

ANTI-CD19 ANTIBODIES AND METHODS OF USING AND MAKING THEREOF

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of the filing date of U.S. Provisional Application Ser. No. 62/984,731 filed March 3, 2020 under 35 U.S.C. 119(e), the entire disclosures of which are incorporated by reference herein.

TECHNICAL FIELD

The present disclosure generally relates to the technical field of biologic therapeutics, and more particularly relates to making and using multi-specific antibodies.

BACKGROUND

Lymphoma represents 4.3% of all cancers diagnosed annually in the United States, with B cell malignancies comprising approximately 90% of all lymphoma diagnoses. CD19 is a B-lymphocyte-specific member of the immunoglobulin superfamily expressed by B lymphocytes at different stages of differentiation, from the onset of V(D)J rearrangement until B cell maturation into plasma cells at which time the surface expression of CD19 seems to be lost. While CD19 is widely used as a pan-B cell marker, CD19 is found to be highly expressed in many forms of leukemia and lymphoma with characters of B-cell origins. CD19 has been a focus of immunotherapy development for over 30 years. Pharmaceutical companies are actively pursuing anti-CD19 strategies as they have the promise of directly targeting those B-cell malignancies corresponding to early B-cell differentiation stages. Targeting CD19 has been approved to be an excellent strategy of immune therapies, especially when the antibody therapies targeting CD22, another pan-B cell marker expressed by B-cell malignancies, were not successful.

CD19 is an important cell surface marker on normal B-cells and cancers of B-cell origins. As such it is highly desirable to have an antibody targeting CD19 for use in anti-cancer therapeutics. Reports in the literature demonstrate that it is difficult to identify anti-CD19 antibodies which also cross-react to the CD19 found in cynomolgus monkeys, a property which greatly facilitates therapeutic pharmacological and toxicological studies. The historic antibody BU12 has been shown to possess high affinity to human CD19 and cross reactivity to cynomolgus CD19, however this antibody was discovered from mouse hybridoma and does not comprise a human framework sequence. Therefore, a humanized variant of BU12 is highly desirable for therapeutic use.

SUMMARY

The application provides anti-CD19 peptides, proteins, protein complexes, antibodies and methods of making and using thereof.

In one aspect, the application provides peptides having a binding specificity to human CD19. In one embodiment, the peptide has an amino acid sequence having at least 70%, 80%, 85%, 90%, 95%, 97%, 98% or 99% of sequence identity to SEQ ID NO. 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 91, or 93.

In one embodiment, the peptide is a scFv peptide. In one embodiment, the scFv peptide may have a binding affinity to human CD19 with a KD not greater than 1nM, 2nM, 3nM, 5nM, 10nM, 15nM, 20nM, 30nM, 40nM, or 50 nM.

In one aspect, the application provides an antibody or antigen-binding fragment thereof having a binding specificity to human CD19. In one embodiment, the isolated antibody or antigen-binding fragment comprises an amino acid sequence having at least 70%, 80%, 85%, 90%, 95%, 97%, 98% or 99% of sequence identity to SEQ ID NO. 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 91, or 93. In one embodiment, the antibody comprises an isolated monoclonal antibody (mAb).

In one embodiment, the antibody is a bi-specific antibody. In one embodiment, the antibody is a multi-specific antibody. In one embodiment, the antibody is a tri-specific antibody, tetra-specific antibody, penta-specific antibody, or hexa-specific antibody.

In one embodiment, the antibody comprises a scFv, wherein the scFv comprises an amino acid sequence having at least 70%, 80%, 85%, 90%, 95%, 97%, 98% or 99% of sequence identity to SEQ ID NO. 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 91, or 93.

In one embodiment, the antibody comprises a Fab, wherein the Fab comprises an amino acid sequence having at least 70%, 80%, 85%, 90%, 95%, 97%, 98% or 99% of sequence identity to SEQ ID NO. 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 91, or 93.

In one embodiment, the application provides a multi-specific antibody-like protein. In one embodiment, the protein comprises the peptide having an amino acid sequence having at least 70%, 80%, 85%, 90%, 95%, 97%, 98% or 99% of sequence identity to SEQ ID NO. 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 91, or 93. In one embodiment, the multi-specific antibody-like protein has a N-terminal and a C-terminal, comprising in tandem from the N-terminal to the C-terminal, a first binding domain (D1) at the N-terminal, a second binding domain (D2) comprising a light chain moiety, a Fc region, a third binding domain (D3), and a fourth binding domain (D4) at the C-terminal. The light chain moiety comprises a fifth binding domain (D5) covalently attached to the C-terminal, a sixth binding domain (D6) covalently attached to the N-terminal, or both, and the D1, D2, D3, D4, D5 and D6 each has a binding specificity to a tumor antigen, an immune signaling antigen, or a combination thereof.

In one embodiment, the multi-specific antibody-like protein is penta-specific. In one embodiment, the antibody-like protein comprises binding domains including D1, D2, D3, D4 and D6.

In one embodiment, the multi-specific antibody-like protein is hexa-specific.

In one embodiment, D1 comprises the peptide comprising an amino acid sequence having at least 70%, 80%, 85%, 90%, 95%, 97%, 98% or 99% of sequence identity to SEQ ID NO. 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 91, or 93.

In one embodiment D1 comprises a peptide having an amino acid sequence with 95% sequence identity to SEQ ID NO. 7 or 19.

In one embodiment, D2 comprises the peptide an amino acid sequence having at least 70%, 80%, 85%, 90%, 95%, 97%, 98% or 99% of sequence identity to SEQ ID NO. 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 91, or 93.

In one embodiment, D2 comprises a peptide having an amino acid sequence with 95% sequence identity to SEQ ID NO. 91 or 93.

In one embodiment, D6 comprises the peptide having an amino acid sequence having at least 70%, 80%, 85%, 90%, 95%, 97%, 98% or 99% of sequence identity to SEQ ID NO. 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 91, or 93.

In one embodiment, D6 comprises a peptide having an amino acid sequence with 95% sequence identity to SEQ ID NO. 7 or 19.

In one embodiment, the application provides multi-specific monoclonal antibody, comprising the multi-specific antibody-like protein as claimed herein.

In one embodiment, the multi-specific monoclonal antibody may have a binding affinity to human CD19 with a K_d not greater than 1nM, 5nM, 10nM, 20nM, 30nM, 40nM or 50 nM.

In one embodiment, the antibody is a humanized antibody. In one embodiment, the multi-specific monoclonal antibody is an IgG.

In one embodiment, the application provides isolated nucleic acid encoding the isolated mAb or an antigen-binding fragment, the IgG1 heavy Chain, the kappa light chain, the variable light chain, or the variable heavy chain, as disclosed thereof.

In one aspect, the application provides isolated nucleic acid sequence encoding an amino acid sequence of the multi-specific monoclonal antibody as disclosed herein.

In one embodiment, the application provides an expression vector comprising the isolated nucleic acid, as disclosed thereof.

In one embodiment, the application provides host cells comprising the nucleic acid as disclosed thereof. In one embodiment, the host cell is a prokaryotic cell or a eukaryotic cell.

In one aspect, the application provides methods of producing an antibody comprising culturing the host cell so that the antibody is produced.

In one aspect, the application provides immuno-conjugates. In one embodiment, the immunoconjugate comprises the isolated mAb or an antigen-binding fragment thereof and a drug unit, wherein the drug unit is linked to the isolated mAb or an antigen-binding fragment through a linker, and 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.

In one embodiment, the drug unit comprises 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, camptothecin, 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 radionuclide, a fluorescent agent, a quantum dots, or a combination thereof.

In one aspect, the application provides pharmaceutical composition. In one embodiment, the pharmaceutical composition comprises the isolated mAb or an antigen-binding fragment thereof a pharmaceutically acceptable carrier. In one embodiment, the pharmaceutical composition may further include 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 aspect, the application provides a pharmaceutical composition including an immune-conjugate as disclosed herein and a pharmaceutically acceptable carrier.

In one aspect, the application provides methods of treating a subject with a cancer. In one embodiment, the method comprises administering to the subject an effective amount of the isolated mAb or an antigen-binding fragment as disclosed thereof. In one embodiment, the method may further include co-administering an effective amount of a therapeutic agent, wherein the therapeutic agent comprises an antibody, a chemotherapy agent, an enzyme, or a combination thereof. In one embodiment, the subject is a human.

In a further aspect, the application provides a solution comprising an effective concentration of the multi-specific monoclonal antibody as disclosed herein. In one embodiment, the solution is blood plasma in a subject.

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 shows an increase in humanness scores (Z-score) from mouse sequence (grey line) to the humanized framework (dark line) in the variable regions of humanized BU12, H4 (Vk for kappa light chain in **1A**, and VH for heavy chain in **1B**) and H5 (Vk for kappa light chain in **1C** and VH for heavy chain in **1D**);

Figure 2 shows the sequence alignment of the variable regions (VL for light chain in **2A** and VH for heavy chain in **2B**) of humanized mouse BU12 (H1-H6, and H7) and human antibody (21D4);

Figure 3 shows DLS thermal stability for SI-63C1 (BU12-chimeric), SI-63C2 (humanized BU12, H1) and SI-34C1 (human antibody, 21D4);

Figure 4 shows the histograms depicting the cross reactivity of the SI-63C2 antibody to human, cynomolgus, and rhesus CD20+ B cells (**4A**) and CD20- lymphocytes (**4B**);

Figure 5 shows the dose-response curve of the SI-63C2 antibody binding to human (**5A**), cynomolgus (**5B**), and rhesus (**5C**) CD20+ lymphocytes, as compared to its parental control (SI-63C1) and mouse anti-human CD19 antibody controls (SJ25C, LT19, HIB19, and 4G7);

Figure 6 shows an analytical SEC profile of SI-63R1(H1), the protein-A purified recombinant anti-CD19 scFv-HIS protein (**6A**) and DLS Thermal Stability of SI-63R1(H1) with unfolding temperature at about 58.8°C (**6B**);

Figure 7 shows analytical SEC profile of the protein-A purified recombinant anti-CD19 scFv-monoFc proteins (H1 through H6) with 90% protein of interest (POI);

Figure 8 depicts a schematic diagram of six binding domains (D1-D6) in hexaGNC antibodies that comprise the core Fab (D2) and Fc regions and the additional D1, D3, and D4 on heavy chain (HC) and D5 and D6 on light chain;

Figure 9 shows the ExpiCHO expression and purification of three hexaGNC antibodies SI-77H3, SI-77H6, and SI-55H11 with their humanized anti-CD19 domains, H4 at D1, H7 at D2 (Fab), and H4 at D6, respectively;

Figure 10 shows the dose-response curves of an antibody (SI-38E17, SI-55H11, SI-77H3, and SI-77H6, respectively) direct cellular cytotoxicity (ADCC) to either human (**10A**) or cynomolgus (**10B**) PBMC; and

Figure 11 shows that the humanized CD19 binding domain of hexaGNC antibodies, such as SI-77H, SI-77H6, and SI-55H11, mediates the cytolysis of Raji lymphoma cells that express only CD19 but no other tumor antigens (**11A**) with a potent dose-response curve comparable to that of SI-38E17, a human anti-CD19 antibody (21D4) (**11B**).

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 present disclosure provides, among others, isolated antibodies, methods of making such antibodies, monoclonal and/or recombinant monospecific antibodies, multi-specific antibodies, antibody-drug conjugates and/or immuno-conjugates composed from such

antibodies or antigen binding fragments, pharmaceutical compositions containing the antibodies, monoclonal and/or recombinant monospecific antibodies, multi-specific antibodies, antibody-drug conjugates and/or immuno-conjugates, the methods for making the antibodies and compositions, and the methods for treating cancer using the antibodies and compositions disclosed herein. Specifically, the present disclosure provides isolated monoclonal antibodies (mAb) or antigen-binding fragments thereof having a binding specificity to human CD19 (**Table 1**), wherein the isolated mAb or antigen-binding fragments comprise an amino acid sequence having an identity with a sequence selected from SEQ ID NO. 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 91, or 93.

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.

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 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.

The terms “antigen- or epitope-binding portion or fragment”, “variable region”, “variable region sequence”, or “binding domain” refer to fragments of an antibody that are capable of binding to an antigen (such as CD19 in this application). 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 variable light chain (VL) and variable heavy chain (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 sub-fragments 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 can be screened for utility using the same techniques employed with intact antibodies.

The “antigen- or epitope-binding portion or fragment”, “variable region”, “variable region sequence”, or “binding domain” may 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. 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 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.

The term "antibody" is used in the broadest sense and specifically covers single monoclonal antibodies and/or recombinant 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, multi-specific or multi-effective, 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 a Fab immunoglobulin expression library and epitope-binding fragments of any of the antibodies and fragments mentioned above.

The term "Fv" refers to 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.

In some embodiments, antibody may include immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, i.e. molecules that contain a binding site and that immunospecifically bind an antigen. 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 light chains of antibodies (immunoglobulins) from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains. 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.

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 alpha, delta, epsilon, gamma, and mu, respectively. The subunit structures and three-dimensional configurations of different classes of immunoglobulins are well known.

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

Monoclonal antibodies can be produced using various methods, including without limitation, mouse hybridoma, phage display, recombinant DNA, molecular cloning of antibodies directly from primary B cells, and antibody discovery methods (see Siegel. *Transfus. Clin. Biol.* 2002; Tiller. *New Biotechnol.* 2011; Seeber et al. *PLOS One.* 2014). 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]).

The term “multi-specific” antibody as used herein denotes an antibody that has at least two binding sites each having a binding affinity to an epitope of an antigen. The term “bi-specific, tri-specific, tetra-specific, penta-specific, or hexa-specific” antibody as used herein denotes an antibody that has two, three, four, five, or six antigen-binding sites. For example, the antibodies disclosed herein with five binding sites are penta-specific, with six binding sites are hexa-specific.

The term “guidance and navigation control (GNC)” protein refers to a multi-specific protein capable of binding to at least one effector cell (such as immune cell) antigen and at least one target cell (such as tumor cell, immune cell, or microbial cell) antigen. The GNC protein may adopt an antibody-core structure including a Fab region and Fc region with various binding domains attached to the antibody-core, in which case the GNC protein is also termed GNC antibody. The GNC protein may adopt an antibody-like structure, in which case the Fv fragment may be replaced with a non-antibody based binding domain such as NKG2D, 4-1BBL (a 4-1BB receptor ligand), 4-1BBL trimer for 4-1BB, or a receptor.

The term “GNC antibody” refers to a GNC protein had an antibody structure that is capable of binding to at least one effector cell (such as immune cell) and at least one target cell (such as tumor cell, immune cell, or microbial cell) simultaneously. The term “biGNC, triGNC, tetraGNC, pentaGNC, or hexaGNC” antibody as used herein denotes a GNC antibody that has two, three, four, five, or six antigen-binding sites, of which at least one antigen-binding site has the binding affinity to an immune cell and at least one antigen-binding site has the binding affinity to a tumor cell. In one embodiment, the GNC antibodies disclosed herein have four to six binding sites (or binding domain) and are tetraGNC, pentaGNC, and hexaGNC antibodies, respectively. In some embodiments, the GNC antibodies include antibody binding domains (such as Fab and scFv) without the requirement for additional protein engineering in the Fc region. In one embodiment, the GNC antibodies additionally have the advantage of retaining bivalency for each targeted antigen. Further in one embodiment, the GNC antibodies have the advantage of avidity effects that result in higher affinity for antigens and slower dissociation rates. This bivalency for each antigen is in contrast to many multi-specific platforms that are monovalent for each targeted antigen, and thus often lose the beneficial avidity effects that make antibody binding so strong.

The term “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 “isolated” or “purified” refers to a biological molecule free from at least some of the components with which it naturally occurs. Either “Isolated” or “purified,” 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, a purified polypeptide will be prepared by at least one purification step. An “isolated” or a “purified” antibody refers to an antibody which is substantially free of other antibodies having different antigenic a binding specificity.

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. While the immunogenic response generally includes both cellular (T cell) and humoral (antibody) arms of the immune response, antibodies directed against therapeutic proteins (anti-drug antibodies, ADA) may consist of IgM, IgG, IgE, and/or IgA isotypes.

The terms "specific binding", "specifically binds to", or "is specific for a particular antigen or an epitope" means that the binding 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.

The present disclosure may be understood more readily by reference to the following detailed description of specific embodiments and examples 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. Designing humanized anti-CD19 sequences.

All computational steps were performed in the Discovery Studio package (Dassault Systemes). First, a structural model was generated using the mouse BU12 sequence (McDonagh et al., 2009). Antibody framework regions in the input sequence were identified and aligned to a database of antibody variable domains using Hidden Markov Models (HMM), and this alignment was used to build and score models using the MODELLER software. CDR loop modelling was performed by a structural mapping of the CDRL1, CDRL2, CDRL3, CDRH1, and CDRH2 regions to known canonical classes and loop models were built similarly to the framework.

The framework regions from the mouse BU12 antibody were aligned and matched to the closest human germline sequence, and CDRs regions were copied into the human sequence except for important structural residues (Vernier residues [Almagro and Fransson, 2008]). Mutations predicted to stabilize the previously build structural model were evaluated computationally by 1000 steps of Steepest Descent with a RMS gradient tolerance of 3, followed by Conjugate Gradient minimization and stabilizing mutations matching frequent human residues were chosen based on individual and combined $-\Delta\Delta G$ versus the initial model. Mutational stabilization energy analysis on discovery studio was performed by using sequence H1 as the reference. Version H2, H3 and H4 are mutational variants which had negative values for mutational energy ($\Delta\Delta G$ was -0.8, -1.5, and -1.1 kCal, respectively) and hypothesized to be more stable than version H1. The resulting humanized sequence (H1, **SEQ ID NO. 1 and 13**) was tested for humanness using the Abysis webserver based on the method of Abhinandan and Martin (2007). Using H4 as an example for its light chain (Vk) and heavy chain (VH) as shown in **Figure 1A and 1B**, the humanized sequences show a higher humanness score than the corresponding mouse sequences (BU12) (**SEQ ID NO. 25 and 27**).

In addition, a direct CDR grafting approach was used to generate humanized versions H5. A reference antibody framework was mutated to analogous human germline residues and CDRs were directly grafted in the mutated framework to generate H5. Using the resulting humanized sequence H5 as the founding sequence, more mutation was made on the H5 framework to improve framework stability which generated humanized sequence (H6). The humanized sequence H5 (**SEQ ID NO. 9 and 21**) was tested for humanness using the Abysis webserver based on the method of Abhinandan and Martin (2007). The humanized sequences show a higher humanness score than the mouse sequence (BU12) (SEQ ID NO. 25, and 27) (**Figure 1C and 1D**).

H1 is the first humanized version originating directly from the variable domains of the Fab sequence of BU12 with a signature amino acid sequence, LEIK, at the C-terminus. As shown in **Figure 2**, the last three residues (EIK) are predominantly present for variable kappa chains present in nature and provides stability when positioned specifically in the Fab domain. In this context, having H4 that ends with VTVL at the Fab position may not be ideal for the stability of the antibody. Version H7 is a modified H4 which is hypothesized to improve protein stability when positioned in the context of a Fab domain (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5058631/>). H7 was created by restoring EIK and introducing a disulfide staple between H7VL and H7VH via a Q to C and a G to C mutation, respectively.

To compare and prioritize these designed sequences, all humanized variable regions (H1, H2, H3, H4, H5, H6, and H7) were aligned with the sequences from a human anti-CD19 antibody, 21D4 (Rao-Naik et al. ,2009), as shown in **Figure 2**. The percentage identities to H1 are 98.1% VL and 99.1-100% VH for H2, H3, H4, and H7, 85% VL and 86% VH for H5 and H6, and 70% VL and

51% VH for 21D4. These findings imply that there are substantial flexibilities in the primary sequences of an anti-CD19 binding domain.

To predict immunogenicity of humanized anti-CD19 sequences, MixMHC2pred algorithm (Gfeller Lab, <https://github.com/GfellerLab/MixMHC2pred>) was used to predict the extent of major histocompatibility complex-II (MHC-II) binding of peptides within mouse and humanized (VH/VL) sequences. The algorithm detects the number of 'core' peptides in a given amino acid sequence that will bind to MHCII with sufficient affinity to form a T cell epitope. The higher the number of MHCII-binding peptides identified in a sequence, the more potential T cell epitopes the sequence contains. A high number of core peptides increases the likelihood of containing some peptides that are pro-immunogenic. Reducing the number of core peptides in the antibody variable regions may thus help to reduce ADA by eliminating potential T cell epitopes.

Anti-CD19 variable sequences were run through the MixMHC2pred algorithm as scFv (VH-(G4S)4-VL). The algorithm includes the option to score among multiple alleles. In this case, "the score from each peptide is taken as its best percentile rank among all the alleles." This scoring strategy allows sequences to be examined to find the strongest ligands to any allele of MHCII. For sequence analysis of antibody variable domains, the number of core peptides was calculated based on the number of peptides in the sequence that could bind to any MHCII allele with a score in the top 0.2% of interactions. As shown in **Table 1**, most of humanized sequences have lower scores than their parental mouse sequences, indicative of weaker MHCII binding peptides and lower risk of immunogenicity. Herein, the total score of core peptides in the variable regions that were predicted to bind strongly to MHCII decreased from 9 for mouse sequences to 5 for humanized sequences (H1 through H4, and H7, no change for H5 and H6). The humanness scores for light and heavy chains were calculated using the humanness Z score analysis algorithm (Abhinandan & Andrew, 2007). For VH sequences, versions H1-H4 had similar humanness as 21D4, while H5 and H6 had higher humanness and H7 had lower humanness. For VK sequences, H1-H7 all had similar humanness which was slightly lower than that of 21D4. Notably, all humanized sequences (H1-H7, VH and Vk) had significantly higher humanness scores than the original mouse sequences (**Table 1**). Considering both humanness and MHC-II peptide binding scores, H1-H4 and H7 were the candidates for generating humanized anti-CD19 antibodies.

