGTEFTLTISSLQPD
DFATYYCLGVWNYWGDDGTAFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:172

418E10 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

DIQMTQSPSTLSASVGDRVTITCQASQSIGSNLNWYQQKPGKAPKLLIYYVSTLASGVPSRFSGSGSGTEFTLTISSLQPD
DFATYYCLGVWNYWGDDGTAFGGGTKVEIK

SEQ ID NO:173

418E10 HUMANIZED HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTC
TGGATTCTCCCTCAGTACCTATTATATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAAG
TATTTATGATAGTGGTGCCGCATACTACGCGACCTCCGCGAAGGGCAGATTCACCATCTCCAGAGACAATTCCAAG
AACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCCTATT
AATAATGCCATCTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCC
CTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAA
CCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCA
GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGA
ATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCAC
CGTGCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGAT
CTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTA
CGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTG

GTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCC
CTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCC
CCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATC
GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGG
CTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTG
ATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:174

418E10 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTC
TGGATTCTCCCTCAGTACCTATTATATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAAG
TATTTATGATAGTGGTGCCGCATACTACGCGACCTCCGCGAAGGGCAGATTCACCATCTCCAGAGACAATTCCAAG
AACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCCTATT
AATAATGCCATCTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

SEQ ID NO:175

418E10 HUMANIZED HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

EVQLVESGGGLVQPGGSLRLSCAASGFSLSTYYMSWVRQAPGKGLEWIGSIYDSGAAYYATSAKGRFTISRDNSKNTLY
LQMNSLRAEDTAVYYCARDPINNAIWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS
GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSV
FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
YKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL
DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:176

418E10 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

EVQLVESGGGLVQPGGSLRLSCAASGFSLSTYYMSWVRQAPGKGLEWIGSIYDSGAAYYATSAKGRFTISRDNSKNTLY
LQMNSLRAEDTAVYYCARDPINNAIWGQGTLVTVSS

SEQ ID NO:177

418E4 HUMANIZED LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCA
GTCAGAGTATTGCTACTAACTTGAACTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATTATAC
ATCCAGTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGC
AGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCTAGGTGTTTGGAATTATTGGGGTGATGATGGTACTGCTTT
CGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGA

GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGG
AAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTA
CAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCA
TCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:178

418E4 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCA
GTCAGAGTATTGCTACTAACTTGAACTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATTATAC
ATCCAGTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGC
AGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCTAGGTGTTTGGAATTATTGGGGTGATGATGGTACTGCTTT
CGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID NO:179

418E4 HUMANIZED LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

DIQMTQSPSTLSASVGDRVTITCQASQSIATNLNWYQQKPGKAPKLLIYYTSSLASGVPSRFSGSGSGTEFTLTISSLQPD
DFATYYCLGVWNYWGDDGTAFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:180

418E4 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

DIQMTQSPSTLSASVGDRVTITCQASQSIATNLNWYQQKPGKAPKLLIYYTSSLASGVPSRFSGSGSGTEFTLTISSLQPD
DFATYYCLGVWNYWGDDGTAFGGGTKVEIK

SEQ ID NO:181

418E4 HUMANIZED HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTC
TGGATTCTCCCTCAGTAGCTACTACATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAA
GTATTTATGCTAGTGGTAGCGCATACTACGCGAGTTCCGCGAAGGGCAGATTCACCATCTCCAGAGACAATTCCAA
GAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCCTAT
TAACAATGACATCTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCC
CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGA
ACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC
AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTG
AATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCA
CCGTGCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA

TCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGT
ACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGT
GGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGC
CCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCC
CCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATC
GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGG
CTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTG
ATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:182

418E4 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTC
TGGATTCTCCCTCAGTAGCTACTACATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAA
GTATTTATGCTAGTGGTAGCGCATACTACGCGAGTTCCGCGAAGGGCAGATTCACCATCTCCAGAGACAATTCCAA
GAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCCTAT
TAACAATGACATCTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

SEQ ID NO:183

418E4 HUMANIZED HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

EVQLVESGGGLVQPGGSLRLSCAASGFSLSSYYMSWVRQAPGKGLEWIGSIYASGSAYYASSAKGRFTISRDNSKNTLYL
QMNSLRAEDTAVYYCARDPINNDIWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS
GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSV
FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
YKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL
DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:184

418E4 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

EVQLVESGGGLVQPGGSLRLSCAASGFSLSSYYMSWVRQAPGKGLEWIGSIYASGSAYYASSAKGRFTISRDNSKNTLYL
QMNSLRAEDTAVYYCARDPINNDIWGQGTLVTVSS

SEQ ID NO:185

418H5 HUMANIZED LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGTCAGTCCA
GTCCGAGTGTTTATAAGAACAACCAATTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTA
TCTGGCATCTACTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACC

ATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTGCAGGCGGTTATAGTAGTAGTAGTGATACTGCTT
TCGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATG
AGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTG
GAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCT
ACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCC
ATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:186

418H5 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGTCAGTCCA
GTCCGAGTGTTTATAAGAACAACCAATTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTA
TCTGGCATCTACTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACC
ATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTGCAGGCGGTTATAGTAGTAGTAGTGATACTGCTT
TCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID NO:187

418H5 HUMANIZED LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

DIQMTQSPSSVSASVGDRVTITCQSSPSVYKNNQLAWYQQKPGKAPKLLIYLASTLASGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCAGGYSSSSDTAFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS
GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:188

418H5 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

DIQMTQSPSSVSASVGDRVTITCQSSPSVYKNNQLAWYQQKPGKAPKLLIYLASTLASGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCAGGYSSSSDTAFGGGTKVEIK

SEQ ID NO:189

418H5 HUMANIZED HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAGCCTC
TGGAATCGACCTCAGTGCCTACCACATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTACATCGGGA
TGATTGGTAGTAGTGGTACCATACACTACGCGAACTCCGCGAAAGGCAGATTCACCATCTCCAAAGACAATACCAA
GAACACGGTGGATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACAGTT
ATAATAGTGATTATGCCTTTAACTTATGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCC
ATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGA
CTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTC
CTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACA

TCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTC
ACACATGCCCACCGTGCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGA
CACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAA
GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCA
CGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCT
CCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
ACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCC
CAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGG
ACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTC
ATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:190

418H5 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAGCCTC
TGGAATCGACCTCAGTGCCTACCACATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTACATCGGGA
TGATTGGTAGTAGTGGTACCATACACTACGCGAACTCCGCGAAAGGCAGATTCACCATCTCCAAAGACAATACCAA
GAACACGGTGGATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACAGTT
ATAATAGTGATTATGCCTTTAACTTATGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

SEQ ID NO:191

418H5 HUMANIZED HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

EVQLVESGGGLVQPGGSLRLSCTASGIDLSAYHMSWVRQAPGKGLEYIGMIGSSGTIHYANSAKGRFTISKDNTKNTVD
LQMNSLRAEDTAVYYCARDSYNSDYAFNLWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV
SWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAA
GAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW
LNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:192

418H5 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

EVQLVESGGGLVQPGGSLRLSCTASGIDLSAYHMSWVRQAPGKGLEYIGMIGSSGTIHYANSAKGRFTISKDNTKNTVD
LQMNSLRAEDTAVYYCARDSYNSDYAFNLWGQGTLVTVSS

SEQ ID NO:193

419D9 HUMANIZED LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCA
GTCAGAGTGTTTATAGTAACTGGTTATCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGAGACTGATCTATTC
TGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATC
AGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCGCAGGCGGTTATAATACTGTTACTGATACTTTTGCTTT
CGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGA
GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGG
AAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTA
CAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCA
TCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:194

419D9 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCA
GTCAGAGTGTTTATAGTAACTGGTTATCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGAGACTGATCTATTC
TGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATC
AGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCGCAGGCGGTTATAATACTGTTACTGATACTTTTGCTTT
CGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID NO:195

419D9 HUMANIZED LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

DIQMTQSPSTLSASVGDRVTITCQSSQSVYSNWLSWYQQKPGKAPKRLIYSASTLASGVPSRFSGSGSGTEFTLTISSLQP
DDFATYYCAGGYNTVTDTFAFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS
GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:196

419D9 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

DIQMTQSPSTLSASVGDRVTITCQSSQSVYSNWLSWYQQKPGKAPKRLIYSASTLASGVPSRFSGSGSGTEFTLTISSLQP
DDFATYYCAGGYNTVTDTFAFGGGTKVEIK

SEQ ID NO:197

419D9 HUMANIZED HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAGCCTCT
GGATTCTCCTTCAGTAGCAGGCACTACATGTGTTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCA
TGCATTTATACTGGTAGTAGTGGTACTCCTCACTACGCGAGCTCCGCGAAAGGCCGGTTCACCATCTCCCAAGACA
ATTCCAAGAACACGGTGACTCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGAG
AAGGTAACCTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCCC

TGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAAC
CGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAG
GACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAA
TCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACC
GTGCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATC
TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTAC
GTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGG
TCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCCC
TCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCC
CATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCG
CCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGC
TCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGA
TGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:198

419D9 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAGCCTCT
GGATTCTCCTTCAGTAGCAGGCACTACATGTGTTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCA
TGCATTTATACTGGTAGTAGTGGTACTCCTCACTACGCGAGCTCCGCGAAAGGCCGGTTCACCATCTCCCAAGACA
ATTCCAAGAACACGGTGACTCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGAG
AAGGTAACCTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