Example 2. Expression of humanized anti-CD19 monoclonal antibodies

To characterize the humanized light chain CDR and heavy chain CDR and framework regions, the DNA sequences encoding H1 and other peptides were synthesized in overlapping fragments and cloned into linearized pTT5 vector (NE Builder) containing a C-terminal human kappa sequence, or human IgG CH1 and Fc region respectively to create a mAb format (**SEQ ID NO. 37** and **39**). The DNA sequences for 21D4 and Mouse (BU12) variable regions were also synthesized and cloned into linearized pTT5 vector containing a C-terminal human kappa sequence, or IgG CH1 and Fc region respectively to generate a chimeric mAb format (**SEQ ID NO. 33, 35, 83, and 85**). The plasmid DNA containing the antibody sequences were expressed using

the ExpiCHO expression system (ThermoFisher). The three recombinant antibodies, SI-63C1 (with BU12 mouse parental anti-CD19 variable sequence), SI-63C2 (with H1 humanized anti-CD19 variable sequence, also known as SI-huCD19), and SI-34C1 (with 21D4 human anti-CD19 variable sequence), were purified from the culture supernatant by using a Protein-A affinity chromatography column (mabSelect Resin, Ge healthcare) with PBS (5X Cv) for washing followed by 20mM Glycine pH 3.5 for elution. The resulting proteins were neutralized with 100X Tris pH 8.5 and dialyzed overnight into PDB buffer. To check for stability and monodispersity, purified antibodies were concentrated to 1mg/ml and injected onto an analytical HPLC (waters, column waters BEH200A 300mm column). The purified anti-CD19 antibodies showed a sharp monodispersed peak with the correct size with 1.8-2.5% aggregate (**Table 2**).

Example 3. Characterization of SI-63C2

The purified SI-63C1, SI-63C2, and SI-34C1 antibodies were tested for their binding affinity using biolayer interferometry (ForteBio OctetRED 384). The antibodies were bound to anti-human Fc biosensors, and human CD19 protein (R&D Biosystems Cat #9269-CD-050) was used as the analyte in a 4-point series of 2-fold dilutions with the highest concentration starting at 200nM. The results of Octet analysis indicated that the binding affinity of SI-63C3 (also known as SI-huCD19) to human and cynomolgus CD19 were at 3.8nM and 3.6nM, comparable to that of the human anti-CD19 antibody (21D4) at 2.1nM and 3.8nM, respectively. Furthermore, the humanized anti-CD19 variable sequences of SI-63C2 not only retain the binding specificity to human and cynomolgus CD19 but also exhibited comparable binding affinity (KD) to SI-63C1 (with BU12 variable sequences) and SI-34C1 (with 21D4 variable sequences) (**Table 2**).

To test the thermal stability of SI-63C2, dynamic light scattering was used while the temperature was ramped from 25°C to 75°C at 0.5°C/min, and the radius of the proteins (1 mg/ml) was monitored by using Wyatt DynaPro Plate Reader III. As shown in **Figure 3** and **Table 2**, the results indicated that SI-63C2 and SI-63C1 displayed similar unfolding temperature, as measured by DLS T_m, which was higher than that of SI-34C1.

Example 4. The binding specificity of SI-63C2

Non-human primates (NHPs), such as the cynomolgus or rhesus macaque, are currently necessary to provide risk assessment data for antibody drug development because of their similarity to humans, predictable metabolic stability, and historically established toxicity profiles. To minimize the use of NHPs and to increase the efficiency, antibody drug candidate should have high target specificity and cross-reactivity. In this context, CD19 is a pan-B cell marker and is expressed by the majority of malignant B cells. CD19 has a broader coverage to B cell development and differentiation than CD20, which is another pan-B cell marker for lymphocytes from human and NHPs, such as cynomolgus and rhesus macaque. Of many mouse anti-human CD19 antibodies, BU12 can cross react with B lymphocytes derived from cynomolgus macaque with lower binding affinity (Liu et al., 2016).

To determine if the humanization alters the cross reactivity, the flow cytometry was carried out. The SI-63C2 antibody was used to bind the peripheral blood mononuclear cells derived from human, cynomolgus, and rhesus, respectively. Lymphocytes were gated based on forward and side scatter, followed by single cells based on the ratio of forward scatter signal height and area. Viable CD20+ B-cell and CD20- lymphocytes are gated based on the exclusion of membrane permeable amine reactive dye and the binding level of CD20 antibody (clone 2H7, Biolegend). Binding of the labelled antibody was determined as the geometric mean fluorescence intensity (gMFI) of the cell population for the fluorescent conjugate's emission channel. As shown in the histogram analysis in **Figure 4**, the SI-63C2 antibody binds to CD20+ B cells from human, cynomolgus, and rhesus (**4A**) but not to their CD20- lymphocytes (**4B**). When a panel of anti-CD19 antibodies (namely, SJ25C, LT19, HIB19, and 4G7) were used for comparison, only SI-63C2 and its the parental antibody, SI-63C1, displayed significant binding affinity to CD20+ B cells from human, cynomolgus, and rhesus (**Figure 5**). These data confirmed the binding specificity of SI-63C2 to human, cynomolgus, and rhesus B cells was retained, however, its cross reactivity to cynomolgus, as measured by EC50, remains lower than its response to human CD19 (**Table 3**).

Example 5. His-tagged humanized anti-CD19 scFv proteins.

To characterize humanized anti-CD19 binding domain as a scFv unit, the DNA sequences encoding humanized anti-CD19 variable regions (H1) were cloned into a His-tagged scFv expression vector containing the residues GSHHHHHH at the C-terminal of the scFv (SEQ ID NO. 41). Using the ExpiCHO expression system, the humanized anti-CD19 scFv-His-tagged protein was expressed, purified via protein L affinity chromatography, and named as SI-63R1. The data from analytical SEC indicated that SI-63R1 had 70% protein of interest, and DLS thermal stability test measured the unfolding temperature for SI-63R1 at 58.8°C (**Figure 6**).

To assess the binding affinity of SI-63R1, Octet binding assay was used. The SI-63R1 protein was loaded via covalent coupling onto AR2G sensors at 10 ug/ml and bound to a serial dilution of His-tagged human CD19 (1:2.5 dilutions from the highest concentration of 200 nM). The result shows that SI-63R1 has a binding affinity to human CD19 in the low nanomolar range (**Table 2**).

Example 6. Humanized anti-CD19 scFv monoFc fusion proteins.

To further screen and compare all humanized peptides, the DNA sequences encoding humanized CD19 binding variants (H1, H2, H3, H4, H5 and H6) were configured to a scFv-monoFc format and cloned (Dimitrov et al. 2012.) (**SEQ ID NO.55,57,59,61,63,65**). Using the ExpiCHO expression system, each of 6 humanized anti-CD19 scFv monoFc fusion proteins was expressed and purified via protein-A affinity chromatography. They were given names as SI-63SF1(H1), SI-63SF2(H2), SI-63SF4(H3), SI-63SF5(H4), SI-63SF6(H5), and SI-63SF7(H6). Following the expression and purification processes, all six proteins were characterized for their physical characters, including yields (titer), purity (% HMW and aSEC), binding affinity (KD, Kon, and Kdis)

to human CD19, and thermal stability. For Octet assay, the scFv-monoFc fusion proteins were loaded via AHC sensors at 10 ug/ml and bound to a serial dilution of His-tagged human CD19 (1:2.5 dilutions starting from the highest concentration of 200 nM), and the resulting global fit to a 1:1 binding model. For the DLS analysis, the temperature was ramped from 25°C to 75°C at 0.5°C/min while the radius of the scFv-monoFc fusion proteins (at 1 mg/ml) was monitored by a Wyatt DynaPro Plate Reader III. The analytical SEC profiles are shown in **Figure 7**, and all the measurements are listed in **Table 4**.

The data revealed that SI-63SF5 (H4) has the highest DLS melting temperature (T_m) at 51.8°C (**Table 4**). Due to its higher thermal stability, humanized anti-CD19 variable region with H4 peptide was selected for further investigation in the GNC antibody platform.

Example 7. Humanized anti-CD19 scFv or Fab domain in GNC antibodies

The Guidance and Navigation Control (GNC) antibodies refer to a multi-specific antibody capable of binding to antigen(s) expressed by at least one target cell (including but not limited to a tumor cell, an immune cell, or a microbial cell) and the antigen expressed by at least one effector cell (such as immune cell) (see Applicant's application WO/2019/005642, incorporated herein in its entirety). A GNC antibody comprises an antibody structure of Fab and Fc regions with various additional binding domains attached to the antibody-core, such as one or more single chain fragment variable domains, also known as scFv. GNC antibodies are capable of targeting tumor antigens, engaging immune-activating receptors, and directing immune effector cell-mediated killing of tumors at a fraction of the cost. For example, it has been shown that tetra-specific GNC (tetra-GNC) antibodies exert desirable multi-facet effects with structurally and functionally diverse but relatively independent binding domains (see Applicant's application WO/2019/191120, incorporated herein in its entirety). In this context, the humanized anti-CD19 variable domain may be added to any GNC antibody as either a Fab or scFv domain.

To characterize the humanized CD19 binding domain in GNC antibodies, the DNA sequences encoding H4 and H7 were configured and cloned into the GNC antibody format in one of five scFv positions and the Fab position, respectively (**Figure 8** shows the configuration scheme). A mutation R19S (Kabat numbering) was optionally incorporated into the FR1 region of the humanized (H4) VH domain for VH3-containing scFvs on the GNC light chain, e.g. SI-55H11. When scFvs containing VH3 are attached to the GNC light chain, the V_H domain can bind to protein A resin during purification, causing formation of light chain monomers and dimers to contaminate the desired heavy-light chain heterotetramer. In order to rationally disrupt protein A binding of VH3 family members, a structural approach was taken to interrupt the binding interface. Crystal structure 1DEE (Graille M. et al. Proc. Nat. Acad. Sci. 2000.) showed that residue R19 in VH3 (Kabat numbering) is in direct contact with two side chains of protein A domain D. In particular, contact with Q32 and D36 could be eliminated to significantly weaken the interaction. Thus, R19 was mutated to serine, which does not form these interactions due to its shorter side-chain. Additionally, S19 exists naturally in other VH family members, suggesting that it may be

less immunogenic than other substitutions. For hexaGNC antibodies, which may contain up to two VH3 scFvs per chain, this mutation is especially important in allowing efficient purification of the desired product.

Table 5 listed the hexaGNC antibodies having a humanized CD19 binding domain H4 at D1 of SI-77H3 (SEQ ID NO. 67 and 69), at D2 (Fab) of SI-77H6 (SEQ ID NO. 71, 73), and at D6 of SI-55H11 (SEQ ID NO. 75 and 77); and the pentaGNC antibody having a humanized CD19 binding domain H4 at D6 of SI-38P12 (SEQ ID NO. 87 and 89). The expression vectors encoding these GNC antibodies were transfected and expressed in the ExpiCHO system and all GNC antibodies were purified via protein-A affinity chromatography. The results of yields and purity as measured by titer and aSEC demonstrated that the GNC antibodies with a humanized CD19 binding domain, as either a scFv or a Fab, can be expressed and purified (**Figure 9** and **Table 6**).

To determine the binding affinity of the hexa and pentaGNC antibodies to human CD19, the Octet binding assay was used. The GNC antibodies were loaded via AHC sensors at 10 ug/ml and bound to a serial dilution (1:2.5 dilutions starting from the highest concentration of 200 nM) or a single 100-nM concentration of His-tagged human CD19. The resulting global fit to a 1:1 binding model demonstrated that these GNC antibodies bind to CD19 with affinities in the low nanomolar range (**Table 6**).

Example 8. The positional effect of a humanized CD19 binding domain in GNC antibodies

To evaluate the humanized CD19 binding domain mediated antibody-dependent cellular cytotoxicity, peripheral blood mononuclear cells (PBMCs) from human and cynomolgus macaque were used. T cell engagers were added to human or cynomolgus PBMC and cultured for 5 days. After 5 days, the culture cells are collected, and both viable and non-viable CD20+ B cell were counted by FACS. Analyses of both viable single B cells and viable all B cells (singlets, doublets, or other cells in the gate) were independently evaluated. Relative total cell counts are quantified using spiked in counting bead controls. In this study, the hexaGNC antibodies being tested included SI-77H3 (H4 at D1), SI-77H6 (H7 at D2, i.e. Fab), SI-55H11 (H4 at D6), and the control was a tetraGNC antibody, SI-38E17 (SEQ ID NO. 79 and 81), which has a human CD19 binding domain (21D4) at the Fab region (D2) (**Table 5**).

The single cell analysis by FACS tends to miss the effect of T cell engagers on the formation of non-cytolytic complexes, most of which seem to fall outside the gate for single cells. In contrast, the analysis that is inclusive of doublet cells covers more events, thereby provides more complete understanding of cell-cell interactions. **Figure 10** shows the results of ADCC analyses using the gate on viable all B cells. The control antibody, SI-38E17, displayed the binding specificity to human CD19 but not to cynomolgus CD19. As a comparison, all three hexaGNC antibodies showed similar responses to both human and cynomolgus PBMC. Unexpectedly, SI-77H6 seemed not to mediate the ADCC to both human and cynomolgus PBMC despite the presence of a humanized CD19 binding affinity (**Table 6**). As shown in **Table 5**, in SI-77H6, the humanized CD19 binding domain is the Fab region of the antibody-core structure, whereas in both SI-77H3 and SI-

55H11, the humanized CD19 binding domain is an added scFv domain to the antibody-core structure. A hexa-GNC antibody possesses at least 6 binding specificities, thereby is capable of binding at least two different types of cells *in vivo* and at the same time, which is a different situation from assessing the affinity of individual binding domains. This observed correlation of position and effect suggested that there are biologically distinct outcomes mediated by the positional effect of the humanized anti-CD19 Fab domain in a GNC antibody, and that SI-77H6 may not be able to support the proper formation of cytolytic immune synapses between activated T cells and target B cells. Since CD19 is expressed by both normal and neoplastic B cells, the positional effect may be useful when assigning each binding domain for the benefit of treating different types of cancer, i.e. solid versus liquid tumors. For example, a SI-77H6 liked GNC antibody may still be useful for treating solid tumors with higher efficacy but lower cytotoxicity to normal B cells. In another example the SI-77H6 liked GNC antibody could be useful for engagement of B cell help to T cells in cytolytic interaction directed toward other tumor associated antigens.

Example 9. RTCC by hexa-GNC antibodies having a humanized CD19 binding domain

To demonstrate the cytotoxic effect of hexaGNC antibodies having a humanized CD19 binding domain, the analysis of re-directed T cell cytotoxicity (RTCC) was carried out using Raji cells. The Raji line of lymphoblast-like cells was derived from a Burkitt's lymphoma. Since each of the three hexaGNC antibodies can bind to multiple tumor antigens other than CD19, such as EGFR, HER3, and PD-L1 (**Table 5**), the Raji cells expressing mKate2 fluorescent protein were stained by labeled monoclonal antibodies against individual tumor antigens and analyzed by FACS. The histogram results confirmed that the Raji cells expresses CD19, and that no expression of EGFR, HER3, or PD-L1 can be detected (**Figure 11A**).

The Raji cells expressing mKate2 fluorescent protein were co-cultured with human CD8 T cells at a ratio of 5 T cells per Raji cell for 81 hours in the presence of T cells engager proteins at concentrations ranging from 10nM to 1fM in triplicate. Target cell fluorescent signal was evaluated as a measure of specific cytolysis by quantitative microscopy and dose response curves modelled using 5 parameter asymmetric sigmoidal nonlinear regression and least squares fit method using Graphpad Prism 8. As shown in **Figure 11B**, the humanized CD19 binding domain in each of SI-55H11 (EC50, 2pM), SI-77H3 (EC50, 8pM), and SI-77H6 (EC50, 30pM) mediated the potent cytolysis of tumor cells, and the potency of SI-55H11 was the same as that of SI-38E17 (EC50, 2pM), a human anti-CD19 antibody (21D4) (**Table 6**). SI-77H6 displayed suboptimal cytolysis with reduced potency, a phenomenon in parallel to its effect of CD19 binding to normal B cells without cytolysis induction. SI-77H3 was able to complete killing tumor cells but at a reduced EC50. Thus, with optimized configuration and treatment conditions (such as the ratio of activated T cells to target cells), the disclosed humanized CD19 binding domain may exert the same potency as the human CD19 binding domain in multi-specific GNC antibodies with an added feature of cross-reactivity to cynomolgus macaque CD19.

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

Reference:

1. Watkins MP, Bartlett NL. CD19-targeted immunotherapies for treatment of patients with non-Hodgkin B-cell lymphomas. *Expert Opin Investig Drugs*. 2018;27(7):601–611. doi:10.1080/13543784.2018.1492549.
2. (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5058631/>.)
3. McDonagh, Charlotte et. Al. CD19 Binding agents and Uses Thereof. US 20090136526 A1.
4. Rao-Naik et. al. CD19 Antibodies and their uses. US 20090142349 A1.
5. Dimitrov et al. 2012: <https://www.frontiersin.org/articles/10.3389/fimmu.2017.01545/full>.
6. (Graille M. et al. *Proc. Nat. Acad. Sci.* 2000.)

TABLES

Table 1. Computational calculation of humanized variable domains for total MHCII binding scores and humanness scores using MixMHC2pred and Z score analysis algorithm, respectively.

Name of Peptides (VH/VL)	Sequence Type	Core peptides (MHCII Binding)	Humanness Score (Vk) (Z score)	Humanness Score (VH) (Z score)
BU12 (VH/VL)	Mouse	9	-1.40	-1.94
H1VH-H1VL	Humanized	5	-0.77	-0.03
H2VH-H2VL	Humanized	5	-0.75	-0.03
H3VH-H3VL	Humanized	5	-0.77	-0.03
H4VH-H4VL	Humanized	5	-0.75	-0.03
H5VH-H5VL	Humanized	9	-0.70	0.58
H6VH-H6VL	Humanized	9	-0.70	0.57
H7VH-H7VL	Humanized	6	-0.56	-0.55
21D4	Human	12	0.86	-0.06

Table 2. The purity, binding affinity, and thermal stability of SI-63C1 (with mouse parental BU12 variable sequences), SI-63C2 (with H1 humanized anti-CD19 variable sequences), SI-34C1 (with 21D4 human anti-CD19 variable sequences), and SI-63R1 (humanized anti-CD19 scFv-His-tagged protein).

Sample ID	Format	α CD19 domain (VH/VL)	Titer (ug/ml)	% aSEC	KD (nM)	Kon (1/ms)	Kdis (1/s)	DLS Tm (°C)
SI-63C1	mAb	BU12	250	98%	3.06	6.81E+04	2.09E-04	75.09
SI-63C2	mAb	H1	235	99%	3.77	6.08E+04	2.29E-04	75.02
SI-34C1	mAb	21D4	60	96.45%	1.56	6.44E+04	1.01E-04	69.07
SI-63R1	ScFv	H1	120	70%	1.33	4.99E+04	9.15E-05	58.8

Table 3. The cross reactivity of recombinant antibodies (SI-63C1 and SI-63C2) and mouse anti-human CD19 antibodies (SJ25C, LT19, HIB19, and 4G7) to CD20+ lymphocytes of human, cynomolgus, and rhesus origins, as measured by EC50.

Anti-CD19 mAb EC50 (μg/ml)		Human CD20+	Cynomolgus CD20+	Rhesus CD20+
SI-63C2-AF647	Humanized	0.03974	2.901	0.6665
SI-63C1-AF647	Mouse	0.2314	0.9093	0.9907
SJ25C-BV421	Mouse	0.2088	N/A	N/A
LT19-FITC	Mouse	0.008687	N/A	N/A
HIB19-APC	Mouse	0.05441	N/A	N/A
4G7-FITC	Mouse	0.5492	N/A	N/A

Table 4. The purity, binding affinity, and thermal stability of humanized anti-CD19 scFv monoFc fusion proteins, SI-63SF1 (H1), SI-63SF2 (H2), SI-63SF4(H3), SI-63SF5 (H4), SI-63SF6 (H5), and SI-63SF7 (H6).

scFv-Fc ID	α CD19 domain (VH/VL)	Titer (ug/ml)	% HMW	% aSEC	KD (nM)	Kon (1/ms)	Kdis (1/s)	DLS Tm (°C)
SI-63SF1	H1	130	20%	80%	6.89	4.41E+04	1.84E-03	46.9
SI-63SF2	H2	121	15%	85%	4.22	4.28E+04	1.81E-03	45.1
SI-63SF4	H3	174	12%	89%	4.18	4.56E+04	1.91E-03	51.2
SI-63SF5	H4	110	11%	88%	5.02	3.72E+04	1.87E-03	51.8
SI-63SF6	H5	101	8%	92%	5.68	5.97E+04	3.39E-04	49.8
SI-63SF7	H6	97	7%	91%	5.37	7.02E+04	3.77E-04	50.1

Table 5. The positions of the humanized CD19 binding domain and other antigen binding domains in GNC antibodies.

GNC Ab ID	Multi-Specificity	D1	D2 (Fab)	D3	D4	D5	D6
SI-77H3	Hexa	H4	α EGFR	α PD-L1	α 4-1BB	α HER3	α CD3
SI-77H6	Hexa	α HER3	H7	α PD-L1	α 4-1BB	α HER3	α CD3
SI-55H11	Hexa	α EGFR	α CD3	α PD-L1	α 4-1BB	α HER3	H4
SI-38P12	Penta	α CD20	α CD3	α PD-L1	α 4-1BB	-	H4
SI-38E17	Tetra	α CD3	21D4	α PD-L1	α 4-1BB	-	-

Table 6. The physical and functional characters of the GNC antibodies having a humanized anti-CD19 scFv domain or Fab region.