SEQ ID NO:199

419D9 HUMANIZED HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

EVQLLESGGGLVQPGGSLRLSCTASGFSFSSRHYMCWVRQAPGKGLEWIACIYTGSSGTPHYASSAKGRFTISQDNSKN
TVTLQMNSLRAEDTAVYYCAREGNLWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN
SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPS
VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG
KEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP
VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:200

419D9 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

EVQLLESGGGLVQPGGSLRLSCTASGFSFSSRHYMCWVRQAPGKGLEWIACIYTGSSGTPHYASSAKGRFTISQDNSKN
TVTLQMNSLRAEDTAVYYCAREGNLWGQGTLVTVSS

SEQ ID NO:201

420H5 HUMANIZED LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GCCCTTGTGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAGGCCA
GTGAGGACATTGATACCTATTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTTTTATGC
ATCCGATCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGC
AGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAAGGCGGTTACTATACTAGTAGTGCTGATACGAGGGGTG
CTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGA
TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAG
TGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCAC
CTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCAC
CCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:202

420H5 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GCCCTTGTGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAGGCCA
GTGAGGACATTGATACCTATTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTTTTATGC
ATCCGATCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGC
AGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAAGGCGGTTACTATACTAGTAGTGCTGATACGAGGGGTG
CTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID NO:203

420H5 HUMANIZED LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

ALVMTQSPSTLSASVGDRVTINCQASEDIDTYLAWYQQKPGKAPKLLIFYASDLASGVPSRFSGSGSGTEFTLTISSLQPD
DFATYYCQGGYYTSSADTRGAFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ
SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:204

420H5 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

ALVMTQSPSTLSASVGDRVTINCQASEDIDTYLAWYQQKPGKAPKLLIFYASDLASGVPSRFSGSGSGTEFTLTISSLQPD
DFATYYCQGGYYTSSADTRGAFGGGTKVEIK

SEQ ID NO:205

420H5 HUMANIZED HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

CAGTCGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGG
ATTCTCCTTCAGTAGCAACTACTGGATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATG
CATTTATGTTGGTAGTAGTGGTGACACTTACTACGCGAGCTCCGCGAAAGGCCGGTTCACCATCTCCAGAGACAAT

TCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGAGAT
AGTAGTAGTTATTATATGTTTAACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGC
CCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGG
ACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTG
TCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTA
CATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAAC
TCACACATGCCCACCGTGCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG
GACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC
AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACA
GCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGG
TCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGG
TGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTA
TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGC
TGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCT
TCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:206

420H5 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

CAGTCGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGG
ATTCTCCTTCAGTAGCAACTACTGGATATGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATG
CATTTATGTTGGTAGTAGTGGTGACACTTACTACGCGAGCTCCGCGAAAGGCCGGTTCACCATCTCCAGAGACAAT
TCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGAGAT
AGTAGTAGTTATTATATGTTTAACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

SEQ ID NO:207

420H5 HUMANIZED HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

QSLVESGGGLVQPGGSLRLSCAASGFSFSSNYWICWVRQAPGKGLEWIACIYVGSSGDTYYASSAKGRFTISRDNSKNT
LYLQMNSLRAEDTAVYYCARDSSSYYMFNLWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAA
GAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW
LNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:208

420H5 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

QSLVESGGGLVQPGGSLRLSCAASGFSFSSNYWICWVRQAPGKGLEWIACIYVGSSGDTYYASSAKGRFTISRDNSKNT
LYLQMNSLRAEDTAVYYCARDSSSYYMFNLWGQGTLVTVSS

SEQ ID NO:209

420H6 HUMANIZED LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCA
GTCAGAGTGTTTATAGTAACTGGTTATCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATTC
TGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATC
AGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCGCAGGCGGTTACAATACTGTAATTGATACTTTTGCTTT
CGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGA
GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGG
AAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTA
CAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCA
TCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:210

420H6 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCA
GTCAGAGTGTTTATAGTAACTGGTTATCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATTC
TGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATC
AGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCGCAGGCGGTTACAATACTGTAATTGATACTTTTGCTTT
CGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID NO:211

420H6 HUMANIZED LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

DIQMTQSPSTLSASVGDRVTITCQASQSVYSNWLSWYQQKPGKAPKLLIYSASTLASGVPSRFSGSGSGTEFTLTISSLQP
DDFATYYCAGGYNTVIDTFAFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS
GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:212

420H6 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

DIQMTQSPSTLSASVGDRVTITCQASQSVYSNWLSWYQQKPGKAPKLLIYSASTLASGVPSRFSGSGSGTEFTLTISSLQP
DDFATYYCAGGYNTVIDTFAFGGGTKVEIK

SEQ ID NO:213

420H6 HUMANIZED HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCT
GGAATCGACTTCAGTAGTAGTTACTACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGC

ATGCATTTATACTGGTGGTAGTGGTACTCCTCACTACGCGAGCTCCGCGAAAGGCCGGTTCACCATCTCCAGAGAC
AATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGA
GAAGGTAGCCTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCC
CTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAA
CCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCA
GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGA
ATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCAC
CGTGCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGAT
CTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTA
CGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTG
GTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCC
CTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCC
CCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATC
GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGG
CTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTG
ATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:214

420H6 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCT
GGAATCGACTTCAGTAGTAGTTACTACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGC
ATGCATTTATACTGGTGGTAGTGGTACTCCTCACTACGCGAGCTCCGCGAAAGGCCGGTTCACCATCTCCAGAGAC
AATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGA
GAAGGTAGCCTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

SEQ ID NO:215

420H6 HUMANIZED HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

EVQLLESGGGLVQPGGSLRLSCAASGIDFSSSYYMCWVRQAPGKGLEWIACIYTGGSGTPHYASSAKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAREGSLWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS
GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSV
FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
YKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL
DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:216

420H6 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

EVQLLESGGGLVQPGGSLRLSCAASGIDFSSSYYMCWVRQAPGKGLEWIACIYTGGSGTPHYASSAKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAREGSLWGQGTLVTVSS

SEQ ID NO:217

459F1 HUMANIZED LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCA
GTCAGAGTGTTTATAGTAACTGGTTCTCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATTC
TGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATC
AGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCGCAGGCGGTTACAATACTGTAACTGATACTTTTGCTTT
CGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGA
GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGG
AAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTA
CAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCA
TCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:218

459F1 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCA
GTCAGAGTGTTTATAGTAACTGGTTCTCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATTC
TGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATC
AGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCGCAGGCGGTTACAATACTGTAACTGATACTTTTGCTTT
CGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID NO:219

459F1 HUMANIZED LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

DIQMTQSPSTLSASVGDRVTITCQSSQSVYSNWFSWYQQKPGKAPKLLIYSASTLASGVPSRFSGSGSGTEFTLTISSLQP
DDFATYYCAGGYNTVTDTFAFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS
GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:220

459F1 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

DIQMTQSPSTLSASVGDRVTITCQSSQSVYSNWFSWYQQKPGKAPKLLIYSASTLASGVPSRFSGSGSGTEFTLTISSLQP
DDFATYYCAGGYNTVTDTFAFGGGTKVEIK

SEQ ID NO:221

459F1 HUMANIZED HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCT
GGAATCGACTTCAGTAGGAGATACTACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGC
ATGCATGTATACTGGTAGCCGCGATACTCCTCACTACGCGAGCTCCGCGAAAGGCCGGTTCACCATCTCCAGAGAC
AATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGA
GAAGGTAACCTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCC
CTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAA
CCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCA
GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGA
ATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCAC
CGTGCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGAT
CTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTA
CGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTG
GTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCC
CTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCC
CCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATC
GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGG
CTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTG
ATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:222

459F1 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCT
GGAATCGACTTCAGTAGGAGATACTACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGC
ATGCATGTATACTGGTAGCCGCGATACTCCTCACTACGCGAGCTCCGCGAAAGGCCGGTTCACCATCTCCAGAGAC
AATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGA
GAAGGTAACCTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

SEQ ID NO:223

459F1 HUMANIZED HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

EVQLLESGGGLVQPGGSLRLSCAASGIDFSRRYYMCWVRQAPGKGLEWIACMYTGSRDTPHYASSAKGRFTISRDNSK
NTLYLQMNSLRAEDTAVYYCAREGNLWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW
NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAP
SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG
KEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP
VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:224

459F1 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

EVQLLESGGGLVQPGGSLRLSCAASGIDFSRRYYMCWVRQAPGKGLEWIACMYTGSRDTPHYASSAKGRFTISRDNSK
NTLYLQMNSLRAEDTAVYYCAREGNLWGQGTLVTVSS

SEQ ID NO:225

460C3 HUMANIZED LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCA
GTCAGAGTGTTTATAGTAACTGGTTCTCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATTC
TGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATC
AGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCGCAGGCGGTTACAATACTGTTATTGATACTTTTGCTTT
CGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGA
GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGG
AAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTA
CAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCA
TCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:226

460C3 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCA
GTCAGAGTGTTTATAGTAACTGGTTCTCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATTC
TGCATCCACTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATC
AGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCGCAGGCGGTTACAATACTGTTATTGATACTTTTGCTTT
CGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID NO:227

460C3 HUMANIZED LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

DIQMTQSPSTLSASVGDRVTITCQSSQSVYSNWFSWYQQKPGKAPKLLIYSASTLASGVPSRFSGSGSGTEFTLTISSLQP
DDFATYYCAGGYNTVIDTFAFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS
GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:228

460C3 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

DIQMTQSPSTLSASVGDRVTITCQSSQSVYSNWFSWYQQKPGKAPKLLIYSASTLASGVPSRFSGSGSGTEFTLTISSLQP
DDFATYYCAGGYNTVIDTFAFGGGTKVEIK

SEQ ID NO:229

460C3 HUMANIZED HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCT
GGAATCGACTTCAGTAGGAGATACTACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGC
ATGCATATATACTGGTAGCCGCGATACTCCTCACTACGCGAGCTCCGCGAAAGGCCGGTTCACCATCTCCAGAGAC
AATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGA
GAAGGTAGCCTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCC
CTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAA
CCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCA
GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGA
ATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCAC
CGTGCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGAT
CTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTA
CGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTG
GTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCC
CTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCC
CCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATC
GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGG
CTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTG
ATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:230

460C3 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCT
GGAATCGACTTCAGTAGGAGATACTACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGC
ATGCATATATACTGGTAGCCGCGATACTCCTCACTACGCGAGCTCCGCGAAAGGCCGGTTCACCATCTCCAGAGAC
AATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGA
GAAGGTAGCCTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

SEQ ID NO:231

460C3 HUMANIZED HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

EVQLLESGGGLVQPGGSLRLSCAASGIDFSRRYYMCWVRQAPGKGLEWIACIYTGSRDTPHYASSAKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAREGSLWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS
GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSV
FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
YKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL
DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:232

460C3 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

EVQLLESGGGLVQPGGSLRLSCAASGIDFSRRYYMCWVRQAPGKGLEWIACIYTGSRDTPHYASSAKGRFTISRDNSKN
TLYLQMNSLRAEDTAVYYCAREGSLWGQGTLVTVSS

SEQ ID NO:233

464C11 HUMANIZED LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCA
GTCAGAGTGTTTATAGTAACAGCTTCTTATCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTA
TTCTGCATCCGATCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACC
ATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCGCAGGCGTTTATAGTGATAATACTTATGTTTTCGG
CGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCA
GTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAG
GTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAG
CCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCA
GGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:234

464C11 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCA
GTCAGAGTGTTTATAGTAACAGCTTCTTATCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTA
TTCTGCATCCGATCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACC
ATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCGCAGGCGTTTATAGTGATAATACTTATGTTTTCGG
CGGAGGGACCAAGGTGGAGATCAAA

SEQ ID NO:235

464C11 HUMANIZED LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

DIQMTQSPSTLSASVGDRVTITCQSSQSVYSNSFLSWYQQKPGKAPKLLIYSASDLASGVPSRFSGSGSGTEFTLTISSLQP
DDFATYYCAGVYSDNTYVFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG
NSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:236

464C11 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

DIQMTQSPSTLSASVGDRVTITCQSSQSVYSNSFLSWYQQKPGKAPKLLIYSASDLASGVPSRFSGSGSGTEFTLTISSLQP
DDFATYYCAGVYSDNTYVFGGGTKVEIK

SEQ ID NO:237

464C11 HUMANIZED HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGCCGTCCCTGAGACTCTCCTGTACAGCTTCT
GGATTCTCCCTCAGTCACTACTGGATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTACATCGGATTC
ATTAATGTTGGTGGTGACACATCTTACGCGAGCTCTGTGAAAGGCAGATTCACCATCTCAAGAGATGATTCCAAAA
GCATCGCCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTACTGTGGCAGAGGTGGTCTGA
CTTTTGGTTGGGACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCT
TCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCC
CGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTC
CTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAAC
GTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGC
CCACCGTGCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCA
TGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACT
GGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCG
TGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAA
AGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCT
GCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGA
CATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCG
ACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTC
CGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:238

464C11 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCAGGGCCGTCCCTGAGACTCTCCTGTACAGCTTCT
GGATTCTCCCTCAGTCACTACTGGATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTACATCGGATTC
ATTAATGTTGGTGGTGACACATCTTACGCGAGCTCTGTGAAAGGCAGATTCACCATCTCAAGAGATGATTCCAAAA
GCATCGCCTATCTGCAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTACTGTGGCAGAGGTGGTCTGA
CTTTTGGTTGGGACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

SEQ ID NO:239

464C11 HUMANIZED HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

EVQLVESGGGLVQPGPSLRLSCTASGFSLSHYWMTWVRQAPGKGLEYIGFINVGGDTSYASSVKGRFTISRDDSKSIAYL
QMNSLKTEDTAVYYCGRGGLTFGWDLWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW
NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAP
SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG

KEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP
VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:240

464C11 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

EVQLVESGGGLVQPGPSLRLSCTASGFSLSHYWMTWVRQAPGKGLEYIGFINVGGDTSYASSVKGRFTISRDDSKSIAYL
QMNSLKTEDTAVYYCGRGGLTFGWDLWGQGTLVTVSS

SEQ ID NO:241

466F6 HUMANIZED LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GACGTTGTGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACCTGTCAGGCCA
GTCAGAACATTAGGACTTACTTATCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCTGC
AGCCAATCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGC
GACCTGGAGCCTGGCGATGCTGCAACTTACTATTGTCAGTCTACCTATCTTGGTACTGATTATGTTGGCGGTGCTTT
CGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGA
GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGG
AAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTA
CAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCA
TCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:242

466F6 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GACGTTGTGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACCTGTCAGGCCA
GTCAGAACATTAGGACTTACTTATCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCTGC
AGCCAATCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGC
GACCTGGAGCCTGGCGATGCTGCAACTTACTATTGTCAGTCTACCTATCTTGGTACTGATTATGTTGGCGGTGCTTT
CGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID NO:243

466F6 HUMANIZED LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

DVVMTQSPSSVSASVGDRVTITCQASQNIRTYLSWYQQKPGKAPKLLIYAAANLASGVPSRFSGSGSGTDFTLTISDLEP
GDAATYYCQSTYLGTDYVGGAFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:244

466F6 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

DVVMTQSPSSVSASVGDRVTITCQASQNIRTYLSWYQQKPGKAPKLLIYAAANLASGVPSRFSGSGSGTDFTLTISDLEP
GDAATYYCQSTYLGTDYVGGAFGGGTKVEIK

SEQ ID NO:245

466F6 HUMANIZED HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

CGGTCGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAGCCTCTGGA
TTCACCATCAGTAGCTACCACATGCAGTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTACATCGGAACCATT
AGTAGTGGTGGTAATGTATACTACGCGAGCTCCGCGAGAGGCAGATTCACCATCTCCAGACCCTCGTCCAAGAAC
ACGGTGGATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACTCTGGTTAT
AGTGATCCTATGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCCC
CTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAA
CCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCA
GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGA
ATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCAC
CGTGCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGAT
CTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTA
CGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTG
GTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGCC
CTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCC
CCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATC
GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGG
CTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTG
ATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:246

466F6 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

CGGTCGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTACAGCCTCTGGA
TTCACCATCAGTAGCTACCACATGCAGTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTACATCGGAACCATT
AGTAGTGGTGGTAATGTATACTACGCGAGCTCCGCGAGAGGCAGATTCACCATCTCCAGACCCTCGTCCAAGAAC
ACGGTGGATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACTCTGGTTAT
AGTGATCCTATGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

SEQ ID NO:247

466F6 HUMANIZED HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

RSLVESGGGLVQPGGSLRLSCTASGFTISSYHMQWVRQAPGKGLEYIGTISSGGNVYYASSARGRFTISRPSSKNTVDLQ
MNSLRAEDTAVYYCARDSGYSDPMWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS
GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAPSV
FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
YKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL
DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:248

466F6 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

RSLVESGGGLVQPGGSLRLSCTASGFTISSYHMQWVRQAPGKGLEYIGTISSGGNVYYASSARGRFTISRPSSKNTVDLQ
MNSLRAEDTAVYYCARDSGYSDPMWGQGTLVTVSS

SEQ ID NO:249

470B6 HUMANIZED LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCA
GTCAGAGCATTAGTACTAACTTGAACTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATTATGC
ATCCAGTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGC
AGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCTAGGTGTTTGGAATTATTGGGGTGATGATGGTACTGATTT
CGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGA
GCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGG
AAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTA
CAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCA
TCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:250

470B6 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCCA
GTCAGAGCATTAGTACTAACTTGAACTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATTATGC
ATCCAGTCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGC
AGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCTAGGTGTTTGGAATTATTGGGGTGATGATGGTACTGATTT
CGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID NO:251

470B6 HUMANIZED LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

DIQMTQSPSTLSASVGDRVTITCQASQSISTNLNWYQQKPGKAPKLLIYYASSLASGVPSRFSGSGSGTEFTLTISSLQPD
DFATYYCLGVWNYWGDDGTDFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL
QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:252

470B6 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

DIQMTQSPSTLSASVGDRVTITCQASQSISTNLNWYQQKPGKAPKLLIYYASSLASGVPSRFSGSGSGTEFTLTISSLQPD
DFATYYCLGVWNYWGDDGTDFGGGTKVEIK

SEQ ID NO:253

470B6 HUMANIZED HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTC
TGGATTCTCCCTCAGTAGCTACTACATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAA
GTATTTATGGTAGTGGTGCCGCATACTACGCGAGCTCCGCTAAAGGCAGATTCACCATCTCCAGAGACAATTCCAA
GAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCCTAT
TAACAATGCCATGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCGGTCTTCCC
CCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGA
ACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTC
AGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTG
AATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCA
CCGTGCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA
TCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGT
ACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGT
GGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCAACAAAGC
CCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCC
CCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATC
GCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGG
CTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTG
ATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:254