GNC Ab ID	Multi-Specificity	α CD19 Position	α CD19 domain (VH/VL)	Titer (μ g/ml)	aSEC %POI	α CD19 KD (nM)	EC50 (pM)
SI-77H3	Hexa	D1	H4	68.4	86.91	7.53	8.1
SI-77H6	Hexa	D2	H4	58.6	78.51	5.25	30.2
SI-55H11	Hexa	D6	H4	61.9	76.95	4.54	2.5
SI-38P12	Penta	D6	H4	101.2	79.05	1.11	n/a
SI-38E17	Tetra	D2	21D4	61.1	80.54	1.48	2.1

SEQUENCE LISTING

Sample ID	Annotation	SEQ ID NO.	
		Protein	DNA
H1VH	Humanized version 1 variable heavy chain	1	2
H2VH	Humanized version 2 variable heavy chain	3	4
H3VH	Humanized version 3 variable heavy chain	5	6
H4VH	Humanized version 4 variable heavy chain	7	8
H5VH	Humanized version 5 variable heavy chain	9	10
H6VH	Humanized version 6 variable heavy chain	11	12
H7VH	Humanized version 7 variable heavy chain	91	92
H1VL	Humanized version 1 variable light chain	13	14
H2VL	Humanized version 2 variable light chain	15	16
H3VL	Humanized version 3 variable light chain	17	18
H4VL	Humanized version 4 variable light chain	19	20
H5VL	Humanized version 5 variable light chain	21	22
H6VL	Humanized version 6 variable light chain	23	24
H7VL	Humanized version 7 variable light chain	93	94
BU12VH	Mouse anti-CD19 heavy chain variable sequence	25	26
BU12VL	Mouse anti-CD19 light chain variable sequence	27	28
21D4VH	Human anti-CD19 heavy chain variable sequence	29	30
21D4VL	Human anti-CD19 light chain variable sequence	31	32
SI-63C1HC	BU12 version mAb heavy chain	33	34
SI-63C1LC	BU12 version mAb kappa light chain	35	36
SI-63C2HC	Humanized version 1 mAb heavy chain	37	38
SI-63C2LC	Humanized version 1 mAb light chain	39	40
SI-63R1	Humanized version 1 ScFv His-tagged	41	42
SI-63SV1	Humanized version 1 ScFv	43	44
SI-63SV2	Humanized version 2 ScFv	45	46
SI-63SV3	Humanized version 3 ScFv	47	48
SI-63SV4	Humanized version 4 ScFv	49	50
SI-63SV5	Humanized version 5 ScFv	51	52
SI-63SV6	Humanized Version 6 ScFv	53	54
SI-63SV7	Humanized Version 7 ScFv	95	96
SI-63SF1	Humanized version 1 ScFv monoFc	55	56
SI-63SF2	Humanized version 2 ScFv monoFc	57	58

SI-63SF4	Humanized version 3 ScFv monoFc	59	60
SI-63SF5	Humanized version 4 ScFv monoFc	61	62
SI-63SF6	Humanized version 5 ScFv monoFc	63	64
SI-63SF7	Humanized version 6 ScFv mono Fc	65	66
SI-77H3HC	hexaGNC heavy chain	67	68
SI-77H3LC	hexaGNC light chain	69	70
SI-77H6HC	hexaGNC heavy chain	71	72
SI-77H6LC	hexaGNC Light Chain	73	74
SI-55H11HC	hexaGNC Heavy Chain	75	76
SI-55H11LC	hexaGNC light chain	77	78
SI-38E17HC	tetraGNC Heavy chain	79	80
SI-38E17LC	tetraGNC Light Chain	81	82
SI-34C1	21D4 mAb Heavy Chain	83	84
SI-34C1	21D4 mAb Light Chain	85	86
SI-38P12 LC	pentaGNC Light Chain	87	88
SI-38P12 HC	pentaGNC Heavy Chain	89	90

>Sequence ID 1: Humanized Version 1(H1VH) Amino Acid Sequence

QVTLKESGPGVLVQPGQTLRLTCAFSGFSLSTSGMGVGVIRQPPGKGLEWLAHIWDDDKRYNPALKSRLTISKDTSKNQVYLQMNS
LDAEDTAVYYCARMELWSYFDYWGGQTLVTVSS

>Sequence ID 2: Humanized Version 1(H1VH) Nucleotide Sequence

CAGGTCACATTGAAGGAATCTGGCCCCGGCCTTGTTTCAGCCAGGACAGACCCTTAGGCTCACCTGTGCCTTCAGTGGTTTTCTCT
TAGCACTAGCGGTATGGGGGTCTGGCTGGATTCGGCAGCCTCCCGGCAAAGGTCTTGAGTGGTTGGCTCACATTTGGTGGGACGACG
ACAAACGGTATAATCCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATACCTCAAAAATCAAGTGACTTGCAAATGAATAGC
CTTGACGCCGAGGATACGGCTGTATATTATTGCGCGCGGATGGAACCTCTGGTCTTACTACTTTGATTATTGGGGGCAGGGGACTCT
CGTCACGGTCTCGAGT

>Sequence ID 3: Humanized Version 2(H2VH) Amino Acid Sequence

QVTLKESGPGVLVQPGQTLRLTCAFSGFSLSTSGMGVGVIRQPPGKGLEWLAHIWDDDKRYNPALKSRLTISKDTSKNQVYLQMNS
LDAEDTAVYYCARMELWSYFDYWGGQTLVTVSS

>Sequence ID 4: Humanized Version 2(H2VH) Nucleotide Sequence

CAGGTCACATTGAAGGAATCTGGCCCCGGCCTTGTTTCAGCCAGGACAGACCCTTAGGCTCACCTGTGCCTTCAGTGGTTTTCTCT
TAGCACTAGCGGTATGGGGGTCTGGCTGGATTCGGCAGCCTCCCGGCAAAGGTCTTGAGTGGTTGGCTCACATTTGGTGGGACGACG
ACAAACGGTATAATCCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATACCTCAAAAATCAAGTGACTTGCAAATGAATAGC
CTTGACGCCGAGGATACGGCTGTATATTATTGCGCGCGGATGGAACCTCTGGTCTTACTACTTTGATTATTGGGGGCAGGGGACTCT
CGTCACGGTCTCGAGT

>Sequence ID 5: Humanized Version 3(H3VH) Amino Acid Sequence

QVTLKESGPGVLVQPGQTLRLTCAFSGFSLSTSGMGVGVIRQPPGKGLEWLAHIWDDDKRYNPALKSRLTISKDTSKNQVYLQMNS
LDAEDTAVYYCARMELWSYFDYWGGQTLVTVSS

>Sequence ID 6: Humanized Version 3(H3VH) Nucleotide Sequence

CAGGTCACATTGAAGGAATCTGGCCCCGGCCTTGTTTCAGCCAGGACAGACCCTTAGGCTCACCTGTGCCTTCAGTGGTTTTCTCT
TAGCACTAGCGGTATGGGGGTCTGGCTGGATTCGGCAGCCTCCCGGCAAAGGTCTTGAGTGGTTGGCTCACATTTGGTGGGACGACG
ACAAACGGTATAATCCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATACCTCAAAAATCAAGTGACTTGCAAATGAATAGC

CTTGACGCCGAGGATACGGCTGTATATTATTGCGCGCGGATGGAACCTCTGGTCTTACTACTTTGATTATTGGGGGCAGGGGACTCT
CGTCACGGTCTCGAGT

>Sequence ID 7: Humanized Version 4(H4VH) Amino Acid Sequence
QVTLKESGPGLVQPGQTLRLTCAFSGFSLSTSGMGVGVWRQPPGKGLEWLAHIWDDDKRYNPALKSRLTISKDTSKNQVYLQMNS
LDAEDTAVYYCARMELWSYFDYWGGTLVTVSS

>Sequence ID 8: Humanized Version 4(H4VH) Nucleotide Sequence
CAGGTACACATTGAAGGAATCTGGCCCCGGCCTTGTTCAGCCAGGACAGACCCTTAGGCTCACCTGTGCCTTCAGTGGTTTTCTCT
TAGCACTAGCGGTATGGGGGTCGGGTGGATTCGGCAGCCTCCCGCCAAAGGTCTTGAGTGGTTGGCTCACATTTGGTGGGACGACG
ACAAACGGTATAATCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATACCTCAAAAATCAAGTGACTTGCAAATGAATAGC
CTTGACGCCGAGGATACGGCTGTATATTATTGCGCGCGGATGGAACCTCTGGTCTTACTACTTTGATTATTGGGGGCAGGGGACTCT
CGTCACGGTCTCGAGT

>Sequence ID 9: Humanized Version 5(H5VH) Amino Acid Sequence
EVQLVESGGGLVQPGGSLRLSCVSGFSLSTSGMGVGVWRQAPGKGLEWVGHIIWDDDKRYNPALKSRFTISRDTSKNTVYLQMNS
LRAEDTAVYYCARMELWSYFDYWGGTLVTVSS

>Sequence ID 10: Humanized Version 5(H5VH) Nucleotide Sequence
GAGGTGCAACTTGTGAAAGCGGCGCGGGTGGTGCAACCTGGCGGTTCACTTCGGCTCTCATGTGTGTTCACTGGTTTTCCCT
TAGCACAAGCGGGATGGGTGTCGGGTGGGTCCGCCAAGCGCCTGGCAAAGGTCTGGAATGGGTGGTTCACATTTGGTGGGATGATG
ACAAAAGGTATAATCCCGCGCTGAAATCTAGATTACTATTAGTCGGGATACGAGTAAGAACACGGTGTATCTGCAAATGAACAGT
CTCAGGGCAGAGGATACAGCGGTATATTATTGTGCTCGAATGGAGCTGTGGTCTTACTATTTTGATTACTGGGGCCAGGGCACGTT
GGTAACGGTCTCGAGT

>Sequence ID 11: Humanized Version 6(H6VH) Amino Acid Sequence
EVQLVESGGGLVQPGGSLRLSCSFSGFSLSTSGMGVGVWRQAPGKGLEWVGHIIWDDDKRYNPALKSRFTISRDTSKNTVYLQMNS
LRAEDTAVYYCARMELWSYFDYWGGTLVTVSS

>Sequence ID 12: Humanized Version 6(H6VH) Nucleotide Sequence
GAGGTGCAACTTGTGAAAGCGGCGCGGGTGGTGCAACCTGGCGGTTCACTTCGGCTCTCATGTAGCTTCAGTGGTTTTCCCT
TAGCACAAGCGGGATGGGTGTCGGGTGGGTCCGCCAAGCGCCTGGCAAAGGTCTGGAATGGGTGGTTCACATTTGGTGGGATGATG
ACAAAAGGTATAATCCCGCGCTGAAATCTAGATTACTATTAGTCGGGATACGAGTAAGAACACGGTGTATCTGCAAATGAACAGT
CTCAGGGCAGAGGATACAGCGGTATATTATTGTGCTCGAATGGAGCTGTGGTCTTACTATTTTGATTACTGGGGCCAGGGCACGTT
GGTAACGGTCTCGAGT

>Sequence ID 13: Humanized Version 1(H1VL) Amino Acid Sequence
ENVLTQSPASLSASPGERVITITCSASSSVSYMHWYQQKPGQAPKLWIYDTSKSLASGVPSRFSGSGSGNDHTLTISSMEPEDFATYY
CFQGSVYPFTFGQGTKLEIK

>Sequence ID 14: Humanized Version 1 (H1VL) Nucleotide Sequence
GAAAATGTATTGACACAGAGCCCCGCTCCCTCAGTGCCTCACCTGGGGAAAGGGTAACTATCACTTGCTCTGCATCAAGCAGCGT
CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
CTAGCCGCTTCAGTGGTTCGGCTCAGGCAACGATCACACCCTTACGATTTCAGTATGGAACCCGAAGATTTGCAACTATTAT
TGTTTCCAGGGGAGCGTGTACCCATTCATTTCCGGGCAGGGGACAAAATTGGAGATAAAG

>Sequence ID 15: Humanized Version 2 (H2VL) Amino Acid Sequence
ENVLTQSPASLSASPGERVITITCSASSSVSYMHWYQQKPGQAPKLWIYDTSKSLASGVPSRFSGSGSGNDHTLTISSMEPEDFATYY
CFQGSVYPFTFGQGTKITIL

>Sequence ID 16: Humanized Version 2 (H2VL) Nucleotide Sequence
GAAAATGTATTGACACAGAGCCCCGCTCCCTCAGTGCCTCACCTGGGGAAAGGGTAACTATCACTTGCTCTGCATCAAGCAGCGT
CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
CTAGCCGCTTCAGTGGTTCGGCTCAGGCAACGATCACACCCTTACGATTTCAGTATGGAACCCGAAGATTTGCAACTATTAT
TGTTTCCAGGGGAGCGTGTACCCATTCATTTCCGGGCAGGGGACAAAATTACGATACTG

>Sequence ID 17: Humanized Version 3 (H3VL) Amino Acid Sequence
ENVLTQSPASLSASPGERVITITCSASSSVSYMHWYQQKPGQAPKLWIYDTSKSLASGVPSRFSGSGSGNDHTLTISSMEPEDFATYY
CFQGSVYPFTFGQGTKLTVL

>Sequence ID 18: Humanized Version 3 (H3VL) Nucleotide Sequence
GAAAATGTATTGACACAGAGCCCCGCTCCCTCAGTGCCTCACCTGGGGAAAGGGTAACTATCACTTGCTCTGCATCAAGCAGCGT
CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC

CTAGCCGCTTCAGTGGTTCGGGCTCAGGCAACGATCACACCCTTACGATTTCAGTATGGAACCCGAAGATTTTGCAACTTATTAT
TGTTTCCAGGGGAGCGTGTAACCATTTCACTTTCGGGCAGGGGACAAAAGTTACGGTACTG

>Sequence ID 19: Humanized Version 4 (H4VL) Amino Acid Sequence
ENVLTQSPASLSASPGERVITITCSASSSVSYMHWYQQKPGQAPKLIYDTSKLAGVPSRFRSGSGSGNDHTLTISSMEPEDFATYY
CFQGSVYPFTFGQGTKVTVL

>Sequence ID 20: Humanized Version 4 (H4VL) Nucleotide Sequence
GAAATAGTATTGACACAGAGCCCCGCTCCCTCAGTGCCTCACCTGGGGAAAGGTAACATCACTTGCTCTGCATCAAGCAGCGT
CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
CTAGCCGCTTCAGTGGTTCGGGCTCAGGCAACGATCACACCCTTACGATTTCAGTATGGAACCCGAAGATTTTGCAACTTATTAT
TGTTTCCAGGGGAGCGTGTAACCATTTCACTTTCGGGCAGGGGACAAAAGTTACGGTACTG

>Sequence ID 21: Humanized Version 5 (H5VL) Amino Acid Sequence
EIVMTQSPSTLSASVGDRIITCSASSSVSYMHWYQQKPGKAPKLLIYDTSKLAGVPSRFRSGSGSGAEFTLTISLQPDDEFATYY
CFQGSVYPFTFGQGTKLTVL

>Sequence ID 22: Humanized Version 5 (H5VL) Nucleotide Sequence
GAAATAGTGTATGACGAGTCACCTAGCACCTTAGTGCTTCTGTAGGAGACAGGGTTATAATTACCTGCAGTGCTAGTTCCCTCAGT
GTCATACATGCACTGGTATCAGCAGAAACCGGGAAAAGCTCCAAAGCTGCTTATATACGACACGTCCAAATTGGCATCAGGTGTCC
CCAGTCGATTAGTGGCTCTGGCTCAGGGGCTGAATTTACGCTCACAATCTCCAGCCTCCAACAGATGACTTCGCCACATACTAC
TGTTTTCAGGGCTCAGTGTATCCGTTTACTTTCCGCCAGGGGACAAAGTTGACTGTACTT

>Sequence ID 23: Humanized Version 6 (H6VL) Amino Acid Sequence
EIVMTQSPSTLSASVGDRIITCSASSSVSYMHWYQQKPGKAPKLLIYDTSKLAGVPSRFRSGSGSGAEFTLTISLQPDDEFATYY
CFQGSVYPFTFGQGTKLTVL

>Sequence ID 24: Humanized Version 6 (H6VL) Nucleotide Sequence
GAAATAGTGTATGACGAGTCACCTAGCACCTTAGTGCTTCTGTAGGAGACAGGGTTATAATTACCTGCAGTGCTAGTTCCCTCAGT
GTCATACATGCACTGGTATCAGCAGAAACCGGGAAAAGCTCCAAAGCTGCTTATATACGACACGTCCAAATTGGCATCAGGTGTCC
CCAGTCGATTAGTGGCTCTGGCTCAGGGGCTGAATTTACGCTCACAATCTCCAGCCTCCAACAGATGACTTCGCCACATACTAC
TGTTTTCAGGGCTCAGTGTATCCGTTTACTTTCCGCCAGGGGACAAAGTTGACTGTACTT

>Sequence ID 25: BU12 VH: Mouse anti-CD19 VH Amino Acid Sequence
QVTLKESGPGILQPSQTLSTCSFSGFSLSTSGMGVGIWVRQPSGKGLEWLAHIWDDDKRYNPALKSRITISKDTSSNQVFLKIAS
VDTADTAAYYCARMELWSYFDYWQGTTTLTVSS

>Sequence ID 26: BU12 VH: Mouse anti-CD19 VH Nucleotide Sequence
CAGGTGACCTGAAAGAAAGCGGGCCGGGCATTCTGCAGCCGAGCCAGACCCTGAGCCTGACCTGCAGCTTTAGCGGCTTTAGCCT
GAGCACCAGCGGCATGGGCGTGGGCTGGATTGCGCAGCCGAGCGGCAAGGCCTGGAATGGCTGGCGCATATTTGGTGGGATGATG
ATAAAGCTATAACCCGGGCGCTGAAAAGCCGCTGACCATTAGCAAAGATACCAGCAGCAACAGGTGTTTCTGAAAATTGCGAGC
GTGGATACCGCGGATACCGGCGCTATTATTGCGCGCGCATGGAAGTGTGGAGCTATTATTTGATTATTGGGGCCAGGGCACCAC
CTGACCGTGAGCAGC

>Sequence ID 27: BU12 VL: Mouse anti-CD19 VL Amino Acid Sequence
ENVLTQSPAIMASAPGEKVTMTCSASSSVSYMHWYQQKSSTSPKLWIYDTSKLAGVPSRFRSGSGSGNSHFLTISSEAEADVATYY
CFQGSVYPFTFGSGTKLEIK

>Sequence ID 28: BU12 VL: Mouse anti-CD19 VL Nucleotide Sequence
GAAACGTGCTGACCCAGAGCCCGCGGATTATGAGCGCGAGCCCGGGCGAAAAAGTGACCATGACCTGCAGCGCGAGCAGCGGT
GAGCTATATGCATTGGTATCAGCAGAAAAGCAGCACCAGCCCCGAACTGTGGATTATGATACCAGCAAAGTGGCGAGCGGCGTGC
CGGGCCGCTTTAGCGGCAGCGGCAGCGGCAACAGCCATTTCTGACCATTAGCAGCATGGAAGCGGAAGATGTGGCGACCTATTAT
TGCTTTCAGGGCAGCGTGATCCGTTTACCTTTGGCAGCGGCACCAAACTGGAAATTAAA

>Sequence ID 29: 21D4 human antibody VH Amino Acid Sequence
EVQLVQSGAEVKKPGESLKISCKGSGYSFSSWIGWVRQAPGKGLEWMGI IYPDDSDTRYSPSFQGVITISADKSIRTAYLQWSSL
KASDTAMYYCARHVTMIWGVIIIDFWGQGLTVTVSS

>Sequence ID 30: 21D4 human antibody VH Nucleotide Sequence
GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAGAAACCAGGAGAGTCTCTGAAGATCTCCTGTAAGGGTTCTGGATACAGCTT
TAGCAGTTTCATGGATCGGCTGGGTGCGCCAGGCACCTGGGAAAGGCCTGGAATGGATGGGGATCATCTATCCTGATGACTCTGATA
CCAGATACAGTCCATCCTTCCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGGACTGCCTACCTGCAGTGGAGTAGCCTG

AAGGCCTCGGACACCGCTATGTATTACTGTGCGAGACATGTTACTATGATTTGGGGAGTTATTATTGACTTCTGGGGCCAGGGAAC
CCTGGTCACCGTCTCCTCA

>Sequence ID 31: 21D4 human antibody VL Amino Acid Sequence
AIQLTQSPSSLSASVGRVTITCRASQGISSALAWYQKPKGAPKLLIYDASSLESVPSRFSGSGSGTDFTLTISLQPEDFATY
YCQQFNSYPFTFGPGTKVDIK

>Sequence ID 32: 21D4 human antibody VL Nucleotide Sequence
GCCATCCAGTTGACCCAGTCTCCATCCTCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAGGGCAT
TAGCAGTGCTTTAGCCTGGTATCAGCAGAAACAGGGAAGCTCCTAAGCTCCTGATCTATGATGCCTCCAGTTTGAAAGTGGGG
TCCCATCAAGGTTACGCGGCAGTGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTGCAACTTAT
TACTGTCAACAGTTTAATAGTTACCCATTCACTTTCGGCCCTGGGACCAAGTGATATCAAA

>Sequence ID 33: SI-63C1 Heavy Chain Amino Acid Sequence
QVTLKESGPGILQPSQTLSTLCSFSGFSLSTSGMGVWIRQPSGKGLEWLAHIWDDDKRYNPALKSRLTISKDTSNQQVFLKIAS
VDTADTAAYYCARMELWSYFYDYWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT
FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRT
PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTIVLHQLDNLNGKEYKCKVSNKALPAPIEKTI SKAKGQ
PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRWQQGNVVFSCSV
HEALHNHYTQKSLSLSPGK