470B6 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTC
TGGATTCTCCCTCAGTAGCTACTACATGAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGGAA
GTATTTATGGTAGTGGTGCCGCATACTACGCGAGCTCCGCTAAAGGCAGATTCACCATCTCCAGAGACAATTCCAA
GAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCCTAT
TAACAATGCCATGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

SEQ ID NO:255

470B6 HUMANIZED HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

EVQLVESGGGLVQPGGSLRLSCAASGFSLSSYYMSWVRQAPGKGLEWIGSIYGSGAAYYASSAKGRFTISRDNSKNTLY
LQMNSLRAEDTAVYYCARDPINNAMWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW
NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAGAP
SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG
KEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP
VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:256

470B6 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

EVQLVESGGGLVQPGGSLRLSCAASGFSLSSYYMSWVRQAPGKGLEWIGSIYGSGAAYYASSAKGRFTISRDNSKNTLY
LQMNSLRAEDTAVYYCARDPINNAMWGQGTLVTVSS

SEQ ID NO:257

470C6 HUMANIZED LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GCCCTTGTGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAGGCCA
GTGAGGACATTGATAACTATTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTTTTATGC
ATCCGATCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGC
AGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAAGGCGGTTACTATACTAGTAGTACTGATACGAGGGGTG
CTTTCGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGA
TGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAG
TGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCAC
CTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCAC
CCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:258

470C6 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GCCCTTGTGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAGGCCA
GTGAGGACATTGATAACTATTTAGCCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTTTTATGC
ATCCGATCTGGCATCTGGGGTCCCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGC
AGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAAGGCGGTTACTATACTAGTAGTACTGATACGAGGGGTG
CTTTCGGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID NO:259

470C6 HUMANIZED LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

ALVMTQSPSTLSASVGDRVTINCQASEDIDNYLAWYQQKPGKAPKLLIFYASDLASGVPSRFSGSGSGTEFTLTISSLQPD
DFATYYCQGGYYTSSTDTRGAFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ
SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:260

470C6 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

ALVMTQSPSTLSASVGDRVTINCQASEDIDNYLAWYQQKPGKAPKLLIFYASDLASGVPSRFSGSGSGTEFTLTISSLQPD
DFATYYCQGGYYTSSTDTRGAFGGGTKVEIK

SEQ ID NO:261

470C6 HUMANIZED HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

CAGTCGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGG
ATTCTCCTTCACTAGCAGCTACTACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATG
CATTTATACTGGTAGTAGTGGTAGCACTTACTACGCGAACTCCGCGAAAGGCCGGTTCACCATCTCCAGAGACAAT
TCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGAGAT
AGTAGTAGTTATTATATGTTTAACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGC
CCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGG
ACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTG
TCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTA
CATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAAC
TCACACATGCCCACCGTGCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG
GACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTC
AAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACA
GCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGG
TCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGG
TGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTA
TCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGC
TGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCT
TCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:262

470C6 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

CAGTCGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGG
ATTCTCCTTCACTAGCAGCTACTACATGTGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATG
CATTTATACTGGTAGTAGTGGTAGCACTTACTACGCGAACTCCGCGAAAGGCCGGTTCACCATCTCCAGAGACAAT
TCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGAGAT
AGTAGTAGTTATTATATGTTTAACTTGTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

SEQ ID NO:263

470C6 HUMANIZED HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

QSLVESGGGLVQPGGSLRLSCAASGFSFTSSYYMCWVRQAPGKGLEWIACIYTGSSGSTYYANSAKGRFTISRDNSKNT
LYLQMNSLRAEDTAVYYCARDSSSYYMFNLWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAA
GAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW
LNGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:264

470C6 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

QSLVESGGGLVQPGGSLRLSCAASGFSFTSSYYMCWVRQAPGKGLEWIACIYTGSSGSTYYANSAKGRFTISRDNSKNT
LYLQMNSLRAEDTAVYYCARDSSSYYMFNLWGQGTLVTVSS

SEQ ID NO:265

472E4 HUMANIZED LIGHT CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCA
GTCAGAGTGTTTATAATAACAATGCTTTAGCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTA
TTTGGCTTCCACTCTGGCATCTGGGGTCCCATCTCGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCA
TCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCTAGGTGTTTATAATGATGATGTTGATAATGGTTTC
GGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAG
CAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGA
AGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTAC
AGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCAT
CAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

SEQ ID NO:266

472E4 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN NUCLEOTIDE SEQUENCE

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGTCCA
GTCAGAGTGTTTATAATAACAATGCTTTAGCCTGGTATCAGCAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTA

TTTGGCTTCCACTCTGGCATCTGGGGTCCCATCTCGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCA
TCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACTGTCTAGGTGTTTATAATGATGATGTTGATAATGGTTTC
GGCGGAGGGACCAAGGTGGAGATCAAA

SEQ ID NO:267

472E4 HUMANIZED LIGHT CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN KAPPA CONSTANT DOMAIN IS UNDERLINED

DIQMTQSPSSLSASVGDRVTITCQSSQSVYNNNALAWYQQKPGKVPKLLIYLASTLASGVPSRFSGSGSGTDFTLTISSLQ
PEDVATYYCLGVYNDDVDNGFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ
SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO:268

472E4 HUMANIZED LIGHT CHAIN VARIABLE LIGHT CHAIN AMINO ACID SEQUENCE. COMPIMENTARITY DETERMINING REGIONS ARE UNDERLINED

DIQMTQSPSSLSASVGDRVTITCQSSQSVYNNNALAWYQQKPGKVPKLLIYLASTLASGVPSRFSGSGSGTDFTLTISSLQ
PEDVATYYCLGVYNDDVDNGFGGGTKVEIK

SEQ ID NO:269

472E4 HUMANIZED HEAVY CHAIN FULL-LENGTH NUCLEOTIDE SEQUENCE

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTC
TGGATTCTCCCTCAATAACAATGCAATAAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTGCAAT
CATACAAAATACTGGTACCACAGACTACGCGAGGTCCGCTAAAGGCAGATTCACCATCTCCAGAGACAATTCCAAG
AACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGGTATGGT
TTTGAGTCGGAGCTTGTCATCTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCAAGGGCCCATCG
GTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACT
TCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTAC
AGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTG
CAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACAC
ATGCCCACCGTGCCCAGCACCTGAAGCCGCGGGGGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACC
CTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTC
AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGT
ACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCGCGGTCTCCA
ACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACA
CCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAG
CGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACT
CCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCAT
GCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

SEQ ID NO:270

472E4 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN NUCLEOTIDE SEQUENCE

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTC
TGGATTCTCCCTCAATAACAATGCAATAAGCTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTGCAAT
CATACAAAATACTGGTACCACAGACTACGCGAGGTCCGCTAAAGGCAGATTCACCATCTCCAGAGACAATTCCAAG
AACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGGTATGGT
TTTGAGTCGGAGCTTGTCATCTGGGGCCAGGGAACCCTGGTCACCGTCTCGAGC

SEQ ID NO:271

472E4 HUMANIZED HEAVY CHAIN FULL-LENGTH AMINO ACID SEQUENCE. HUMAN GAMMA-1 CONSTANT DOMAIN IS UNDERLINED

EVQLVESGGGLVQPGGSLRLSCAASGFSLNNNAISWVRQAPGKGLEWVAIIQNTGTTDYARSAKGRFTISRDNSKNTLY
LQMNSLRAEDTAVYYCARGYGFESELVIWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPEAAG
APSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL
NGKEYKCAVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

SEQ ID NO:272

472E4 HUMANIZED HEAVY CHAIN VARIABLE HEAVY CHAIN AMINO ACID SEQUENCE. COMPLIMENTARITY DETERMINING REGIONS ARE UNDERLINED

EVQLVESGGGLVQPGGSLRLSCAASGFSLNNNAISWVRQAPGKGLEWVAIIQNTGTTDYARSAKGRFTISRDNSKNTLY
LQMNSLRAEDTAVYYCARGYGFESELVIWGQGTLVTVSS

CLAIMS

What is claimed is:

1. An isolated monoclonal antibody (mAb) or antigen-binding fragment thereof that binds specifically to human or cynomolgus 4-1BB, comprising an amino acid sequence having at least 90% identity with SEQ ID NO:4, SEQ ID NO:8, SEQ ID NO:12, SEQ ID NO:16, SEQ ID NO:20, SEQ ID NO:24, SEQ ID NO:28, SEQ ID NO:32, SEQ ID NO:36, SEQ ID NO:40, SEQ ID NO:44, SEQ ID NO:48, SEQ ID NO:52, SEQ ID NO:56, SEQ ID NO:60, SEQ ID NO:64, SEQ ID NO:68, SEQ ID NO:72, SEQ ID NO:76, SEQ ID NO:80, SEQ ID NO:84, SEQ ID NO:88, SEQ ID NO:88, SEQ ID NO:92, SEQ ID NO:96, SEQ ID NO:100, SEQ ID NO:104, SEQ ID NO:108, SEQ ID NO:112, SEQ ID NO:116, SEQ ID NO:120, SEQ ID NO:124, SEQ ID NO:128, SEQ ID NO:132, SEQ ID NO:136, SEQ ID NO:140, SEQ ID NO:144, SEQ ID NO:148, SEQ ID NO:152, SEQ ID NO:156, SEQ ID NO:160, SEQ ID NO:164, SEQ ID NO:168, SEQ ID NO:172, SEQ ID NO:176, SEQ ID NO:180, SEQ ID NO:184, SEQ ID NO:188, SEQ ID NO:192, SEQ ID NO:196, SEQ ID NO:200, SEQ ID NO:204, SEQ ID NO:208, SEQ ID NO:212, SEQ ID NO:216, SEQ ID NO:220, SEQ ID NO:224, SEQ ID NO:228, SEQ ID NO:232, SEQ ID NO:236, SEQ ID NO:240, SEQ ID NO:244, SEQ ID NO:248, SEQ ID NO:252, SEQ ID NO:256, SEQ ID NO:260, SEQ ID NO:264, SEQ ID NO:268, or SEQ ID NO:272.

2. An isolated monoclonal antibody (mAb) or antigen-binding fragment thereof that binds specifically to human or cynomolgus 4-1BB, wherein the antibody or antigen-binding fragment comprises an amino acid sequence having at least 98% identity with SEQ ID NO:4, SEQ ID NO:8, SEQ ID NO:12, SEQ ID NO:16, SEQ ID NO:20, SEQ ID NO:24, SEQ ID NO:28, SEQ ID NO:32, SEQ ID NO:36, SEQ ID NO:40, SEQ ID NO:44, SEQ ID NO:48, SEQ ID NO:52, SEQ ID NO:56, SEQ ID NO:60, SEQ ID NO:64, SEQ ID NO:68, SEQ ID NO:72, SEQ ID NO:76, SEQ ID NO:80, SEQ ID NO:84, SEQ ID NO:88, SEQ ID NO:88, SEQ ID NO:92, SEQ ID NO:96, SEQ ID NO:100, SEQ ID NO:104, SEQ ID NO:108, SEQ ID NO:112, SEQ ID NO:116, SEQ ID NO:120, SEQ ID NO:124, SEQ ID NO:128, SEQ ID NO:132, SEQ ID NO:136, SEQ ID NO:140, SEQ ID NO:144, SEQ ID NO:148, SEQ ID NO:152, SEQ ID NO:156, SEQ ID NO:160, SEQ ID NO:164, SEQ ID NO:168, SEQ ID NO:172, SEQ ID NO:176, SEQ ID NO:180, SEQ ID NO:184, SEQ ID NO:188, SEQ ID NO:192, SEQ ID NO:196, SEQ ID NO:200, SEQ ID NO:204, SEQ ID NO:208, SEQ ID NO:212, SEQ ID NO:216, SEQ ID NO:220, SEQ ID NO:224, SEQ ID NO:228, SEQ ID NO:232, SEQ ID NO:236, SEQ ID NO:240, SEQ ID NO:244, SEQ ID NO:248, SEQ ID NO:252, SEQ ID NO:256, SEQ ID NO:260, SEQ ID NO:264, SEQ ID NO:268, or SEQ ID NO:272.

3. The isolated mAb or antigen-binding fragment according to Claim 1, having a binding affinity to human or cynomolgus 4-1BB with a Kd not greater than 70nM.

4. The isolated mAb or antigen-binding fragment according to Claim 1, exhibiting one or more functional properties selected from high affinity binding to human or cynomolgus 4-1BB, inhibiting human or cynomolgus 4-1BB activity, enhancing T cell activation, survival and cytolytic activity, stimulating antibody response, reversing the suppressive function of an immunosuppressive cell, or a combination thereof.

5. The isolated mAb or antigen-binding fragment according to Claim 4, wherein the immunosuppressive cell comprises a regulatory cell.

6. The isolated mAb or antigen-binding fragment according to Claim 4, wherein the enhancing T-cell activation comprises T-cell proliferation, IFN-γ and/or IL-2 secretion, or a combination thereof.

7. The isolated mAb or antigen-binding fragment thereof according to claim 1, further comprising a human framework region.

8. The isolated mAb or antigen-binding fragment thereof according to claim 1, wherein the isolated mAb is a humanized antibody, a chimeric antibody, or a recombinant antibody.

9. The isolated mAb or antigen-binding fragment thereof according to claim 1, wherein the isolated mAb is an IgG.

10. The isolated mAb or antigen-binding fragment thereof according to claim 1, wherein the antigen-binding fragment is a Fv, a Fab, a F(ab')2, a scFV or a scFV2 fragment.

11. The isolated mAb or antigen-binding fragment thereof according to claim 1, wherein the isolated mAb is a bispecific antibody, tri-specific antibody, or multi-specific antibody.

12. An IgG1 heavy chain for the isolated mAb or antigen-binding fragment thereof according to claim 1, comprising an amino acid sequence having at least 90% identity with SEQ ID NO:7, SEQ ID NO:15, SEQ ID NO:23, SEQ ID NO:31, SEQ ID NO:39, SEQ ID NO:47, SEQ ID NO:55, SEQ ID NO:63, SEQ ID NO:71, SEQ ID NO:79, SEQ ID NO:87, SEQ ID NO:95, SEQ ID NO:103, SEQ ID NO:111, SEQ ID NO:119, SEQ ID NO:127, SEQ ID NO:135, SEQ ID NO:143, SEQ ID NO:151, SEQ ID NO:159, SEQ ID NO:167, SEQ ID NO:175, SEQ ID NO:183, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:207, SEQ ID NO:215, SEQ ID NO:223, SEQ ID NO:231, SEQ ID NO:239, SEQ ID NO:247, SEQ ID NO:255, SEQ ID NO:263, or SEQ ID NO:271.

13. A kappa light chain for the isolated mAb or antigen-binding fragment thereof according to claim 1, comprising an amino acid sequence having at least 90% identity with SEQ ID NO:3, SEQ ID NO:11, SEQ ID NO:19, SEQ ID NO:27, SEQ ID NO:35, SEQ ID NO:43, SEQ ID NO:51, SEQ ID NO:59, SEQ ID NO:67, SEQ ID NO:75, SEQ ID NO:83, SEQ ID NO:91, SEQ ID NO:99, SEQ ID NO:107, SEQ ID NO:115, SEQ ID NO:123, SEQ ID NO:131, SEQ ID NO:139, SEQ ID NO:147, SEQ ID NO:155, SEQ ID NO:163, SEQ ID NO:171, SEQ ID NO:179, SEQ ID NO:187, SEQ ID NO:195, SEQ ID NO:203, SEQ ID NO:211, SEQ ID NO:219, SEQ ID NO:1 SEQ ID NO:227, SEQ ID NO:235, SEQ ID NO:243, SEQ ID NO:257, or SEQ ID NO:263.

14. A variable light chain for the isolated mAb or antigen-binding fragment thereof according to claim 1, comprising an amino acid sequence having at least 90% identity with SEQ ID NO:4, SEQ ID NO:12, SEQ ID NO:20, SEQ ID NO:28, SEQ ID NO:36, SEQ ID NO:44, SEQ ID NO:52, SEQ ID NO:60, SEQ ID NO: 68, SEQ ID NO:76, SEQ ID NO:84, SEQ ID NO:92, SEQ ID NO:100, SEQ ID NO:108, SEQ ID NO:116, SEQ ID NO:124, SEQ ID NO:132, SEQ ID NO:140, SEQ ID NO:148, SEQ ID NO:156, SEQ ID NO:164, SEQ ID NO:172, SEQ ID NO:180, SEQ ID NO:188, SEQ ID NO:196, SEQ ID NO:204, SEQ ID NO:212, SEQ ID NO:220, SEQ ID NO:228, SEQ ID NO:236, SEQ ID NO:244, SEQ ID NO:252, SEQ ID NO:260, or SEQ ID NO:268.

15. A variable heavy chain for the isolated mAb or antigen-binding fragment thereof according to claim 1, comprising an amino acid sequence having at least 90% identity with SEQ ID NO:8, SEQ ID NO:16, SEQ ID NO:24, SEQ ID NO:32, SEQ ID NO:40, SEQ ID NO:48, SEQ ID NO:56, SEQ ID NO:64, SEQ ID NO:72, SEQ ID

NO:80, SEQ ID NO:88, SEQ ID NO:96, SEQ ID NO:104, SEQ ID NO:112, SEQ ID NO:120, SEQ ID NO:128, SEQ ID NO:136, SEQ ID NO:144, SEQ ID NO:152, SEQ ID NO:160, SEQ ID NO:168, SEQ ID NO:176, SEQ ID NO:184, SEQ ID NO:192, SEQ ID NO:200, SEQ ID NO:208, SEQ ID NO:216, SEQ ID NO:224, SEQ ID NO:232, SEQ ID NO:240, SEQ ID NO:248, SEQ ID NO:256, SEQ ID NO:264, or SEQ ID NO:272.

16. An isolated nucleic acid encoding the isolated mAb or antigen-binding fragment according to Claim 1, the IgG1 heavy Chain of Claim 12, the kappa light chain of Claim 13, the variable light chain of Claim 14, or the variable heavy chain of Claim 15.

17. An expression vector comprising the isolated nucleic acid of Claim 16, wherein the vector is expressible in a cell.

18. A host cell comprising the nucleic acid of Claim 16, wherein the host cell is a prokaryotic cell or a eukaryotic cell.

19. A method of producing an antibody comprising culturing the host cell of one of Claim 18, so that the antibody is produced.

20. An immuno-conjugate, comprising the isolated mAb or antigen-binding fragment thereof according to Claim 1 and a drug unit through a linker, wherein the linker comprises a covalent bond selected from an ester bond, an ether bond, an amine bond, an amide bond, a disulphide bond, an imide bond, a sulfone bond, a phosphate bond, a phosphorus ester bond, a peptide bond, a hydrazone bond or a combination thereof.

21. The immuno-conjugate according to claim 21, wherein the drug unit comprises a cytotoxic agent, an immune regulatory reagent, a combination thereof.