>Sequence ID 34: SI-63C1 Heavy Chain Nucleotide Sequence
CAGGTGACCTGAAAGAAAGCGGCCCGGGCATTCTGCAGCCGAGCCAGACCCTGACCTGCAGCTTTAGCGGCTTTAGCCT
GAGCACCAGCGGCATGGGCGTGGGCTGGATTGCGCAGCCGAGCGGCAAGGCCCTGGAATGGCTGGCGCATATTTGGTGGGATGATG
ATAAACGCTATAACCCGGCGCTGAAAAGCCGCTGACCATTAGCAAAGATACCAGCAGCAACCAGGTGTTTCTGAAAATTGCGAGC
GTGGATACCGCGGATACCGCGCGCTATTATTGCGCGCGCATGGAAGTGTGGAGCTATTATTTTATTATTGGGGCCAGGGCACCAC
CCTGACCGTGAGCAGCGCTAGCACCAAGGGCCCATCTGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCTG
CCCTGGGCTGCCTGGTCAAGGACTACTTCCCTGAACCTGTGACAGTGTCTTGAAGTCAAGGAGCCCTGACCAGCGCGTGCACACC
TTCCCGGCTGCTTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTA
CATCTGCAACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCCAAATCTTGTGACAAAACCTCACACATGCC
CACCCTGCCCAGCACCTCCTGTAGCAGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACC
CCTGAGGTACATGCGTGGTGGTGGAGCTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCA
TAATGCCAAGACAAAGCCGCGGAGGAGCAGTACGCCAGCAGTACCGTGTGGTCAAGCTCCTCACCCTCCTGCACAGGACTGGC
TGAATGGCAAGGAGTACAAGTGAAGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAG
CCCCGAGAACCACAGGTGTACACCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGACCTGCTGCTCAAAGG
CTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTCTGGACT
CCGACGGCTCCTTCTCTCTACAGCAAGCTCACCCTGGACAAGAGCAGGTGGCAGCAGGGGAACGCTCTCTCATGCTCCGTGATG
CATGAGGCTCTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGCAAA

>Sequence ID 35: SI-63C1 Light Chain Amino Acid Sequence
ENVLTQSPAIMASAPGEKVTMTCSASSSVSYMHYQQKSSSTPKLWIYDTSKLASGVPGRFSGSGSGNSHFLTISSEAEADVATYY
CFQGSVYPTFTGSGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSY
SLSSLTTLTKADYIEKHVYACEVTHQGLSSPVTKSFNRGEC

>Sequence ID 36: SI-63C1 Light Chain Nucleotide Sequence
GAAACGTGCTGACCCAGAGCCCGCGGATTATGAGCGCGAGCCCGGGCGAAAAAGTGACCATGACCTGCAGCGCGAGCAGCAGCGT
GAGCTATATGCATTGGTATCAGCAGAAAAGCAGCACAGCCCGAAACTGTGGATTATGATACAGCAAACCTGGCGAGCGCGTGC
CGGGCCGCTTTAGCGGCAGCGGCAGCGGCAACAGCCATTTTCTGACCATTAGCAGCATGGAAGCGGAAGATGTGGCGACCTATTAT
TGCTTTACGGGACGCTGTATCCGTTTACCTTTGGCAGCGGCACCAAACTGGAAATTAACGTACGGTGGCTGCACCATCTGTCTT
CATCTTCCCGCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCTGCTGAATAACTTCTATCCCAGAGAGGCCA
AAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTAC
AGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCTGCGAAGTACCCATCAGGGCCTGAG
CTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

>Sequence ID 37: SI-63C2 Heavy Chain Amino Acid Sequence
QVTLKESGPGILVQPGQTLRLTCAFSGFSLSSTSGMGVWIRQPPGKGLEWLAHIWDDDKRYNPALKSRLTISKDTSKNQVYLQMNS
LDAEDTAVYYCARMELWSYFYDYWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT
FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKHTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRT
PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRVVSVLTIVLHQLDNLNGKEYKCKVSNKALPAPIEKTI SKAKGQ
PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRWQQGNVVFSCSV
HEALHNHYTQKSLSLSPGK

>Sequence ID 38: SI-63C2 Heavy Chain Nucleotide Sequence

CAGGTCACATTGAAGGAATCTGGCCCCGGCCTTGTTAGCCAGGACAGACCCTTAGGCTCACCTGTGCCTTCAGTGGTTTTCTCT
TAGCACTAGCGGTATGGGGGTCGGCTGGATTTCGGCAGCCTCCCGGCAAAGGCTTGAGTGGTTGGCTCACATTTGGTGGGACGACG
ACAAACGGTATAATCCTGCCCTGAAAAGTCGGCTGACCATTAGTAAGGATACCTCAAAAAATCAAGTGACTTGCAAATGAATAGC
CTTGACGCCGAGGATACGGCTGTATATTATTGCGCGCGGATGGAACCTCTGGTCTTACTACTTTGATTATGGGGGCAGGGGACTCT
CGTCACGGTGCTCTGCTAGCACCAAGGGCCCATCTGTCTTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACAGCTG
CCCTGGGCTGCCTGGTCAAGGACTACTTCCCTGAACCTGTGACAGTGTCTTGGAACTCAGGAGCCCTGACCAGCGGCGTGACACCC
TTCCGGCTGCTCCTACAGTCTCAGGACTCTACTCCCTCAGCAGGTGGTGACCGTGCCCTCCAGCAGCTTGGGCAACCCAGACCTA
CATCTGCAACGTGAATCAACAGCCAGCAACACCAAGGTGGACAAGAAAGTTGAGCCCCAAATCTGTGACAAAACCTCACACATGCC
CACCGTGCCAGCACCTCCTGTAGCAGGACCGTCAGTCTTCTCTTCCCCCAAACCCAAAGGACACCTCATGATCTCCCGGACC
CCTGAGGTACATGCGTGGTGGTGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGAGGTGCA
TAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACGCCAGCACGTACCGTGTGGTCAGCGTCTCACCCTGACACGAGGACTGGC
TGAATGGCAAGGAGTACAAGTGCAAGGTCTCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAG
CCCCGAGAACCACAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCAAGAACCAGGTGACGCTGACCTGGCTGGTCAAAGG
CTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGTGGACT
CCGACGGCTCCTTCTTCTTACAGCAAGCTACCGTGGACAAGCAGGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATG
CATGAGGCTCTGCACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCCGGGCAA

>Sequence ID 39: SI-63C2 Light Chain Amino Acid Sequence

ENVLTQSPASLSASPGERVITCSASSSVSYMHWYQQKPGQAPKLWIYDTSKLASGVPSRFSGSGSGNDHTLTISSEMPEDFATYY
CFQGSVYPFTFGQGTKLEIKRTVAAPSVFI FPPSDEQLKSGTASVVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSY
SLSLTLTLKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC

>Sequence ID 40: SI-63C2 Light Chain Nucleotide Sequence

GAAATGTATTGACACAGAGCCCCGCCTCCCTCAGTGCCTCACCTGGGGAAAGGGTAACATCACTTGCTCTGCATCAAGCAGCGT
CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
CTAGCCGCTTCAGTGGTTCGGGCTCAGGCAACGATCACACCCTTACGATTTCCAGTATGGAACCCGAAGATTTTGCAACTTATTAT
TGTTTCCAGGGGAGCGTGATCCCATTTCACTTTCGGGCAGGGGACAAAATTGGAGATAAAGCGTACGGTGGCTGACCATCTGTCTT
CATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAATGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCAGAGAGGCCA
AAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTAC
AGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCTGCGAAGTACCCATCAGGGCCTGAG
CTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTG

>Sequence ID 41: SI-63R1 (H1 ScFv-His) Amino Acid Sequence

ENVLTQSPASLSASPGERVITCSASSSVSYMHWYQQKPGQAPKLWIYDTSKLASGVPSRFSGSGSGNDHTLTISSEMPEDFATYY
CFQGSVYPFTFGQGTKLEIKGGGSGGGGSGGGGSGGGGSGVTLKESGPGLVQPGQTLRLTCAFSGFSLSSTSGMGVGVIRQPPGKG
LEWLAHIWDDDKRYNPALKSRLTISKDTSKNQVYLQMNSLDAEDTAVYYCARMELWSYFDYWQGTLLVTVSSGSHHHHHH

>Sequence ID 42: SI-63R1 (H1 ScFv-His) Nucleotide Sequence

GAAATGTATTGACACAGAGCCCCGCCTCCCTCAGTGCCTCACCTGGGGAAAGGGTAACATCACTTGCTCTGCATCAAGCAGCGT
CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
CTAGCCGCTTCAGTGGTTCGGGCTCAGGCAACGATCACACCCTTACGATTTCCAGTATGGAACCCGAAGATTTTGCAACTTATTAT
TGTTTCCAGGGGAGCGTGATCCCATTTCACTTTCGGGCAGGGGACAAAATTGGAGATAAAGGGCGGTGGCGGTAGTGGGGGAGGCGG
TTCTGGCGGCGGAGGTCGGCGGTGGAGGATCACAGGTACATTTGAAGGAATCTGGCCCCGGCTTGTTAGCCAGGACAGACCC
TTAGGCTCACCTGTGCCTTCAGTGGTTTTCTCTTAGCACTAGCGGTATGGGGGTCGGCTGGATTCCGCAGCCTCCCGGCAAAGGT
CTTGAGTGGTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATAC
CTCAAAAAATCAAGTGACTTGCAATGAATAGCCTTGACGCCGAGGATACGGCTGTATATTATTGCGCGCGGATGGAACCTCTGGT
CTTACTACTTTGATTATTGGGGGACGGGACTCTCGTCACGGTCTCGAGTGGATCCCATCATCACCATCACCATTGA

>Sequence ID 43: SI-63SV1 Amino Acid Sequence

ENVLTQSPASLSASPGERVITCSASSSVSYMHWYQQKPGQAPKLWIYDTSKLASGVPSRFSGSGSGNDHTLTISSEMPEDFATYY
CFQGSVYPFTFGQGTKLEIKGGGSGGGGSGGGGSGGGGSGVTLKESGPGLVQPGQTLRLTCAFSGFSLSSTSGMGVGVIRQPPGKG
LEWLAHIWDDDKRYNPALKSRLTISKDTSKNQVYLQMNSLDAEDTAVYYCARMELWSYFDYWQGTLLVTVSS

>Sequence ID 44: SI-63SV1 Nucleic Acid Sequence

GAAATGTATTGACACAGAGCCCCGCCTCCCTCAGTGCCTCACCTGGGGAAAGGGTAACATCACTTGCTCTGCATCAAGCAGCGT
CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
CTAGCCGCTTCAGTGGTTCGGGCTCAGGCAACGATCACACCCTTACGATTTCCAGTATGGAACCCGAAGATTTTGCAACTTATTAT
TGTTTCCAGGGGAGCGTGATCCCATTTCACTTTCGGGCAGGGGACAAAATTGGAGATAAAGGGCGGTGGCGGTAGTGGGGGAGGCGG
TTCTGGCGGCGGAGGTCGGCGGTGGAGGATCACAGGTACATTTGAAGGAATCTGGCCCCGGCTTGTTAGCCAGGACAGACCC
TTAGGCTCACCTGTGCCTTCAGTGGTTTTCTCTTAGCACTAGCGGTATGGGGGTCGGCTGGATTCCGCAGCCTCCCGGCAAAGGT
CTTGAGTGGTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATAC
CTCAAAAAATCAAGTGACTTGCAATGAATAGCCTTGACGCCGAGGATACGGCTGTATATTATTGCGCGCGGATGGAACCTCTGGT
CTTACTACTTTGATTATTGGGGGACGGGACTCTCGTCACGGTCTCGAGTGGATCCCATCATCACCATCACCATTGA

>Sequence ID 45: SI-63SV2 Amino Acid Sequence

ENVLTQSPASLSASPGERVITITCSASSSVSYMHVYQQKPGQAPKLIYDTSKLASGVPSRFSGSGSGNDHTLTISSEMPEDFATYY
CFQGSVYPFTFGQGTKITILGGGSGGGGSGGGGSGGGGSGVTLKESGPGLVQPGQTLRLTCAFSGFSLSSTSGMGVGVIRQPPGKG
LEWLAHIWDDDKRNPALKSRLTISKDTSKNQVYLQMNSLDAEDTAVYYCARMELWSYFDYWGGQGLVTVSS

>Sequence ID 46: SI-63SV2 Nucleic Acid Sequence

GAAATGTATTGACACAGAGCCCCGCCTCCCTCAGTGCCTCACCTGGGGAAAGGGTAACATCACTTGCTCTGCATCAAGCAGCGT
CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
CTAGCCGCTTCAGTGGTTCGGGCTCAGGCAACGATCACACCCTTACGATTTCAGTATGGAACCCGAAGATTTTGCAACTTATTAT
TGTTTTCCAGGGGAGCGTGTACCCATTCACTTTCGGGCAGGGGACAAAATTGACGGTACTGGGCGGTGGCGGTAGTGGGGGAGGCGG
TTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAGGTCACATTGAAGGAATCTGGCCCCGGCCTTGTTTCAGCCAGGACAGACCC
TTAGGCTCACCTGTGCCTTCAGTGGTTTTTCTCTTAGCACTAGCGGTATGGGGGTCGGCTGGATTCGGCAGCCTCCCGGCAAAGGT
CTTGAGTGGTTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATAC
CTCAAAAATCAAGTGTAAGTGTCAATGAATAGCCTTGACGCCGAGGATACGGCTGTATATTATGCGCGCGGATGGAACCTCTGGT
CTTACTACTTTGATTATTGGGGGAGGGGACTCTCGTCACGGTCTCGAGT

>Sequence ID 47: SI-63SV3 Amino Acid Sequence

ENVLTQSPASLSASPGERVITITCSASSSVSYMHVYQQKPGQAPKLIYDTSKLASGVPSRFSGSGSGNDHTLTISSEMPEDFATYY
CFQGSVYPFTFGQGTKITLVLGGGSGGGGSGGGGSGGGGSGVTLKESGPGLVQPGQTLRLTCAFSGFSLSSTSGMGVGVIRQPPGKG
LEWLAHIWDDDKRNPALKSRLTISKDTSKNQVYLQMNSLDAEDTAVYYCARMELWSYFDYWGGQGLVTVSS

>Sequence ID 48: SI-63SV3 Nucleic Acid Sequence

GAAATGTATTGACACAGAGCCCCGCCTCCCTCAGTGCCTCACCTGGGGAAAGGGTAACATCACTTGCTCTGCATCAAGCAGCGT
CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
CTAGCCGCTTCAGTGGTTCGGGCTCAGGCAACGATCACACCCTTACGATTTCAGTATGGAACCCGAAGATTTTGCAACTTATTAT
TGTTTTCCAGGGGAGCGTGTACCCATTCACTTTCGGGCAGGGGACAAAATTGACGGTACTGGGCGGTGGCGGTAGTGGGGGAGGCGG
TTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAGGTCACATTGAAGGAATCTGGCCCCGGCCTTGTTTCAGCCAGGACAGACCC
TTAGGCTCACCTGTGCCTTCAGTGGTTTTTCTCTTAGCACTAGCGGTATGGGGGTCGGCTGGATTCGGCAGCCTCCCGGCAAAGGT
CTTGAGTGGTTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATAC
CTCAAAAATCAAGTGTAAGTGTCAATGAATAGCCTTGACGCCGAGGATACGGCTGTATATTATGCGCGCGGATGGAACCTCTGGT
CTTACTACTTTGATTATTGGGGGAGGGGACTCTCGTCACGGTCTCGAGT

>Sequence ID 49: SI-63SV4 Amino Acid Sequence

ENVLTQSPASLSASPGERVITITCSASSSVSYMHVYQQKPGQAPKLIYDTSKLASGVPSRFSGSGSGNDHTLTISSEMPEDFATYY
CFQGSVYPFTFGQGTKITLVLGGGSGGGGSGGGGSGGGGSGVTLKESGPGLVQPGQTLRLTCAFSGFSLSSTSGMGVGVIRQPPGKG
LEWLAHIWDDDKRNPALKSRLTISKDTSKNQVYLQMNSLDAEDTAVYYCARMELWSYFDYWGGQGLVTVSS

>Sequence ID 50: SI-63SV4 Nucleic Acid Sequence

GAAATGTATTGACACAGAGCCCCGCCTCCCTCAGTGCCTCACCTGGGGAAAGGGTAACATCACTTGCTCTGCATCAAGCAGCGT
CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
CTAGCCGCTTCAGTGGTTCGGGCTCAGGCAACGATCACACCCTTACGATTTCAGTATGGAACCCGAAGATTTTGCAACTTATTAT
TGTTTTCCAGGGGAGCGTGTACCCATTCACTTTCGGGCAGGGGACAAAATTGACGGTACTGGGCGGTGGCGGTAGTGGGGGAGGCGG
TTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAGGTCACATTGAAGGAATCTGGCCCCGGCCTTGTTTCAGCCAGGACAGACCC
TTAGGCTCACCTGTGCCTTCAGTGGTTTTTCTCTTAGCACTAGCGGTATGGGGGTCGGCTGGATTCGGCAGCCTCCCGGCAAAGGT
CTTGAGTGGTTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATAC
CTCAAAAATCAAGTGTAAGTGTCAATGAATAGCCTTGACGCCGAGGATACGGCTGTATATTATGCGCGCGGATGGAACCTCTGGT
CTTACTACTTTGATTATTGGGGGAGGGGACTCTCGTCACGGTCTCGAGT

>Sequence ID 51: SI-63SV5 Amino Acid Sequence

EIVMTQSPSTLSASVGDRIITCSASSSVSYMHVYQQKPGKAPKLLIYDTSKLASGVPSRFSGSGSGAEFTLTISLQPDDEFATYY
CFQGSVYPFTFGQGTKITLVLGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCVFSGFSLSSTSGMGVGVVRQAPGKG
LEWVGHIWDDDKRNPALKSRFTISRDTSKNTVYLQMNSLRAEDTAVYYCARMELWSYFDYWQQGGLVTVSS

>Sequence ID 52: SI-63SV5 Nucleic Acid Sequence

GAAATAGTGATGACGAGTCACCTAGCACCTTAGTGCTTCTGTAGGAGACAGGGTTATAATTACCTGCAGTGCTAGTTCTCTCAGT
GTCATACATGCACTGGTATCAGCAGAAACCGGGAAAAGCTCAAAGCTGCTTATATACGACACGTCCAAATTGGCATCAGGTGTCC
CCAGTCGATTTAGTGGCTCTGGCTCAGGGGCTGAATTTACGCTCACAATCTCCAGCCTCAACAGATGACTTCGCCACATACTAC
TGTTTTTCAGGGCTCAGTGTATCCGTTTACTTTCGGCCAGGGGACAAAAGTTGACTGTACTTGGCGGTGGCGGTAGTGGGGGAGGCGG
TTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCAGAGGTCAACTTGTGGAAGCGGCGGCGGGTTGGTGCAACCTGGCGGTTAC
TTCGGCTCTCATGTGTGTTTCAGTGGTTTTTCCCTTAGCAACAAGCGGATGGGTGTCGGGTGGGTCCGCCAAGCGCTGCGCAAAGGT
CTGGAATGGGTTGGTCACATTTGGTGGGATGATGACAAAAGGTATAATCCCGCGCTGAAATCTAGATTTACTATTAGTCGGGATAC

GAGTAAGAACACGGTGTATCTGCAAAATGAACAGTCTCAGGGCAGAGGATACAGCGGTATATTATTGTGCTCGAATGGAGCTGTGGT
CTTACTATTTTGATTACTGGGGCCAGGGCACGTTGGTAACGGTCTCGAGT

>Sequence ID 53: SI-63SV6 Amino Acid Sequence

EIVMTQSPSTLSASVGRVITCSASSSVSYMHYQQKPKAPKLLIYDTSKLASGVPSRFSGSGSGAEFTLTISLQPDFFATYY
CFQGSVYPFTFGQGTGLTLVGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLRLSCSFSGFSLSTSGMGVGVWRQAPGKG
LEWVGHIWDDDKRYNPALKSRFTISRDTSKNTVYLQMNSLRAEDTAVYYCARMELWSYFDYWGQGLVTVSS

>Sequence ID 54: SI-63SV6 Nucleic Acid Sequence

GAAATAGTGATGACGACAGTACCTAGCACCCCTAGTGCTTCTGTAGGAGACAGGGTTATAATTACCTGCAGTGCTAGTTCCCTCAGT
GTCATACATGCAGTGGTATCAGCAGAAACCGGGAAAAGCTCCAAGCTGCTTATATACGACACGTCCAATTGGCATCAGGTGTCC
CCAGTCGATTAGTGGCTCTGGCTCAGGGGCTGAATTTACGCTCACAATCTCCAGCCTCCAACCAGATGACTTCGCCACATACTAC
TGTTTTTCAGGGCTCAGTGTATCCGTTTACTTTCCGCCAGGGGACAAAGTTGACTGTACTTGGCGGTGGCGGTAGTGGGGGAGGCGG
TTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCAGAGGTGCAACTTGTGGAAAGCGGCGGCGGGTGGTGCAACCTGGCGGTTAC
TTCGGCTCTCATGTAGTTCAGTGGTTTTTCCCTTAGCACAAAGCGGATGGGTGTGCGGTGGGTCCGCCAAGCGCTGGCAAAGGT
CTGGAATGGGTTGGTCACATTTGGTGGGATGATGACAAAGGTATAATCCCGCGCTGAAATCTAGATTTACTATTAGTCGGGATAC
GAGTAAGAACACGGTGTATCTGCAAAATGAACAGTCTCAGGGCAGAGGATACAGCGGTATATTATTGTGCTCGAATGGAGCTGTGGT
CTTACTATTTTGATTACTGGGGCCAGGGCACGTTGGTAACGGTCTCGAGT