22. The immuno-conjugate according to claim 22, wherein the cytotoxic agent is selected from a growth inhibitory agent or a chemotherapeutic agent from a class of tubulin binders, DNA intercalators, DNA alkylators, enzyme inhibitors, immune modulators, antimetabolite agents, radioactive isotopes, or a combination thereof.

23. The immuno-conjugate according to claim 22, wherein the cytotoxic agent is selected from a calicheamicin, ozogamicin, monomethyl auristatin E, emtansine, a derivative or a combination thereof.

24. The immuno-conjugate according to claim 22, wherein the immune regulatory reagents activate or suppress immune cells, T cell, NK cell, B cell, macrophage, or dendritic cell.

25. A pharmaceutical composition, comprising the isolated mAb or antigen-binding fragment thereof of Claim 1 or the immuno-conjugate of Claim 23 and a pharmaceutically acceptable carrier.

26. The pharmaceutical composition of Claim 25, further comprising a radioisotope, a radionuclide, a toxin, a therapeutic agent, a chemotherapeutic agent or a combination thereof.

27. The pharmaceutical composition of Claim 26, wherein the therapeutic agent comprises an anti-estrogen agent, a receptor tyrosine kinase inhibitor, a kinase inhibitor, a cell cycle inhibitor, a DNA, RNA or protein synthesis inhibitor, a RAS inhibitor, or a combination thereof.

28. A method of treating a subject with a cancer, comprising administering to the subject an effective amount of the isolated mAb or antigen-binding fragment thereof according to Claim 1.

29. The method of Claim 28, wherein the cancer comprises cells expressing 4-1BB.

30. The method of Claim 28, wherein the cancer comprises breast cancer, colorectal cancer, pancreatic cancer, head and neck cancer, melanoma, ovarian cancer, prostate cancer, non-small lung cell cancer, glioma, esophageal cancer, nasopharyngeal cancer, anal cancer, rectal cancer, gastric cancer, bladder cancer, cervical cancer, or brain cancer.

31. The method of Claim 28, further comprising co-administering an effective amount of a therapeutic agent.

32. The method of Claim 31, wherein the therapeutic agent comprises an antibody, a chemotherapy agent, an enzyme, anti-estrogen agent, a receptor tyrosine kinase inhibitor, a kinase inhibitor, a cell cycle inhibitor, a DNA, RNA or protein synthesis inhibitor, a RAS inhibitor, or a combination thereof.

33. The method of Claim 28, wherein the subject is a human.

34. A solution comprising an effective concentration of the isolated mAb or an antigen-binding fragment thereof according to Claim 1, wherein the solution is blood plasma in a subject.

FIGURE 1 Immunization schedule for rabbit cohorts no.1 and 2 with human 41BB or cynomolgus 41BB transiently transfected HEK293 cells.

Day	Cohort	Antigen	Adjuvant
0	1	Human 41BB transfected 293 cells	Titermax
7	1	Cynomolgus 41BB transfected 293 cells	Alyhrodgel 2% + CpG 2007
14	1	Human 41BB transfected 293 cells	Titermax
21	1	Cynomolgus 41BB transfected 293 cells	Alyhrodgel 2% + CpG 2007
27	1	Serum collection	
28	1	Human 41BB transfected 293 cells	Titermax
37	1	Cynomolgus 41BB transfected 293 cells	Alyhrodgel 2% + CpG 2007
44	1	Serum collection	
	1	Human 41BB transfected 293 cells	Titermax
51	1	Cynomolgus 41BB transfected 293 cells	Alyhrodgel 2% + CpG 2007
58	1	Human 41BB transfected 293 cells	Titermax
62	1	Serum collection	

Day	Cohort	Antigen	Adjuvant
0	2	Human 41BB transfected 293 cells	Complete Freund's
7	2	Cynomolgus 41BB transfected 293 cells	Alyhrodgel 2% + CpG 2007
14	2	Human 41BB transfected 293 cells	Incomplete Freund's
21	2	Cynomolgus 41BB transfected 293 cells	Alyhrodgel 2% + CpG 2007
27	2	Serum collection	
28	2	Human 41BB transfected 293 cells	Incomplete Freund's
37	2	Cynomolgus 41BB transfected 293 cells	Alyhrodgel 2% + CpG 2007
44	2	Serum collection	
	2	Human 41BB transfected 293 cells	Incomplete Freund's
51	2	Cynomolgus 41BB transfected 293 cells	Alyhrodgel 2% + CpG 2007
58	2	Human 41BB transfected 293 cells	Titermax
62	2	Serum collection	

FIGURE 2 41BB-specific rabbit IgG antibodies in B cell culture supernatant enhance activation of anti-CD3 activated human T cells and corresponding binding of chimeric rabbit/human IgG 41BB-specific antibodies rescued from the parental B cell culture wells to recombinant human and cynomolgus 41BB protein.

		B cell culture supernatant		Transfection Supernatant	
		Proliferation	Gamma Interferon	Octet Binding to recombinant 41BB kdis(1/s)	
	Original BCC well ID	RLU	OD_{450}	Human	Cynomolgus
1	419D9	8.0E+07	2.2	6.3E-04	1.4E-03
2	418H5	8.9E+07	1.8	1.4E-03	1.6E-03
3	411H11	3.3E+07	2.2	1.0E-03	1.5E-03
4	413F3	1.8E+07	0.3	5.4E-04	7.9E-04
5	416G1	9.0E+07	2.0	1.4E-03	1.9E-03
6	416H5	7.8E+07	2.1	1.1E-02	3.2E-03
7	418E10	7.6E+07	1.5	1.1E-03	1.5E-03
8	418E4	9.4E+07	2.5	3.6E-03	5.0E-03
9	420H6	7.0E+07	2.5	9.4E-04	2.0E-03
10	459F1	3.2E+07	0.3	7.5E-04	7.5E-03
11	464C11	5.5E+07	1.0	4.5E-03	8.3E-03
12	470B6	1.4E+08	2.4	1.3E-03	1.2E-03
13	472E4	8.8E+07	1.9	1.1E-03	1.8E-03
14	418E8	9.8E+07	3.0	3.0E-03	3.6E-03
15	468C11	6.6E+07	2.2	2.7E-03	1.2E-03
16	470H2	5.5E+07	2.2	4.3E-03	6.9E-03
17	460C3	3.6E+07	0.3	6.7E-04	4.1E-03
18	413G3	2.4E+07	0.5	4.2E-04	7.9E-04
19	414A8	2.2E+07	0.4	2.9E-04	3.9E-04
20	415E8	5.4E+07	2.2	2.2E-03	5.8E-04
21	416G6	8.0E+07	2.5	7.0E-04	5.6E-03
22	416H7	8.1E+07	2.4	3.1E-03	2.5E-03
23	418H1	1.5E+08	2.4	1.4E-02	1.0E-02
24	420A11	7.6E+07	1.1	3.1E-03	1.1E-01
25	420G12	0.0E+00	2.2	1.4E-02	1.1E-03
26	459E8	4.4E+07	0.9	3.1E-04	6.4E-04
27	459H12	5.5E+07	2.2	1.4E-03	1.4E-03
28	464B12	7.5E+07	2.4	1.3E-03	6.4E-04
29	466G10	4.4E+07	0.3	2.8E-03	2.3E-03
30	468E5	0.0E+00	0.4	4.2E-04	1.1E-03
31	416F8	7.7E+07	1.8	4.3E-03	3.0E-03
32	420H5	8.1E+07	1.7	1.3E-03	2.3E-03
33	466F6	8.6E+07	1.7	2.1E-03	2.6E-03
34	470C6	8.1E+07	2.3	1.0E-03	1.4E-03

FIGURE 3 Chimeric rabbit/human IgG antibodies specific for 41BB enhance T cell activation, proliferation, and gamma interferon secretion.