>Sequence ID 55: SI-63SF1 (H1 ScFv-monoFc) Amino Acid Sequence

ENVLTQSPASLSASPGERVITCSASSSVSYMHYQQKPGQAPKLIYDTSKLASGVPSRFSGSGSGNDHTLTISSEMPEDFATYY
CFQGSVYPFTFGQGTGLEIKGGGSGGGGSGGGGSGGGGSGVTLKESGPGLVQPGQTLRLTCAFSGFSLSSTSGMGVGVWRQPPGKG
LEWLAHIWDDDKRYNPALKSRFTISKDTSKNQVYLQMNSLDAEDTAVYYCARMELWSYFDYWGQGLVTVSS
GGSSGSGSGSTGLVPRGSTSSSGTGTSAGTFVAGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
KPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLRCHVKGFYPS
DIAVEWESNGQPENNYKTTKPVLDSDGSFFLYSTLTVDKSRWQQGNVFCFVLSVLEALHNHYTQKSLSLSPGKSGSLNDIFEAQKIEWHE

>Sequence ID 56: SI-63SF1 (H1 ScFv-monoFc) Nucleotide Sequence

GAAATGTATTGACACAGAGCCCCGCCTCCCTCAGTGCCTCACCTGGGGAAAGGGTAACATCACTTGCTCTGCATCAAGCAGCGT
CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
CTAGCCGCTTCAGTGGTTCGGGCTCAGGCAACGATCACACCCCTTACGATTTCCAGTATGGAACCCGAAGATTTTGCAACTATTAT
TGTTTCCAGGGGAGCGTGATCCCATTCATTTCCGGGCGAGGGGACAAAATTTGGAGATAAAGGGCGGTGGCGGTAGTGGGGGAGGCGG
TTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAGGTCACATTGAAGGAATCTGGCCCCGGCCTTGTTTCAGCCAGGACAGACCC
TTAGGCTCACCTGTGCTTCAGTGGTTTTTCTCTTAGCAGCTAGCGGTATGGGGTTCGGCTGGATTCCGGCAGCCTCCCGGCAAGGT
CTTGAGTGGTTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATAC
CTCAAAAATCAAGTGACTTGCAAAATGAATAGCCTTGACGCGGAGGATACGGCTGTATATTATGCGCGCGGATGGAACCTCTGGT
CTTACTACTTTGATTATTGGGGGCGAGGGGACTCTCGTCACGGTCTCGAGT
GGGGGATCCTCTGGAAGTGGCTCCGGCAGCACTGGGCTCGTACCAAGGGGGTCCACATCCAGTAGCGGTACTGGCACATCCGCGGG
AACCCTCGCTGGACCGTCACTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACAT
GCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA
AAGCCGCGGAGGAGCAGTACGCTAGCACGTACCGTGTGGTCAAGCTCCTCACCCTCTGCACACGAGTGGCTGAATGGCAAGGA
GTACAAGTGCAAGGTCTCCACAAAAGCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGAGACACAC
AGGTGTACACCTGCCCCATCCCGGATGAGCTGACCAAGAACCAGGTGAGCTGAGATGCCACGTCAAAGGCTTCTATCCCAGC
GACATCGCCGTGGAGTGGGAGAGCAATGGGCGAGCGGAGAACAACTACAAGACCACGAAGCCCGTGGTGGACTCCGACGGCTCCTT
CTTCTCTACAGCACCTCACCCTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGCTCCATGAGGCTCTGC
ACAACCACTACACAGAAAGACCTCTCCCTGTCTCCGGGCAAGGTTGAGGCTGAACGATATTTTTGAAGCGCAGAAAATTGAA
TGGCATGAA

>Sequence ID 57: SI-63SF2 (H2 ScFv-monoFc) Amino Acid Sequence

ENVLTQSPASLSASPGERVITCSASSSVSYMHYQQKPGQAPKLIYDTSKLASGVPSRFSGSGSGNDHTLTISSEMPEDFATYY
CFQGSVYPFTFGQGTKITILGGGSGGGGSGGGGSGGGGSGVTLKESGPGLVQPGQTLRLTCAFSGFSLSSTSGMGVGVWRQPPGKG
LEWLAHIWDDDKRYNPALKSRFTISKDTSKNQVYLQMNSLDAEDTAVYYCARMELWSYFDYWGQGLVTVSSGSSGSGSGSTG
LVPRGSTSSSGTGTSAGTFVAGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
KPREEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLRCHVKGFYPS
DIAVEWESNGQPENNYKTTKPVLDSDGSFFLYSTLTVDKSRWQQGNVFCFVLSVLEALHNHYTQKSLSLSPGKSGSLNDIFEAQKIEWHE

>Sequence ID 58: SI-63SF2 (H2 ScFv-monoFc) Nucleotide sequence

GAAATGTATTGACACAGAGCCCCGCCTCCCTCAGTGCCTCACCTGGGGAAAGGGTAACATCACTTGCTCTGCATCAAGCAGCGT
CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
CTAGCCGCTTCAGTGGTTCGGGCTCAGGCAACGATCACACCCCTTACGATTTCCAGTATGGAACCCGAAGATTTTGCAACTATTAT
TGTTTCCAGGGGAGCGTGATCCCATTCATTTCCGGGCGAGGGGACAAAATTTACGATACTGGCGGTGGCGGTAGTGGGGGAGGCGG
TTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAGGTCACATTTGAAGGAATCTGGCCCCGGCCTTGTTTCAGCCAGGACAGACCC

TTAGGCTCACCTGTGCCTTCAGTGGTTTTTCTCTTAGCACTAGCGGTATGGGGTTCGGCTGGATTCCGGCAGCCTCCCGGCAAAGGT
 CTTGAGTGGTTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATAC
 CTCAAAAAATCAAGTGTACTTGCAAATGAATAGCCTTGACGCCGAGGATACGGCTGTATATTATTGCGCGCGGATGGAACCTCTGGT
 CTTACTACTTTGATTATTGGGGGACGGGGACTCTCGTCACGGTCTCGAGT
 GGGGATCCTCTGGAAGTGGCTCCGGCAGCACTGGGCTCGTACCAAGGGGGTCCACATCCAGTAGCGGTACTGGCACATCCCGGGG
 AACCCCGTCTGCTGACCGTCACTCTTCTCTTCCCCCAAACCCAGGACACCTCATGATCTCCCGGACCCCTGAGGTACAT
 GCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCTGGAGGTGCATAATGCCAAGACA
 AAGCCGCGGGAGGAGCAGTACGTAGCACGTACCGTGTGGTCAGCGTCTCACCGTCTGCACCCAGGACTGGCTGAATGGCAAGGA
 GTACAAGTGAAGGTCTCCAAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCAC
 AGGTGTACACCTGCCCCCATCCCGGGATGAGCTGACCAAGAACAGGTGAGCTGAGATGCCACGTCAAAGGCTTCTATCCAGC
 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGAAGCCCGTCTGGACTCGGACGGCTCTT
 CTTCTCTACAGCACCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGCTCCATGAGGCTCTGC
 ACAACCACTACACAGAAAGACCTCTCCCTGTCTCCGGGCAAAGGTTCAAGCCTGAACGATATTTTTGAAGCGCAGAAATTGAA
 TGGCATGAA

>Sequence ID 59: SI-63SF4 (H3 ScFv-monoFc) Amino Acid Sequence

ENVLTQSPASLSASPERVITITCSASSSVSYMHWYQQKPKQAPKLIYDTSKLASGVPSRFSGSGSGNDHTLTISSEMPEDFATYY
 CFQGSVYPFTFGQGTKLTLVGGGSGGGGSGGGGSGGGGSGVTLKESGPGLVQPGQTLRLTCAFSGFSLSTSGMGVWIRQPPGKG
 LEWLAIHWDDDKRYNPALKSRLTISKDTSKNQVYLQMNSLDAEDTAVYYCARMELWSYFDYWQGTLLVTVSSGGSSGSGSGTG
 LVPRGSTSSSGTGTSAITPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYR
 VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKQPREPQVYTLPPSRDELTKNQVSLRCHVKGFYPSDIAVEWESNGQP
 ENNYKTTKPVLDSDGSFFLYSTLTVDKSRWQQGNVFCFVLEALHNHYTQKSLSLSPGKSGSLNDIFEAQKIEWHE

>Sequence ID 60: SI-63SF4 (H3 ScFv-monoFc) Nucleotide Sequence

GAAAATGTATTGACACAGAGCCCCGCTCCCTCAGTGCCTCACCTGGGGAAAGGGTAACATCACTTGCTCTGCATCAAGCAGCGT
 CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
 CTAGCCGCTTCAGTGGTTCGGCTCAGGCAACGATCACACCTTACGATTTCAGTATGGAACCCGAAGATTTTGCACCTTATTAT
 TGTTCAGGGGAGCGTGTACCCATTCACTTTCCGGGACGGGACAAAACCTTACGGTACTGGGCGGTGGCGGTAGTGGGGAGGCGG
 TTCTGGCGGCGGAGGTCGGCGGTGGAGGATCACAGGTACATTTGAAGGAATCTGGCCCCGGCCTTGTTCAGCCAGGACAGAGCC
 TTAGGCTCACCTGTGCCTTCAGTGGTTTTTCTCTTAGCACTAGCGGTATGGGGTTCGGCTGGATTCCGGCAGCCTCCCGGCAAAGGT
 CTTGAGTGGTTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATAC
 CTCAAAAAATCAAGTGTACTTGCAAATGAATAGCCTTGACGCCGAGGATACGGCTGTATATTATTGCGCGCGGATGGAACCTCTGGT
 CTTACTACTTTGATTATTGGGGGACGGGGACTCTCGTCACGGTCTCGAGT
 GGGGATCCTCTGGAAGTGGCTCCGGCAGCACTGGGCTCGTACCAAGGGGGTCCACATCCAGTAGCGGTACTGGCACATCCCGGGG
 AACCCCGTCTGCTGACCGTCACTCTTCTCTTCCCCCAAACCCAGGACACCTCATGATCTCCCGGACCCCTGAGGTACAT
 GCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCTGGAGGTGCATAATGCCAAGACA
 AAGCCGCGGGAGGAGCAGTACGTAGCACGTACCGTGTGGTCAGCGTCTCACCGTCTGCACCCAGGACTGGCTGAATGGCAAGGA
 GTACAAGTGAAGGTCTCCAAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCAC
 AGGTGTACACCTGCCCCCATCCCGGGATGAGCTGACCAAGAACAGGTGAGCTGAGATGCCACGTCAAAGGCTTCTATCCAGC
 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGAAGCCCGTCTGGACTCCGACGGCTCTT
 CTTCTCTACAGCACCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGCTCCATGAGGCTCTGC
 ACAACCACTACACAGAAAGACCTCTCCCTGTCTCCGGGCAAAGGTTCAAGCCTGAACGATATTTTTGAAGCGCAGAAATTGAA
 TGGCATGAA

>Sequence ID 61: SI-63SF5 (H4 ScFv-monoFc) Amino Acid Sequence

ENVLTQSPASLSASPERVITITCSASSSVSYMHWYQQKPKQAPKLIYDTSKLASGVPSRFSGSGSGNDHTLTISSEMPEDFATYY
 CFQGSVYPFTFGQGTKVTTLVGGGSGGGGSGGGGSGGGGSGVTLKESGPGLVQPGQTLRLTCAFSGFSLSTSGMGVWIRQPPGKG
 LEWLAIHWDDDKRYNPALKSRLTISKDTSKNQVYLQMNSLDAEDTAVYYCARMELWSYFDYWQGTLLVTVSSGGSSGSGSGTG
 LVPRGSTSSSGTGTSAITPVAGPSVFLFPPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYR
 VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIKAKQPREPQVYTLPPSRDELTKNQVSLRCHVKGFYPSDIAVEWESNGQP
 ENNYKTTKPVLDSDGSFFLYSTLTVDKSRWQQGNVFCFVLEALHNHYTQKSLSLSPGKSGSLNDIFEAQKIEWHE

>Sequence ID 62: SI-63SF5 (H4 ScFv-monoFc) Nucleotide Sequence

GAAAATGTATTGACACAGAGCCCCGCTCCCTCAGTGCCTCACCTGGGGAAAGGGTAACATCACTTGCTCTGCATCAAGCAGCGT
 CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
 CTAGCCGCTTCAGTGGTTCGGCTCAGGCAACGATCACACCTTACGATTTCAGTATGGAACCCGAAGATTTTGCACCTTATTAT
 TGTTCAGGGGAGCGTGTACCCATTCACTTTCCGGGACGGGACAAAAGTTACGGTACTGGGCGGTGGCGGTAGTGGGGAGGCGG
 TTCTGGCGGCGGAGGTCGGCGGTGGAGGATCACAGGTACATTTGAAGGAATCTGGCCCCGGCCTTGTTCAGCCAGGACAGAGCC
 TTAGGCTCACCTGTGCCTTCAGTGGTTTTTCTCTTAGCACTAGCGGTATGGGGTTCGGCTGGATTCCGGCAGCCTCCCGGCAAAGGT
 CTTGAGTGGTTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATAC
 CTCAAAAAATCAAGTGTACTTGCAAATGAATAGCCTTGACGCCGAGGATACGGCTGTATATTATTGCGCGCGGATGGAACCTCTGGT
 CTTACTACTTTGATTATTGGGGGACGGGGACTCTCGTCACGGTCTCGAGT

GGGGATCCTCTGGAAGTGGCTCCGGCAGCACTGGGCTCGTACCAAGGGGGTCCACATCCAGTAGCGGTACTGGCACATCCGCGGG
 AACCCCGTCTGACCGTCACTCTTCTTCCCCAAAACCAAGGACACCTCATGATCTCCCGACCCCTGAGGTACAT
 GCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA
 AAGCCGCGGGAGGAGCAGTACGCTAGCACGTACCGTGTGGTCAGCGTCTCACCGTCTGCACCGAGGACTGGCTGAATGGCAAGGA
 GTACAAGTGAAGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCAC
 AGGTGTACACCTGCCCCCATCCCGGGATGAGCTGACCAAGAACAGGTGAGCTGAGATGCCACGTCAAAGGCTTCTATCCAGC
 GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCAGAAAGCCCGTGGTGGACTCCGACGCTCCTT
 CTTCTCTACAGCACCTCACCGTGGACAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTCTCATGAGGCTCTGC
 ACAACCACTACACAGAAAGACCTCTCCCTGTCTCCGGCAAAGGTTGAGGCTGAACGATATTTTTGAAGCGCAGAAATTGAA
 TGGCATGAA

>Sequence ID 63: SI-63SF6 (H5 ScFv-monoFc) Amino Acid Sequence

EIVMTQSPSTLSASVGDRVIITCSASSSVSYMHVYQQKPKGKAPKLLIYDTSKLASGVPSTRFSGSGSGAEFTLTISLQPDFFATYY
 CFQGSVYPTFFGQGTGLTLVGGGGSGGGSGGGSGGGSEVQLVESGGGLVQPGGSLRLSCVFSFGFSLSTSGMGVGVWRQAPGKG
 LEWVGHIIWDDDKRNPALKSRFTISRDTSKNTVYLQMNLAEDTAVYICARMELWSYFDYWGQGLTVTVSSGSGSGSGSTGL
 VPRGSTSSSGTGTSAGTPVAGPSVFLFPPKPKDLMISRTEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRV
 VSVLTVLHQDLNNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSRDELTKNQVSLRCHVKGFYPSDIAVEWESNGQPE
 NNYKTKPKVLDSGDSFFLYSTLTVDKSRWQQGNVFSCSVLHEALHNHYTQKLSLSLSPGKSGSLNDI FEAQKIEWHE

>Sequence ID 64: SI-63SF6 (H5 ScFv-monoFc) Nucleotide Sequence

GAAATAGTGATGACGAGTCACCTAGCACCTTAGTGCTTCTGTAGGAGACAGGGTTATAATTACCTGCAGTGCTAGTTCTCTCAGT
 GTCATACATGCACTGGTATCAGCAGAAACCGGGAAAAGCTCCAAAGCTGCTTATATACGACACGTCCAAATTGGCATCAGGTGTCC
 CCAGTCGATTAGTGGCTCTGGCTCAGGGGCTGAATTTACGCTCACAATCTCCAGCCTCCAACACAGATGACTTCGCCACATACTAC
 TGTTTTCAGGGCTCAGTGTATCCGTTTACTTTCCGCCAGGGGACAAAGTTGACTGTACTTGGCGGTGGCGGTAGTGGGGGAGGCGG
 TTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCAGAGGTGCAACTTGTGGAAAGCGGCGCGGGTGGTGCAACTGGCGGTTTAC
 TTCCGCTCTCATGTGTGTTTCACTGGTTTTTCCCTTAGCACAAGCGGGATGGGTGTCGGGTGGTCCGCCAAGCGCTGGCAAAGGT
 CTGGAATGGGTGGTGCACATTTGGTGGGATGATGACAAAAGGTATAATCCCGCGCTGAAATCTAGATTACTATTAGTCGGGATAC
 GAGTAAGAACACCGGTGTATCTGCAAATGAACAGTCTCAGGGCAGAGGATACAGCGGTATATTATTGTGCTCGAATGGAGCTGTGGT
 CTTACTATTTTGTATTACTGGGGCCAGGGCAGGTTGGTAACGGTCTCGAGTGGATCCTCTGGAAGTGGCTCCGGCAGCACTGGGCTC
 GTACCAAGGGGGTCCACATCCAGTAGCGGTACTGGCACATCCGCGGGAACCCCGTCTGCTGGACCGTCACTTCTCTTCCCCC
 AAAACCCAAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCAGAACCCCTGAGGTCA
 AGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACGCTAGCACGTACCGTGTG
 GTGACGCTCTCACCGTCTGACACAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCC
 CATCGAGAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCA
 AGAACCAGGTGAGCTGAGATGCCACGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG
 AACAACACAGACCGAAGCCCGTCTGGACTCCGACGGCTCCTTCTCTCTACAGCACCTCACCGTGGACAAGAGCAGGTG
 GCAGCAGGGGAACGCTTCTCATGCTCCGTGCTCCATGAGGCTCTGCAACCACTACACAGAAAGACCTCTCCCTGTCTCCGG
 GCAAAGGTTACGGCTGAACGATATTTTTGAAGCGCAGAAATTGAATGGCATGAA

>Sequence ID 65: SI-63SF7 (H6 ScFv-monoFc) Amino Acid Sequence

EIVMTQSPSTLSASVGDRVIITCSASSSVSYMHVYQQKPKGKAPKLLIYDTSKLASGVPSTRFSGSGSGAEFTLTISLQPDFFATYY
 CFQGSVYPTFFGQGTGLTLVGGGGSGGGSGGGSGGGSEVQLVESGGGLVQPGGSLRLSCSFSFGFSLSTSGMGVGVWRQAPGKG
 LEWVGHIIWDDDKRNPALKSRFTISRDTSKNTVYLQMNLAEDTAVYICARMELWSYFDYWGQGLTVTVSSGSGSGSGSTGL
 VPRGSTSSSGTGTSAGTPVAGPSVFLFPPKPKDLMISRTEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYASTYRV
 VSVLTVLHQDLNNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSRDELTKNQVSLRCHVKGFYPSDIAVEWESNGQPE
 NNYKTKPKVLDSGDSFFLYSTLTVDKSRWQQGNVFSCSVLHEALHNHYTQKLSLSLSPGKSGSLNDI FEAQKIEWHE

>Sequence ID 66: SI-63SF7 (H6 ScFv-monoFc) Nucleotide Sequence

GAAATAGTGATGACGAGTCACCTAGCACCTTAGTGCTTCTGTAGGAGACAGGGTTATAATTACCTGCAGTGCTAGTTCTCTCAGT
 GTCATACATGCACTGGTATCAGCAGAAACCGGGAAAAGCTCCAAAGCTGCTTATATACGACACGTCCAAATTGGCATCAGGTGTCC
 CCAGTCGATTAGTGGCTCTGGCTCAGGGGCTGAATTTACGCTCACAATCTCCAGCCTCCAACACAGATGACTTCGCCACATACTAC
 TGTTTTCAGGGCTCAGTGTATCCGTTTACTTTCCGCCAGGGGACAAAGTTGACTGTACTTGGCGGTGGCGGTAGTGGGGGAGGCGG
 TTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCAGAGGTGCAACTTGTGGAAAGCGGCGCGGGTGGTGCAACTGGCGGTTTAC
 TTCCGCTCTCATGTAGCTTCACTGGTTTTTCCCTTAGCACAAGCGGGATGGGTGTCGGGTGGTCCGCCAAGCGCTGGCAAAGGT
 CTGGAATGGGTGGTGCACATTTGGTGGGATGATGACAAAAGGTATAATCCCGCGCTGAAATCTAGATTACTATTAGTCGGGATAC
 GAGTAAGAACACCGGTGTATCTGCAAATGAACAGTCTCAGGGCAGAGGATACAGCGGTATATTATTGTGCTCGAATGGAGCTGTGGT
 CTTACTATTTTGTATTACTGGGGCCAGGGCAGGTTGGTAACGGTCTCGAGTGGATCCTCTGGAAGTGGCTCCGGCAGCACTGGGCTC
 GTACCAAGGGGGTCCACATCCAGTAGCGGTACTGGCACATCCGCGGGAACCCCGTCTGCTGGACCGTCACTTCTCTTCCCCC
 AAAACCCAAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCAGAACCCCTGAGGTCA
 AGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACGCTAGCACGTACCGTGTG
 GTGACGCTCTCACCGTCTGACACAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCC
 CATCGAGAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCA
 AGAACCAGGTGAGCTGAGATGCCACGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG

AACAACACAAAGACCAGAACGCCGTGCTGGACTCCGACGGCTCCTTCTTCTCTACAGCACCCCTACCGTGGACAAGAGCAGGTG
GCAGCAGGGGAACGCTTCTCATGCTCCGTGCTCCATGAGGCTCGCACAACCACTACACACAGAAGAGCCTCTCCCTGTCTCCGG
GCAAAGGTTTCAGGCTGAACGATATTTTTGAAGCGCAGAAAATTGAATGGCATGAA

>Sequence ID 67: SI-77H3 Heavy Chain Amino Acid Sequence

ENVLTQSPASLSASGERVITITCSASSSVSMHWYQQKPKQAPKLIWYDTSKLASGVPSRFSGSGSGNDHTLTITSSMEPEDFATYY
CFQGSVYPTFTFGQGTQKVTVLGGGSGGGGSGGGGSGGGGSGVTLKESGPGLVQPGQTLTSLTCAFSGFSLSTSGMGVWIRQPPGKG
LEWLAIHWDDDKRNPALKSRLTISKDTSKNQVYLQMNSLDAEDTAVYYCARMELWSYFDYWGQGTLLVTVSSGGGSGGGGSGV
QLQSGPGLVKPSSETLSITCTVSGFSLTNYGVHWIRQAPGKCLEWLGVIWSGGNTDYNTPFTSRFTITKDNSKNQVYFKLRSVRAD
DTAIYYCARALTYDYEFAYWGQGTLLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
VLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRTPE
VTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTI SKAKGQPR
EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSGSEFFLYSKLTVDKSRWQQGNVFSVCSVMHE
ALHNHYTQKSLSLSPGSGGGSGGGGSEVQLLESGGGLVPGGSLRLSCAASGFSFSGYDMCWVRQAPGKGLEWIAICIAAGSAGIT
YDANWAKGRFTISRNSTKYLQMNSLRAEDTAVYYCARSAFTGCDYAMDLDWGQGTLLVTVSSGGGSGGGGSGGGGSGGGGSDIQM
TQSPSTLSASVGDRTITCQASQSISSHLNHWYQQKPKAPKLLIYKASTLASGVPSRFSGSGSGTEFTLTISLQPDFFATYYCQQ
GYSWGNVDNVFGGKVEIKGGGSGGGGSGGRSLVESGGGLVQPGGSLRLSCTASGFTISSYHMQWVRQAPGKLEYIGTISGGN
VYYASSARGRFTISRPSKNTVDLQMNSLRAEDTAVYYCARDGYSDFPMWGQGTLLVTVSSGGGSGGGGSGGGGSGGGGSDVMTQ
SPSSVSASVGDRTITCQASQNIITYLSWYQQKPKAPKLLIYAAANLASGVPSRFSGSGSGTDFTLTISDLEPGDAATYYCQSTY
LGTDYVGGAFGGGTKEIK

>Sequence ID 68: SI-77H3 Heavy Chain Nucleic Acid Sequence

GAAATGTATTGACACAGAGCCCCGCTCCCTCAGTGCCTCACCTGGGGAAGGTAACATCACTTGTCTGCATCAAGCAGCGT
CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
CTAGCGCTTCAGTGGTTCGGGCTCAGGCAACGATCACACCCTTACGATTTCAGTATGGAACCGAAGATTTTGCAACTTATTAT
TGTTTCAGGGGAGCGGTACCCATTCACTTTCGGGCGAGGGACAAAAGTGACCGTCTAGGCGGTGGCGGTAGTGGGGGAGGCGG
TTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAGTACATGAGTGAAGGAATCTGGCCCCGGCTTGTTCAGCCAGGACAGACCT
TTAGCCTCACCTGTGCCTCAGTGGTTTTTCTCTTAGCACTAGCGGTATGGGGGTGGCTGGATTCCGGCAGCCTCCCGGCAAGGT
CTTGAGTGGTTCGCTACATTTGGTGGGACGACGACAAACGGTATAATCCTGCCTTGAAAAGTGGCTGACCATAGTAAAGGATAC
CTCAAAAAATCAAGTGTACTTGCAATGAATAGCCTTGACGCCGAGGATACGGCTGTATATTATTCGCTCGGATGGAACCTCTGGT
GACACTGCGATCTACTATTGTGGGGGCGAGGGGACTCTCGTCACGGTTCGAGTGGCGGTGGAGGGTCCGGCGGTGGATCACAAAGTA
CAGTTGCAGCAATCCGGTCCCGGTCTCGTCAAACCGAGTGAGACGCTTAGTATAACGTGTACTGTTTCAGGCTTTAGCCTTACGAA
CTATGGAGTTCAGTGGATTCCGGCAGGCACCCGGCAAAATGTTTGAATGGCTGGGTGTTATTTGGTCAGTGGAAATACAGACTATA
ACACCCCTTTACAAGTCCGGTTACAATTACGAAAGATAATCCAAAAATCAAGTTTATTTCAAGTTGAGATCCGTCCGCGCGGAC
GACACTGCGATCTACTATTGTGGGGGCGAGGGGACTCTCGTACGATTTACGATTACGAATTTGCGTATTGGGGGCAAGGGACTCTTTGAACAGT
CTCCAGTGTAGCACCAAGGGCCCATCGGTCTTCCCTGGCACCTCTCCAAGAGCACCTCTGGGGGACAGCGGCCCTGGGCT
GCCTGGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGGAACCTCAGCGGCCCTGACACGCGCGTGCACACCTTCCCGGCT
GTCTTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAA
CGTGAATCACAGCCACGACCAACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAACTCACAGATGCCACCGTGGC
CAGCACCTGAAGCCGCGGGGACCGTCACTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAG
GTACATGCGTGGTGGTGGAGCTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGGTGGAGGTGCATAATGC
CAAGACAAAGCCGCGGGGAGGAGTACAACAGCAGTACCGTGTGGTCAAGCTCTCACCGTCTGCACAGGACTGGCTGAATG
GCAAGGAGTACAAGTCCGCGGTCTCCAAACAAAGCCCTCCAGCCCCATCGAGAAAAACCATCTCCAAAGCCAAAGGCCCAAGGCA
GAACCACAGGTGTACACCTGCCCCATCCCGGATGAGCTGACCAAGAACAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTA
TCCCAGCGACATCGCGTGGAGTGGGAGAGCAATGGGACGCCGAGAACAACTACAAGACCACGCTCCCGTGTGAGTCCGAGC
GCTCCTTCTTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAG
GCTCTGCAACAACCACTACACGACAGAGAGCCTCTCCCTGTCTCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGAGGTGCA
GCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCTCCTTCAGTAGCG
GGTACGACATGTGCTGGGTCCGCCAGGCTCCAGGAAGGGGCTGGAGTGGATCGCATGCATTGCTGCTGGTAGTGTGTTACTACT
TACGACGCGAAGTGGGCGAAAGGCCGCTTACCATCTCCAGAGACAATCCAAAGAACACGCTGTATCTGCAATGAACAGCCTGAG
AGCCGAGGACACGGCCGTATATTACTGTGCGAGATCGGGGTTTTGCTTCGACTACGCCATGGACCTCTGGGGCCAGGGAACCTGG
TCACCGTGTGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCGGCGGTGGCGGTCCGGTGGAGGCGGCTCTGACATCCAGATG
ACCCAGTCTCCTTCCACCTGTCTGCATCTGTAGGAGACAGAGTACCATCACTTGCCAGGCCAGTCAGAGCATTAGTCCCACCT
AACTGGTATCAGCAGAAACAGGGAAGCCCCCTAAGCTCCTGATCTATAAGGCATCCACTCTGGCATCTGGGGTCCCATCAAGGT
TCAGCGGAGTGGATCTGGGACAGAATTTACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGCCAACAG
GGTTATAGTTGGGGTAATGTTGATAATGTTTTCGCGGAGGACCAAGGTGGAGATCAAAGGCGGTGGAGGGTCCGGCGGTGGTGG
CTCCGACGGTCTGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGTCCCTGAGACTCTCCTGACTGCCTCTGGATTCA
CCATCAGTAGCTACACATGCAAGTGGGTCGGCAGGCTCCAGGAAGGGGTGGAGTACATCGGAACCATAGTAGTGGTGGTAAT
GTATACTACGCAAGCTCCGCTAGAGGCAAGTTACCATCTCCAGACCCCTCGTCCAAGAACACGGTGGATCTTCAAATGAACAGCCT
GAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACTCTGGTTATAGTGATCCTATGTGGGGCCAGGGAACCTGGTACCG
TCTCTTCAGCGGTGGCGGTAGTGGGGGAGGCGGTTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCAGACGTTGTGATGACCCAG
TCTCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTACCATCACCTGTAGGCCAGTCAGAACATTAGCACTTACTTATCCTG
GTATCAGCAGAAACAGGGAAGCCCTAAGCTCCTGATCTATGCTGACGCCAATCTGGCATCTGGGGTCCCATCAAGGTTACGCG

GCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCGACCTGGAGCCTGGCGATGCTGCAACTTACTATTGTAGTCTACCTAT
CTTGGTACTGATTATGTTGGCGGTGCTTTTCGGCGGAGGGACCAAGGTGGAGATCAAATGA

>Sequence ID 69: SI-77H3 Light Chain Amino Acid Sequence
EIVMTQSPSTLSASVGRVITTCQASESISWLAHYQQKPKGKAPKLLIYEASKLASGVPSRFSGSGSGAEFTLTISLQPDFFATY
YCQGYFYFISRTYVNSFGQTKLTVLGGGSGGGGSGGGGSGGGGSEVQLVESGGGLVQPGGSLSLSCAASGFTISTNAMSWSVRQA
PGKLEWVGVIITGRDITYYASWAKGRFTISRDTSKNTVYLQMNSLRAEDTAVYYCARDGSSAITSNNIWGGQGLTVTVSSGGGSGG
GGSEIVLTQSPSTLSVSPGERATFSCRASQSIGTNIHWYQQKPKGKPPRLLIKYASESISGIPDRFSGSGSGTEFTLTISLQSED
FAVYYCQNNNWPFTFGCGTKLTVLRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS
KDSYSLSSLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGECGGGSGGGGSGGGGSSQALTQPASVSGSPGQSITISCTGT
SSDVGGYNFVSWYQQHPGKAPKLMYDVSDRPSGVSDRFSGSKSNTASLIISGLQADDEADYYCSYSGSSSTHVI FGGGTGKTVL
GGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGG
RFTISRDDAKNSLYLQMNSLRAEDTAVYYCARDRGVGYFDLWGRGLTVTVSS

>Sequence ID 70: SI-77H3 Light Chain Nucleotide Sequence
GAAATCGTTATGACGCAGAGTCCCTCCACGCTCTCCGCTAGTGTGCGGGATCGCGTCATTATCACATGCCAGGCCCTCCGAGTCAAT
CAGCAGCTGGCTTGCATGGTATCAACAGAAAGCGGGAAGCTCCTAAATTGCTGATCTATGAAGCGTCAAAATGGCGCTCTGGTG
TCCCCTAGTGTCTCCGGCTCTGGGTCTGGTGCGGAATTTACTTTGACAATCTCCAGTCTTCAACCAGACGATTTTCGTACCTAC
TAGCCGCGATACTTCAAAGAATACCGTTTACCTTCAAATGAATAGCTTGGGGCGGAAGACACAGCTGTGTATTACTGCGCGAGGG
AGGCAGTGGTGGCGGGGCGAGCGAGGTGGTGGTTCAGGGGGTGGTGGGAGCGAAGTCCAATTGGTAGAAAGTGGCGGTGGTCTGG
TGCAACCTGGTGGATCTCTTAGCCTCTCATGCGCGCTAGTGGCTTTACTATTTCAACTAATGCGATGAGCTGGGTTCGCCAGGCC
CCCGGCAAAGGACTTGAGTGGGTCTCGGCTCATCACCGGCGAGGACATTACATACTATGCGAGTTGGGCAAAGGGCAGGTTACGAT
TAGCCGCGATACTTCAAAGAATACCGTTTACCTTCAAATGAATAGCTTGGGGCGGAAGACACAGCTGTGTATTACTGCGCGAGGG
ATGGAGGTAGTTCGCCATAACTTCCAACAACATATGGGACAAAGGCAGCTGGTACTGTCTCGAGTGGCGGTGGAGGGTCCGGC
GGTGGTGGATCAGAAATCGCTTACACAATCTCTAGCACACTGAGTGTGAGCCCCGCGCAACGCGGACTTTCTCTGCGAGGGC
AAGTCAATCCATAGGACTAATATACATTGGTATCAACAAAAGCCAGGTAAACCACCCAGGCTTTTGATTAAGTATGCAAGTGAGT
CTATTTCCGCTATCCCTGACCGCTTCTCTGGATCAGGCTGAGGACAGAGTTCACTACCATATCTAGTGTGCAATCAGAGGAC
TTCCGCGTGTATTACTGCCAACAGAATAATAACTGGCCGACTACCTTCGGATGCGGTACAAAGCTGACCGTTTTACGTACGGTGGC
TGCAACATCTGTCTCATCTTCCCGCATCTGATGAGCAGTTGAAATCTGGAATGCGCTCTGTTGTGTGCTGCTGTAATAACTTCT
ATCCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGC
AAGGACAGCACTACAGCCTCAGCAGCACCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCTTCCGAAAGTAC
CCATCAGGGCTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTGGCGGTGGCGGTAGCGGTGGCGGCGGAAGTGGTG
GCGGAGGATCCAGTCTGCCCTGACTCAGCTGCTCCGTGTCTGGGTCTCCTGGACAGTCTGATCACCATCTCCTGCACTGGAACC
AGCAGTGACGTTGGTGGTTATACTTTGTCTCCTGGTACCAACACCCAGGCAAAGCCCCAACTCATGATCTATGATGTCAG
TGATCGCGCTCAGGGGTGCTGATCGCTTCTCCGCTCCAAGTCTGGCAACACGGCCTCCCTGATCATCTGTGCAATCAGAGGCTG
ACGACGAGGCTGATTATTACTGCAGCTCATATGGGAGCAGCAGCTCATGTGATTTTCGGCGGAGGGACCAAGGTGACCGTCTTA
GGTGGAGGCGGTTCAGGCGGAGGTGGTTCGGCGGTGGCGGCTCCGCTGAGGCGGCTCTCAGGTGCAATTGCAAGGAGTGGGGGG
AGGCCTGGTCAAGCTGGAGGGTCCCTGAGTCTCTCCTGTGAGCCTCTGGATTACCTTTAGTAGTTATTGGATGAGCTGGGTCC
GCCGCTCCAGGGAAGGGCTGGAGTGGGTGGCCAAACATTAACCGCGAGTGGAAAGTGGAGTTACTATGTGGACTCTGTGAAGGAC
CGATTACCATCTCCAGAGACGACGCCAAGAACTCACTGTATCTGCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTA
CTGTGCGAGAGATCGTGGGTGGGCTACTTCGATCTCTGGGCGCTGGCACCTGGTACCGCTCTCTAGC

>Sequence ID 71: SI-77H6 Heavy Chain Amino Acid Sequence
EIVLTQSPSTLSVSPGERATFSCRASQSIGTNIHWYQQKPKGKPPRLLIKYASESISGIPDRFSGSGSGTEFTLTISLQSEDFAVY
YCQNNNWPFTFGPGTKLTVLGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGGSGGGG
EWLGVWISGNTDYNTPFTSRFTITKDNSKNQVYFKLSVRADDTAIYYCARALTYDYEFAYWQGTGLTVTVSSGGGSGGGGSGV
TLKESGPGLVQPGQTLRLTCAFSGFSLSTSGMGVWIRQPPGKCLEWLAHIWDDDKRYNPALKSRLTISKDTSKNQVYLQMNSLD
AEDTAVYYCARMELWSYFYDWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGLVKDYFPEPTVSWNSGALTSVHTFP
AVLQSSGLYSLSSVTVPSLSTGTYICNVNHKPSNTKVDKREPKSCDKHTHTCPCPAPEAAGAPSVFLFPPKPKDLMISRTF
EVTCTVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTIKAKGQP
REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVSCVMH
EALHNHYTQKLSLSLSPGGGSGGGGSEVQLLESGLLVQPGGSLRLSCAASGFSFSSGYDMCWVRQAPGKLEWIAICIAAGSAGI
TYDANWAKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARSAFSDYAMDLDWGQGLTVTVSSGGGSGGGGSGGGGSGGGGSDIQ
MTQSPSTLSASVGRVITTCQASQSISSHLNHYQQKPKGKAPKLLIYKASTLASGVPSRFSGSGSGTEFTLTISLQPDFFATYYCQ
QGYSWGNVDNVFGGGTKVEIKGGGSGGGGSGGSLVESGGGLVQPGGSLRLSCTASGFTISSYHMQWVRQAPGKLEYIGTISGGG
NVYYASSARGRFTISRPSKNTVDLQMNSLRAEDTAVYYCARDGSDPMWQGLTVTVSSGGGSGGGGSGGGGSGGGGSDVVM
QSPSSVSAVGRVITTCQASQNIIRTYLSWYQQKPKGKAPKLLIYAAANLASGVPSRFSGSGSGTDFTLTISDLEPGDAATYYCQST
YLGTDYVGAFFGGGKVEIK

>Sequence ID 72: SI-77H6 Heavy Chain Nucleotide Sequence
GAAATCGTCTTACACAATCTCTAGCACTGAGTGTGAGCCCCGCGCAACGCGGACTTTCTCTTGCAGGGCAAGTCAATCCAT
AGGACTAATATACATTGGTATCAACAAAAGCCAGGTAAACCACCCAGGCTTTTGATTAAGTATGCAAGTGAGTCTATTTCCGGTA
TCCCTGACCGCTTCTCTGGATCAGGCAGTGGCACAGAGTTCACACTACCATATCTAGTGTGAATCAGAGGACTTCGCCGTGTAT

>Sequence ID 74: SI-77H6 Light Chain Nucleotide sequence
GAAATCGTTATGACGCAGAGTCCCTCCACGCTCTCCGCTAGTGTCGGGGATCGCGTCATTATCACATGCCAGGCCCTCCGAGTCAAT
CAGCAGCTGGCTTCGATAGGATATCAACAGAAGCCGGGAAAAGCTCTTAAATTTGCTGATCTATGAAGCGTCAAATTTGGCGTCTGGTG
TCCCATCTAGGTTCTCCGGCTCTGGGTCTGGTGCAGAAATTTACTTTGACAACTCTCCAGTCTTCAACAGACGATTTCCGTACTACTAC
TACTGCCAAGGGTATTTCTATTTTATAAGCCGGACATATGTAACTCCTTCGGCCAAGGAACAAAGTTGACTGTTCTTGGTGGCGG
AGGCAGTGGTGGCGGGGCGACGGAGGTGGTGGTTCAGGGGGTGGTGGGAGCAAGTCCAATTGGTAGAAAGTTGGCGGTGGTCTGG
TGCAACCTGGTGATCTCTAGCCTCTCATCGCCGCTAGTGGGCTTTACTATTTCAACTAATCGCATGAGCTGGGTTCGCCAGGCC
CCCCGCAAGAGCTTTGAGTGGTCCGCGTCATACCCGACAGGACATTACATCTACTGCGAGTTGGGCAAGGCGAGTTCCAGTAC
TAGCGCGCATACTTTCAAAGATAACCGTTTACCTTTCAAATGAATAGCTTGAGGGCGGAAGACACAGCTGTGTATTATCGCGCAGGGG
ATGGAGGTAGTTTCGCCATACTTCCAAACATATGGGGACAAGCGACGCTGGTTACTGTCTCAGCGCGGCTGGAGGGTCCGGC
GGTGGTGGATCAGAAATGTATTGACACAGAGCCCGCCCTCCCTCAGTGCCTCACTGGGGAAAGGTTAACTACATCTGCTCTG

ATCAAGCAGCGTCTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCAAGCTCTGGATATACGATACGAGCAAGCTGG
 CTTCGCGCGTACCTAGCCGCTTCAGTGGTTCGCGCTCAGGCAACGATCACACCTTACGATTTCCAGTATGGAACCCGAAGATTTT
 GCAACTTATTATTGTTTCCAGGGGAGCGTGATCCCATTCACCTTTCCGGTGTGGGACAAAAGTGGAGATCAAGCGTACGGTGGCTGC
 ACCATCTGCTCTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCCTCTGTTGTGTGCTGCTGAATAACTTCTATC
 CCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCCGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAG
 GACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTACCCCA
 TCAGGCATCTGAGCTGCCTGCTCACAAGAGCTTCAACAGGGGAGAGTGTGCGCGTGGCGGTAGCGGTGGCGGCGGAAGTGGTGGCG
 GAGGATCCCAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGTCTCTGGACAGTTCGATCACCATCTCCTGCACTGGAACGAGC
 AGTGAGCTTGGTGGTTATAACTTTGTCTCCTGGTACCAACAACCCAGGCAAGCCCCAACTCATGATCTATGATGTCAGTGA
 TCGGCCCTCAGGGGTGTCTGATCGCTTCTCCGGCTCCAAGTCTGGCAACACGGCCTCCCTGATCATCTCTGGCCTCAGGCTGACG
 ACGAGGCTGATTATTACTGCAGCTCATATGGGAGCAGCAGCACTCATGTATTTTCGGCGGAGGACCAAGGTGACCGTCTAGGT
 GGAGCGGTTTCCAGGCGAGGTGGTTCGCGCGGTGGCGGTCCGGTGGAGCGGCTCTCAGGTGCAATTGACAGGAGTCCGGGGGAGG
 CCTGTGCAAGCCTGAGGGTCCCTGAGTCTCTCCTGTGACGCTCTGGATTACCTTTAGTAGTTATTGGATGAGCTGGTCCGCC
 AGGCTCCAGGGAAGGGGCTGGAGTGGGTGGCAACATAAACCGCGATGGAAGTGCAGTACTATGTGGACTCTGTGAAGGGCCGA
 TTCACCATCTCCAGAGACGCGCAAGAACTCACTGTATCTGCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTG
 TCGGAGAGATCGTGGGTGGGCTACTTCGATCTCTGGGCGCTGGCACCTGGTCACCGTCTCTAGC