		First agonist assay										
		Proliferation (Fold change over background)										
		Concentration of 41BB-specific chimeric antibody [ng/ml]										
Original BCC well ID	Gamma-interferon EC_{50} [ng/ml]	3000	1000	333.3	111.1	37.0	12.3	4.1	1.4	0.5	0.2	0
411H11	18.9	2.9	2.4	2.2	2.7	2.5	1.8	1.4	1.5	1.4	1.3	1.0
413F3	11.3	1.4	1.4	1.3	1.2	1.5	1.3	1.1	1.1	1.0	1.1	1.0
413G3	23.7	1.3	1.4	1.3	1.4	1.3	1.2	1.0	1.0	1.1	0.9	1.0
414A8	90.3	1.1	1.5	1.2	1.4	1.4	1.2	1.2	1.1	1.2	1.1	1.0
415E8	10.3	1.7	1.6	1.8	1.8	1.5	1.4	1.2	1.0	1.0	1.0	1.0
416F8	7.3	1.3	1.6	1.6	1.8	1.6	2.2	1.3	1.1	1.2	1.2	1.0
416G1	11.9	1.3	1.6	1.1	1.5	1.6	1.0	1.0	1.1	1.1	1.0	1.0
416G6	7.3	1.5	1.8	1.8	1.8	1.9	1.8	1.7	1.1	1.1	1.1	1.0
416H5	39.1	1.5	1.6	1.5	1.6	1.5	1.2	1.0	1.0	1.0	1.1	1.0
416H7	17.1	1.9	1.9	2.3	2.6	1.9	1.7	1.2	1.3	1.2	1.2	1.0
418E10	20.9	1.6	1.6	1.7	1.7	1.8	1.3	1.0	0.8	1.0	1.0	1.0
418E4	24.4	2.3	1.6	1.5	1.5	1.5	1.8	1.0	1.1	0.8	0.9	1.0
418E8	5.6	1.7	1.5	1.5	1.5	1.6	1.6	1.5	1.3	1.2	1.0	1.0
418H1	28.9	1.7	1.6	1.9	1.8	1.7	1.4	1.0	1.3	1.1	1.1	1.0
418H5	25.5	1.6	1.4	1.8	2.0	1.9	1.1	1.1	1.1	1.1	1.1	1.0
419D9	17.6	1.1	1.6	1.7	1.8	1.8	1.3	1.0	1.1	1.1	1.1	1.0
420A11	23.8	1.4	1.4	1.6	1.6	1.6	1.2	0.9	0.7	0.9	0.9	1.0
420G12	5.7	1.6	1.9	1.6	1.6	1.7	1.6	1.4	1.3	1.2	1.1	1.0
420H5	5.2	1.6	1.9	2.1	2.2	2.2	2.2	1.7	1.4	1.5	1.3	1.0
420H6	17.1	1.2	1.8	2.0	2.0	2.0	1.4	1.3	1.1	1.3	1.2	1.0
459E8	71.9	1.1	1.3	1.2	1.5	1.3	1.1	1.1	1.1	1.1	1.1	1.0
459F1	23.7	1.6	1.9	2.2	2.3	2.3	1.5	1.5	1.4	1.3	1.3	1.0
459H12	8.4	1.1	1.3	1.3	1.4	1.3	1.4	0.9	0.8	1.0	1.0	1.0
460C3	8.8	1.4	1.7	1.9	2.6	1.7	1.6	1.4	1.1	1.0	1.2	1.0
464B12	18.1	1.9	1.8	2.0	1.9	1.7	1.3	1.0	1.0	1.0	1.1	1.0
464C11	25.3	1.2	1.4	1.5	1.5	1.6	1.3	1.6	1.1	1.1	1.1	1.0
466F6	8.8	1.7	1.7	1.8	1.9	2.1	1.5	1.3	1.1	1.2	1.0	1.0
466G10	11.1	2.5	2.1	2.5	2.3	1.9	2.1	1.4	1.3	1.3	1.3	1.0
468C11	12.4	1.8	1.9	1.9	1.9	1.8	1.5	1.2	1.1	1.0	1.1	1.0
468E5	22.7	0.9	1.3	1.2	1.4	1.5	1.2	1.4	1.1	1.1	1.2	1.0
470B6												
470C6	6.9	2.3	2.5	2.4	2.8	2.8	2.4	1.7	1.6	1.4	1.4	1.0
470H2	10.5	1.4	1.6	1.7	1.7	1.9	1.6	1.5	1.1	0.9	1.1	1.0
472E4	14.1	1.9	1.4	1.5	1.5	1.5	1.3	0.9	1.0	0.9	1.0	1.0
Positive control.1	14.1	1.9	1.9	2.1	2.7	2.7	1.7	1.3	1.1	1.0	1.1	1.0

FIGURE 3 (Continued)

		Second agonist assay										
		Proliferation (Fold change over background)										
		Concentration of 41BB-specific chimeric antibody [ng/ml]										
Original BCC well ID	Gamma-interferon EC_{50} [ng/ml]	3000	1000	333.3	111.1	37.0	12.3	4.1	1.4	0.5	0.2	0
411H11	14.6	1.1	2.0	1.7	2.1	2.1	1.5	1.2	1.0	0.9	1.0	1.0
413F3	44.7	0.7	0.8	0.9	1.0	0.9	0.9	0.9	0.9	0.9	1.0	1.0
413G3	21.3	0.9	1.0	1.4	2.0	1.7	1.2	0.9	1.0	0.9	1.0	1.0
414A8	71.3	1.1	1.3	1.4	1.3	1.1	1.1	0.8	0.8	0.8	1.0	1.0
415E8	17.5	0.8	1.1	1.4	1.6	1.5	1.0	0.8	0.7	0.6	0.8	1.0
416F8	11.2	1.0	1.0	1.3	1.2	1.4	1.2	0.9	0.7	0.6	0.7	1.0
416G1	12.8	0.9	1.3	1.4	2.3	2.3	1.6	1.1	1.0	0.8	1.0	1.0
416G6	13.1	0.6	1.4	1.3	2.0	1.7	1.1	0.6	0.7	0.7	0.9	1.0
416H5	44.5	1.6	1.6	1.8	1.8	1.4	1.1	0.9	0.7	0.8	0.9	1.0
416H7	28.0	0.9	1.5	1.6	1.5	1.6	1.0	0.7	0.8	0.7	0.9	1.0
418E10	20.4	2.0	2.2	2.2	2.1	2.0	1.2	1.0	0.9	0.9	0.7	1.0
418E4	31.0	1.2	1.6	1.8	1.7	1.7	1.0	0.9	0.9	0.8	1.0	1.0
418E8	12.8	1.2	1.8	1.6	2.2	1.9	1.4	1.0	0.9	0.8	0.9	1.0
418H1	25.0	0.8	1.2	1.3	1.4	1.4	1.0	0.9	0.7	0.8	0.8	1.0
418H5	37.5	2.2	1.8	1.6	2.0	1.1	1.0	0.7	0.9	0.9	1.1	1.0
419D9	13.0	1.5	1.4	1.5	2.0	1.8	1.2	0.7	0.9	0.7	0.8	1.0
420A11	25.3	2.3	1.7	1.9	1.7	1.4	1.0	0.8	0.8	0.9	0.8	1.0
420G12	20.8	1.0	1.2	1.4	1.7	1.6	1.1	0.8	0.8	0.8	0.9	1.0
420H5	8.9	3.2	2.6	2.3	2.4	3.0	1.9	1.2	1.0	0.9	1.0	1.0
420H6	14.9	1.5	1.9	1.7	2.8	1.9	1.2	1.0	0.9	0.9	1.0	1.0
459E8	42.3	1.1	1.2	1.6	1.4	1.2	1.0	0.8	0.8	1.0	1.1	1.0
459F1	17.4	1.1	1.7	1.9	2.4	2.1	1.6	1.0	1.1	1.2	0.8	1.0
459H12	19.2	1.8	1.1	1.2	1.5	1.3	1.2	0.9	0.8	1.0	0.8	1.0
460C3	10.4	1.1	1.4	1.7	2.0	2.3	1.5	1.1	0.9	1.1	0.8	1.0
464B12	13.1	0.8	1.3	1.2	1.9	1.7	1.3	0.9	0.8	0.9	0.6	1.0
464C11	40.3	1.5	1.4	1.1	1.6	1.3	1.1	1.0	0.9	0.9	0.9	1.0
466F6	8.2	1.1	1.7	2.0	3.1	2.8	2.3	1.6	1.0	1.2	1.1	1.0
466G10	15.8	0.8	1.1	1.1	1.4	1.5	1.2	1.0	1.0	0.9	0.9	1.0
468C11	15.2	0.7	1.5	1.3	2.2	2.0	1.4	0.9	0.8	0.8	0.8	1.0
468E5	22.1	1.2	1.0	1.2	0.8	1.2	0.9	0.8	0.8	0.7	0.8	1.0
470B6	24.1	0.7	1.5	1.6	2.1	1.5	1.3	1.0	1.0	0.9	0.8	1.0
470C6	7.2	1.0	1.5	1.4	2.1	3.2	2.6	1.4	1.2	1.0	1.1	1.0
470H2	22.0	2.4	2.0	1.9	2.6	2.0	1.2	1.2	1.2	1.2	1.1	1.0
472E4	16.4	0.7	1.1	1.2	1.4	1.4	1.1	1.0	0.8	1.0	0.8	1.0
Positive control.1	12.5	0.7	1.5	2.1	2.1	2.7	1.7	1.2	1.0	0.9	0.9	1.0

FIGURE 4 Octet analysis of dissociation rate for humanized 41BB-specific IgG antibodies.

Antibody ID	Humanized Variant	Binding off-rate kdis(1/s)
411H11	VHv1VLv1	1.79E-03
413F3	VHv1VLv1	2.24E-03
416F8	VHv3VLv1	6.45E-03
416G1	VHv1VLv1	1.66E-03
418E10	VHv1VLv1	9.58E-04
418E4	VHv1VLv1	2.77E-03
418H5	VHv2VLv1	2.45E-03
419D9	VHv3VLv3	2.84E-03
420H5	VHv3VLv3	1.78E-03
420H6	VHv1VLv1	1.28E-03
459F1	VHv1VLv1	1.31E-03
460C3	VHv1VLv1	7.28E-04
464C11	VHv1VLv1	7.84E-04
466F6	VHv2VLv5	2.54E-03
470B6	VHv1VLv1	9.10E-04
470C6	VHv3VLv3	1.83E-03
472E4	VHv1VLv1	2.65E-03

FIGURE 5 Humanized 41BB-specific IgG antibodies enhance T cell activation, proliferation, and gamma interferon secretion.