>Sequence ID 75: SI-55H11 Heavy Chain Amino Acid Sequence

EIVLTQSPSTLSVSPGERATFSCRASQSIGTNIHWYQQKPKPRLLIKYASESISGIPDRFSGSGSGTEFTLTISVQSEDFAVY
 YCQQNNWPPTTFPGTKLTVLGGGSGGGSGGGSGGGSGVQLQQSGPLVKPSETLSITCTVSGFSLTNYGVHWIRQAPGKGL
 EWLGLVIWSGGNTDYNTPFTSRFTITKDN SKNQVYFKLR SVRADDTAIYYCARALTYDYEFAYWGQGLTVTVSSGGGSGGGSGG
 GSGGGGSEVQLVSESGGLVQPGGSLRLSCAASGFTISTNAMS WVRQAPGKCLEWIGVITGRDITYYASWAKGRFTISRDN SKNTL
 YLQMNSLRAEDTAVYYCARDGGSSAITSNNI WQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGLVKDYFPEPVTVSWNSG
 ALTS GVHTFPAVLQSSGLYSLSSVTVPS SSSLTGTQYICNVNHKPSNTKVDKRVFKSCDKHTHTCPCPAPEAAGAPSVFLFPKP
 KDTLMI SRTPEVTCTVVDVSHEDPEVKFNWYVDGVEVHNAKT KPREQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIE
 KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQ
 GNVFSCVMHEALHNHYTQKSLSLSPGGGGSGGGGSEVQLLES GGGLVQPGGSLRLSCAASGFSFSSGYDMCWVRQAPGKLEWI
 ACIAAGSAGITYDANWAKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARSAFSDYAMD LWGQGLTVTVSSGGGSGGGSGGG
 GSGGGSDIQMTQSPSTLSASVGRVTITCQASQSISSHLN WYQQKPKAPKLLIYKASTLASGVPSRFSGSGSGTEFTLTISLQ
 PDDFATYYCQGGYSWGNVDNVFGGGTKEIKGGGSGGGSGSRLVESGGGLVQPGGSLRLSCTASGFTISSYHMQWVRQAPGKGL
 EYIGTISSGGNVYYASARGRFTISRPSKNTVDLQMNSLRAEDTAVYYCARD SGYS DPMWQGLTVTVSSGGGSGGGSGGGSGG
 GGGSDVVMQTPSPSSVSASVGRVTITCQASQNI RTYLSWYQQKPKAPKLLIYAAANLASGVPSRFSGSGSGTDFTLTISDLEPG
 DAATYYCQSTYLGTDYVGAFAFGGKVEIK

>Sequence ID 76: SI-55H11 Heavy Chain Nucleotide Sequence

GAAATCGTCTTACACAATCTCCTAGCACACTGAGTGTGAGCCCCGGCGAAGCGCGACTTTCTCTTGCAGGGCAAGTCAATCCAT
 AGGGACTAATATACATTGGTATCAACAAAAGCCAGGTAACACCCAGGCTTTTGATTAAAGTATGCAAGTGAGTCTATTTCGGTA
 TCCCTGACCGCTTCTCTGGATCAGGCAGTGGCACAGAGTTCACTACCATATCTAGTGTGCAATCAGAGGACTTCGCGGTGTAT
 TACTGCCAACAGTAATACTGGCCGACTACCTTCGGACCGGTCAAAAGCTGACCGTTTTCAGCGGTGGCGGTAGTGGGGAGG
 CGGTCTTGGCGGGGAGGGTCCGGCGGTGGAGGATCACAAGTACAGTTGCAGCAATCCGGTCCCGGTCTCGTCAAACCGAGTGAGA
 CGCTTAGTATAACGTGTACTGTTT CAGGCTTTAGCCTTACGAACATATGGAGTTCACTGGATTCCGCGAGGACCCGGCAAAGGTTTG
 GAATGGCTGGGTGTTATTTGGT CAGGTGGAATACAGACTATAACACCCCTTTTACAAGTCCGGTTCACAATTACGAAAGATAATTC
 CAAAATCAAGTTTATTTTCAAGTTGAGATCCGTCCGCGCGGACGACACTGCGATCTACTATTGTGCGAGGGCACTGACCTACTACG
 ATTACGAATTTGCGTATTGGGGGCAAGGGACTCTTGTAAACAGTCTCAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCGGCGGT
 GGCGGCTCCGGTGGAGGCGGTCTGAGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTCCAGCCTGGGGGCTCCCTGAGACTCTC
 CTGTGCAGCCTCTGGATTACCATCAGTACCAATGCAATGAGCTGGGTCCGCCAGGCTCCAGGGAAGTGTCTGGAGTGGATCGGAG
 TCATTACTGGTCTGTGATATCACATACTACGCGAGCTGGGCGAAAGGCGAGATTACCATCTCCAGAGACAATCCAAAGAACCGCTG
 TATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACGGTGGTCTTCTGCTATTACTAGTAA
 CAACATTTGGGGCCAGGGAACCTGGTCACCGTGTCTCAGCTAGCACCAAGGGCCATCGGTCTTCCCTGGCACCTCCTCCA
 AGAGCACCTCTGGGGGACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGC
 GCCCTGACCAGCGGCTGCACACCTTCCCGGCTGTCTACAGTCTCAGGACTTACTCCCTCAGCAGCGTGGTGACCTGGCCCTC
 CAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCAGCAACCAAGGTGGACAAGAGAGTTGAGCCCAAT
 CTTGTGACAAAACCTCACATGCCCACCGTGCACGACCTGAAGCCGCGGGGGCACCGTCAGTCTTCTTCCCCCAAAACCC
 AAGGACACCTCATGATCTCCCGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAA
 CTGGTACGTGGACGCGGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAAGC
 TCCTCACCGTCTTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTGC CGGTCTCCAACAAAGCCCTCCAGCCCCATCGAG
 AAAACCATCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCATCCCGGATGAGCTGACCAAGAACA
 GGTACGCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCACATCGCGTGGAGTGGGAGAGCAATGGGCAGCCGAGAACAACT
 ACAAGACCACGCTCCCGTCTGGACTCCGACGGCTCCTTCTCTATAGCAAGCTCACCGTGGACAGAGCAGGTGGCAGCAG
 GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGAGAAGAGCCTCTCCCTGTCTCCGGGTGGCGG
 TGGAGGGTCCGGCGGTGGTGGATCCGAGGTGCAGTGTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGAGACTCT
 CTTGTGCAGCCTCTGGATTCTCTTACGTAGCAGCATGTGCTGGTCCGCCAGGCTCCAGGAGGCTCCAGGAGGCTGGATCGATC
 GCATGCATTGCTGCTGAGTGTGGTACTTACGACGCGAAGTGGGCGAAAGGCGGTTCCACATCTCCAGAGACAATCCAA

GAACACGCTGTATCTGCAAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGATCGGCGTTTTTCGTTCTGACT
 ACGCCATGGACCTCTGGGGGCCAGGGAACCCCTGGTCACCGTGTGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCCGGCGGTTGGC
 GGCTCCGGTGGAGGCGGCTCTGACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC
 TTGCCAGGCCAGTCAGAGCATTAGTTCCCACTTAACTGGTATCAGCAGAAACCAGGGAAAGCCCTAAGCTCCTGATCTATAAGG
 CATCCACTCTGGCATCTGGGGTCCCATCAAGGTTGAGCGGCAGTGGATCTGGGACAGAAATTTACTCTCACCATCAGCAGCCTGCAG
 CCTGATGATTTTGAACCTTATTACTGCCAACAGGGTTATAGTTGGGGTAATGTTGATAATGTTTTCGGCGGAGGGACCAAGGTGGA
 GATCAAAGGCGGTGGAGGTCGGCGGTTGGTGGCTCCGGACGCTGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGT
 CCCTGAGACTCTCCTGTACTGCCTCTGGATTACCATCAGTAGTACCACATGCAGTGGGTCCGCCAGGCTCCAGGGAAGGGGCTG
 GAGTACATCGGAACCATTAGTAGTGGTGGTAATGTATACTACGCAAGCTCCGCTAGAGGCGAGATTACCATCTCCAGACCTCGTC
 CAAGAACACGGTGGATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACTCTGGTTATAGTG
 ATCCTATGTGGGGCCAGGGAACCCCTGGTCACCGTCTCTTACGGCGGTGGCGGTAGTGGGGGAGGCGGTTCTGGCGGCGGAGGGTCC
 GGCGGTGGAGGATCAGACGTTGTGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACCTGTCA
 GGCCAGTCAGAACATTAGGACTTACTTATCCTGGTATCAGCAGAAACCAGGGAAAGCCCTAAGCTCCTGATCTATGCTGCAGCCA
 ATCTGGCATCTGGGGTCCCATCAAGGTTGAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCGACCTGGAGCCTGGC
 GATGCTGCAACTTACTATTGTCTAGTCTACCTATCTTGGTACTGATTATGTTGGCGGTGCTTTCGGCGGAGGGACCAAGTGGAGAT
 CAAA

>Sequence ID 77: SI-55H11 Light Chain Amino Acid Sequence

ENVLTQSPASLSASPGERVITCSASSSVSYMHVYQKPKQAPKLIYDTSKLASGVPSRFSGSGSGNDHTLTITSSMEPEDFATYY
 CFQGSVYPFTFGQGTQVTVLGGGGSGGGSGGGSGGGSGVTLKESGPGLVQPGQTLSTLCAFSGFSLSSTSGMGVWIRQPPGKG
 LEWLAIHWDDDKRNPALKSRLTISKDTSKNQVYLQMSLDAEDTAVYYCARMELWSYFYFDYWGQGLVTVSSGGGGSGGGSDV
 VMTQSPSTLSASVGRVTINQASESISSWLAWYQKPKGAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISLQPDFFATYYC
 QGYFYFISRTYVNSFGGCTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSK
 DSTYLSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECGGGGSGGGSGGGGSQALTQPASVSGSPGQSITISCTGTS
 SDVGGYNFVSWYQQHPGKAPKLMIDVSDRPSGVSDRFSGSKSNTASLIISGLQADDEADYYCSSYSSSTHVIFFGGGTQVTVL
 GGGSGGGSGGGSGGGSGVQLQESGGGLVPGGSLSLSCAASGFTFFSSYWMSWVRQAPGKGLEWVANINRDGSASYVDSVKGR
 FTISRDDAKNSLYLQMNSLRAEDTAVYYCARDRGVGYFDLWGRGTLVTVSS

>Sequence ID 78: SI-55H11 Light Chain Nucleotide Sequence

GAAATGTATTGACACAGAGCCCCGCTCCCTCAGTGCCTCACCTGGGGAAAGGTAACATCACTTGCTCTGCATCAAGCAGCGT
 CTCATATCATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
 CTAGCCGCTTCAGTGGTCCGGCTCAGGCAACGATCACACCCCTTACGATTTCAGTATGGAACCCGAAGATTTTGCAACTTATTAT
 TGTTCAGGGGAGCGTGATCCCATTCACCTTCGGGCGAGGGACAAAAGTGACCGTCTTAGGCGGTGGCGGTAGTGGGGGAGGCGG
 TTCTGGCGGCGGAGGGTCCGGCGGTGGAGGATCACAGGTCACATTGAAGGAATCTGGCCCCGGCCTTGTTTCAGCCAGGACAGACCC
 TAGCCTCACCTGTGCTCCTCAGTGGTTTTTCTCTTAGCACTACGGGTATGGGGGTGCGGTGGATTTCGGCAGCCTCCCGGCAAGGT
 CTTGAGTGGTTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATAC
 CTCAAAAATCAAGTGTACTTGCAAATGAATAGCCTTGACGCGGAGGATACGGCTGTATATTATGCGCTCGGATGGAACCTCTGGT
 CTTACTACTTTGATTATTTGGGGGCGAGGGACTCTCGTCACGGTCTCAGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGACGTC
 GTAGCTCACCTGTGCTCCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGGAACCTGGAACCTGGAACCTGGAACCTGGA
 TTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAGCCCTAAGCTCCTGATCTATGAAGCATCCAACTGGCATCTGGGGTCCCAT
 CAAGGTTACGGCGGAGTGGATCTGGGACAGAATTTACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCAACTTATTACTGC
 CAAGGCTATTTTATTTTATAGTCTGACTTATGTAAATTTCTTCGGCTGTGGGACCAAGGTGGAGATCAAACGTACCGTGGCTGC
 ACCATCTGCTCTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGGAACCTGGAACCTGGAACCTGGAACCTGGA
 CCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAG
 GACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACAAAGTCTACGCCTGCGAAGTACCCCA
 TCAGGCGCTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTGGCGGTGGCGGTAGCGGTGGCGGCGGAAGTGGTGGCG
 GAGGATCCCAAGTCTGCCCTGACTCAGCCTGCCTCCGTGTCTGGTCTCCTGGACAGTCTGATCACCATCTCTGCACTGGAACAGC
 AGTGACGTTGGTGGTTATACTTTGTCTCCTGGTACCAACAACACCCAGGCAAGCCCCAACTCATGATCTATGATGTCACTGA
 TCGGCCCTCAGGGGTGTCTGATCGCTTCTCGGCTCCAAGTCTGGCAACACGGCCTCCCTGATCATCTCTGGCTCCAGGCTGACG
 ACAGGCTGATTATTACTGCAGCTCATATGGGAGCAGCAGCACTCATGTGATTTTCGGCGGAGGGACCAAGGTGACCGTCTTAGGT
 GGAGGCGGTTACGGCGGAGGTGGTTCGGCGGCTGGCGGCTCCGGTGGAGGCGGCTCTCAGGTGCAATTGCAGGAGTGGGGGGAGG
 CCTGGTCAAGCCTGGAGGGTCCCTGAGTCTCTCCTGTGCAGCCTCTGGATTACCTTTAGTAGTTATTGGATGAGCTGGGTCCGCC
 AGGCTCCAGGGAAGGGGCTGGAGTGGGTGGCCAAACATAAACCAGGATGGAAGTGGAGTTACTATGTGACTCTGTGAAGGGCCGA
 TTTACCATCTCCAGAGACGACGCCAAGAACTCACTGTATCTGCAAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTG
 TCGGAGAGATCTGGGGTGGGCTACTTCGATCTCTGGGCGGCTGGCACCCCTGGTCAACCTCTCTAGCTGA

>Sequence ID 79: SI-38E17 Heavy Chain Amino Acid Sequence

DVMTQSPSTLSASVGRVTINQASESISSWLAWYQKPKGAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISLQPDFFATYY
 YCQGYFYFISRTYVNSFGGGTKVEIKGGGSGGGSGGGSGGGSGGGSEVQLVESGGGLVQPGGSLRLSCAASGFTISTNAMS
 PGKLEWIGVITGRDITYYASWAKGRFTISRDNKNTLYLQMSLRAEDTAVYYCARDGSSAITSNNIWGQGLVTVSSGGGGSG
 GGGSEVQLVQSGAEVKKPESLKISCKGSGYSFSSWIWVRQAPGKGLEWMIIPDDSDTRYSPFQGVVTSADKSIIRTA
 YLQWSLKSADTAMYYCARHVMIGVLIIDFWGQGLTVTVSSASTKGPSVFLAPSSKSTSGGTAALGLVKDYFPEPVTVSWNSGALT
 SGVHTFPFVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVPEKSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKD

LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNV
FSCSVMEALHNHYTQKSLSLSPGGGGSGGGGSEVQLLESGLVQPGGSLRLSCAASGFSFSSGYDMCWVRQAPGKGLEWIAICI
AAGSAGITYDANWAKGRFTISRDN SKNTLYLQMNSLRRAEDTAVYYCARSAFSDYAMD LWGQGLTVTVSSGGGSGGGGSGGGSGG
GGSDIQMTQSPSTLSASVGRVITITCQASQSISSHLNWKYQKPKAPKLLIYKASTLASGVPSRFSGSGSGTEFTLTISLQPD
FATYYCQQGYSWGNVDNVFGGKTKVEIKGGGSGGGGSRSLVESGGGLVQPGGSLRLSTASGFTISSYHMQWVRQAPGKGLEIYI
TISGGNVYASSARGRFTISRPSKNTVDLQMNLSRAEDTAVYYCARD SGYSDPMWGQGLTVTVSSGGGSGGGGSGGGSGGGG
SDVMTQSPSSVSASVGRVITITCQASQNI RTYLSWYQKPKAPKLLIYAAANLASGVPSRFSGSGSGTDFTLTISDLEPGDAAT
YYCQSTYLGTDYVGGAFGGGTKVEIK

>Sequence ID 80: SI-38E17 Heavy Chain Amino Acid Sequence

GACGTCGTGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAAGCCAGTGAGAGCAT
TAGCAGTTGGTTAGCTTGGTATCAGCAGAAACAGGGAAGCCCCCTAAGCTCCTGATCTATGAAGCATCAAACCTGGCATCTGGGG
TCCCATCAAGGTTTCCAGCGGAGTGGATCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGCACCTTAT
TACTGCCAAGGCTATTTTATTTATAGTCGTACTTATGATAAATCTTTTCGGCGGAGGAGACCAAGGTGGAGATCAAAGCGCGTGG
CGGTAGTGGGGAGCGGTTCTGGCGCGGAGGGTCCGGCGGTGGAGGATCAGAGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGG
TCCAGCCTGGGGGTTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCATCAGTACCAATGCAATGAGCTGGGTCCGCCAGGCT
CCAGGGAAGGGGCTGGAGTGGATCGGAGTCATTACTGGTCGTGATATCACATACTACCGGAGCTGGGCGAAAGGCAGATTACCAT
CTCCAGAGACAATTCCAAGAACACGCTGTATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGCTGTGTATTACTGTGCGCGG
ACGGTGGATCATCTGCTATTACTAGTAACAACATTTGGGGCCAAAGGAACCTGGTCACCGTTTCTTCAGGCGGTGGAGGGTCCGGC
GGTGGTGGATCCGAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAGAACACAGGAGAGTCTCTGAAGATCTCCTGTAAAGGTTT
TGGATACAGCTTTAGCAGTTTATGGATCGGCTGGGTGCGCCAGGCACCTGGGAAGGCCTGGAATGGATGGGGATCATCTATCTG
ATGATCTGTATACCATGATACAGTCCATCCTTCCAAGGCCAGGTCAACATCTCAGCCGACAAGTCCATCAGGACTGCCTACCTGCAG
TGGAGTAGCCTGAAGGCTCGGACACCGCTATGTATTACTGTGCGAGACATGTTACTATGATTGGGGAGTTATTATTGACTTCTG
GGGCGAGGGAACCTGGTCACCGTCTCCTCAGCTAGCACCAAGGCCCATCGGTCTTCCCTCGGACCGCTCCTCCAAGAGCAGCT
CTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAAGTCAAGGCGCCCTGACC
AGCGCGGTGCACACCTTCCGGCTGTCTTACAGTCTCAGGACTCTACTTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTT
GGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAACTCTTGTGACA
AACTCACACATGCCACCGTGCAGCAGCTGAAGCCGCGGGGACCGTCAGTCTTCTTCTTCCCCCAAAACCCAAAGGACACC
CTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGT
GGACGGCTGGAGGTGCTATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAGCTACCGTGGTGGTCAAGGCTCCTCACCG
TCCTGCACCGAGTGGCTGAATGGCAAGGAGTACAAGTGCAGGCTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATC
TCCAAGGCCAAAGGCGAGCCCGAGAACACAGGTGTATACCCTGCCCCATCCCGGATGAGCTGACCAAGAACAGGTGAGCCT
GACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCGAGCCGAGAACAACTACAAGACCA
CGCTCCCGTGTGATGCTGGTACCTTACGACGCGAAGTGGGCGAGGAGCCGCTTACCATCTCCAGAGACAATTCCAAGAACACGCT
TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAACAGGCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGT
CGGCGGTGGTGGATCCGAGGTGCAGCTGTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGTTCCCTGAGACTCTCCTGTGCAG
CCTCTGGATTCTCCTTCACTAGCGGGTACGACATGTGCTGGGTCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATT
GCTGTGGTGTGCTGGTACCTTACGACGCGAAGTGGGCGAGGAGCCGCTTACCATCTCCAGAGACAATTCCAAGAACACGCT
GTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAGATCGGCGTTTTCGTTGACTACGCCATGG
ACCTCTGGGCGAGGGAACCTGGTCACCGTCTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCGGCGGTGGCGGCTCCGGT
GGAGGCGGCTCTGACATCCAGATGACCCAGTCTCCTTCCACCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCAGGC
CAGTCAGAGCATTAGTTCCCACTTAACTGGTATCAGCAGAAACAGGGAAGCCCTAAGCTCCTGATCTATAAGGCATCCACTC
TGGCATCTGGGGTCCCATCAAGGTTTCCAGCGGAGTGGATCTGGGACAGAATTTACTCTCACCATCAGCAGCCTGCAGCCTGATGAT
TTTGCAACTTATTACTGCCAACAGGTTATAGTTGGGTAATGTTGATAATGTTTTCGGCGGAGGGAACAGGTGGAGATCAAAGG
CGGTGGAGGTCGGCGGTGGTGGATCCCGGTGCTGGTGGAGTCTGGGGAGGCTTGGTCCAGCCTGGGGGTTCCCTGAGACTCT
CCTGTACAGCCTCTGGATTACCATCAGTAGCTACACATGCAAGTGGGTCCGCGAGGCTCCAGGGAAGGGGCTGGAGTACATCGGA
ACCATAGTAGTGGTGGTAATGTATACTACGCGAGCTCCGCGAGAGGAGATTACCATCTCCAGACCCTCGTCCAAGAACACGGT
GGATCTTCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACTCTGGTTATAGTGATCCTATGTGG
GCCAGGGAACCTGGTCACCGTCTCGAGCGCGGTGGCGGTAGTGGGGAGGCGGTCTGGCGGCGGAGGGTCCGGCGGTGGAGGA
TCAGACGTTGTGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACCTGTGAGGCCAGTCAGAA
CATTAGGACTTACTTATCCTGGTATCAGCAGAAACAGGGAAGCCCTAAGCTCCTGATCTATGCTGCAGCCAATCTGGCATCTG
GGGTCCCATCAAGGTTTCCAGCGGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCGACCTGGAGCCTGGCGATGCTGCAACT
TACTATTGTCTAGTCTACCTATCTTGGTACTGATTATGTTGGCGGTGCTTTCGGCGGAGGGAACAGGTGGAGATCAAA

>Sequence ID 81: SI-38E17 Light Chain Amino Acid Sequence

AIQLTQSPSSLSASVGRVITITCRASQGISSALAWYQKPKAPKLLIYDASSLESQVPSRFSGSGSGTDFTLTISLQPEDFATY
YQCFNSYPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS
YLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC

>Sequence ID 82: SI-38E17 Light Chain Nucleotide Sequence

GCCATCAGTTGACCCAGTCCATCCTCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGGCGGGCAAGTCAGGGCAT
TAGCAGTGCTTTAGCTTGGTATCAGCAGAAACAGGGAAGCTCCTAAGCTCCTGATCTATGATGCCTCAGTTTGGAAAGTGGGG

TCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGATTCTACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTAT
TACTGTCAACAGTTTAATAGTTACCCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAACGTACGGTGGCTGCACCATTCTGT
CTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCAGAGAGG
CCAAAGTACAGTGGAAAGTGGATAACGCCCTCCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACC
TACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCTGCGAAGTACCCATCAGGCGCT
GAGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

>Sequence ID 83: SI-34C1 Heavy Chain Amino Acid Sequence

EVQLVQSGAEVKKPGESLKI SCKGSGYSFSSSWIGWVRQAPGKGLEWMGIIYPDDSDTRYSPSFQGVVTSADKSI RTAYLQWSSL
KASDTAMYYCARHVTMIWGVII DFWGQGLTVTVSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH
TFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKHTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS
RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
GQPRFPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS DGSFFLYSKLTVDKSRWQQGNVFCSS
VMHEALHNHYTQKSLSLSPG

>Sequence ID 84: SI-34C1 Heavy Chain Nucleotide Sequence

GAGGTGCAGTGGTGCAGTCTGGAGCAGAGGTGAAGAAACCAGGAGAGTCTCTGAAGATCTCCTGTAAGGGTCTGGATACAGCTT
TAGCAGTTCATGGATCGGCTGGGTGCGCCAGGCACCTGGGAAAGGCCTGGAATGGATGGGGATCATCTATCCTGATGACTCTGATA
CCAGTACAGTCCATCCTTCCAAGGCCAGGTACCATCTCAGCGACCAAGTCCATCAGGACTGCCTACCTGCAGTGGAGTAGCCTG
AAGGCCTCGGACACCGCTATGTATTACTGTGCGAGACATGTTACTATGATTTGGGGAGTTATTATTGACTTCTGGGGCCAGGGAAC
CCTGGTCACCGTCTCTCAGCTAGCACCAAGGGGCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACAG
CGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCGAACCGGTGACGGTGTCTGTTGGAATCAGGCGCCCTGACCAGCGCGGTGCAC
ACCTTCCCGCTGTCTTACAGTCTCAGGACTCTACTCCCTCAGGACCGTGGTGACCGTGCCTCCAGCAGCTTGGGACCCAGAC
CTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACAT
GCCCCACCGTCCCAGCACCTGAATCTCCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCC
CGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGGA
GGTGACATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAAGCTCCTCACCGTCTGCACCAAG
ACTGGCTGAATGGCAAGGAGTACAAGTGAAGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCAAAGGCCAAA
GGGACGCCCCGAGAACCAAGGTGTACACCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCTGACCTGCCTGGT
CAAAGGCTTCTATCCAGGCACATCGCGTGGAGTGGGAGAGCAATGGGACGCGGAGAACCACTACAAGACCACCGCTCCCGTGC
TGGACTCCGACGGCTCCTTCTTCTCTATAGCAAGCTCACCCTGGACAAGAGCAGGTGGCAGCAGGGGACGCTTCTCATGCTCC
GTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGT

>Sequence ID 85: SI-34C1 Light Chain Amino Acid Sequence

AIQLTQSPSSLSASVGDRTVITCRASQGISSALAWYQQKPGKAPKLLIYDASSLESQVPSRFSGSGSGTDFTLTISLQPEDFATY
YCQQFNSYPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS
TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>Sequence ID 86: SI-34C1 Light Chain Nucleotide Sequence

GCCATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTACCATCACTTGCCTGGGCAAGTCAAGGCAT
TAGCAGTGTCTTAGCTGTGATCAGCAGAAACCAGGGAAGCTCCTAAGCTCCTGATCTATGATGCCTCCAGTTTGGAAAGTGGGG
TCCCATCAAGGTTTCAGCGGCAGTGGATCTGGGACAGATTCTACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTAT
TACTGTCAACAGTTTAATAGTTACCCATTCACTTTCGGCCCTGGGACCAAAGTGGATATCAAACGTACGGTGGCTGCACCATCTGT
CTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCAGAGAGG
CCAAAGTACAGTGGAAAGTGGATAACGCCCTCCAATCGGGTAACCTCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACC
TACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCTGCGAAGTACCCATCAGGCGCT
GAGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

>Sequence ID 87: SI-38P12 Heavy Chain Amino Acid Sequence

QIVLSQSPAILASAPGEKVTMTCRASSSVSYIHFQKQKPGSSPKPIYATSNLASGVPRVFRSGSGSGTSYSLTISRVEAEDAATYY
CQQWTSNPPFTFGGKTLTVLGGGSGGGGSGGGSGGGGSGVQLQPGAEVLVKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLE
WIGAIYPGNGDTSYNQKFKGKATLTADKSSSTAYMQLSLTSSEDSAVYYCARSTYYGGDWYFNVWAGTTVTVSSGGGSGGGGSE
VQLVESGGGLVQPGGSLRLSCAASGFTISTNAMS WVRQAPGKLEWIGVITGRDITYYASWAKGRFTISRDN SKNTLYLQMNSLRA
EDTAVYYCARDGGSSAITSNNIWGQGLTVTVSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
PAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKHTHTCPPCPAPEAAGAPSVFLFPPKPKDTLMISRT
PEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCAVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDS DGSFFLYSKLTVDKSRWQQGNVFCSSVM
HEALHNHYTQKSLSLSPGGGGSGGGGSEVQLLES GGGLVQPGGSLRLSCAASGFTSSSGYDMCWVRQAPGKLEWIAIAGSAG
ITYDANWAKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARSAFSDYAMD LWGQGLTVTVSSGGGSGGGGSGGGGSGGGGSDI
QMTQSPSTLSASVGDRTVITCQASQSISSHLN WYQQKPKAPKLLIYKASTLASGVPSRFSGSGSGTEFTLTISLQPD FATTYYC
QQGYSWGNVDNVFGGTGKVEIKGGGSGGGGSGRSLVESGGGLVQPGGSLRLSCTASGFTISSYHMQWVRQAPGKLEYIGTISSG
GNVYYASSARGRFTISRPS SKNTVDLQMNSLRAEDTAVYYCARD SGYS DPMWGQGLTVTVSSGGGSGGGGSGGGGSGGGGSDVVM

TQSPSSVSASVGDVRTITCQASQNIPTYLSWYQQKPKAPKLLIYAAANLASGVPSRFSGSGSGTDFTLTISDLEPGDAATYYCQS
TYLGTDYVGGAFGGGTKVEIK

>Sequence ID 88: SI-38P12 Heavy Chain Nucleotide Sequence

CAGATCGTGCTGAGCCAGAGCCCCGCCATCCTGAGCGCCAGCCCCGGCGAGAAGGTGACCATGACCTGCCGGGCCAGCAGCAGCGT
GAGCTACATCCACTGGTTCAGCAGAAAGCCCCGAGCAGCCCCAAGCCCTGGATCTACGCCACCAGCAACCTGGCCAGCGCGTGC
CCGTGCGGTTTCAGCGCAGGGCAGCGGCACCAGCTACAGCCTGACCATCAGCCGGGTGGAGGCCGAGGACGCCGCCACCTACTAC
TGCCAGCAGTGGACCAGCAACCCCCCACCTTCGGCGGGCGGCACCAAGCTGACCGTGCTGGGTGGTGGTGGCTCTGGAGGAGGCGG
GAGCGGGGGTGGTGGCTCAGTGGTGGAGGTTCCAGAGTGCAGCTGCAGCAGCCCGCGCGGAGCTGGTGAAGCCCGGGGCCAGGG
TGAAGATGAGCTGCAAGGCCAGCGCTACACCTTCACAGCTACAACATGCACTGGGTGAAGCAGACCCCCGGCGGGGCTGGAG
TGGATCGGGCCCATACCCCCGGCAACGGCGACACCAGCTACAACCAGAAGTTCAAGGGCAAGGCCACCTGACCGCCGACAAGAG
CAGCAGCACCGCTACATGCACTGAGCAGCTGACGAGCCTGACGAGCAGGACAGCGCCGTGTAATACTGCGCCCCGAGCAGCTACTACGGCG
GCGACTGGTACTTCAACGTGTGGGCGCCGGCACCACCTGACCGTCTCGAGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCAGAG
GTGCACTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTACCATCAG
TACGATGCAATGAGTGAAGTTCAGGAGTCCAGGGAAGGCTGAGGGTGGATCGGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAGT
ACGCGAGCTGGGCGAAAGGAGGATTCACCATCTCCAGAGACAATTCAGAAGACAGCTGTATCTTCAAATGAACAGCCTGAGAGCC
GAGGACACGGCTGTGTATTACTGTGCGAGAGACGGTGGTCTTCTGTGCTATTACTAGTAACAACATTTGGGGCCAGGGAACCTGGT
CACCGTGTCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGGCC
TGGGTATGCCAATGAGTGAAGTACTTCCCCGAACCGGTGAGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT
CCGGCTGTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT
CTGCAACGTGAATCAAGCCAGCAACCAAGGTGGACAAGAGAGTTGAGCCCAAATCTTGTGACAAAACCTCACACATGCCAC
CGTGCCAGCACCTGAAGCCCGGGGGGACCGCTCAGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACC
CCTGAGGTCACATGCTGGT
TAATGCCAAGACAAGCCGCGGGAGGAGCAGTACAACAGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT
TGAATGGCAAGGAGTACAAGTGGCGGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAGGCCAAAGGGGAG
CCCCGAGAACCACAGGTGTACACCTGCCCCATCCCGGATGAGCTGACCAAGAACCAGGTGACGCTGACCTGCCTGGTCAAAGG
CTTCTATCCAGCGCATCGCCGTGGAGTGGGAGAGCAATGGGAGCGCGGAGAGCAACTACAAGACACGCTCCCGTCTGGACT
CCGACGGCTCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATG
CATGAGGCTCTGCAACAACCTACACGCAAGAGCCTCTCCCTGTCTCCGGGTGGCGGTGGAGGGTCCGGCGGTGGTGGATCCGA
GGTGCACTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTCTCCTTCA
GTAGCGGTGAGTCAAGTGTGCTGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGATCGCATGCATGCTGCTGGTGGTGGTGGT
ATCACTTACGACGCAACTGGGCGAAAGGCCGTTACCATCTCCAGAGACAATTCAGAAGACAGCTGTATCTGCAATGAACAG
CCTGAGAGCCGAGGACACGCCCTATATTACTGTGCGAGATCGCGGTTTTCTGTTGACTACGCCATGGACCTCTGGGGCCAGGGAA
CCCTGGTACCGGTGTCGAGCGGTGGAGGCGGATCTGGCGGAGGTGGTTCGGCGGTGGCGGCTCCGGTGGAGGCGGCTCTGACATC
CAGATGACCCAGTCTCCTTCCACCTGTCTGCATCTGTAGGAGCAGAGTCAACATCACTTGCCAGGCCAGTCAAGCATTAGTTC
CCACTTAACTGGTATCAGCAGAAACCAGGGAAGCCCCTAAGCTCCTGATCTATAAGGCATCCACTCTGGCATCTGGGGTCCCAT
CAAGGTTACGCGGAGTGGATCTGGGACAGAATTACTCTACCATCAGCAGCCTGCAGCCTGATGATTTGCAACTTATTACTGC
CAACAGGGTTATAGTTGGGGTAATGTTGATAATGTTTTCGGGGAGGGACCAAGGTGGAGATCAAAGGCGGTGGAGGGTCCGGCGG
TGGTGGTCCGGACGCTGCTGGT
GATTACCATCAGTAGCTACCATGCACTGAGTGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTACATCGGAACCATTAGTAGTGGT
GGTAATGTATCTAGCAGAGCTCCGCTAGAGGAGATTACCATCTCCAGACCTCGTCCAAGAACACGGTGGATCTTCAAATGAA
CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACTCTGGTTATAGTATCTATGTGGGGCCAGGGAACCTGG
TCACCGTCTCTTACGGCGGTGGCGGTAGTGGGGGAGGCGGTTCTGGCGGCGAGGGTCCGGCGGTGGAGGATCAGACGTTGTGATG
ACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCAACATCACCTGTGAGGCCAGTCAAGACATTAGGACTTACTT
ATCCTGGTATCAGCAGAAACCAGGGAAGCCCCTAAGCTCCTGATCTATGCTGCAGCCAATCTGGCATCTGGGGTCCCATCAAGGT
TCAGCGGAGTGGATCTGGGACAGATTTCACTCTACCATCAGCGACCTGGAGCCTGGCGATGCTGCAACTTACTATTGTAGTCT
ACCTATCTTGGTACTGATTATGTTGGCGGTGCTTTCGGCGGAGGGACCAAGGTGGAGATCAAATGA

>Sequence ID 89: SI-38P12 Light Chain Amino Acid Sequence

ENVLTQSPASLSASPERVITITCSASSSVSYMHYQQKPGQAPKLIYDTSKLASGVPSRFSGSGSGNDHTLTISSEMPEDFATYY
CFQGSVYPFTFGQTKVTVLGGGSGGGGSGGGGSGGGGSGVTLKESGPGLVQPGQTLRLTCAFSGFSLSSTSGMGVWIRQPPGKG
LEWLAHIWDDDKRYNPALKSRLTISKDTSKNQVYLQMNSLDAEDTAVYYCARMELWSYFDYWQGTLLTVSSGGGSGGGGSDV
VMTQSPSTLSASVGDVRTINCQASESISWLAHYQQKPKAPKLLIYEASKLASGVPSRFSGSGSGTEFTLTISLQPDFFATYYC
QGYFYFISRTYVNSFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNFPYPRKRVQWKVDNALQSGNSQESVTEQDSK
DSTYLSLSTLTLSKADYKEHKVYACEVTHQGLSSPVTKSFNRGEC

>Sequence ID 90: SI-38P12 Light Chain Nucleotide Sequence

GAAAATGTATTGACACAGAGCCCCGCCCTCCCTCAGTGCCTACCTGAGGGGAAGGTAACATCACTTGCTCTGCATCAAGCAGCGT
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CTAGCCGCTTCAGTGGTTCGGCTCAGGCAACGATCACACCTTTACGATTTCCAGTATGGAACCCGAAGATTTTCAACTTATTAT
TGTTTCCAGGGGAGCGTGTACCATTTCTTCCGGGAGGGGACAAAAGTGACGGTACTGGGTGGAGGCGGTTCCAGCGGAGGTTGG
TCCGGCGGTGGCGCTCCGGTGGAGGCGGCTCTCAGTACATTGAAGGAATCTGGCCCCGGCCTTGTTCAGCAGGACAGACCC
TTAGGCTCACCTGTGCTTCCAGTGGTCTTCTTAGCACTAGCGGTATGGGGGTGGGCTGGATTCGGGACGCTCCCGGCAAGGT

CTTGAGTGGTTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATAC
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CTTACTACTTTGATTATTGGGGGCAGGGGACTCTCGTCACGGTCTCGAGCGCGGTGGAGGGTCCGGCGGTGGTGGATCAGACGTC
GTGATGACCCAGTCTCCTTCCACCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAATTGCCAAGCCAGTGAGAGCATTAGCAG
TTGGTTAGCCTGGTATCAGCAGAAACCAGGGAAGCCCCAAGCTCCTGATCTATGAAGCATCCAACTGGCATCTGGGGTCCCAT
CAAGGTTACAGCGGAGTGGATCTGGGACAGAATCACTCTCACCATCAGCAGCCTGCAGCCTGATGATTTTGAACCTTATTACTGC
CAAGGCTATTTTTATTATTAGTCTGTAATTTCTTTGGCGGAGGGACCAAGGTGGAGATCAAACGTACGGTGGCTGC
ACCATCTGTCTTCACTTCCCGCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTGTAATAACTTCTATC
CCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAAATCGGGTAACTCCAGGAGAGTGTACAGAGCAGGACAGCAAG
GACAGCACCTACAGCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACAAAGTCTACGCCTGCGAAGTACCCCA
TCAGGGCCTGAGCTCGCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT

>Sequence ID 91: Humanized Version 7 (H7VH) Amino Acid Sequence

QVTLKESGPGVLVQPGQTLRLTCAFSGFSLSSTSGMGVWIRQPPGKCLEWLAHIWDDDKRYNPALKSRLTISKDTSKNQVYLQMN
SLDAEDTAVYYCARMELWSYFDYWQGLTVTVSS

>Sequence ID 92: Humanized Version 7 (H7VH) Nucleotide Sequence

CAGGTCACATTGAAGGAATCTGGCCCCGGCCTTGTTACGCCAGGACAGACCCCTTAGGCTCACCTGTGCCTTCAGTGGTTTTCTCT
TAGCCTAGCGGTATGGGGTTCGGCTGGATTCGGCAGCCTCCCGGCAATGTCTTGAGTGGTTGGCTCACATTTGGTGGGACGACG
ACAAACGGTATAATCCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATACCTCAAAAAATCAAGTGTACTTGCAATGAATAGC
CTTGACGCCGAGGATACGGCTGTATATTATTGCGCTCGGATGGAACCTCTGCTTACTACTTTGATTATTGGGGGCAGGGGACTCT
CGTCACGGTGTCTGAGT

>Sequence ID 93: Humanized Version 7 (H7VL) Amino Acid Sequence

ENVLTQSPASLSASPGERVITCSASSSVSYMHWYQKPGQAPKLWIYDTSKLASGVPSRFRSGSGSGNDHTLTISSEMPEDFATYY
CFQGSVYPFTFGCGTKVEIK

>Sequence ID 94: Humanized Version 7 (H7VL) Nucleotide Sequence

GAAAATGTATTGACACAGAGCCCCGCCTCCCTCAGTGCCTCACCTGGGGAAAGGGTAACATCACTTGCTCTGCATCAAGCAGCGT
CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
CTAGCCGCTTCAGTGGTTCCGGCTCAGGCAACGATCACACCCTTACGATTTCAGTATGGAACCCGAAGATTTTGAACCTATTAT
TGTTTCCAGGGGAGCGTGTACCCATTCACTTTCCGGGTGTGGGACAAAAGTGGAGATCAAG

>Sequence ID 95: SI-63SV7 Amino Acid Sequence

ENVLTQSPASLSASPGERVITCSASSSVSYMHWYQKPGQAPKLWIYDTSKLASGVPSRFRSGSGSGNDHTLTISSEMPEDFATYY
CFQGSVYPFTFGCGTKVEIKGGGSGGGSGGGSGGGSGGGSGVTLKESGPGVLVQPGQTLRLTCAFSGFSLSSTSGMGVWIRQPPGK
CLEWLAHIWDDDKRYNPALKSRLTISKDTSKNQVYLQMNSLDAEDTAVYYCARMELWSYFDYWQGLTVTVSS

>Sequence ID 96: SI-63SV7 Nucleic Acid Sequence

GAAAATGTATTGACACAGAGCCCCGCCTCCCTCAGTGCCTCACCTGGGGAAAGGGTAACATCACTTGCTCTGCATCAAGCAGCGT
CTCATACATGCATTGGTATCAACAAAAGCCTGGACAGGCCCCCAAGCTCTGGATATACGATACGAGCAAGCTGGCTTCCGGCGTAC
CTAGCCGCTTCAGTGGTTCCGGCTCAGGCAACGATCACACCCTTACGATTTCAGTATGGAACCCGAAGATTTTGAACCTATTAT
TGTTTCCAGGGGAGCGTGTACCCATTCACTTTCCGGGTGTGGGACAAAAGTGGAGATCAAGGGTGGCGGAGGCAGTGGTGGCGGGG
CAGCGGAGGTGGTGGTTCAAGGGGTGGTGGGAGCCAGGTACATTGAAGGAATCTGGCCCCGGCCTTGTTACGCCAGGACAGACCC
TTAGGCTCACCTGTGCCTTCAGTGGTTTTCTCTTAGCACTAGCGGTATGGGGTGGCTGGATTCGGCAGCCTCCCGGCAATGT
CTTGAGTGGTTGGCTCACATTTGGTGGGACGACGACAAACGGTATAATCCTGCCTTGAAAAGTCGGCTGACCATTAGTAAGGATAC
CTCAAAAAATCAAGTGTACTTGCAATGAATAGCCTTGACGCCGAGGATACGGCTGTATATTATTGCGCTCGGATGGAACCTCTGGT
CTTACTACTTTGATTATTGGGGGCAGGGGACTCTCGTCACGGTGTCTGAGT