		Proliferation (Fold change over background)										
		Concentration of Humanized 41BB-specific antibody [ng/ml]										
Original BCC well ID	Gamma-interferon EC_{50} [ng/ml]	3000	1000	333.3	111.1	37.0	12.3	4.1	1.4	0.5	0.2	0
411H11	5.8	0.9	1.3	1.2	1.3	1.3	1.3	1.3	0.9	1.0	0.8	1.0
413F3	139.4	0.8	1.5	1.3	0.9	1.0	1.1	1.3	1.1	1.3	1.0	1.0
416F8	37.5	1.1	1.4	1.7	2.1	1.4	1.6	1.2	1.6	0.8	1.2	1.0
416G1	36.7	1.5	1.7	2.4	2.3	1.7	1.8	1.4	1.6	1.5	1.2	1.0
416H5	-	0.5	0.7	0.6	0.7	0.7	1.1	0.9	1.3	1.1	0.9	1.0
418E4	12.3	1.1	1.7	1.7	1.6	2.3	1.4	1.1	1.3	1.2	1.2	1.0
418E10	7.1	0.9	1.3	1.8	1.5	2.2	2.2	1.4	1.4	1.0	1.1	1.0
418H5	14.5	1.2	2.0	1.5	2.1	2.2	1.4	1.3	0.9	1.2	0.7	1.0
419D9	13	1.0	1.1	1.4	1.5	1.9	1.3	1.0	0.9	1.1	0.8	1.0
420H5	50.7	1.8	1.8	1.3	1.3	1.7	1.3	1.0	1.4	1.1	1.1	1.0
420H6	26	0.9	1.4	1.7	1.8	1.5	1.5	1.3	0.9	1.0	1.0	1.0
459F1	21.2	0.5	0.7	0.8	1.1	1.3	1.4	0.9	1.2	0.9	0.8	1.0
460C3	11.5	0.7	0.9	1.2	1.4	1.8	1.6	1.2	1.6	1.4	1.1	1.0
464C11	8.4	1.1	1.4	1.8	2.0	2.1	1.8	1.0	1.0	1.1	0.9	1.0
466F6	9.8	1.1	0.9	1.8	1.4	1.4	2.0	1.4	1.2	0.8	1.1	1.0
470B6	17.8	1.1	2.2	1.4	1.3	1.8	1.8	1.2	1.1	1.0	1.0	1.0
470C6	5.7	1.6	2.1	2.0	2.3	2.6	2.2	2.1	1.7	1.4	1.4	1.0
472E4	11.6	1.2	2.0	1.9	2.4	2.0	1.6	1.2	1.2	1.4	0.9	1.0
Positive control.1	4.3	1.5	1.8	1.5	1.5	1.7	1.7	1.4	1.4	1.2	1.3	1.0

FIGURE 6 Serum from rabbits immunized with human or cynomolgus 41BB expressing HEK293's analyzed for 41BB-specific IgG antibody binding to parental CHO or human or cynomolgus 41BB-transfected CHO cells.

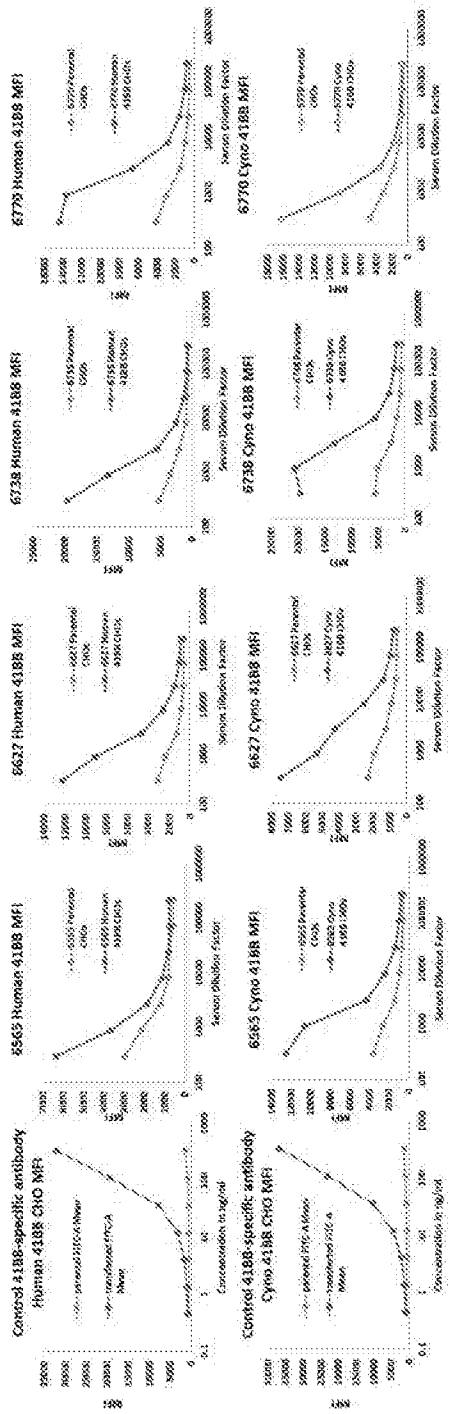
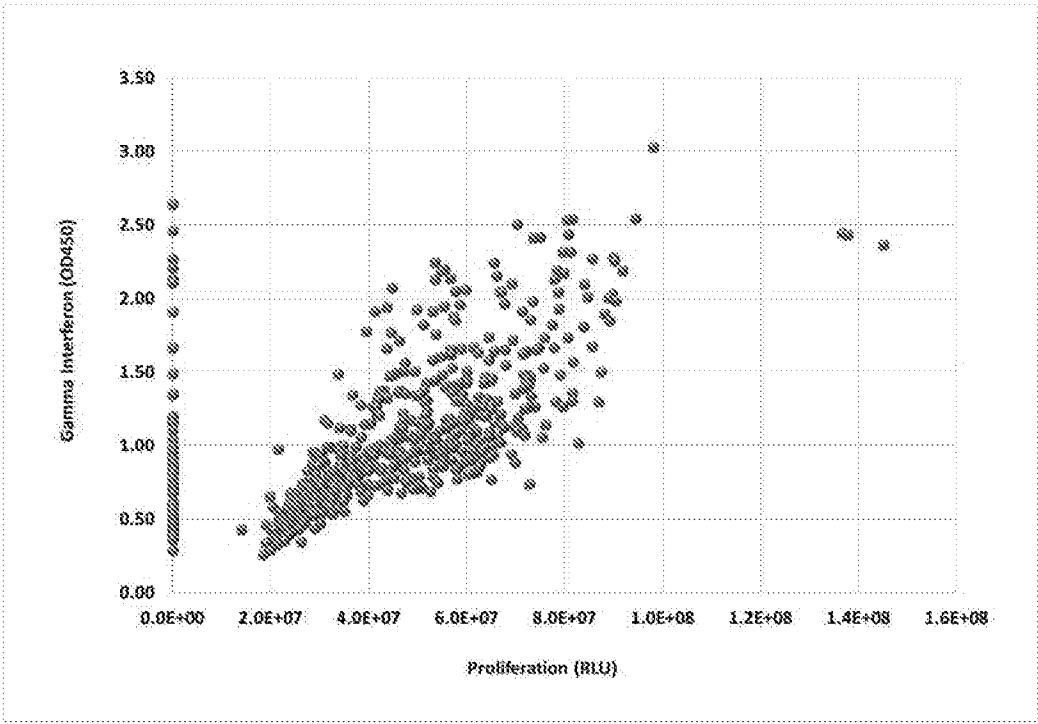


FIGURE 7 Correlation of 41BB-specific IgG antibody in B cell culture supernatant enhancement of Gamma interferon secretion versus proliferation of human T cells.



PATENT COOPERATION TREATY

PCT

DECLARATION OF NON-ESTABLISHMENT OF INTERNATIONAL SEARCH REPORT
(PCT Article 17(2)(a), Rules 13*ter*.1(c) and (d) and 39)

Applicant's or agent's file reference SIBA028PCT	**IMPORTANT DECLARATION**	Date of mailing *(day/month/year)* 07 SEP 2018
International application No. PCT/US18/39155	International filing date *(day/month/year)* 22 June 2018	(Earliest) Priority Date *(day/month/year)* 25 June 2017
International Patent Classification (IPC) or both national classification and IPC IPC: C12Q 1/68; CPC: C12Q 2600/158		
Applicant SYSTIMMUNE, INC.		

This International Searching Authority hereby declares, according to Article 17(2)(a), that **no international search report will be established** on the international application for the reasons indicated below.

1. ☐ The subject matter of the international application relates to:
   - a. ☐ scientific theories
   - b. ☐ mathematical theories
   - c. ☐ plant varieties
   - d. ☐ animal varieties
   - e. ☐ essentially biological processes for the production of plants and animals, other than microbiological processes and the products of such processes
   - f. ☐ schemes, rules or methods of doing business
   - g. ☐ schemes, rules or methods of performing purely mental acts
   - h. ☐ schemes, rules or methods of playing games
   - i. ☐ methods for treatment of the human body by surgery or therapy
   - j. ☐ methods for treatment of the animal body by surgery or therapy
   - k. ☐ diagnostic methods practised on the human or animal body
   - l. ☐ mere presentations of information
   - m. ☐ computer programs for which this International Searching Authority is not equipped to search prior art
2. ☐ The failure of the following parts of the international application to comply with prescribed requirements prevents a meaningful search from being carried out:
   ☐ the description ☐ the claims ☐ the drawings
3. ☒ A meaningful search could not be carried out without the sequence listing; the applicant did not, within the prescribed time limit:
   - ☒ furnish a sequence listing in the form of an Annex C/ST.25 text file, and such listing was not available to the International Searching Authority in a form and manner acceptable to it; or the sequence listing furnished did not comply with the standard provided for in Annex C of the Administrative Instructions.
   - ☐ furnish a sequence listing on paper or in the form of an image file complying with the standard provided for in Annex C of the Administrative Instructions, and such listing was not available to the International Searching Authority in a form and manner acceptable to it; or the sequence listing furnished did not comply with the standard provided for in Annex C of the Administrative Instructions.
   - ☐ pay the required late furnishing fee for the furnishing of a sequence listing in response to an invitation under Rule 13*ter*.1(a) or (b).
4. Further comments:
   Applicant failed to submit a valid electronic seq. listing in respone to the ISA/225.

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